Adam, Eve and Population Genetics: A Reply to Dr. Richard Buggs (Part 1)

Blog Posts

system (system) 2017-11-03 07:09:53 UTC #1
It's impossible to prove that we didn't descend from just two individuals. But the genetic evidence makes that scenario extremely unlikely.

This is a companion discussion topic for the original entry at **https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/adam-eve-and-population-genetics-a-reply-to-dr-richard-buggs-part-1**

Adam and Eve had Perfect Genomes (The Genetic Entropy Argument)

What about embodied cognition?

TedDavis (Dr. Ted Davis) 2017-11-03 13:52:59 UTC #2

Dennis,

I appreciate the great clarity of your reply to Dr. Buggs–not that an absence of clarity has ever been something I would associate with your work. 🙂

I hope that Discovery also tweets your reply to Dr. Buggs. They owe it to fair discourse to do exactly that much, since they are responsible for bringing Buggs' concerns out of the academic tent and into their own, much larger tent. Otherwise, they might be skirting with the same danger that Buggs is worried about: that "of alienating Christians from science on the basis of a wrong interpretation of the current literature."

I resonate with that concern. That's one of the main reasons why I decided to devote my professional life to helping Christians (and others too) understand the *history* better. Thank you for helping us understand the *science* better.

DennisVenema (Dennis Venema) 2017-11-08 23:09:37 UTC #5

Thanks for your kind words, Ted. I've learned a lot from you over the past several years - I'm glad that I've been able to return the favour.

John_Rood (John Rood) 2017-11-10 06:24:00 UTC #6

Thanks for this Dennis! The work you're doing here is timely and invaluable. I'm glad to see you thoroughly engaging Dr. Buggs' points, and I also appreciate the distinction between the matter of Adam's existence and of being sole-progenitor. Many of us have, at one time or another, believed and/or put forward the idea that scripture says Adam is the sole-progenitor. I have the impression that scripture does not actually make that claim. (although, I think the meaning of Eve being the "mother of all the living" deserves some explanation…maybe that's been addressed somewhere else on this site.) Maybe we would have double-checked our exegesis sooner if we had thought sooner about the sort of science being highlighted in this article. These implications from population genetics might not be obvious to many in my generation, but I imagine they might be obvious to many in the next generation…a generation that grows up in a world of CRISPR innovations and consumer genetic analysis like 23andMe. I really would hate to set them up for an unnecessary science vs faith crisis. For that reason, I'm especially thankful for your work.

I'm currently still leaning toward affirming, not only that Adam was a real person, but more specifically the "de novo" creation of him. That seems like it's compatible with what you've said, assuming Adam and Eve's children intermarried into the existing hominid population.

Daniel_Justesen (Daniel Lamdahl Justesen) 2017-11-10 08:53:17 UTC #7

Awesome response 🙂 I was wondering myself why heterozygosity even mattered in this discussion since reducing the human species to just two people would restrict the max. of alleles pr. gene to 4.
Knowing how YECs have responded to the decay rates of radioactive isotopes (used for radiometric dating) and how light could have reached us from stars millions of light years away, I imagine their response to the data put forward by Venema would be something like this:" well what if the mutation rate were a lot higher in the past?".
But wouldn't it require a highly hazardous(if not life-prohibiting) environment to produce mutation rates high enough to account for our current genetic diversity if we only descended from two people a few thousand years ago (or even several thousands)? I imagine it would.

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tallen_1 (Tim) 2017-11-10 14:39:51 UTC #8

Dennis,

Quick question. There's something I'm trying to wrap my head around and I'm not quite succeeding. Richard Buggs is a biologist who seems very well steeped in genetics. He has a number of publications in plant genetics in respected journals, including one in Nature (albeit not as a lead researcher). Yet he seems to make a rookie mistake in confusing heterozygosity with genetic diversity. Which, having read your response seems exactly the case. How does this happen? How does one progress through years of study and research only to fundamentally misunderstand a basic scientific tenet in their specialized field? I'm at a loss, so hoping you can connect some dots for me here. Thanks!

RichardBuggs (Richard Buggs) 2017-11-10 15:46:06 UTC #10

Hi Dennis, Thank you for beginning to reply to my concerns. I very much look forward to continuing this discussion now that you have so graciously replied to my email. As you know, I blogged about this issue, reviewing chapter three of your book on 28th October at the **Nature Ecology and Evolution Community**. This allowed me to tackle the issue in more depth than I did in my email to you in May. This blog has already dealt with some of the issues you mention above. I have also responded to some comments on my blog at the Skeptical Zone **here** which provides further information. When I have more time I will post a longer response to your blog here on Biologos, but meanwhile, would refer you and your readers to the two links above. Best wishes, Richard

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DennisVenema (Dennis Venema) 2017-11-10 20:55:19 UTC #11

Thanks, Richard - and welcome to BioLogos! I very much appreciate your patience in waiting for this reply.

RichardBuggs (Richard Buggs) 2017-11-12 21:38:43 UTC #12

Note:
I have also published this text here in order to provide a stable and easily findable record:
http://richardbuggs.com/response_to_Dennis_Venema_Biologos_PartI_Adam_Eve.html

Dear Dennis,

I am glad that we are now establishing a dialogue about the scientific credibility of a bottleneck of two at some point in the history of the human lineage. I am hoping that during the course of this discussion we will be able to examine in

detail the claims that you make in chapter three of *Adam and the Genome*, and that you will respond to all the critiques and questions that I have raised in my **email** to you and my **blog at Nature Ecology and Evolution Community**.

This Part I of your response is helpful in that it clears up some areas of potential misunderstanding between us, and points me to two arguments that are not made explicitly in your book chapter. I trust I can look forward to the subsequent Parts for your responses to the majority of the issues I have raised.

I will work through your blog in this comment, seeking to be as constructive as possible in my reading of it.

Scientific Confidence vs. Scientific Certainty

I am happy to take your point that you do not believe that science has DISPROVEN that a bottleneck of two individuals could have happened in the human lineage. Your position is that you are as certain that it has not happened as you are certain that the earth rotates around the sun. I am sorry if I mischaracterised your position as being more certain than it actually is.

10,000 individuals?

In your blog you say: “I do not claim this [heliocentric level of] certainty for the oft-cited ~10,000 figure, as Buggs seems to imply”.

I am happy to take this point, but I should explain why I got the impression from your book chapter that you hold pretty strongly to the 10,000 figure. In your book chapter
you argue that multiple independent methods converge on a figure of 10,000, and even predict that one method that gives a lower figure is likely to be revised upwards. Here are the relevant quotations from your chapter:

> it is worth at least sketching out a few of the methods geneticists use that support the conclusion that we descend from a population that has never dipped below about 10,000 individuals.

Then you mention evidence from allelic diversity, and state:

> these methods indicate an ancestral population size for humans right around that 10,000 figure.

Then you present an argument from linkage disequilibrium, and state:

> The results indicate that we come from an ancestral population of about 10,000 individuals— the same result we obtained when using allele diversity alone.

Then you say more about linkage disequilibrium and state:

> The researchers found that, during this period, humans living in sub-Saharan Africa maintained a minimum population of about 7,000 individuals, and that the ancestors of all other humans maintained a minimum population of about 3,000—once again, adding up to the same value other methods arrive at.

Then you describe the PSMC method and state:

> Taken together, this is in good agreement with previous, less powerful methods, with a combined minimum size of around 6,900 individuals. These numbers may shift upward, however, as we sequence more and more individuals from both groups.

This is why I got the impression that you attached a high degree of certainty to the 10,000 figure. This impression came across especially strongly in the last two statements above, when you were (I think incorrectly, as I argue in my blog) adding up numbers from two populations to come to a 10,000 figure, and then suggesting that the PSMC method's result might be revised upwards (towards 10,000, presumably). I think that if you re-read your chapter yourself you will agree that the 10,000 figure comes across quite strongly, and sounds to the reader like a very precise measurement of past human population size.

However, I am willing to take your point that you do not attach such a high level of certainty to the 10,000 figure as you attach to there never having been a bottleneck of two. That seems a reasonable position to hold.

Heterozygosity and population bottlenecks

The majority of your blog is taken up with the topic of genetic diversity. I think that we are largely in agreement here. I am glad that you agree with the points I made about the amount of heterozygosity that can be carried through a short, sharp bottleneck. I do not dispute that allelic diversity can provide stronger evidence for a past bottleneck than heterozygosity can. In my blog I stated this clearly: "A sharp bottleneck will affect allelic richness more than heterozygosity". I am grateful that you have helped out non-scientists who are seeking to follow our debate by giving a simple "Genetics 101" explanation of why this is so in your blog.

Although we are in agreement about the relative merits of heterozygosity and allelic diversity in detecting bottlenecks, misunderstanding between us has arisen for two reasons: (1) ambiguous usage of the term "genetic variability" in your book chapter, and (2) the choice of Tasmanian Devils in your book chapter as an example of the consequences of a population bottleneck. I will explain both of these below.

(1) I commented on heterozygosity in my email and blog because in your book chapter you refer many times to "genetic variability". As you know, in scientific population genetics literature the term "genetic variability" does not refer only to allelic diversity. Genetic variability of populations is measured in many ways: heterozygosity, allelic diversity, private allele frequency, gene diversity, fixation indices, inbreeding coefficients etc. I did not realise that when you use the term in your chapter you intend only to refer to allelic diversity. That is not the way the term is normally used in the field. I therefore assumed that you were also referring to heterozygosity. It is a pity that this ambiguity was present, but I understand that it is hard to write about science at a popular level without the occasional ambiguity slipping in that a specialist will stumble on.

(2) I also got the impression you are including heterozygosity within your definition of genetic variability because of your choice of Tasmanian Devils as an exemplar of a species that has undergone a bottleneck. This exemplar takes up quite a large proportion of the early part of your chapter. It is well known that Tasmanian devils have **low heterozygosity** as well as low allelic diversity - they have much lower levels of heterozygosity than humans (see this **paper**). The low heterozygosity within Tasmanian Devils appears to be partly responsible for the low fitness of their populations, likely due to several prolonged bottlenecks. In fact, you say of the Tasmanian Devils: "most of them have exactly the same alleles with only rare differences." That sounded to me as I read the chapter to be popular-science-level statement that they have low heterozygosity.

For these reasons, I thought you were including heterozygosity in your chapter as one aspect of genetic variability. However I am willing to take your point that you were not, now that you have clearly stated this. I am happy to put this down to a communication issue. I misread your chapter, and did not realise you mean "allelic diversity" whenever you say "genetic variability". I did not realise that when you bring up the example of Tasmanian Devils you are leaving to one side the issue of their low heterozygosity.

Now that we have cleared up this point, I think we can leave the issue of heterozygosity behind us, as we seem to be in full agreement about it.

Allelic diversity and bottlenecks

Now to look in more detail at the points you raise about allelic diversity. This is where I think your argument is strongest, so I would like to examine it in some detail. To do this full justice, I want to start with what you say about this in your book chapter. One of your most explicit statements about this in your book chapter is as follows:

> …scientists have many other methods at their disposal to measure just how large our population has been over time. One simple way is to select a few genes and measure how many alleles of that gene are present in present-day humans. Now that the Human Genome Project has been completed and we have sequenced the DNA of thousands of humans, this sort of study can be done simply using a computer. Taking into account the human mutation rate, and the mathematical probability of new mutations spreading in a population or being lost, these methods indicate an ancestral population size for humans right around that 10,000 figure. In fact, to generate the number of alleles we see in the present day from a starting point of just two individuals, one would have to postulate mutation rates far in excess of what we observe for any animal.

As I note in my blog, you give no citation to the scientific literature to back up this point, so it is hard for me to interact with you on it. I would invite you again to make such a citation so that we can discuss this point further.

In your recent blog you have now made a similar claim, and given more detail:

> So, a bottleneck to two individuals would leave an enduring mark on our genomes – and one part of that mark would be a severe reduction in the number of alleles we have - down to a maximum of four alleles at any given gene. Humans, however, have a large number of alleles for many genes – famously, there are **hundreds of alleles** for some genes involved in immune system function. These alleles take time to generate, because the mutation rate in humans is very low. This high allele diversity is thus the first indication that we did not pass through a severe population bottleneck, but rather a relatively mild one (estimated, as we have discussed, at about 10,000 individuals by current methods).

Would I be correct in assuming that this statement in your blog is intended to illuminate the passage I quoted above from your book chapter? If so, this is helpful as you give a link in the blog to an **online primer** about Human leukocyte antigen (HLA) genes, suggesting that your argument relates to these genes. But the online primer has nothing in it about models of past human bottlenecks. I would invite you to make a more explicit argument on this point, as I think this is the strongest argument that is available to you against a bottleneck of two. As you mention HLA genes in your blog, it sounds to me as if your argument may rest on **Ayala et al (1994)** but this paper was published before the human genome project, so I assume you must have a more up to date source that you drew on for your book chapter. Please could you let me know what it is so that I can follow up your argument?

I realise that some of your non-biologist readers may think I am being rather pedantic in asking for a citation when you are making what appears to be a very straightforward case from allele numbers. But biologist readers will know that very few things in this area are straightforward, and without a citation I have to treat your claims as unsubstantiated. For example, if your argument is from HLA genes, I have already mentioned these briefly in my blog, and why their rapid rates of evolution may prevent them from making strong argument against a bottleneck::

> Hyper-variable loci like MHC genes [of which HLA genes are a type] or microsatellites have so many alleles that they seem to defy the idea of a single couple bottleneck until we consider that they have very rapid rates of evolution, and could have evolved very many alleles since a bottleneck.

Also as I wrote in a comment on the **Skeptic Zone**:

> MHC loci are pretty exotic. Several studies show that they evolve fast and may be under sexual selection, pathogen-mediated selection, and frequency-dependent selection; they may also have heterozygote advantage

> (see e.g. **http://rspb.royalsocietypublishing.org/content/277/1684/979**). The maintenance of MHC polymorphism is still “an evolutionary puzzle” (**https://www.nature.com/articles/ncomms1632**). There is some evidence for convergent evolution of HLA genes (**https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1918223/**, **http://onlinelibrary.wiley.com/doi/10.1111/j.1600-065X.1999.tb01381.x/full**, **https://link.springer.com/article/10.1007/BF00189233**, **https://link.springer.com/article/10.1007%2Fs002510050028**). If the whole case for large human ancestral population sizes rests on MHC loci, I think this is inadequate to prove the point, given our current state of knowledge on MHC evolution.

I look forward to hearing more from you on this topic in future blog posts.

Rare alleles

Finally in your blog you make an argument from frequencies of rare alleles. This is an argument that is not mentioned in your book chapter, as far as I am aware. You state in your blog:

> Another effect that a bottleneck to two individuals would produce is that there would be no rare alleles after the bottleneck. All alleles would have a frequency of at least 25%. As the population expanded after such an event, those alleles would stay common, and only new mutations would produce less common alleles. What we observe in humans in the present day is that many alleles are rare - even exceedingly rare. The distribution of alleles in present-day humans looks like it comes from an old, large population - not one that passed through an extreme bottleneck within the last few hundred thousand years, which is when our species is found in the fossil record. Thus the observation that we have many alleles of certain genes and the distribution of allele frequencies both support the hypothesis that humans come from a population, rather than a pair.

I agree with everything you are saying, up until the full stop after “exceedingly rare”. That is my understanding of the patterns of human genetic diversity also. However, beyond this point I need you to give a citation to the scientific literature to support your claims that the distribution of alleles in humans is inconsistent with “an extreme bottleneck within the last few hundred thousand years”. This is an interesting claim and one I would like to follow up, but without a citation this is an unsubstantiated assertion. I think I may have partly anticipated this argument in my blog when I wrote: “We need to bear in mind that explosive population growth in humans has allowed many new mutations to rapidly accumulate in human populations (A. Keinan and A. G. Clark (2012) Science 336: 740-743).”

Conclusion

I am grateful to you for beginning to respond to the objections I have raised to his book chapter in my email and Nature Eco Evo blog. I am glad we have cleared up the issue of heterozygosity and appear to be in agreement about it. I invite you to make clear citations to the scientific literature to back up several key points that you make in your book chapter and in this current blog. I note that you have not yet addressed the majority of my criticisms of your book chapter. I look forward to your responses to the objections I have raised to your use of: (1) the example of the Tasmanian Devils, (2) PSMC analysis, (3) the linkage disequilibrium study by Tenesa and colleagues, and (4) incomplete lineage sorting.

Note:
I have also published this text here in order to provide a stable and easily findable record:
http://richardbuggs.com/response_to_Dennis_Venema_Biologos_PartI_Adam_Eve.html

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DennisVenema (Dennis Venema) 2017-11-13 15:03:27 UTC #13

Hello Richard,

Thanks for the reply. There's more there than I can quickly respond to, and I'll be busy for the next few days. We might end up talking past each other for a bit, as I am still working on the second part of my reply.

Some of the citations you're looking for are just working familiarity with published data sets. Perhaps **@glipsnort** could also weigh in - he has discussed the allele frequency distribution here previously (and with nice graphs). The human allele frequency distribution as a whole is one very good piece of evidence that we do not come from just two people in the last few hundred thousand years. You could try messing about with a starting pair and mutation frequencies and see for yourself the challenge of generating the distribution we observe.

Also, keep in mind you're asking about a bottleneck to two - not 2,000, not 200, not 20 … you get the picture. Moreover, you're asking for a **census** size of two, not just Ne =2 . It's a long way down from thousands to 2.

More anon - thanks as always for your patience.

RichardBuggs (Richard Buggs) 2017-11-13 21:30:00 UTC #14

Hi Dennis,

Thanks for your brief reply. I look forward to Part II of your response.

It would be great if **@glipsnort** were to join in the discussion - I would like to see more detail of the argument from allele frequency distributions.

> Some of the citations you're looking for are just working familiarity with published data sets.

I think I must check at once that I am not misunderstanding or reading too much into your statement here. Do I understand you to be saying is that you will not be giving me citations to the peer-reviewed literature to back up certain of the claims in *Adam and the Genome* that I am querying? If so, I have to reassess somewhat my expectations for our discussion.

If you really are saying this, does it apply to this statement in chapter 3?

> …scientists have many other methods at their disposal to measure just how large our population has been over time. One simple way is to select a few genes and measure how many alleles of that gene are present in present-day humans. Now that the Human Genome Project has been completed and we have sequenced the DNA of thousands of humans, this sort of study can be done simply using a computer. Taking into account the human mutation rate, and the mathematical probability of new mutations spreading in a population or being lost, these methods indicate an ancestral population size for humans right around that 10,000 figure. In fact, to generate the number of alleles we see in the present day from a starting point of just two individuals, one would have to postulate mutation rates far in excess of what we observe for any animal.

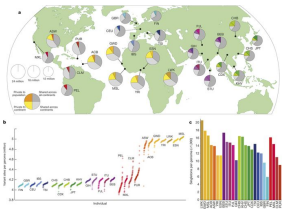
This is a key passage in the chapter, and, as I have said before, I am very keen to read the details of the work.

DennisVenema (Dennis Venema) 2017-11-14 01:38:44 UTC #15

> RichardBuggs:
>
> I think I must check at once that I am not misunderstanding or reading too much into your statement here. Do I understand you to be saying is that you will not be giving me citations to the peer-reviewed literature to back up

> certain of the claims in Adam and the Genome that I am querying? If so, I have to reassess somewhat my expectations for our discussion.

No, I'm not saying that. I am saying this is my understanding of the published literature and the relevant publically-available databases. Li and Durban would be one paper relevant here; moreover the 1,000 genomes consortium papers, papers that estimate the present-day human mutation rate, and so on. For example:



A global reference for human genetic variation

Results for the final phase of the 1000 Genomes Project are presented including whole-genome sequencing, targeted exome sequencing, and genotyping on high-density SNP arrays for 2,504 individuals across 26 populations, providing a global reference...

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tallen_1 (Tim) 2017-11-14 02:05:20 UTC #16

Richard,

Just an observation as a fly on the wall, but your style of communication here may be more offputting than you intend. I think your questions are fair and I share your desire in seeing your exchange with Dennis be as productive as we all hope. But you also seem to be issuing quite a lot of demands on exactly how this exchange needs to happen. As far as I know, it's customary to make your argument, allow your conversational partner to make theirs in rebuttal, and continue as such as the issues are worked through. You seem to be wanting to direct exactly how Dennis needs to proceed as well as pressuring upon him a sense of urgency that at best seems unnecessary and at worst a little churlish or rude. Maybe this is just my own take and it's not shared by Dennis or others reading this thread, but for what it's worth…

That said, I'm looking forward to your continued exchange.

GJDS (GJDS) 2017-11-14 03:46:56 UTC #17

Asking for references and clarification is about as standard and civilised as it gets in the scientific literature - hardly churlish and it is odd to think it rude.

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tallen_1 (Tim) 2017-11-14 03:53:53 UTC #18

CJDS,

Simply asking for references or clarifications is not what I'm referring to.

Christy (Christy Hemphill) 2017-11-14 04:07:09 UTC #19

I think it is easy to read unintended tone into other people's words. As a moderator, I think both Dr. Venema and Dr. Buggs are modeling the graciousness we aspire to here. One person's clarity and forthrightness is another person's demands. Let's not derail the conversation by expecting anyone to defend how their "tone" should have been read.

RichardBuggs (Richard Buggs) 2017-11-14 14:47:58 UTC #20

Hi Dennis,

Thank you for such a quick response to my query, and thank you for the citation to Li and Durbin and to the 1000 genomes project.

> I am saying this is my understanding of the published literature and the relevant publically-available databases.

I had assumed that was the case as this is what one expects from a scientist. This is of course, why, as a fellow scientist, I am asking you - I hope courteously and professionally - to point me to the exact papers in the published literature, and to actual analyses of the public databases that support the claims you are making in *Adam and the Genome*.

> Li and Durban would be one paper relevant here

Thank you. As you know, this is the paper that presents the PSMC method. In my email to you and my blog I have explained why I do not think that the PSMC method is able to detect a short sharp population bottleneck. I assume that you are going to respond to my comments on PSMC in Part II of your response, so I will not press you further on this issue now.

> moreover the 1,000 genomes consortium papers, papers that estimate the present-day human mutation rate, and so on. For example **A global reference for human genetic variation**

I can see how the 1,000 genomes project can provide the raw data for an analysis such as the one I am asking you for clarification on - the one that you mention in the passage from your book that I quoted in my previous post (above).

However, as far as I can see, the 1,000 genomes paper does not do the calculations that you report in that passage. Unless I am missing something, the authors do not report a calculation of ancestral population sizes from the number of alleles found in present day populations. They do present several PSMC analyses (which are based on runs of heterozygosity within genomes) but they do not seem to present the calculation that you mention in the passage I quoted from *Adam and the Genome*. Is there another paper in which they conduct the calculations that you are telling your readers about? As I say, I am very keen to know what genes were used in these calculations and how they generated an ancestral population size of 10,000.

DennisVenema (Dennis Venema) 2017-11-14 16:00:18 UTC #21

> RichardBuggs:
>
> Unless I am missing something, the authors do not report a calculation of ancestral population sizes from the number of alleles found in present day populations. They do present several PSMC analyses (which are based on runs of heterozygosity within genomes) but they do not seem to present the calculation that you mention in the passage I quoted from Adam and the Genome.

What I'm talking about there is a summary of the field as a whole - and the PSMC analyses in the 1,000 genomes paper is certainly one of the relevant experiments. So are LD studies. So are the Li and Durban PSMC results. All are based on examining present-day alleles in present-day populations (of course - it couldn't be otherwise unless we're talking paleogenomics). Some of these analyses use a forward mutation rate (which is also the rate of fixation for neutral alleles, and most variation is neutral). I know you think PMSC studies could miss a bottleneck to two. I disagree, but you're going to have to wait until I have time to write it up and explain why I think you're mistaken. Part II might include PSMC, or it might not. Part of my goal here is to not just explain my reasoning to you as a biologist, but to make it accessible to a non-specialist audience. That takes more time.

glipsnort (Steve Schaffner) 2017-11-14 16:25:23 UTC #22

> RichardBuggs:
>
> I agree with everything you are saying, up until the full stop after “exceedingly rare”. That is my understanding of the patterns of human genetic diversity also. However, beyond this point I need you to give a citation to the scientific literature to support your claims that the distribution of alleles in humans is inconsistent with “an extreme bottleneck within the last few hundred thousand years”. This is an interesting claim and one I would like to follow up, but without a citation this is an unsubstantiated assertion. I think I may have partly anticipated this argument in my blog when I wrote: “We need to bear in mind that explosive population growth in humans has allowed many new mutations to rapidly accumulate in human populations (A. Keinan and A. G. Clark (2012) Science 336: 740-743).”

(For now I just want to comment on this – I should have more to add when I’ve run some simulations (which may take a few days).)

The Keinan and Clark paper is not relevant to the question at hand. The new mutations they describe are indeed rare: 80% of them have frequency < 0.05%. There is no question that large numbers of very rare variants can accumulate in a large, young population. It is the alleles at moderate frequency – roughly 5% to 20% minor allele frequency – that are difficult to explain with a recent bottleneck. As the authors point out in that paper, 92% of neutral alleles at a frequency of 5% are expected to be older than 10,000 years; that is not the historical period they discuss.

DennisVenema (Dennis Venema) 2017-11-14 17:02:13 UTC #23

> glipsnort:
>
> I should have more to add when I’ve run some simulations

Looking forward to what you have to contribute, Steve.

RichardBuggs (Richard Buggs) 2017-11-14 18:34:17 UTC #24

Hi Dennis,

I am very happy to wait for your comments on the PSMC method and why you believe that it would detect a sudden sharp bottleneck of two. Please don’t feel under any pressure; I appreciate your attempts to make all this accessible to non-specialist audiences. That is not always an easy task.

Regarding the passage from chapter 3 of *Adam and the Genome* that I am asking you for citations to support. You have responded in your comment above:

> What I'm talking about there is a summary of the field as a whole - and the PSMC analyses in the 1,000 genomes paper is certainly one of the relevant experiments. So are LD studies. So are the Li and Durban PSMC results.

I am sorry, I am struggling to follow you here. I'm afraid I can't see how that passage is a summary of the field as a whole, and therefore I don't understand how citations of the PSMC and LD studies support it.

Here is the passage that we are discussing in its context in *Adam and the Genome*: I have placed it in italics, and also added some emphases in bold.

> ...given the importance of this question for many Christians— and the strong insistence of many apologists that the science is completely wrong— it is worth at least sketching out a few of the methods geneticists use that support the conclusion that we descend from a population that has never dipped below about 10,000 individuals. While the story of the beleaguered Tasmanian devil provides a nice way to "see" the sort of thing we would expect if in fact the human race began with just two individuals, *scientists have many other methods at their disposal to measure just how large our population has been over time.* ***One simple way*** *is to select a few genes and measure* ***how many alleles of that gene*** *are present in present-day humans. Now that the Human Genome Project has been completed and we have sequenced the DNA of thousands of humans, this sort of study can be done simply using a computer. Taking into account the human mutation rate, and the mathematical probability of new mutations spreading in a population or being lost, these methods indicate an ancestral population size for humans right around that 10,000 figure. In fact, to generate the* ***number of alleles*** *we see in the present day from a starting point of just two individuals, one would have to postulate mutation rates far in excess of what we observe for any animal.* Ah, you might say, these studies require an estimate of mutation frequencies from the distant past. What if the mutation frequency once was much higher than it is now? Couldn't that explain the data we see now and still preserve an original founding couple? Aside from the problems this sort of mutation rate would present to any species, **we have other ways** of measuring ancestral population sizes that do not depend on mutation frequency. **These methods thus provide an independent way** to check our results using allele diversity alone. Let's tackle one of these methods next: estimating ancestral population sizes using something known as "linkage disequilibrium."

Then, after describing the LD study you write:

> The results indicate that we come from an ancestral population of about 10,000 individuals— the same result we obtained **when using allele diversity alone**.

A little later you write

> A **more recent and sophisticated model** that uses a similar approach but also incorporates mutation frequency has recently been published. This paper was significant because the model allows for determining ancestral population sizes over time using the genome of only one individual. [You then describe the PSMC method.]

I am therefore struggling to understand how the passage we are discussing - the one in italics above - could be a "summary of the field as a whole" including linkage disequilibrium and PSMC methods. It seems to just be about the allele frequency method. You clearly distinguish the allele frequency method from the other methods. You say that the linkage disequilibrium method is "an independent way to check our results using allele diversity alone." You say it gives "the same result we obtained when using allele diversity alone". You describe the PSMC methods as "A more recent and sophisticated model".

I am sorry that I am spending so long on this point - this really is not where I had expected our discussion to go. I thought I was making a very straightforward request when I asked for a citation for the calculations in this passage. I am still hoping that you may be able to, now I have reminded you of the context of the passage. I appreciate that it may be a while since you re-read the chapter for yourself, and your recollection of what you wrote could be different from the text of the book. I know that I am sometimes surprised when I re-read something that I wrote myself after several months away from it.

DennisVenema (Dennis Venema) 2017-11-14 19:20:44 UTC #25

Hi Richard,

Allele-based methods: 1000 genomes (including their PSMC), and understanding allele frequency distribution and mutation frequency/fixation
LD: independent of mutation frequency
"recent and sophisticated" = PSMC *on single individuals* (a specific case of allele methods that is somewhat distinct from the prior PSMC work)

So you're right - it's a summary of allele methods, including PSMC, interspersed with the discussion on LD, and then back to a special case of an allele method with the use of PSMC on single genomes. That summary doesn't include LD. I haven't read over that section in some time. Hopefully that clears it up.

DennisVenema (Dennis Venema) 2017-11-14 19:39:32 UTC #26

Another thing to keep in mind is that the vast majority of scientists are not at all interested in (or likely aware of) what evangelical Christians want to "see" from their data. It wouldn't even cross the mind of a group to publish a paper that specifically tackles the question of all humans descending uniquely from just two people. This wouldn't even be on their radar because none of the evidence we have accumulated in the last 30+ years even remotely suggests it.

So, you're not going to see that specifically addressed in the literature. What it takes is people who are tuned to those questions who can interpret the literature in light of those issues.

RichardBuggs (Richard Buggs) 2017-11-14 20:54:48 UTC #27

Hi Dennis

> So you're right - it's a summary of allele methods, including PSMC, interspersed with the discussion on LD, and then back to a special case of an allele method with the use of PSMC on single genomes.

I'm sorry, but that wasn't my reading of the passage. As I say, it seems to me that the passage in italics is about a method based on allele counts, (explicitly not including PSMC). It seems to be describing the kind of study you mention in your "Part I" blog:

> So, a bottleneck to two individuals would leave an enduring mark on our genomes – and one part of that mark would be a severe reduction in the number of alleles we have - down to a maximum of four alleles at any given gene. Humans, however, have a large number of alleles for many genes – famously, there are hundreds of alleles for some genes involved in immune system function. These alleles take time to generate, because the mutation rate in humans is very low. This high allele diversity is thus the first indication that we did not pass through a severe population bottleneck, but rather a relatively mild one (estimated, as we have discussed, at about 10,000 individuals by current methods).

Clearly you have a study in mind that supports the passage in italics and also this paragraph from your blog. All I am requesting is that you share the reference with me. Sorry if I am starting to sound like a broken record!

RichardBuggs (Richard Buggs) 2017-11-14 21:21:19 UTC #28

> DennisVenema:
>
> It wouldn't even cross the mind of a group to publish a paper that specifically tackles the question of all humans descending uniquely from just two people.

> DennisVenema:
>
> So, you're not going to see that specifically addressed in the literature.

Dennis, this is exactly my point! 🙂 This is what my **Nature Ecology and Evolution community blog** is saying.

> DennisVenema:
>
> This wouldn't even be on their radar because none of the evidence we have accumulated in the last 30+ years even remotely suggests it.

I agree it's not on the radar, but I think we are getting ahead of ourselves if we say that none of the evidence even remotely suggests it, given that the hypothesis has not been directly tested.

> DennisVenema:
>
> Another thing to keep in mind is that the vast majority of scientists are not at all interested in (or likely aware of) what evangelical Christians want to "see" from their data.

This is exactly my concern with your book chapter. I think you are seeing things in the studies that are not there, as they never set out to test the bottleneck hypothesis.

So the question is: given that the scientific literature does not specifically address the question of whether or not humans have passed through a bottleneck of two, what further analyses are needed to address this question? This will take more work than just interpretation of the existing literature.

I am really glad that we seem to be finding some common ground.

DennisVenema (Dennis Venema) 2017-11-14 22:29:43 UTC #29

> RichardBuggs:
>
> So the question is: given that the scientific literature does not specifically address the question of whether or not humans have passed through a bottleneck of two, what further analyses are needed to address this question? This will take more work than just interpretation of the existing literature.

I disagree here. Even if the authors themselves do not specifically address it, the data certainly do.

This also crops up in other areas - you will not find a paper where the authors specifically address the idea that the earth is 6,000 years old, for example. Why not? Because the evidence we have doesn't even come close to 6KYA. The data absolutely are relevant to the question.

Or to put it another way, I don't think we need more work - I think the literature is clear. I suppose what would be most convincing to you would be to have the 1000 genomes group, or Li and Durban, etc, run a simulation to see what their PSMC results would look like on an artificial dataset that is instantaneously reduced to 2 people. I think you'd see a result that gets down at least close to Ne=2 (or 20, or 200) even if it spread that result over a longer timescale, like we see in their papers. What you're arguing is that ~1500 and 2 are indistinguishable by their methods. I disagree. More anon.

DennisVenema (Dennis Venema) 2017-11-14 22:33:13 UTC #30

> RichardBuggs:
>
> I'm sorry, but that wasn't my reading of the passage. As I say, it seems to me that the passage in italics is about a method based on allele counts

That passage is a summary statement about allele-based methods. Why would I exclude the 1000 genomes papers (including their PSMC results)? I was primarily thinking about the 1000 genomes work when writing that section.

RichardBuggs (Richard Buggs) 2017-11-15 20:58:11 UTC #31

Hi Dennis,[quote="DennisVenema, post:29, topic:37039"]
Even if the authors themselves do not specifically address it, the data certainly do.
[/quote]

I agree that the genomic data presented in the existing literature are relevant, and sufficient, for an analysis to address the short sharp bottleneck hypothesis. But if the authors have not done an appropriate analysis, someone else needs to. As far as I can see this has not been done. This is what I am saying in my blog.

> DennisVenema:
>
> I suppose what would be most convincing to you would be to have the 1000 genomes group, or Li and Durban, etc, run a simulation to see what their PSMC results would look like on an artificial dataset that is instantaneously reduced to 2 people. I think you'd see a result that gets down at least close to Ne=2 (or 20, or 200) even if it spread that result over a longer timescale, like we see in their papers.

In my blog I refer to a website that reports such a simulation, which found that PSMC could not detect sharp sudden bottlenecks. I also sketch out reasons why this is to be expected. I look forward to discussing this with you in more detail.

Adam, Eve and Population Genetics: A Reply to Dr. Richard Buggs (Part 2)

RichardBuggs (Richard Buggs) 2017-11-15 21:10:36 UTC #32

> DennisVenema:
>
> That passage is a summary statement about allele-based methods. Why would I exclude the 1000 genomes papers (including their PSMC results)? I was primarily thinking about the 1000 genomes work when writing that section.

I am sorry Dennis, but I am not persuaded that this passage in your book is a summary statement that includes the PSMC method. With all due respects to you as author, a plain reading of your chapter, as I have spelt out in detail above, is that this passage refers to an allele counting method that you then later compare the LD and PSMC approaches with. You make a point in your chapter that allele counts, LD and PSMC independently give close to the same result - a population size of 10,000 individuals.

Furthermore, in your Part 1 response blog (which we are discussing here) you make a big point that heterozygosity is little affected by bottlenecks but allele counts are. You go to great length to explain why allele counts are a good way of

detecting bottlenecks. You repeat the claim that the allele counting method indicates that human population sizes have never dropped below 10,000.

But now you seem to be saying to me that allele counting methods are not actually specifically included in your chapter: that the passage about the allele counting method is actually a summary about all methods that use alleles in some way, including PSMC (which does not count alleles, and does not “select a few genes”). Despite my repeated requests, you have not given me any reference or citation, or a description of an analysis that you or someone else has done, where human effective population sizes have been estimated by an allele counting method.

Instead, you are pointing me to the 1000 genomes paper. This is a wonderful paper that I have often referred my students to, and I do not doubt for a moment that the 1000 genomes project provides the raw data necessary for an analysis based on allele counts, but as far as I can see, the authors have not done such an analysis.

If you are not able to give me a citation that includes use of an allele counting method, why did you spend such a large proportion of your Part I blog explaining why the allele counting method is such a good way of detecting bottlenecks? Why do you mention allele counting methods in your book?

I have to admit, I am bemused by this. I think that the allele counting method is one of the best methods available for detecting bottlenecks, and I think it is the biggest challenge to the bottleneck of two hypothesis. I think there is a really interesting discussion to be had here. It has come as a genuine surprise to me that you are not pointing me to a calculation, or a paper, or a textbook, or something else that clearly explains the derivation of a 10,000 effective population size figure.

We seem to have reached an impasse on this point. I will have to let others read through your book chapter and your blog above, and reach their own conclusions.

---

tallen_1 (Tim) 2017-11-16 03:05:28 UTC #33

Richard,

Perhaps you could wait for Dennis to post the next parts of his blog response, as he’s committed to do, before declaring an impasse.

---

gbrooks9 (George Brooks) 2017-11-16 04:57:09 UTC #34

> RichardBuggs:
>
> I have to admit, I am bemused by this. I think that the allele counting method is one of the best methods available for detecting bottlenecks, and I think it is the biggest challenge to the bottleneck of two hypothesis. I think there is a really interesting discussion to be had here. It has come as a genuine surprise to me that you are not pointing me to a calculation, or a paper, or a textbook, or something else that clearly explains the derivation of a 10,000 effective population size figure.

@RichardBuggs ,

Surely **@DennisVenema** is not the only person who can do genome mathematics.

What test or study results can you offer that would indicate an answer closer to 2 than to 10,000? Certainly on a scale of difference that large, it should be relatively easy to offer some general results from your side of the divide.

RichardBuggs (Richard Buggs) 2017-11-16 13:38:06 UTC #35

Hi Tim, I'm not saying we are at an impasse on this whole issue - just the point about what Dennis was saying in that particular, but very important passage of his book.

I would invite you to step in and help us. As far as I can see you are not a biologist, so you can help adjudicate between us about what is the plain meaning of the passage to readers. Perhaps **@TedDavis** could also pitch in to, as he finds Dennis's writing to have great clarity, as he has mentioned above. As a historian, he must be used to looking closely at the meaning of texts. I would also welcome the view of **@glipsnort** as a geneticist, and perhaps **@Christy** could step in as moderator. I would also welcome other readers to pitch in and give their opinion.

The questions I ask you are, when you read the extract from *Adam and the Genome* in bold below, which I show in its context:

- Does the passage make you think that it is referring to a scientific study where a few genes have been selected and the number of alleles of those genes in current day human populations have been measured?
- Does the passage make you think that someone has done calculations on these genes on a computer that have indicated that the ancestral population size for humans is around 10,000?
- Does the passage make you think that this is a different method to the PSMC method?

Here is the passage that we are discussing in its context in *Adam and the Genome*:

> ...given the importance of this question for many Christians— and the strong insistence of many apologists that the science is completely wrong— it is worth at least sketching out a few of the methods geneticists use that support the conclusion that we descend from a population that has never dipped below about 10,000 individuals. While the story of the beleaguered Tasmanian devil provides a nice way to "see" the sort of thing we would expect if in fact the human race began with just two individuals, **scientists have many other methods at their disposal to measure just how large our population has been over time. One simple way is to select a few genes and measure how many alleles of that gene are present in present-day humans. Now that the Human Genome Project has been completed and we have sequenced the DNA of thousands of humans, this sort of study can be done simply using a computer. Taking into account the human mutation rate, and the mathematical probability of new mutations spreading in a population or being lost, these methods indicate an ancestral population size for humans right around that 10,000 figure. In fact, to generate the number of alleles we see in the present day from a starting point of just two individuals, one would have to postulate mutation rates far in excess of what we observe for any animal.** Ah, you might say, these studies require an estimate of mutation frequencies from the distant past. What if the mutation frequency once was much higher than it is now? Couldn't that explain the data we see now and still preserve an original founding couple? Aside from the problems this sort of mutation rate would present to any species, we have other ways of measuring ancestral population sizes that do not depend on mutation frequency. These methods thus provide an independent way to check our results using allele diversity alone. Let's tackle one of these methods next: estimating ancestral population sizes using something known as "linkage disequilibrium." [Then, the text describes the LD study and continues]...The results indicate that we come from an ancestral population of about 10,000 individuals— the same result we obtained when using allele diversity alone... [Then a little later the chapter continues] A more recent and sophisticated model that uses a similar approach but also incorporates mutation frequency has recently been published. This paper was significant because the model allows for determining ancestral population sizes over time using the genome of only one individual. [It then describes the PSMC method, saying of it]... Instead of looking at a given pair of loci in many individuals, this method looks at many pairs of loci within one individual....this is in good agreement with previous, less powerful methods,

I look forward to your and other readers' answers to my questions.

glipsnort (Steve Schaffner) 2017-11-16 13:53:04 UTC #36

Time for me to comment. I'll break this up into pieces, and starting with prior thinking on the subject.

The hypothesis is that there was a bottleneck of size two in the immediate human lineage. For me, the plausibility of the hypothesis (i.e. whether it is one I would think likely enough to be worth investigating) depends critically on the timing of the bottleneck. Here's how I think about it:

1. Population bottlenecks distort the allele frequency distribution in the bottlenecked population. A bottleneck of size two massively distorts it. It takes time for that distortion to be erased by genetic drift.
2. The characteristic timescale (in generations) for genetic drift in diploids is twice the effective population size.
3. Human populations from Africa show allele frequency distributions that are broadly consistent with a constant population size plus relatively recent expansion.
4. The relevant effective population size for humans is roughly 10,000. (Probably higher, actually, given current estimates of the mutation rate.)
5. Human generation time is roughly 25 years. (Again, recent estimates put it higher.)

From these facts, my working assumption is that this kind of bottleneck would be detectable for at least ~500,000 years, and that such a tight bottleneck within the last 250,000 years would leave the kind of evidence that researchers would have seen just by looking at allele frequency data.

That's my intuition. Testing that intuition requires some work, which I will attempt to describe after my malaria genetics meeting.

TedDavis (Dr. Ted Davis) 2017-11-16 14:53:03 UTC #37

> RichardBuggs:
>
> The questions I ask you are, when you read the extract from Adam and the Genome in bold below, which I show in its context:
>
> Does the passage make you think that it is referring to a scientific study where a few genes have been selected and the number of alleles of those genes in current day human populations have been measured?
> Does the passage make you think that someone has done calculations on these genes on a computer that have indicated that the ancestral population size for humans is around 10,000?
> Does the passage make you think that this is a different method to the PSMC method?

I don't have a copy of the book in front of me, but I don't have any reason to think the blocked text is not accurately quoted and edited.

So, my answer to each of your three questions is, Yes.

I am indeed a true ignoramus on these issues, having never studied any biology after one year in high school roughly fifty years ago. My science degree was in physics, and my research lab experience in astrophysics, and none of it at all recent. Nearly all of the science in Dennis' book and in this thread is totally unfamiliar to me. My only point of contact is that I did read Ayala's 1994 paper a few years ago, and I understood the takeaway message about a group of ancestors ca. 10,000 much further back than 6000 years. I can't tell you how he and his team got there, and I can't tell you what the PSMC method is. Like almost everyone else reading this, I don't know what I'm talking about, when it comes to the science. All I can say is that no one in this discussion appears to have made an argument that violates a fundamental physical law. 🙂

I appreciate you coming into this conversation, Dr Buggs and Dr Schaffner. Dennis already devotes a lot of time to helping people like me understand biology, but I wish more biologists would do that. I realize that the demands of running a research laboratory effectively preclude that type of activity as regular thing, and one's peers tend to frown on it. Ditto in the humanities. IMO, however, experts in any field have no right to complain about the dismal state of popular knowledge about their field, if they haven't tried to address it themselves–or, at least, if they haven't properly supported those colleagues who do make the effort.

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tallen_1 (Tim) 2017-11-16 15:13:16 UTC #38

Richard,

As far as I can tell, Dennis makes three claims most relevant to your point: One, that there is a method to estimate minimum ancestral population sizes based upon measurements of number of alleles across various genes present in a population, and that this method indicates a population of approx. 10,000. Two, that an independent method exists that does not rely upon estimates of past mutation rates, involving "linkage disequilibrium," that converges upon the same ancestral population size of 10,000. Three, that there has been a more recent method that is similar (not identical) that is not independent of mutation rate but also converges on similar results, namely the PSMC method.

Of these three approaches, Dennis's support for the first seems to derive mostly from calculations on collected data. Presumably done by himself or others. Of the latter two approaches, that does seem to be something that is published and to which he could (and I think did) direct you. But I'm unclear as to whether the published studies for the latter two methods explicitly state Dennis's conclusions or if he is drawing as well primarily on their collected data for support. I'm perhaps at a bit of a handicap on this as I'm relying on only excerpts of his book here on this thread. But to your point I do believe he describes three distinct methods. I'm eager to hear more about the sort of calculations conducted in these methods and how they may or may not support Dennis's argument. That is what I am looking forward to in his remaining parts to this topic.

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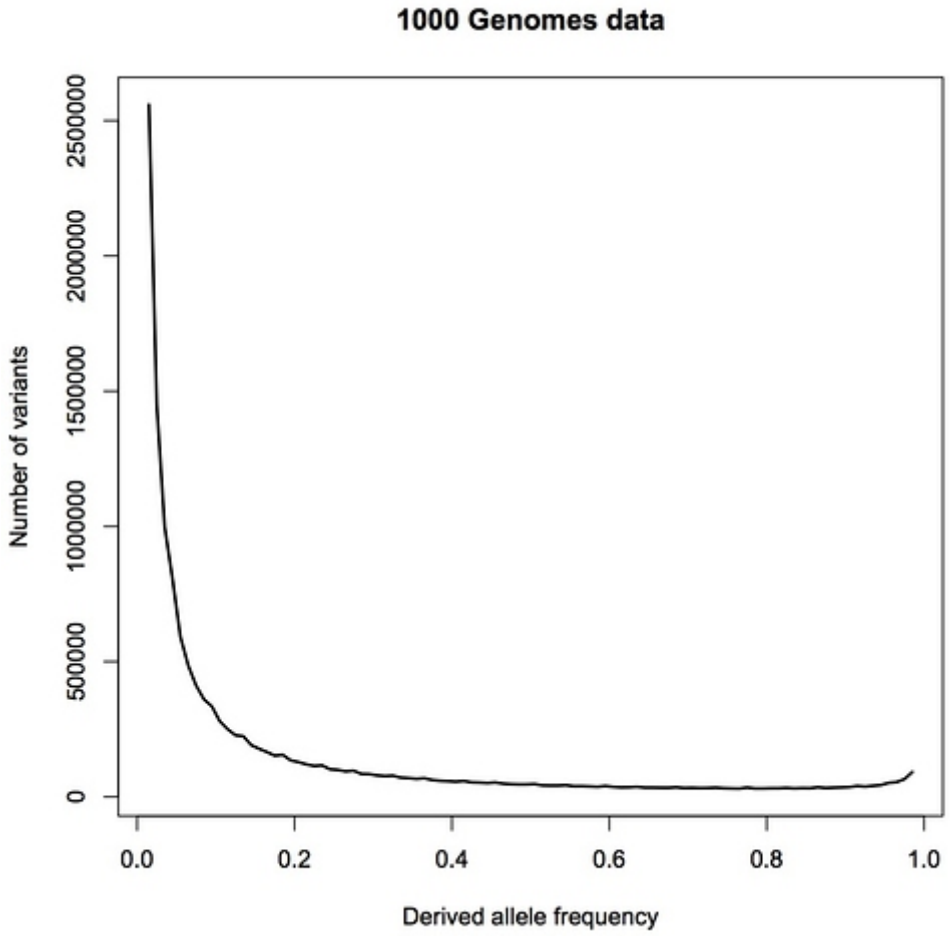
glipsnort (Steve Schaffner) 2017-11-16 15:52:25 UTC #39

First, the data. Here is the allele frequency distribution for the combined African population in 1000 Genomes Project data:

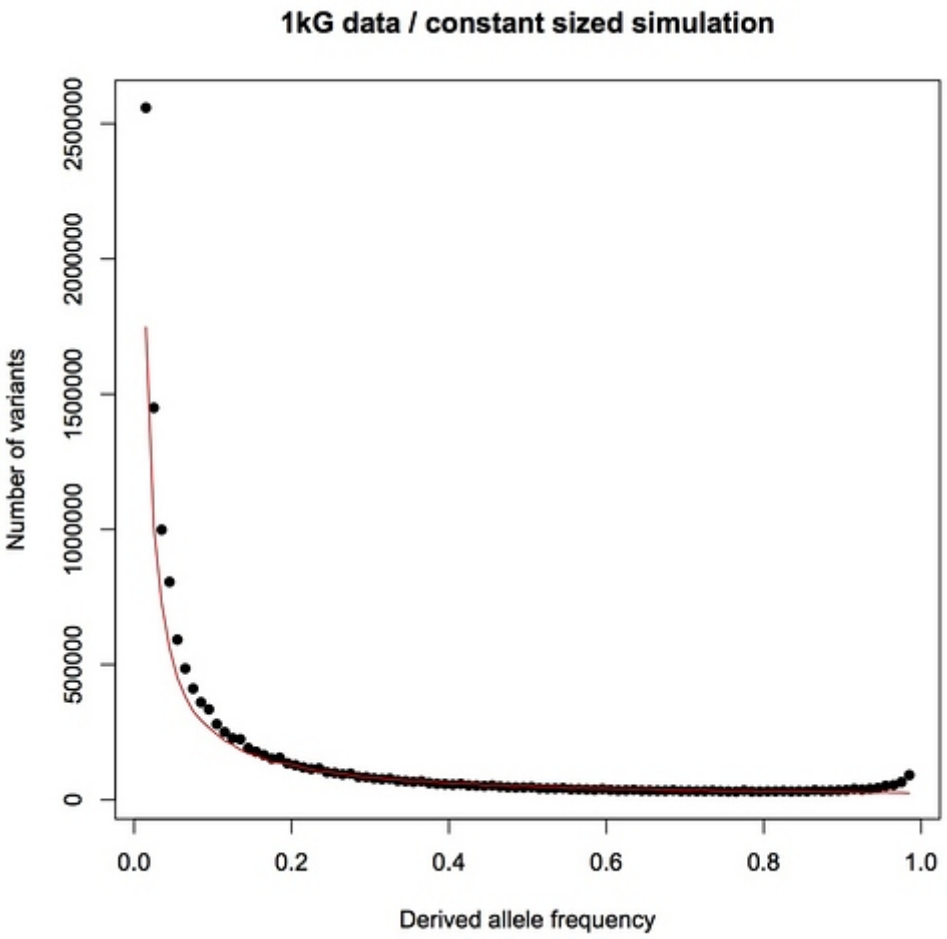


This includes all single-base variant sites from the 22 autosomes that have exactly two alleles in the data, i.e. some people have an A at one site, while others have a T there, and no third variant is found. I have only taken sites with a minor allele frequency greater than 1%. I estimate the effective size of the genome being assayed here to be 2.4 billion base pairs.

The frequency on the x axis is that of the derived allele, i.e. the base that is different from the ancestral state, as inferred from primate relatives. Theoretically, this distribution falls as 1/frequency for an ideal, constant-sized population. New variants appear when a mutation occurs, and initially appear as a single copy, which means an allele frequency of 1/2N, where N is the population size. (It's 2N because each person has two copies of the genome.) The frequency will then wander randomly from generation to generation ("genetic drift"), and in some cases will eventually wander to high values.

The rise near the right edge results primarily from misidentification of the ancestral allele (for ~2% of sites); the true frequency for many of those sites is one minus the frequency shown. The little jiggles along the curve are artifacts from binning, not noise – there is a lot of data here, and very little statistical uncertainty.

Here is the same data (black) compared to the prediction for a population with constant size (red):



The observed distribution follows the prediction very well above 20% frequency, and is higher than predicted as lower frequencies, which is indicative of fairly recent population expansion. I made the predicted curve with a forward simulation (for those who know about genetic simulators), previously published, using an effective population size of 16,384 and a mutation rate (1.6e-8/bp/generation) drawn from David Reich's recent study (**here**). I chose the mutation rate to be conservative, since it is the highest recently published estimate that I know of. (The lower the mutation rate, the longer it takes to generate the diversity lost through a bottleneck, and the easier it is to detect the bottleneck.) I chose the population size because it's a power of two (convenient for when I start modeling the bottleneck) and in the right ballpark for humans. The chosen population size and mutation rate happen to give a predicted curve that's pretty much bang on the empirical data, without any tuning needed.

So. . . the point of this exercise will be to determine whether a model with a recent bottleneck of size two can reproduce the data distribution. Comparisons in next post.

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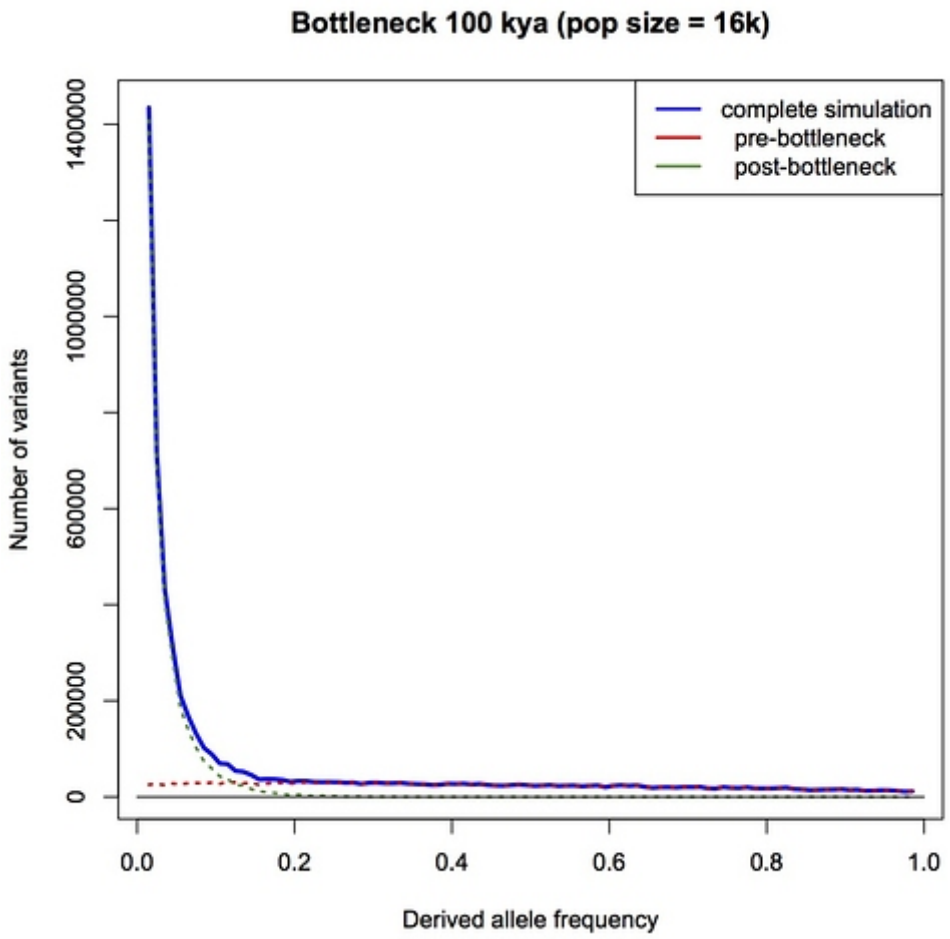
glipsnort (Steve Schaffner) 2017-11-16 16:19:21 UTC #40

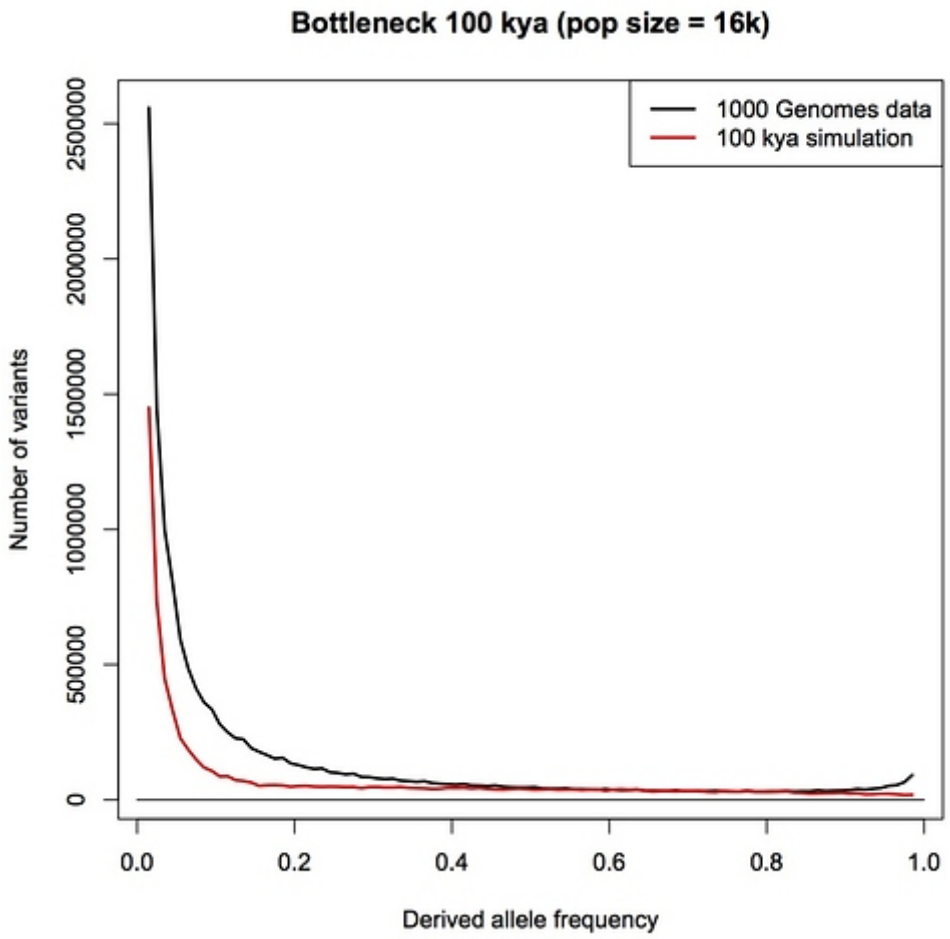
Bottleneck simulations:
I modeled the Adam and Eve bottleneck as a constant-sized population, followed by a sudden collapse to 2 individuals, after which the population doubles every generation until it reaches a new, fixed value. I assume 25 years per generation. Here is the resulting frequency distribution for a bottleneck 100,000 years ago, with a final population size of 16,384:



The two dotted lines show the contribution from genetic variation that survived the bottleneck (red) and from mutations occurring after the bottleneck (green). The distribution for pre-bottleneck variation, which would have had the characteristic 1/frequency appearance originally, is nearly flat after going through the bottleneck; that's what I mean by a massive distortion of the spectrum. That's also why it's not really relevant that a lot of heterozygosity makes it through a bottleneck: the bottleneck still has dramatic effects on diversity.

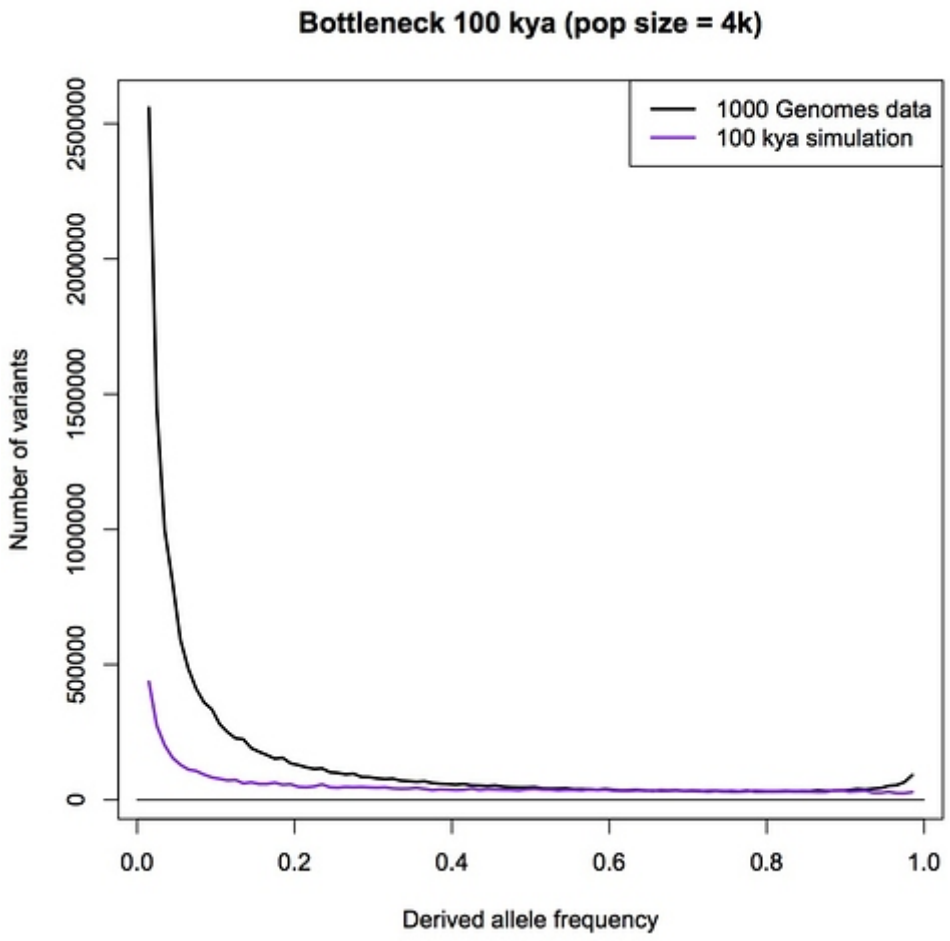
The contributions from before and after the bottleneck are effectively independent. This means I can increase the pre-b contribution by increasing the original population size, pretty much however is needed to agree with the data. For future comparisons with data, then, I will scale ancestral population as needed to match the data in the 60-70% frequency range.

Here is how this particular model compares to the empirical data we've already seen:



It might not look too bad at a glance, but the agreement here is terrible in the region of interest. In places, there are more than three times as many variants as predicted. There simply has not been enough time for mutation to generate new variation, and for genetic drift to increase their frequency substantially. I know of no biologically plausible process that would make this model work. A smaller post-bottleneck population has more drift, so the peak gets smeared out more, but also has half as many variants. Here's what the same simulation looks like with a post-bottleneck population

of 4000:



(More comparisons in a bit, after I go back and edit my last post.)

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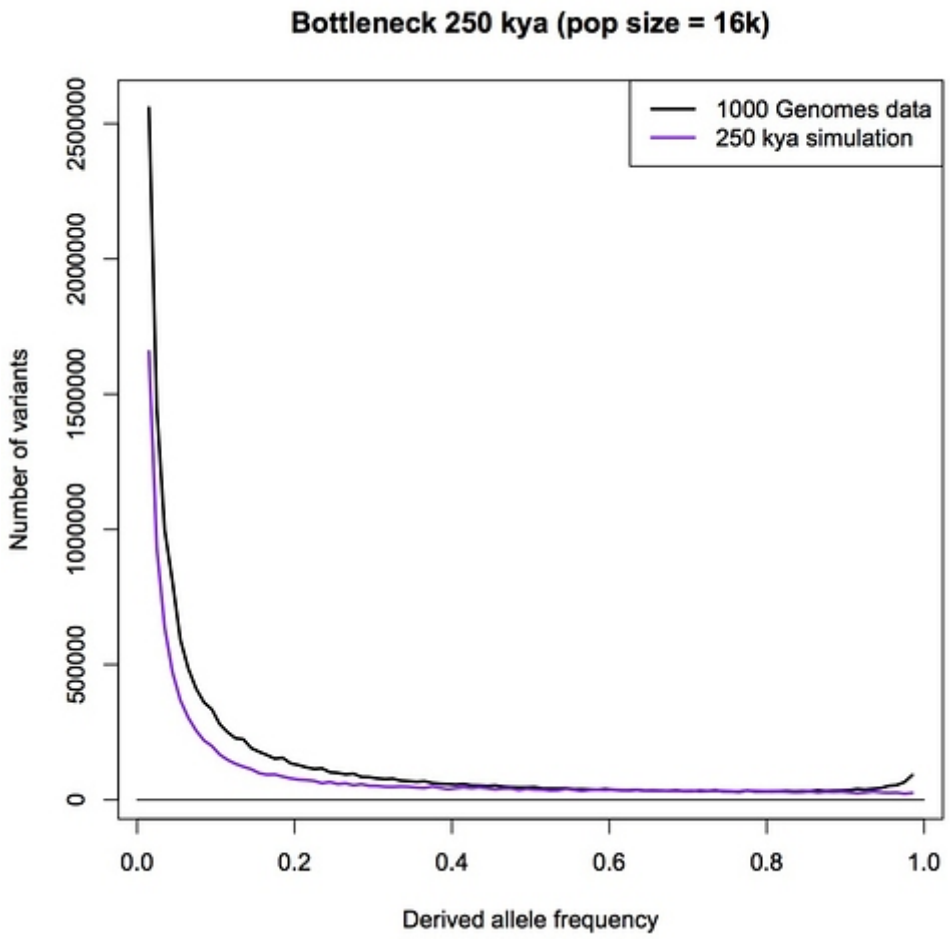
glipsnort (Steve Schaffner) 2017-11-16 16:39:45 UTC #41

Based on the previous results, Adam and Eve (as a unique pair of ancestors) are simply not credible within the last 100,000 years. Not at all. How about longer ago? My intuition was that anything in the last 250,000 years would be easy to rule out – so that's what I modeled.

Here is the comparison for a 250,000 year old bottleneck, with the usual population size of ~16,000:



We're getting a lot closer, but we're still not there. There are still around twice as many observed variant sites as predicted in places, since there still hasn't been time to fill out the depleted part of the distribution. Much larger or smaller final populations make things even worse.

Based on allele frequencies, then, 250,000 years seems to be too recent for a two-person bottleneck, even just judging the distributions by eye. For even earlier dates, I would want to use more rigorous statistical tests, which should also be more sensitive. Exactly how far back you can exclude a single couple gets murky and would require a lot of study, which is why I usually give "several hundred thousand years" as the likely excluded region.

Questions are welcome.

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agauger (Ann Gauger) 2017-11-16 21:02:27 UTC #42

Hi Steve. Thanks for doing this. Can you show what 500,000 or 1 million look like, or is that too computationally intensive?

Ann

GJDS (GJDS) 2017-11-17 06:31:34 UTC #44

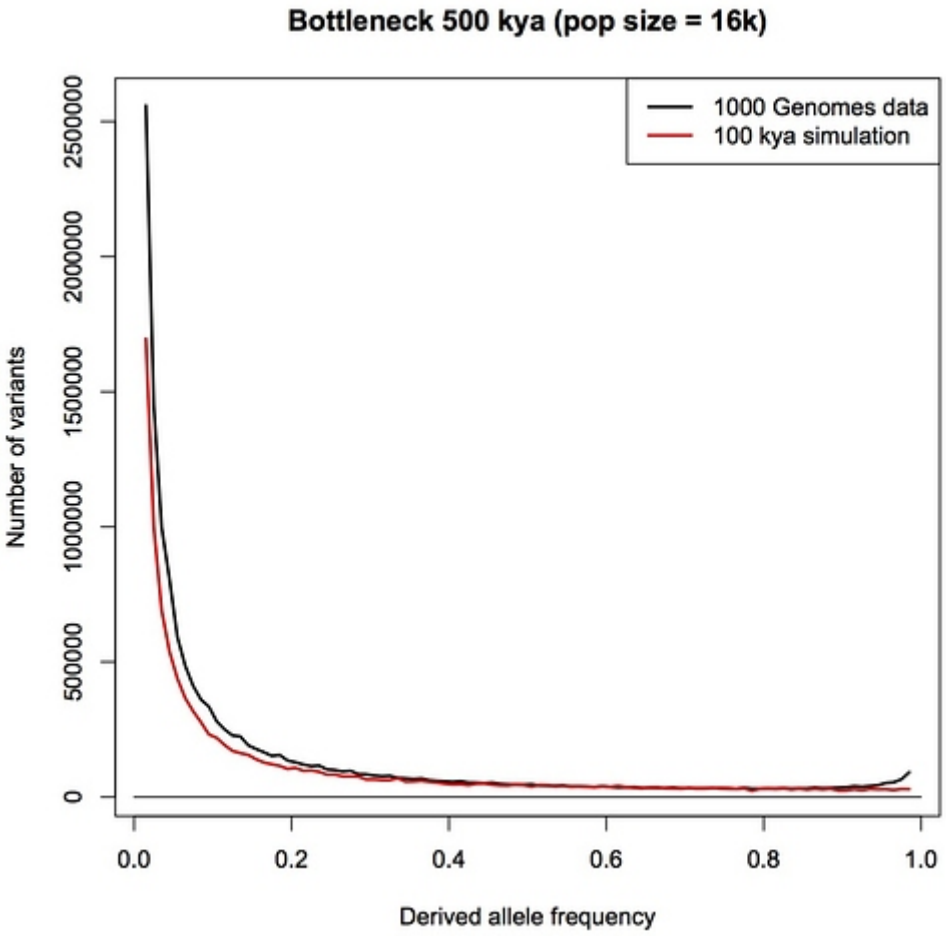
This question is simply out of curiosity and not questioning the nature of the simulation (I have downloaded a couple of papers).

Are your simulations based solely on data on current population(s), or do you have data that directly addresses past populations as well?

glipsnort (Steve Schaffner) 2017-11-17 14:27:22 UTC #45

Here's 500,000 years; I'm running 1 million now. To approximate a constant-sized initial population, I simulate a pop of 10,000 for 100,000 generations to start each simulation, so a million years at 16k pop size isn't much of a computational burden.

As you move the bottleneck date earlier, I start to worry that more complex demographies really should be explored for a better fit. Something like a pop size of 30,000 after the bottleneck for 250,000 years, a second, modest bottleneck, then another 250,000 at 30,000 might be a way to generate lots of mutations and still get enough drift to shift them to higher frequencies. But I don't want to undertake this as a research project.



glipsnort (Steve Schaffner) 2017-11-17 14:33:43 UTC #46

> GJDS:
>
> Are your simulations based solely on data on current population(s), or do you have data that directly addresses past populations as well?

The empirical data I'm trying to match is purely from current population data. The mutation rate is a fixed parameter in the model. It can be estimated from comparison with ancient DNA, or from comparison with another species, but the estimate I'm using is based on data from modern populations. The generation time also comes from data on modern populations.

GJDS (GJDS) 2017-11-17 14:40:20 UTC #47

Thanks for this

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tallen_1 (Tim) 2017-11-17 15:25:37 UTC #48

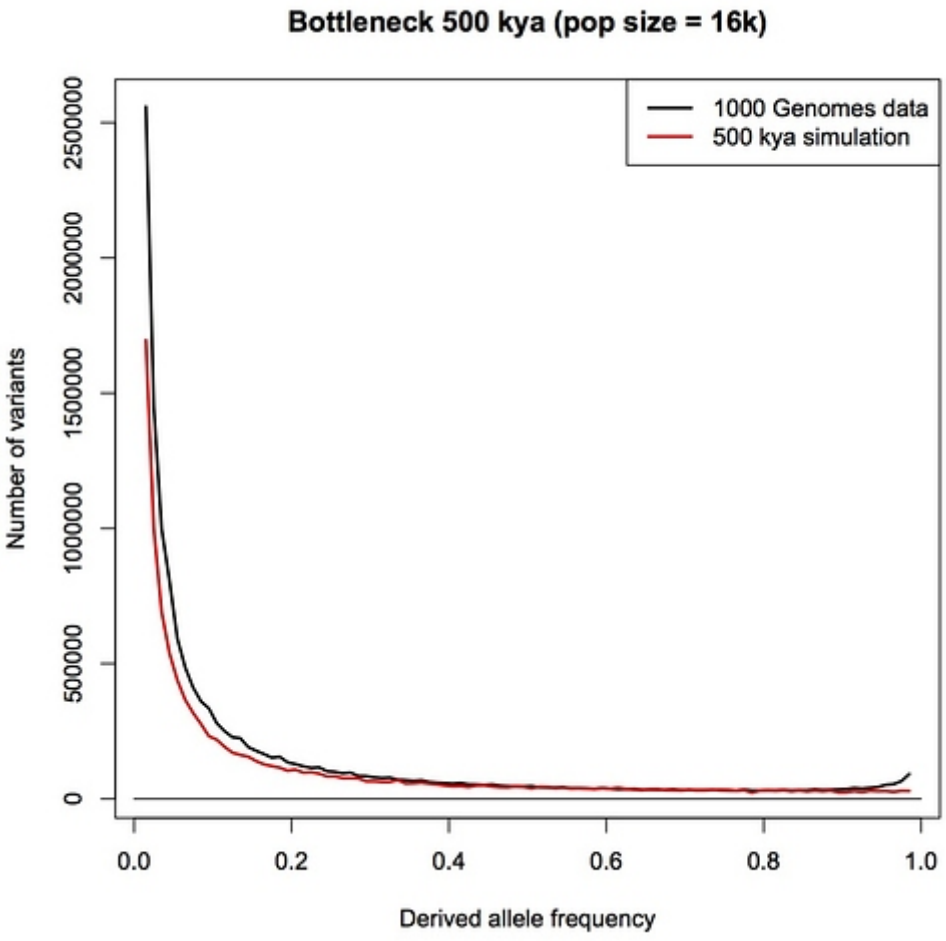
Should the legend say 500 kya simulation instead of 100?

---

glipsnort (Steve Schaffner) 2017-11-17 15:45:50 UTC #49

> tallen_1:
>
> Should the legend say 500 kya simulation instead of 100?

Yes, it should. That's what happens when you cut and paste in your R script.



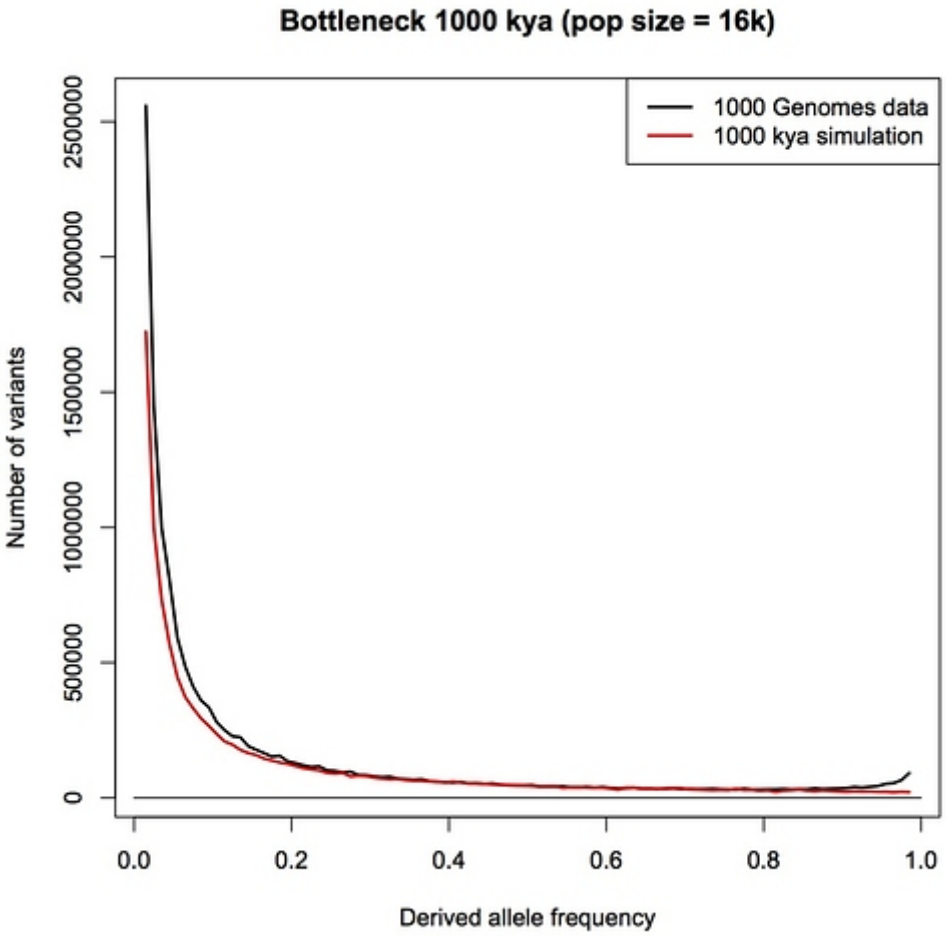
Casper_Hesp (Casper Hesp) 2017-11-17 15:53:15 UTC #50

Classic question: how large would the error bars on that plot be, given the uncertainty in the mutation rate estimate? Don't bother if it costs effort to figure out the answer, I'm already amazed that you have time on your hands to run these simulations.

---

glipsnort (Steve Schaffner) 2017-11-17 16:08:59 UTC #51

1 million years. By eye, this doesn't look any different than the constant-sized population compared to data that I posted earlier. Add a population expansion and it would fit well.

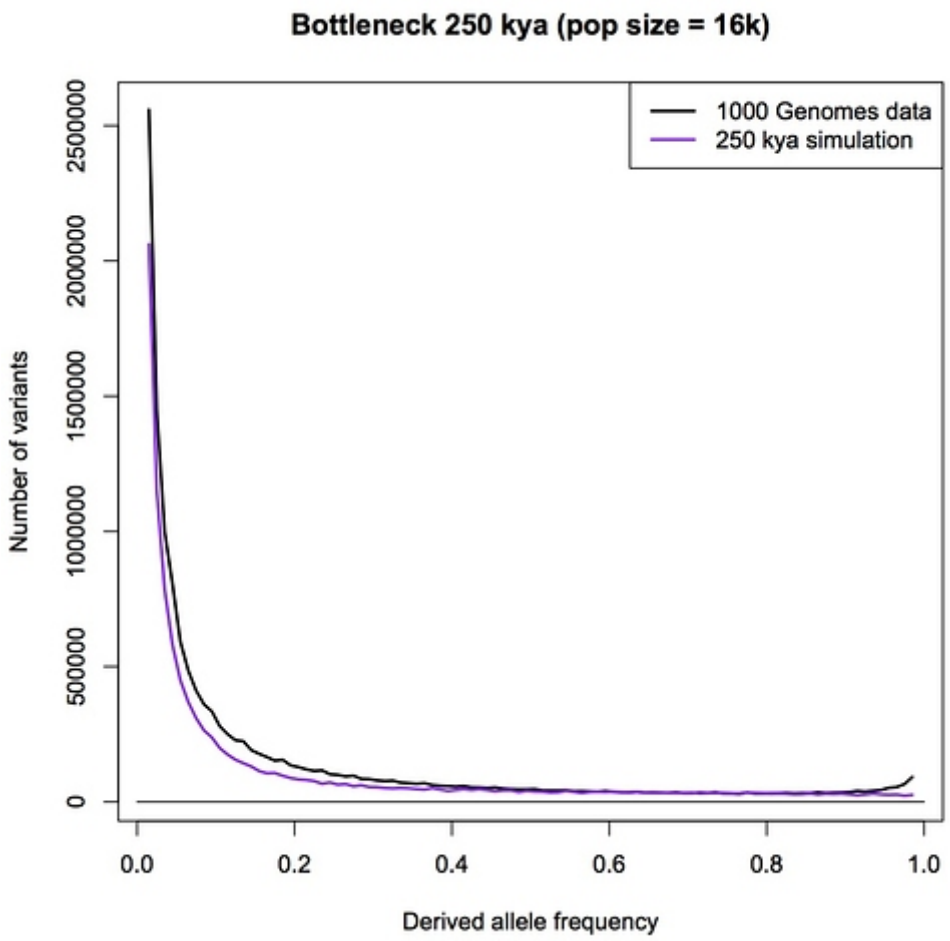


glipsnort (Steve Schaffner) 2017-11-17 16:26:18 UTC #52

> Casper_Hesp:
>
> Classic question: how large would the error bars on that plot be, given the uncertainty in the mutation rate estimate? Don't bother if it costs effort to figure out the answer, I'm already amazed that you have time on your hands to run these simulations.

Not a simple question, in this case. The mutation rate is poorly known, and why it's poorly known is also not well understood. Estimates range over roughly 1.1 to 2.0 x 10^-8; most recent estimates have been near the low end of that range. To a varying extent, changing the mutation rate can be absorbed by changing the population size – completely for a constant-sized population, less so for genetic drift after the bottleneck.

What I have done is run a couple of the simulations using the highest mutation rate within the above range (2.0 x 10^-8). Here is 250,000 years, pop size = 16,000. You can compare it to the plot above for the same age, which was done with mut rate = 1.6 x 10^-8.



RichardBuggs (Richard Buggs) 2017-11-17 18:54:56 UTC #53

Thank you so much for doing these analyses, Steve. I was hoping that my Nature Eco Evo blog would stimulate some studies that set out to explicitly test the bottleneck of two hypothesis, and this is certainly a big step in that direction.

As I begin to comment on this, I think I should say for those reading in who are not in the science world that Steve Schaffner is right at the top of the field when it comes to human genomics, and was one of the authors of the 1,000 genomes paper (and many other highly cited and very significant papers too). It is a real privilege to us all who are interested in this issue to have Steve running simulations on the two person bottleneck hypothesis, and to be taking the time to answer questions on it.

I would also note that the fact that we are discussing these new simulations is in itself very good backing for the point I made in my blog that more research is needed on this issue. It highlights how mistaken it is to declare that we can be as certain that there has not been a two person bottleneck as we can be that the earth rotates around the sun. After all, if I were to question the latter, no one would need to go away and do a simulation to come up with new evidence for it, in order to be persuasive.

Steve, I am very interested in your analyses. I had expected allele counts at polymorphic loci to be the biggest argument I would come across against the bottleneck of two hypothesis. I was not expecting an argument from allele frequency spectra. I am delighted to come across this possible way to test the hypothesis that I had not thought of, and that was not mentioned in Dennis' book chapter.

I am still going to take a bit of convincing that this is a good approach to testing the hypothesis, however. I will explain my reasoning below. I would underline that I know you see what you have done as just a preliminary study and you

yourself are well aware of the approximations and simplifications that you have had to make. I will try to explain my points as simply as I can for our readers.

1. Steve has already highlighted that this approach depends heavily on a correct estimation of mutation rates, and the model presented assumes that these do not vary with time or in different parts of the genome. This may not be the case in reality.

2. Also, as far as I can see (Steve, do correct me if I am wrong), this approach depends on the assumption of a single panmictic population over the timespan that is being examined. I think it would be fair to say that there has been substantial population substructure in Africa over that timespan and that this has varied over time. To my mind, this population substructure could well boost the number of alleles at the frequencies of 0.05 to 0.2.

Let me just try to explain that in a way that is a bit more accessible to our readers. I am saying that Steve's model (at least in its current preliminary form) is making the approximation that there is one single interbreeding population that has been present in Africa throughout history, and that mating is random within that population. However, the actual history is almost certainly very different to this. The population would have been divided into smaller tribal groups which mainly bred within themselves. Within these small populations, some new mutations would have spread to all individuals and reached an allele frequency of 100%. In other tribes these mutations would not have happened at all. Thus if you treated them all as a large population, you would see an allele frequency spectrum that would depend on how many individuals you sampled from each tribe. It is more complicated than this because every-so-often tribes would meet each other after a long time of separation and interbreed, or one tribe would take over another tribe and subsume it within itself. Such a complex history, over tens or hundreds of thousands of years would be impossible to reconstruct accurately, but would distort the allele frequency spectrum away from what we would expect from a single population with random mating. It gets even more complicated if we start also including monogamy, or polygamy.

3. As far as I can see the model currently also assumes no admixture from outside of Africa. A group of people arriving in Africa from another continent would affect the allele frequency spectrum if they interbred, and if their non-African population had diverged from African populations. Obviously this could not have happened at time periods when there were no humans outside Africa. But the data under analysis is obviously of present day Africans after centuries of admixture from outside Africa. Steve may be able to account for this with a more complex model that excluded alleles that are common in non-African populations, although it would be hard to be completely sure about the origins of these alleles.

4. As far as I can see, the model currently assumes no selection. Natural selection will boost the frequency of beneficial alleles (and alleles linked to an allele being selected for). Especially relevant would be alleles selected in one location and not another, and alleles under balancing selection. Steve would know better than me how to try to incorporate selection into the model, but my guess is that it would be very tricky.

Finally, could I ask, Steve, how many allelic variants did you assume in the founding couple, and what proportions of alleles did you put in them at 25% and 50%? Or did you assume that all variants arose through mutation?

---

agauger (Ann Gauger) 2017-11-17 21:30:09 UTC #54

@glipsnort . Thanks very much for doing this. When I asked about it being computationally intensive I had forgotten you only let the population double up to 16K and then held the population fixed.

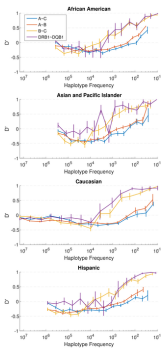
We have planned to test the effects of varying various parameters, as you suggest. No more requests.

---

agauger (Ann Gauger) 2017-11-17 21:59:52 UTC #55

@glipsnort **@RichardBuggs** **@T_aquaticus**

Richard, you have mentioned highly polymorphic genes as posing a major problem to the 2 person bottleneck hypothesis. Perhaps you and Steve are aware of this paper:



HLA class I haplotype diversity is consistent with selection for frequent...

Author summary The adaptive immune system presents antigens derived from pathogenic and normal self proteins on the cell surface using human leukocyte antigen (HLA) molecules. The HLA loci coding for these molecules are found in major...

They surveyed the HLA-A, B, C and DRB1 and DQB1 loci from 6 million individuals, and found purifying selection at the level of haplotype for Class I genes but not Class II. There are clear pairings of alleles which co-occur; in addition recombination appears to be suppressed in the region. Then they looked for selection between alleles and found that new alleles were favored. It is at the level of the allele (usually exon 2) where mutation rates and gene conversion rates are thought to be high.

I'd be interested to get your opinion about this paper and its possible relevance to the bottleneck question.

DennisVenema (Dennis Venema) 2017-11-17 23:23:56 UTC #56

I see the conversation has continued in my absence - I've been away from email for two days. Hunting, actually. Hauling a rifle up and down steep cliffs seeking elusive deer is remarkably therapeutic and very good exercise…

Steve, thanks for those simulations. Very nice.

Richard - I see you're still at me for specific references. The paper that specifically undergirds the "pick a few genes" part of the broad-brush summary statement about allele methods is this one, which like PSMC, is a coalescent-based approach:

http://www.genetics.org/content/genetics/147/4/1977.full.pdf

Darrel Falk and I also discussed that one way back when I first started writing for BioLogos.

Now, is PSMC an allele-based method? Does it "count" alleles? I guess it's a bit semantic at this point - but that's one of the challenges of writing for a non-specialist audience. Explain coalescence, or talk about it in simpler terms? I went with simpler terms. Sorry if it was confusing.

DennisVenema (Dennis Venema) 2017-11-17 23:31:25 UTC #57

Also, for this paper, note that it gives an Ne at about 18,000, not the usual "10,000" - and it's based on polymorphic Alu insertions, and thus not on the standard forward mutation frequency (Mu). So, it's another independent measure of ancestral population sizes that again, does not (at all) support a bottleneck to two.

http://www.genetics.org/content/genetics/147/4/1977.full.pdf

DennisVenema (Dennis Venema) 2017-11-17 23:58:44 UTC #58

Also note this from the paper: they considered, tested, and rejected a strong bottleneck hypothesis in the time frame we are discussing. Note how they cite the allele frequency spectrum for the Alu variant sites:

“The disagreement between the two figures suggests a mild hourglass constriction of human effective size during the last interglacial since 6000 is very different from 18,000. On the other hand our results also deny the hypothesis that there was a severe hourglass contraction in the number of our ancestors in the late middle and upper Pleistocene. If humans were descended from some small group of survivors of a catastrophic loss of population, then the distribution of ascertained Alu polymorphisms would show a pre- ponderance of high frequency insertions (unpublished simulation results). Instead the suggestion is that our ancestors were not part of a world networkof gene flow among archaic human populations but were instead effectively a separate species with effective size of 10,000-20,000 throughout the Pleistocene.”

---

gbrooks9 (George Brooks) 2017-11-18 05:59:39 UTC #59

> RichardBuggs:
>
> Ah, you might say, these studies require an estimate of mutation frequencies from the distant past. What if the mutation frequency once was much higher than it is now? Couldn’t that explain the data we see now and still preserve an original founding couple?

@RichardBuggs ,

Really? Why don’t we conclude that the speed of light gets faster and faster with time while we are at it. 6000 years ago, it took 4 hours for you to see the stampeding wildebeasts… and naturally, you were run over by them before you could literally see them.

For you to assume that mutation rates were different, you would need evidence for why that would be, yes?

Conversely, if we correlated mutation rates across several types of animals and types of phenotypes… if we saw convergence and general agreement, your theory would be proved wrong.

So… instead of “what-if”-ing scientists to death … maybe you could collect the evidence that shows you something?

RichardBuggs (Richard Buggs) 2017-11-18 10:39:45 UTC #60

> gbrooks9:
>
> Really?

George, the quote you are making is from Dennis’ book, which I was quoting. I did not pen those words. However, I would point out there is a considerable literature on the evolution of mutation rate. Michael Lynch has done a lot of work on this. This is very different from the speed of light.

RichardBuggs (Richard Buggs) 2017-11-18 11:21:28 UTC #61

Hi Dennis, good to hear you have had a nice hunting trip. I trust you are enjoying some venison now.

> DennisVenema:
>
> Richard - I see you’re still at me for specific references.

I am indeed. I cannot underline enough how important this issue is. If you are making unsubstantiated or mistaken claims about science in your book, just lines after saying “given the importance of this question for many Christians”, I don’t think it is just me who views that as quite a serious issue. This is why I am so keen to give you every opportunity to substantiate this passage.

For readers struggling to follow all the different threads in this comments stream, let me remind them that this is the passage from Adam and the Genome that we are discussing

> RichardBuggs:
>
> [Quoting Adam and the Genome] “scientists have many other methods at their disposal to measure just how large our population has been over time. One simple way is to select a few genes and measure how many alleles of that gene are present in present-day humans. Now that the Human Genome Project has been completed and we have sequenced the DNA of thousands of humans, this sort of study can be done simply using a computer. Taking into account the human mutation rate, and the mathematical probability of new mutations spreading in a population or being lost, these methods indicate an ancestral population size for humans right around that 10,000 figure. In fact, to generate the number of alleles we see in the present day from a starting point of just two individuals, one would have to postulate mutation rates far in excess of what we observe for any animal.”

So far, these are the attempts you have made to substantiate this passage from your book.[quote=“DennisVenema, post:13, topic:37039”]
Some of the citations you’re looking for are just working familiarity with published data sets.
[/quote]

> DennisVenema:
>
> I am saying this is my understanding of the published literature and the relevant publically-available databases. Li and Durban would be one paper relevant here; moreover the 1,000 genomes consortium papers, papers that estimate the present-day human mutation rate, and so on.

> DennisVenema:
>
> What I’m talking about there is a summary of the field as a whole - and the PSMC analyses in the 1,000 genomes paper is certainly one of the relevant experiments. So are LD studies. So are the Li and Durban PSMC results.

> DennisVenema:
>
> it’s a summary of allele methods, including PSMC

> DennisVenema:
>
> That passage is a summary statement about allele-based methods. Why would I exclude the 1000 genomes papers (including their PSMC results)? I was primarily thinking about the 1000 genomes work when writing that section.

I have argued that the plain meaning of that passage in your book, backed up by your Part I blog, is that it is not a summary statement and not a reference to PSMC and that to merely refer to datasets without the described analyses is not an adequate citation.

I don't know how much time you have had to read through all the posts since your hunting trip. To make sure that others would agree with me about the plain meaning of the passage from your book about allele counting methods, I posed three simple questions for others to answer about it.[quote="RichardBuggs, post:35, topic:37039"]
The questions I ask you are, when you read the extract from Adam and the Genome in bold below, which I show in its context:

Does the passage make you think that it is referring to a scientific study where a few genes have been selected and the number of alleles of those genes in current day human populations have been measured?
Does the passage make you think that someone has done calculations on these genes on a computer that have indicated that the ancestral population size for humans is around 10,000?
Does the passage make you think that this is a different method to the PSMC method?
[/quote]
To which your Biologos colleague Ted Davis answered:

> TedDavis:
>
> So, my answer to each of your three questions is, Yes.

And another reader also agrees with my reading of the passage: [quote="tallen_1, post:38, topic:37039"]
As far as I can tell, Dennis makes three claims most relevant to your point: One, that there is a method to estimate minimum ancestral population sizes based upon measurements of number of alleles across various genes present in a population, and that this method indicates a population of approx. 10,000. Two, that an independent method exists that does not rely upon estimates of past mutation rates, involving "linkage disequilibrium," that converges upon the same ancestral population size of 10,000. Three, that there has been a more recent method that is similar (not identical) that is not independent of mutation rate but also converges on similar results, namely the PSMC method.

Of these three approaches, Dennis's support for the first seems to derive mostly from calculations on collected data. Presumably done by himself or others. Of the latter two approaches, that does seem to be something that is published and to which he could (and I think did) direct you. But I'm unclear as to whether the published studies for the latter two methods explicitly state Dennis's conclusions or if he is drawing as well primarily on their collected data for support. I'm perhaps at a bit of a handicap on this as I'm relying on only excerpts of his book here on this thread. But to your point I do believe he describes three distinct methods. I'm eager to hear more about the sort of calculations conducted in these methods and how they may or may not support Dennis's argument. That is what I am looking forward to in his remaining parts to this topic.
[/quote]
No one, so far, has defended your reading of the passage. This is making me think that your reading of the passage is what you wish you had written, rather than what you actually wrote.

And now in your latest posts you are saying:

> DennisVenema:
>
> The paper that specifically undergirds the "pick a few genes" part of the broad-brush summary statement about allele methods is this one, which like PSMC, is a coalescent-based approach:
>
> **http://www.genetics.org/content/genetics/147/4/1977.full.pdf**

My first response was to think "Well, thank you, why didn't you say so before?" But a quick skim of the paper convinces me that, again, this is not an adequate citation to support the passage we are discussing.

1. It was published before the Human Genome Project, and before we had "sequenced the DNA of thousands of humans"

2. Most of the genes (if we may loosely call a retrotransposon a “gene)” in the paper are monomorphic in the human population studied and a handful are dimorphic. Thus the maximum number of alleles at any locus in the study is two. The allele counting method as described in your book, and elaborated upon in your Part I blog, explicitly requires higher numbers of alleles.

So again, I don’t think this is an adequate citation.

Dennis, I have to say the conclusion I am coming to is that you made a mistake in your book. If so, I would have huge respect for you if you were willing to admit it, then we could all move on and discuss the interesting science of the other methods you have written about, and the work that Steven Schaffner is doing. We all make mistakes, and those of us active in research are very used to having them forcibly pointed out to us when we get back peer review comments on our manuscripts and grant proposals. It is never much fun to have them pointed out, but part of being a good scientist is being willing to correct our mistakes and move on.

DennisVenema (Dennis Venema) 2017-11-18 14:42:27 UTC #62

Richard, I agree the passage is not clear. My mistake was trying to shove too much into a short summary in a way that would be accessible. I was over my word count as it was and things needed to be concise. Obviously that part was too concise to the point of confusion.

Like I said, it’s my (in hindsight poor) attempt of a summary of the field as a whole, for all allele-based methods.

I’m not sure why you continue to insist that that summary excludes PSMC methods. It doesn’t. I was primarily thinking of the 1000 genomes papers, but also all of the older literature prior to the human genome project work. Are you really saying that you know better than I what was in my mind as I wrote that passage?

What should be a bigger issue than my unclear writing is that there is no evidence in the literature that supports your hypothesis, and plenty of evidence that supports my conclusion in the book - which is the whole point that that passage is trying to convey, albeit in too compressed a fashion. Early work and the massive results from the Human Genome Project agree: humans are too diverse to have come from just two people.

So yes, by all means, let’s discuss the science. How about that Alu paper? It specifically tests the hypothesis you’re asking about, which counters your claim that researchers have not considered your hypothesis. Do you think that Alu polymorphisms in present-day humans are compatible with a population bottleneck to two people within the last 200,000 or 300,000 years? Why or why not? My take on it is a resounding “no”. It’s also nice that it’s not based on the nucleotide mutation rate, so it provides a check against papers that have to estimate that. It fits right in with the allele frequency spectrum data for SNPs that Steve is laying out for you. If there had been a human bottleneck, we would see skewed frequency spectrum for Alu insertions as well as for SNPs.

After we’re done discussing that paper, we can also discuss this other older one if you like (and then the 1000 genomes papers, and so on):

http://www.sciencedirect.com/science/article/pii/S004058098571026X

DennisVenema (Dennis Venema) 2017-11-18 15:23:24 UTC #63

And since we’re on the topic of the pre-genome project literature, here are two other papers that I consider “older” papers, although they are sort of genome project papers, since they were published based on studies on specific genome regions when the HGP was underway/nearly done. These papers also were part of the older literature that formed my understanding of the data, and they are based on allelic variation in small genome regions. Even though they are older, they remain relevant. One even explicitly says there was no severe bottleneck in the last 500,000 years.

http://www.pnas.org/content/97/21/11354.full.pdf

Global Patterns of Human DNA Sequence Variation in a 10-kb Region on Chromosome...

Human DNA variation is currently a subject of intense research because of its importance for studying human origins, evolution, and demographic history and for association studies of complex diseases. A ~10-kb region on chromosome 1, which contains...

DennisVenema (Dennis Venema) 2017-11-18 16:05:45 UTC #64

And last, but not least, another early paper that is part of the body of knowledge of the field as a whole.

Allelic genealogy and human evolution. | Molecular Biology and Evolution |...

Genetic variation at most loci examined in human populations indicates that the (effective) population size has been approximately 10(4) for the past 1 Myr and that individuals have been genetically united rather tightly. Also suggested is that the...

These last three papers are also under the surface of the “pick a few genes” statement, FYI.

Edit: a few more early papers, also part of the discussion. Remember, that summary statement is a gloss of the field using allele diversity methods. There might be other papers I’m not remembering at the moment too, but these at least give a sampling.

X chromosome evidence for ancient human histories

National Academy of Sciences

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1712470/

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tallen_1 (Tim) 2017-11-18 17:53:31 UTC #65

Dennis,

As a non-specialist here, I’m doing my best to follow along. But I’m hoping you can clear things up.

In my response to Richard above, I noted you seem to provide three distinct methods to estimate a minimal bottleneck size in human population over the past (presumably) hundreds of thousands of years. With one of them being independent of mutation rate. And all three converging on the same result. In the back-and-forth on this thread, I’m having a difficult time separating evidence and claims presented into these three methods. It seems to muddle together a bit. Again, as a non-specialist. I’m also struggling to gain clarity on how some of the studies tossed around here connects to the distinct methods you discussed in your book, and whether they explicitly back up your claims for at least the latter two methods or if there is some chain of inference and extrapolation that distances us somewhat from the

authors' conclusions in those studies. And perhaps better understand exactly how you intended all of that to come out. Again as a non-specialist. So I'm doing my absolute best here, but am hoping for some help. I presume most other readers with passing familiarity with the material, but no professional expertise, may find themselves in a similar quandary. Looking forward to your thoughts. Thanks Dennis!

DennisVenema (Dennis Venema) 2017-11-18 19:27:15 UTC #66

> tallen_1:
>
> Dennis,
>
> As a non-specialist here, I'm doing my best to follow along. But I'm hoping you can clear things up.
>
> In my response to Richard above, I noted you seem to provide three distinct methods to estimate a minimal bottleneck size in human population over the past (presumably) hundreds of thousands of years. With one of them being independent of mutation rate. And all three converging on the same result. In the back-and-forth on this thread, I'm having a difficult time time separating evidence and claims presented into these three methods. It seems to muddle together a bit. Again, as a non-specialist. I'm also struggling to gain clarity on how some of the studies tossed around here connects to the distinct methods you discussed in your book, and whether they explicitly back up your claims for at least the latter two methods or if there is some chain of inference and extrapolation that distances us somewhat from the authors' conclusions in those studies. And perhaps better understand exactly how you intended all of that to come out. Again as a non-specialist. So I'm doing my absolute best here, but am hoping for some help. I presume most other readers with passing familiarity with the material, but no professional expertise, may find themselves in a similar quandary. Looking forward to your thoughts. Thanks Dennis!

Yes, it does get a little muddled. Let's give this a try, and then maybe you can respond for additional clarification if needed.

Early studies on human variation, prior to the human genome project (HGP) were restricted to working with alleles of single "genes" (in reality, generally short stretches of DNA that included a gene but also some DNA around it). These studies depended on the researchers actually going out and sequencing a large number of people for this specific gene, and then making sense of the allele diversity they found for that region (by modelling using mutation frequency, etc). These are not PSMC methods, but earlier coalescent-based methods.

For example, **this early paper** looks at a few such genes for which data was available at the time and concludes this (from the abstract, my emphases):

"Genetic variation at most loci examined in human populations indicates that the (effective) population size has been approximately 10(4) for the past 1 Myr and that individuals have been genetically united rather tightly. **Also suggested is that the population size has never dropped to a few individuals, even in a single generation.** These impose important requirements for the hypotheses for the origin of modern humans: a relatively large population size and frequent migration if populations were geographically subdivided. **Any hypothesis that assumes a small number of founding individuals throughout the late Pleistocene can be rejected**."

Later pre-HGP papers were in agreement with these results. For example, **this paper** looked at another gene (the PHDA1 gene), and reports a human effective population size of ~18,000.

Another paper from this timeframe looked at allelic diversity of the beta-globin gene and found it to indicate an ancestral effective population size of ~11,000, and conclude that **"There is no evidence for an exponential expansion out of a bottlenecked founding population, and an effective population size of approximately 10,000 has been maintained."** They also state that the allelic diversity they are working with cannot be explained by recent

population expansion - the alleles are too old to be that recent. (This also fits with the genome-wide allele frequency data we see later from the HGP.)

It is in this timeframe that the **Alu paper** is also published. It looks at allelic diversity of a different kind. Alu elements are transposons - mobile DNA - and they can generate "alleles" where they insert. Generally, if an Alu is present, that's an allele, compared to when an Alu is absent (the alternative allele). This paper is also nice because it does not depend on a forward nucleotide substitution rate - i.e. the DNA mutation rate, since Alu alleles are not produced by nucleotide substitutions. This paper concludes that the human effective population size is ~18,000. They also state (my emphases):

"The disagreement between the two figures suggests a mild hourglass constriction of human effective size during the last interglacial since 6000 is very different from 18,000. **On the other hand our results also deny the hypothesis that there was a severe hourglass contraction in the number of our ancestors in the late middle and upper Pleistocene. If humans were descended from some small group of survivors of a catastrophic loss of population, then the distribution of ascertained Alu polymorphisms would show a pre-ponderance of high frequency insertions (unpublished simulation results).** Instead the suggestion is that our ancestors were not part of a world network of gene flow among archaic human populations but were instead effectively a separate species with effective size of 10,000-20,000 throughout the Pleistocene."

From here, we start to get into what are really HGP papers but are focused studies on small DNA regions, rather than genome-wide variation. These are still not PSMC studies. For example, **this paper** looks at a small section of an autosomal chromosome (chromosome 22). They conclude (my emphases):

"The comparable value in non- Africans to that in Africans indicates **no severe bottleneck during the evolution of modern non-Africans**; however, the possibility of a mild bottleneck cannot be excluded because non-Africans showed considerably fewer variants than Africans. The present and two previous large data sets all show a strong excess of low frequency variants in comparison to that expected from an equilibrium population, indicating a relatively recent population expansion. The mutation rate was estimated to be 1.15 10 9 per nucleotide per year. **Estimates of the long-term effective population size Ne by various statistical methods were similar to those in other studies.** "

A **second paper of this type** looked at a region of chromosome 1. They also do a variety of estimates of population size for this region, and they conclude the following (my emphases):

An average estimate of ~12,600 for the long-term effective population size was obtained using various methods; the estimate was not far from the commonly used value of 10,000. Fu and Li's tests rejected the assumption of an equilibrium neutral Wright-Fisher population, largely owing to the high proportion of low-frequency variants. The age of the most recent common ancestor of the sequences in our sample was estimated to be more than 1 Myr. Allowing for some unrealistic assumptions in the model, this estimate would still suggest an age of more than 500,000 years, providing further evidence for a genetic history of humans much more ancient than the emergence of modern humans. The fact that many unique variants exist in Europe and Asia also suggests a fairly long genetic history outside of Africa and argues against a complete replacement of all indigenous populations in Europe and Asia by a small Africa stock. **Moreover, the ancient genetic history of humans indicates no severe bottleneck during the evolution of humans in the last half million years; otherwise, much of the ancient genetic history would have been lost during a severe bottleneck.**

In other words, the alleles we see in the present day cannot be explained as arising after a severe bottleneck in the last 500,000 years.

From here, we're on to the HGP papers and later the 1000 genomes papers as they extend this sort of thing to the genome as a whole, show the allele frequency spectrum for a much, much larger dataset, and now we start seeing PSMC analyses included. There's a lot to summarize in those papers, but the take-home message is those papers support the same conclusions as the previous work, but now using a **massive** data set. No one looked at the HGP/

1000 genomes work and said it's time to revisit the previous conclusion that a sharp bottleneck had been ruled out. On the contrary - the HGP/1000 genomes papers provide additional evidence that the prior work was solid.

So, there's a full treatment of what is glossed as a few sentences in Adam and the Genome.

I'll cover linkage disequilibrium (LD) (which is independent of the nucleotide substitution rate) and the single-genome PSMC approaches in my upcoming replies to Richard. Hopefully this gets you (and everyone else) up to speed thus far. Let me know if you'd like clarification on any of the above.

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glipsnort (Steve Schaffner) 2017-11-18 19:54:44 UTC #67

> RichardBuggs:
>
> 1. Steve has already highlighted that this approach depends heavily on a correct estimation of mutation rates, and the model presented assumes that these do not vary with time or in different parts of the genome. This may not be the case in reality.

No assumption is needed to deal with variation in mutation rate across the genome. Both the mutation rate and the genetic variation data include contributions from (more or less) the entire genome. It doesn't matter whether the different parts of the genome contribute uniformly or not – they're all contributing to both. (Unless you have to worry about multiple mutations at sites, but that's not the case here.)

Variation in mutation rate with time could cause problems, provided the variation were large enough. There are good reasons to think it's not in fact an issue, though. First, the high-end mutation rate I mentioned (2 x 10^-8) was calculated by comparison with the chimpanzee genome, so it would include any previous higher rate. As I showed with one plot, using that rate does not qualitatively change the situation. Second, there is no biologically plausible mechanism for changing rates for different mutational processes in sync. If one process had changed rate, I would expect to see that reflected in the proportions of different kinds of mutation over different time scales, but I don't. In particular, the ratio of mutations at CpG sites to mutations at other sites is the same in intra- and inter-species data, even though they are caused by very different processes.

> RichardBuggs:
>
> 2. Also, as far as I can see (Steve, do correct me if I am wrong), this approach depends on the assumption of a single panmictic population over the timespan that is being examined. I think it would be fair to say that there has been substantial population substructure in Africa over that timespan and that this has varied over time. To my mind, this population substructure could well boost the number of alleles at the frequencies of 0.05 to 0.2.

Structure can indeed be important, but you have the sign wrong. There is a body of theoretical work on the effect of population structure on detecting bottlenecks, and as far as I know, it all points to structure causes spurious signals of bottlenecks, not erasing the signatures of actual bottlenecks. (See **this paper**, for example, and references therein, in particular John Wakeley's 1999 paper, in which he concludes that we underestimate the ancestral human population size when we fail to consider population structure and migration.[quote="RichardBuggs, post:53, topic:37039"]
3) As far as I can see the model currently also assumes no admixture from outside of Africa.
[/quote]
This is really just another version of (2), I think. In general, a fragmented population (inside or outside Africa) creates two classes of parts of the genome: those with genetic ancestry entirely within one population, and those with ancestry from a second population. The former will have coalescence times (and therefore diversities) characteristic of the population of the single population, while the latter will have longer coalescence times and higher diversities; their most recent common ancestor has to lie before the time the populations diverged, or at least far enough back for earlier

migration to have carried the lineage into the second population. This signature – many regions with low diversity, some with much higher diversity – is also the signature of a bottleneck, in which some regions have variation that made it through the bottleneck and some don't.

> RichardBuggs:
>
> 4. As far as I can see, the model currently assumes no selection. Natural selection will boost the frequency of beneficial alleles (and alleles linked to an allele being selected for). Especially relevant would be alleles selected in one location and not another, and alleles under balancing selection. Steve would know better than me how to try to incorporate selection into the model, but my guess is that it would be very tricky.

While positive selection has certainly occurred in the human lineage, its effect on the overall landscape of genetic diversity is actually pretty hard to pick out, and is almost certainly smaller than the effect of background selection (which acts more or less to reduce the effective population size relative to the census size near functional elements in the genome), and even more so than the effect of neutral drift. There has been a debate whether the effect of positive selection is even detectable.

> RichardBuggs:
>
> Finally, could I ask, Steve, how many allelic variants did you assume in the founding couple, and what proportions of alleles did you put in them at 25% and 50%? Or did you assume that all variants arose through mutation?

I assumed that all variants in the founding couple were what they inherited from their ancestors, who were part of a large, constant-sized population. For each simulation, I included as much as was needed to match the predicted and observed data for the higher portion of the allele frequency distribution.

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gbrooks9 (George Brooks) 2017-11-18 23:12:33 UTC #68

> RichardBuggs:
>
> George, the quote you are making is from Dennis' book, which I was quoting. I did not pen those words. However, I would point out there is a considerable literature on the evolution of mutation rate. Michael Lynch has done a lot of work on this. This is very different from the speed of light.

@RichardBuggs ,

But both statements are "Deus Ex Macina" objections… you pull this notion out of nowhere… what if things were different a million years ago? Or just 3000 years ago?

I don't know… what if? When Galileo had the Pope's representatives look through the telescope, he asked if the could see the imperfections to the Lunar sphere - - craters and mountains and jagged hillsides on the supposedly pristine Lunar plains.

Their answer was that they could just detect an invisible layer of Lunar material covering over these imperfections, to render the Moon, once again, as a divinely perfect object.

Galileo, with his eyes flaring, bends over to look through the telescope again. And he steps back and concludes, but gentlemen, I see invisible mountains and craters on top of your invisible perfect lunar planes!

Propose the fringiest fringe ideas you would like … but you have to start showing results that would support these and related contentions.

gbrooks9 (George Brooks) 2017-11-18 23:16:37 UTC #69

> DennisVenema:
>
> "The comparable value in non- Africans to that in Africans indicates no severe bottleneck during the evolution of modern non-Africans; however, the possibility of a mild bottleneck cannot be excluded because non-Africans showed considerably fewer variants than Africans. The present and two previous large data sets all show a strong excess of low frequency variants in comparison to that expected from an equilibrium population, indicating a relatively recent population expansion. The mutation rate was estimated to be 1.15 10 9 per nucleotide per year. Estimates of the long-term effective population size Ne by various statistical methods were similar to those in other studies. "

@DennisVenema

I think it is pretty clear that if there is a bottleneck, it happened within Africa, and not in the out-of-Africa diaspora.

[Typo: “not is the out-of-Africa diaspora” corrected to “not In the out-of-Africa diaspora”]

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tallen_1 (Tim) 2017-11-19 01:01:17 UTC #70

Hi Dennis,

Thank you very much, that clears things up for me considerably. I look forward to your future discussion on the Linkage Disequilibrum and PSMC approaches. Also, does this then leave us with four methods being discussed here? Earlier coalescent-based methods involving (1) allelic diversity via nucleotide polymorphisms (mutation rate dependent) & (2) allelic diversity via Alu insertions (mutation rate independent), as well as (3) linkage disequilibrium (also mutation rate independent) & (4) single-genome PSMC? So (2) & (3) could both be considered independent checks irrespective of mutation rate? Thanks!

DennisVenema (Dennis Venema) 2017-11-19 01:16:17 UTC #71

> tallen_1:
>
> Hi Dennis,
>
> Thank you very much, that clears things up for me considerably. I look forward to your future discussion on the Linkage Disequilibrum and PSMC approaches. Also, does this then leave us with four methods being discussed here? Earlier coalescent-based methods involving (1) allelic diversity via nucleotide polymorphisms (mutation rate dependent) & (2) allelic diversity via Alu insertions (mutation rate independent), as well as (3) linkage disequilibrium (also mutation rate independent) & (4) single-genome PSMC? So (2) & (3) could both be considered independent checks irrespective of mutation rate? Thanks!

You’re welcome. You’ve basically got it, yes, but be aware that there are a variety of related coalescent methods in those papers cited above, but it’s a bit fuzzy to draw sharp distinctions between them. They do, however, use different raw data sets. The PSMC approach in the 1000 genomes papers is also a form of a coalescent analysis, as is single-genome PMSC. But you’re right that the LD and Alu analyses are independent of the nucleotide mutation frequency. They are also independent of each other. So at a minimum, we’re looking at three independent lines of evidence (if we want to lump all coalescent modelling together). Obviously, population geneticists don’t lump them all together, otherwise they wouldn’t keep improving them and applying them to larger and larger data sets.

DennisVenema (Dennis Venema) 2017-11-19 01:22:40 UTC #72

> gbrooks9:
>
> "The comparable value in non- Africans to that in Africans indicates no severe bottleneck during the evolution of modern non-Africans; however, the possibility of a mild bottleneck cannot be excluded because non-Africans showed considerably fewer variants than Africans. The present and two previous large data sets all show a strong excess of low frequency variants in comparison to that expected from an equilibrium population, indicating a relatively recent population expansion. The mutation rate was estimated to be 1.15 10 9 per nucleotide per year. Estimates of the long-term effective population size Ne by various statistical methods were similar to those in other studies. "
>
> **@DennisVenema**
>
> I think it is pretty clear that if there is a bottleneck, it happened within Africa, and not is the out-of-Africa diaspora.

Ah, yes. The point is that if the method is powerful enough to exclude a sharp bottleneck in non-Africans, which have an effective population size (Ne) around 1200, then it is amply able to exclude one for African populations which have a much higher Ne.

RichardBuggs (Richard Buggs) 2017-11-20 11:34:49 UTC #73

Hi Steve, **@glipsnort** , thanks for your responses to the points I raised about your model. I will respond more in due course, but for now I will just focus on the issue of population sub-structure.[quote="RichardBuggs, post:53, topic:37039"]
2) Also, as far as I can see (Steve, do correct me if I am wrong), this approach depends on the assumption of a single panmictic population over the timespan that is being examined. I think it would be fair to say that there has been substantial population substructure in Africa over that timespan and that this has varied over time. To my mind, this population substructure could well boost the number of alleles at the frequencies of 0.05 to 0.2.

Let me just try to explain that in a way that is a bit more accessible to our readers. I am saying that Steve's model (at least in its current preliminary form) is making the approximation that there is one single interbreeding population that has been present in Africa throughout history, and that mating is random within that population. However, the actual history is almost certainly very different to this. The population would have been divided into smaller tribal groups which mainly bred within themselves. Within these small populations, some new mutations would have spread to all individuals and reached an allele frequency of 100%. In other tribes these mutations would not have happened at all. Thus if you treated them all as a large population, you would see an allele frequency spectrum that would depend on how many individuals you sampled from each tribe. It is more complicated than this because every-so-often tribes would meet each other after a long time of separation and interbreed, or one tribe would take over another tribe and subsume it within itself. Such a complex history, over tens or hundreds of thousands of years would be impossible to reconstruct accurately, but would distort the allele frequency spectrum away from what we would expect from a single population with random mating. It gets even more complicated if we start also including monogamy, or polygamy.
[/quote]

> glipsnort:
>
> Structure can indeed be important, but you have the sign wrong. There is a body of theoretical work on the effect of population structure on detecting bottlenecks, and as far as I know, it all points to structure causes spurious signals of bottlenecks, not erasing the signatures of actual bottlenecks. (See this paper, for example, and references therein, in particular John Wakeley's 1999 paper, in which he concludes that we underestimate the ancestral human population size when we fail to consider population structure and migration.

I think you will find that John Wakeley's paper supports the point I am making. My point is only about the approach that you are using: modelling of allele frequency spectra. It is not (for now) about other methods of detecting bottlenecks. The problem for the bottleneck hypothesis that you are posing is the high number of intermediate frequency alleles in present day Africa. I am suggesting that past population structure (post-bottleneck) could explain this. Similarly, Wakeley is seeking in his 1999 paper to explain the fact that in a dataset he is looking at "nuclear loci show an excess of polymorphic sites segregating at intermediate frequencies (Hey 1997). This is illustrated by Tajima's (1989) statistic, D, which is positive…". Wakeley then goes on to explain pattern as "due to a shift from a more ancient subdivided population to one with less structure today". As far as I can see, this supports the point I am making: population subdivision can cause intermediate allele frequencies.

In addition, a paper which built on Wakeley's work shows that ""in simulations with low levels of gene flow between demes… Tajima's D calculated from samples spread among several demes was often significantly positive, as expected for a strongly subdivided population" (Pannell, Evolution 57(5), 2003, pp. 949–961).

Thus I think it is fair to say that strong population sub-structure for a prolonged period at some point subsequent to a bottleneck would shift allele frequency spectra towards having more alleles at intermediate frequencies.

---

glipsnort (Steve Schaffner) 2017-11-20 15:09:17 UTC #74

> RichardBuggs:
>
> I think you will find that John Wakeley's paper supports the point I am making. My point is only about the approach that you are using: modelling of allele frequency spectra. It is not (for now) about other methods of detecting bottlenecks. The problem for the bottleneck hypothesis that you are posing is the high number of intermediate frequency alleles in present day Africa.

No, that's exactly the opposite of the problem. Note that in this context "intermediate frequency" means not close to 0% or 100% (look at the Hey paper Wakeley cites if you doubt this). After your tight bottleneck, you've still got a substantial number of intermediate frequency alleles, but you've lost almost all of the low frequency alleles.

> RichardBuggs:
>
> Similarly, Wakeley is seeking in his 1999 paper to explain the fact that in a dataset he is looking at "nuclear loci show an excess of polymorphic sites segregating at intermediate frequencies (Hey 1997). This is illustrated by Tajima's (1989) statistic, D, which is positive…".
> […]
> In addition, a paper which built on Wakeley's work shows that ""in simulations with low levels of gene flow between demes… Tajima's D calculated from samples spread among several demes was often significantly positive, as expected for a strongly subdivided population" (Pannell, Evolution 57(5), 2003, pp. 949–961).

Tajima's D for the post-bottleneck scenarios *is* positive – very positive initially, because heterozygosity wasn't reduced very much by the bottleneck, while rare alleles were wiped out. The real human population, meanwhile, has a modestly negative D, thanks to the excess rare alleles from population expansion. You're proposing to add a process to the bottleneck scenario that will make D even more positive.

RichardBuggs (Richard Buggs) 2017-11-20 15:57:13 UTC #75

Hi Steve, perhaps I have misunderstood which aspect of you simulations is not fitting with the data. I was going on this comment that you posted near the beginning:

> glipsnort:
>
> It is the alleles at moderate frequency – roughly 5% to 20% minor allele frequency – that are difficult to explain with a recent bottleneck.

Then putting this comment together with this one:

> glipsnort:
>
> 100kya_16k.jpg1050x1050 71.4 KB
>
> It might not look too bad at a glance, but the agreement here is terrible in the region of interest. In places, there are more than three times as many variants as predicted. There simply has not been enough time for mutation to generate new variation, and for genetic drift to increase their frequency substantially. I know of no biologically plausible process that would make this model work.

I got the impression that you were saying that the problem with the model in your 100kya_16K simulation was that between 0.05 and 0.2 on the X axis the model is not predicting enough variants. This is why I suggested that one could invoke population subdivision over part of the last 100Kya to increase the numbers of these intermediate alleles, and if this were included it might be possible to fit the data.

Have you calculated Tajima's D for the data and simulation in the 100kya_16K chart? How do they compare?

I completely agree with you that the immediate effect of the bottleneck would be a positive Tajima's D, but I thought your argument was that 100Kya later the intermediate frequency alleles derived from the bottleneck had a very small - almost negligible effect on the allele frequency spectrum, which was now dominated by new mutations.

I am sure I must be misunderstanding something here.

DennisVenema (Dennis Venema) 2017-11-20 16:20:04 UTC #76

Another thing to keep in mind here is the allele frequency spectrum is a smooth distribution. If you're proposing that it was cobbled together from different demes after a bottleneck you'll have to account for the shape and fit of the curve, not just some explanation that happens to boost the frequency of some alleles due to population structure.

Back to being a fly on the wall (for now).

Casper_Hesp (Casper Hesp) 2017-11-20 16:28:48 UTC #77

At least biology-trained flies on the wall can sort out for themselves what's reasonable or not in this exchange. Being a non-expert fly on the wall is interesting but also pretty confusing.

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glipsnort (Steve Schaffner) 2017-11-20 17:08:07 UTC #78

> RichardBuggs:
>
> I got the impression that you were saying that the problem with the model in your 100kya_16K simulation was that between 0.05 and 0.2 on the X axis the model is not predicting enough variants.

That is the problem. The model doesn't predict enough relative to alleles around 50%, which are also intermediate alleles.

Let's back up and think about it in terms of first principles. After the bottleneck, you have enough alleles around 50% frequency, but a great shortage of lower frequency alleles. These can only be replenished by mutation followed by drift, and you have to get both processes to work in the time allotted. In a panmictic population, drift does not occur fast enough to move new mutations up to ~30% frequency in time.

Subdividing the population doesn't affect the mutation component at all: it's the same number of individuals mutating. Subdivision does affect the drift process, and it *slows* it. You can see this intuitively. When there is one copy of a new allele, it matters hardly at all whether it is in a panmictic population: it will be passed on to zero, one or two descendants regardless of how big the immediate population is. When it becomes more common, though, an increase in frequency is held back if it's in a local deme, because the new number of copies can't exceed the deme size, while there is no such constraint in the panmictic population.

Alternatively, treat it mathematically. Drift speed is governed by the variance of the sampling process; large variance = fast drift. Consider a new mutation in two populations, each with 10,000 individuals, one panmictic and the other divided into 10 demes. When there is one copy of the new allele, the variance is virtually identical for the two populations: Binomial variance = np(1-p). For population 1, n = 10,000, p = 1e-4, variance = .9999. For population 2, n = 1,000, p = 1e-3, variance = .999. (Not surprisingly, both are almost equal to the variance for an equivalent Poisson process, which this almost is.) But when the allele is at a higher frequency, the variances diverge. When there are 500 copies, for pop 1, p = .05 and the variance = 475, while for pop 2, p = .5 and the variance = 250. Drift proceeds faster in the large population.

Migration reduces but does not reverse this effect. If the allele has migrated to a second deme, with say 400 copies in the first and 100 in the second, the variance on the total number is the sum of the variances for the two demes, or 240 + 90, which is still less than the variance for a panmictic population. (The two only drift at the same rate when every deme has the same number of copies.)

Since your basic problem is that you have to speed up drift somehow while still producing lots of new mutations, subdivision cannot help you.

RichardBuggs (Richard Buggs) 2017-11-20 21:43:31 UTC #79

Thanks Steve for your patience.

This was how my argument was working: Immediately after a bottleneck, Tajima's D is positive (due to the intermediate frequency (25% and 50% minor allele frequency) alleles. Some time after the bottleneck, let's call this "Phase 2", Tajima's D is negative (due to the excess of very minor frequency alleles). Longer after this, Tajima's D ends up closer to zero as the population comes to equilibrium. That is my understanding of the expectation - I think we are on the same page here.

The issue of fitting the bottleneck model to the data was that the Tajima's D of the 100kya_16K model seemed more negative than the actual data (I am not sure if the actual data has zero Tajima's D or positive Tajima's D - if it is similar to the data that Wakeley (1999) was looking at then I guess it would have been positive). So we seem to be in "phase 2".

This was a similar problem to that faced by Wakeley: Tajima's D seemed too positive in his data. Wakeley solved this by invoking population sub-division. Similarly in models by Pannell (2003) Tajima's D tended to be more positive in a strongly sub-divided population, when samples were collected from several demes.

Thus it seemed reasonable to me to suggest that population subdivision could be causing more positive Tajima's D in the 1000 genomes project African populations, despite a past extreme bottleneck. Do you disagree with Wakeley's use

of population sub-division to explain a higher Tajima's D, or did he make a mistake, or am I misunderstanding his paper? (I suspect the latter may well be the case, but I would like to know where I am going wrong).

I take your point that if we are thinking in terms of overall allele numbers, drift happens more quickly in a large population. I.e., an allele can get more quickly from 1 copy to 500 copies in a single population of 10,000 individuals than it can in a single population of 1,000 individuals. However, the allele can more quickly go to fixation in the 1,000 population. Once an allele has reached a frequency of 1000 in a population of 1000 it cannot be lost, whereas an allele with a frequency of 1000 in a population of 10,000 can be lost by drift as easily as it arrived. Thus population subdivision will enhance the retention of new mutations as they get fixed in sub-populations. Then if the sub-populations mix again in the future, or if we sample across the sub-populations treating them as a single population, then we will find an excess of intermediate frequency alleles. In addition, it is harder to an allele to go to complete fixation in the whole metapopulation when there is population sub-division - in fact that will be rare. So the number of new mutations that end up neither being lost nor going to complete fixation is higher in a subdivided metapopulation. More of them get stuck at intermediate frequencies. This is my intuitive understanding of Pannell's result. That is the point I have been trying, perhaps not very clearly, to make up until now.

However, I also have another possibility that I would like to raise. What if the high number of intermediate frequency alleles in the African 1000 genomes study were due to a more recent bottleneck. I.e. we were still in the phase where the bottleneck had caused positive Tajima's D? How recent would the bottleneck need to be for that to be the case?

I have a suspicion the answer to my last question would be a date that is so young as to not be able to fit with known archeology. If so, I am wondering if perhaps population subdivision could act to slow down the loss of the intermediate alleles that are derived from the bottleneck itself. If there was a bottleneck of two, followed by rapid expansion of multiple sub-populations of offspring, most of the intermediate frequency alleles could be maintained in the metapopulation as a whole, giving intermediate frequencies long into the future.

This brings me to something that I wanted to follow up on earlier:[quote="glipsnort, post:67, topic:37039"]
I assumed that all variants in the founding couple were what they inherited from their ancestors, who were part of a large, constant-sized population. For each simulation, I included as much as was needed to match the predicted and observed data for the higher portion of the allele frequency distribution.
[/quote]
I was wondering why you could not include as much variation from the pre-bottleneck population as was needed to cause the simulations to fit the data in the 20-50% range? Why only focus on making them match at the 60-70% frequency range? I didn't quite follow the logic here, with your brief description.

Thanks again for your patience. BTW, I accept the point about mutation rates that you made earlier: that you are being quite generous to the model with your mutation rates. I still need to think a bit more about the selection and admixture issues, though I agree with you that the admixture issue is in effect another take on the population sub-division issue.

---

gbrooks9 (George Brooks) 2017-11-20 22:11:54 UTC #80

> RichardBuggs:
>
> I was wondering why you could not include as much variation from the pre-bottleneck population as was needed to cause the simulations to fit the data in the 20-50% range? Why only focus on making them match at the 60-70% frequency range? I didn't quite follow the logic here, with your brief description.
>
> Thanks again for your patience. BTW, I accept the point about mutation rates that you made earlier: that you are being quite generous to the model with your mutation rates. I still need to think a bit more about the selection and admixture issues, though I agree with you that the admixture issue is in effect another take on the population sub-division issue.

@RichardBuggs ,

I think you folks could be playing with these numbers from here to doomsday… trying to see what they **include**!

Wouldn't it be easier to see what they **exclude**?

What if you arranged your data with all of your most optimistic - - but still reasonable - - assumptions.
And use three different baseline rates:

1] the Low Baseline: the average rate for conventional multi-rate alleles;

2] the Medium Baseline: 1.5 x the average rate for conventional multi-rate alleles;

3] the High Baseline: 2 x the average rate for conventional multi-rate alleles.

Run these 3 baselines against 3 time frames:

A] Low, Medium & High for 6000 years;
B] Low, Medium & High for 10,000 years (a 66% longer timeframe); and
C] Low, Medium & High for 500,000 years (an 8200% longer timeframe!).

So, using your most optimistic premises, and a broad range of baseline mutation rates, compare the resulting allele diversity factors for these 9 scenarios to the allele diversity factors that the human population currently presents.

Do all of them meet and exceed current diversity? Or do just a few?
This will at least give you folks something concrete to fiddle with …
Right now, all I see are people with the pointer finger touching their foreheads and winging it.

**These are not deadly radioactive chemicals we are working with here. They are **
Rates of Change and "N's"… oh, and I suppose a few other factors. But it is still a pretty finite universe of numbers to put together.

RichardBuggs (Richard Buggs) 2017-11-21 21:04:01 UTC #81

Hi Dennis, just a quick note to thank you for the five papers that you have pointed out in your recent posts. I have downloaded them and started to work through them. I will come back with comments in due course.

DennisVenema (Dennis Venema) 2017-11-22 01:47:11 UTC #82

Sounds good - a little light reading for you… 🙂

Marty (Marty) 2017-11-22 02:56:13 UTC #83

Hi @glipsnort . A couple of quick questions (I think…).

If the generation times were faster, perhaps closer to puberty at 15 years:
How would that affect the mutation rate per generation? Would it be less per generation because they are younger, or are most of the errors copying errors anyway from when the germ cell first forms so the mutation rate is about the same?
Secondly, if the mutation rate stayed "the same" and the generation time reduced, would that pull the X axis in proportionally? That is, would a 40% reduction in generation times produce a 40% reduction in the X axis?

> gbrooks9:
>
> For you to assume that mutation rates were different, you would need evidence for why that would be, yes?

George - I can't find it now, but I recall Steve pointing out that the graphs assume fairly constant mutation rates, which is a fair place to try. But, for example, if our solar system goes through regions of space that are higher or lower in various types of radiation or other toxicity, they could vary some. I think the point of **@RichardBuggs** is not to just cast doubt, but to draw legitimate boundaries around what can be said with greater or lesser confidence. Scientists don't want to be guilty of assumptions that could be proven false, but if those assumptions are explicit because there is no better option at this time, well, better to identify those areas. I appreciate Steve stating it up front, and I think it appropriate to recognize it as a fair working assumption which could perhaps be open to revision.

Now for the scientists, is there any way to assess variability in historical mutation rates? And for Steve, if the mutation rate halved, for example, would that double the X axis of your graphs?

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gbrooks9 (George Brooks) 2017-11-22 06:36:37 UTC #84

> Marty:
>
> George - I can't find it now, but I recall Steve pointing out that the graphs assume fairly constant mutation rates, which is a fair place to try. But, for example, if our solar system goes through regions of space that are higher or lower in various types of radiation or other toxicity, they could vary some. I think the point of **@RichardBuggs** is not to just cast doubt, but to draw legitimate boundaries around what can be said with greater or lesser confidence. Scientists don't want to be guilty of assumptions that could be proven false, but if those assumptions are explicit because there is no better option at this time, well, better to identify those areas. I appreciate Steve stating it up front, and I think it appropriate to recognize it as a fair working assumption which could perhaps be open to revision.

@Marty

Well, I think we all know that numbers can vary. But to have numbers "seriously challenged" with absolutely no evidence to support the speculation is a bit of a stretch. Frankly, we can speculate that the change is actually in favor of the BioLogos conclusions, rather than the opposite, right? I don't remember seeing any "equal time" on how the wild speculation could go… But, I'll tell you what, Marty, I like your point!

I think we should really put some teeth into it though - don't you? For our sakes and for **@RichardBuggs** as well. Here is a useful article for accomplishing that:

http://curious.astro.cornell.edu/physics/55-our-solar-system/the-sun/the-sun-in-the-milky-way/207-how-often-does-the-sun-pass-through-a-spiral-arm-in-the-milky-way-intermediate

.
.
.

The article provides approximate speeds for our solar system, relative to the entire Milky Way galaxy:

The solar motion on top of its circular orbit about the centre of the Galaxy (which has a period of about 230 million years) can be described by how fast it is going in three different directions:

U = 10 km/s (radially inwards) [< towards the center of the galaxy]
V = 5 km/s (in the direction of Galactic rotation)

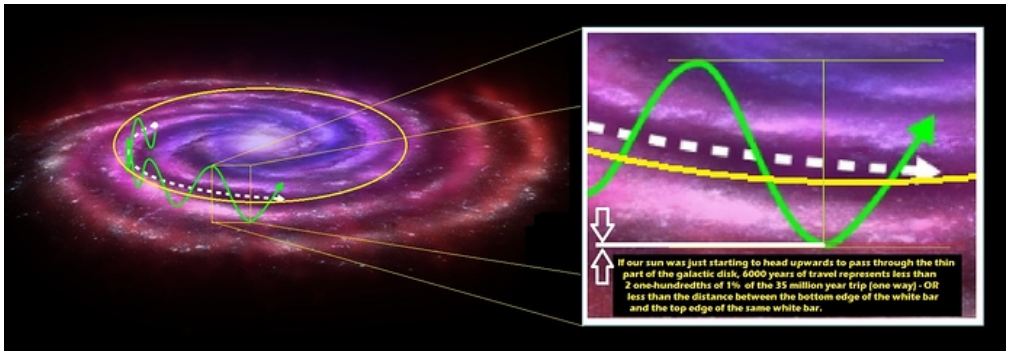
W = 7 km/s (northwards out of the plane of the Galaxy)
. . . . . [moving either up or down, perpendicular to the “flat” disk of the galaxy]

“Of course the Sun won’t keep on going in this direction forever. In fact we approximate its motion by an ‘epicycle’ on top of the mean motion around the Galaxy. The period of oscillation in and out of the plane of the galaxy (up and down) is about 70 million years. This means that we pass through the Galactic midplane about every 35 million years. . .”

I wonder how far @RichardBuggs thinks our solar system can move in just 6,000 years. It’s pretty far in terms of miles, but not very far compared to the rest of galactic space embraced by the arms of the Milky Way!

6000 years as a percentage of 35,000,000 years is the decimal fraction of 0.00017, or less than 0.02%. That’s not 2%. That’s 2 One-Hundredths of just **One Percent!**

I recommend clicking on the image in order to see the image more clearly, especially the white bar in the lower portion of the rectangular inset, with a down arrow and a white arrow pointing to emphasize the top of the white bar and the bottom of the white bar. This white bar is more than 0.02% [or 2 One-Hundredths of 1%] of the full distance our star will travel in 35 million years!



I should point out that Cosmologists, who not only have to traverse the width of the Milky Way to make their observations, but also must measure light and gravity in the immense distances ‘‘between” galaxies … not just the width of galaxies… and they have not detected any inconsistencies in the behavior of light or matter in any direction they look - - other than what is expected from the General Theory of Relativity!

RichardBuggs (Richard Buggs) 2017-11-22 09:31:45 UTC #86

Hi Dennis, I’ve had a read of Zhao et al (2000) PNAS now. Here is what you said about it to @tallen_1 :

> DennisVenema:
>
> From here, we start to get into what are really HGP papers but are focused studies on small DNA regions, rather than genome-wide variation. These are still not PSMC studies. For example, this paper looks at a small section of an autosomal chromosome (chromosome 22). They conclude (my emphases):
>
> "The comparable value in non- Africans to that in Africans indicates **no severe bottleneck during the evolution of modern non-Africans**; however, the possibility of a mild bottleneck cannot be excluded because non-Africans showed considerably fewer variants than Africans. The present and two previous large data sets all show a strong excess of low frequency variants in comparison to that expected from an equilibrium population, indicating a relatively recent population expansion. The mutation rate was estimated to be 1.15 10 9 per nucleotide per year. **Estimates of the long-term effective population size Ne by various statistical methods were similar to those in other studies. "**

I am not sure why you highlighted the words in the abstract about the authors not finding evidence for a bottleneck of modern non-Africans because that is not what we are discussing here. We are discussing the possibility of a bottleneck in the human lineage, not just non-African humans.

The authors estimates of human effective population size are between 8100 and 18800. These estimates are based on present day numbers of segregating sites in the sample sequences, and estimates of mutation rate. This method assumes a fairly constant population size over time. Thus, although they are estimating present effective population size, they are happy to extrapolate this into the past, and call their estimates “long-term effective population size”. This phrase is essentially an expression of their assumption, which is necessary for their method, that population size has remained fairly constant. They say in their discussion: “The lowest value (8,100) suggests that the long-term effective population size of humans is unlikely to be lower than 5,000” but this is 5000 figure is not supported by a calculation: it is seems to be a figure chosen for being a round number. “Long-term” is not defined in terms of number of years. No historical reconstruction of effective population size at different time-points in history is given. I struggle to see this paper as evidence that there was never a short sharp bottleneck in human history.

DennisVenema (Dennis Venema) 2017-11-22 15:33:56 UTC #87

> RichardBuggs:
>
> I am not sure why you highlighted the words in the abstract about the authors not finding evidence for a bottleneck of modern non-Africans because that is not what we are discussing here. We are discussing the possibility of a bottleneck in the human lineage, not just non-African humans.

Because, as I point out to George above, if the authors can exclude a bottleneck for non-Africans they can exclude one all the more for Africans, which have more diversity. [quote=“RichardBuggs, post:86, topic:37039”]

The authors estimates of human effective population size are between 8100 and 18800. These estimates are based on present day numbers of segregating sites in the sample sequences, and estimates of mutation rate. This method assumes a fairly constant population size over time. Thus, although they are estimating present effective population size, they are happy to extrapolate this into the past, and call their estimates “long-term effective population size”. This phrase is essentially an expression of their assumption, which is necessary for their method, that population size has remained fairly constant. They say in their discussion: “The lowest value (8,100) suggests that the long-term effective population size of humans is unlikely to be lower than 5,000” but this is 5000 figure is not supported by a calculation: it is seems to be a figure chosen for being a round number. “Long-term” is not defined in terms of number of years. No historical reconstruction of effective population size at different time-points in history is given. I struggle to see this paper as evidence that there was never a short sharp bottleneck in human history.
[/quote]

Have a look at Table 5, which shows their data for the distribution of TMRCA values. This is the data and analysis they are basing their conclusions on. Bottlenecks increase the probability of coalescence (this is also how PSMC methods work). We see a distribution of TCMRA values for the alleles in the study. This is basically what a PSMC analysis does sequentially for an entire genome to get a much larger sample size.

DennisVenema (Dennis Venema) 2017-11-22 15:34:56 UTC #88

> RichardBuggs:
>
> This method assumes a fairly constant population size over time.

I disagree. The methods used are capable of detecting bottlenecks - that’s why they are used.

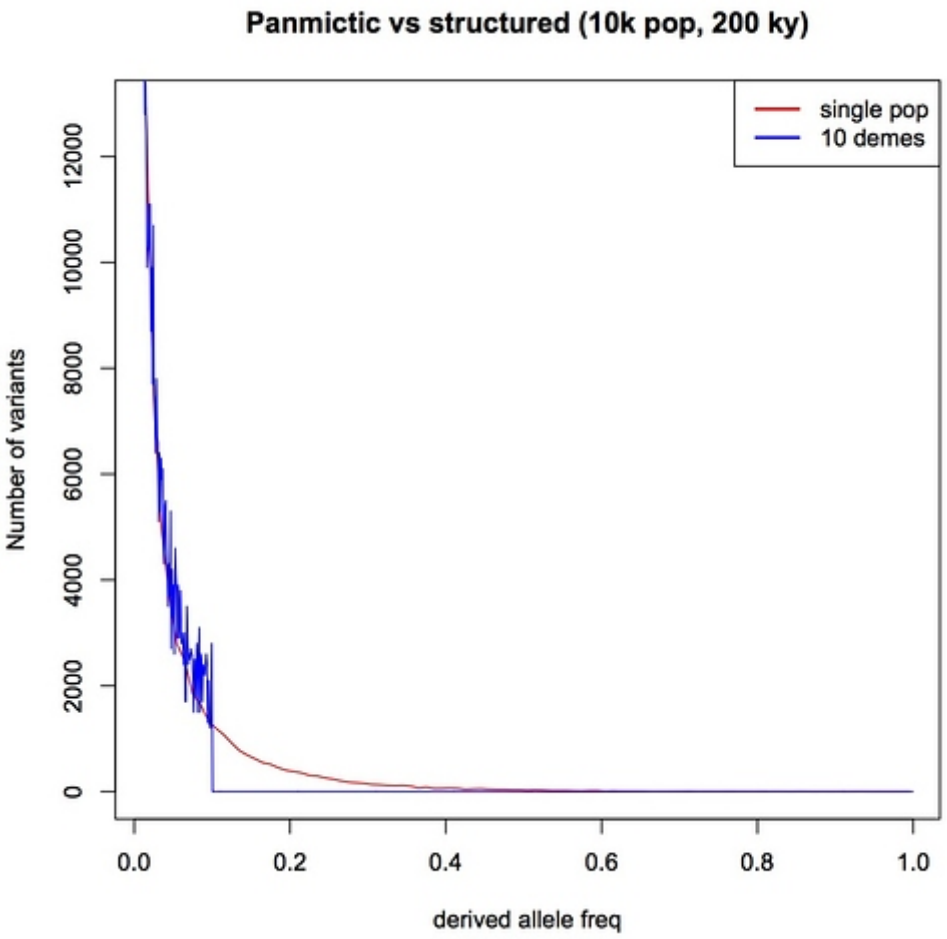
glipsnort (Steve Schaffner) 2017-11-22 16:38:39 UTC #89

> RichardBuggs:
>
> This was how my argument was working: Immediately after a bottleneck, Tajima's D is positive (due to the intermediate frequency (25% and 50% minor allele frequency) alleles. Some time after the bottleneck, let's call this "Phase 2", Tajima's D is negative (due to the excess of very minor frequency alleles). Longer after this, Tajima's D ends up closer to zero as the population comes to equilibrium. That is my understanding of the expectation - I think we are on the same page here.
>
> The issue of fitting the bottleneck model to the data was that the Tajima's D of the 100kya_16K model seemed more negative than the actual data (I am not sure if the actual data has zero Tajima's D or positive Tajima's D - if it is similar to the data that Wakeley (1999) was looking at then I guess it would have been positive). So we seem to be in "phase 2".
>
> This was a similar problem to that faced by Wakeley: Tajima's D seemed too positive in his data. Wakeley solved this by invoking population sub-division. Similarly in models by Pannell (2003) Tajima's D tended to be more positive in a strongly sub-divided population, when samples were collected from several demes.
>
> Thus it seemed reasonable to me to suggest that population subdivision could be causing more positive Tajima's D in the 1000 genomes project African populations, despite a past extreme bottleneck. Do you disagree with Wakeley's use of population sub-division to explain a higher Tajima's D, or did he make a mistake, or am I misunderstanding his paper? (I suspect the latter may well be the case, but I would like to know where I am going wrong).

A couple of comments, since I don't want to go very far down this particular rabbit hole. First, there is no reason to be calculating a summary statistic like Tajima's D here when we're looking at the actual distribution of allele frequencies; the distribution contains more information. Second, Wakeley's paper was looking at a very different scenario than you're proposing. He considered a structured population that had reached a stationary state. You are proposing a population that is very far from stationary, in which allele frequencies are recovering from a tight bottleneck.

> RichardBuggs:
>
> I take your point that if we are thinking in terms of overall allele numbers, drift happens more quickly in a large population. I.e., an allele can get more quickly from 1 copy to 500 copies in a single population of 10,000 individuals than it can in a single population of 1,000 individuals. However, the allele can more quickly go to fixation in the 1,000 population. Once an allele has reached a frequency of 1000 in a population of 1000 it cannot be lost, whereas an allele with a frequency of 1000 in a population of 10,000 can be lost by drift as easily as it arrived. Thus population subdivision will enhance the retention of new mutations as they get fixed in sub-populations.

Very few alleles will be fixed even in a (reasonably sized) subpopulation in this timeframe. The dominant effect will be to stall the drifting alleles at a frequency limited by the deme size. This is easy to simulate, though, so I did. I simulated a constant-sized population (size = 10,000) for 8000 generations (200,000 years), and then simulated a subpopulation of size 1000 for the same period. To compare the two, I scaled down the frequency bins for the subpop by 10 and scaled up the counts by 100 (10x for ten subpopulations in the big population, another 10x since each frequency bin is now 1/10th the width of my usual bin). Here is the result:



It's the same number of variants (slightly less, actually), but bunched at lower frequency. Whatever subpopulation size you pick, the result will be to shift variants to lower frequencies, worsening the fit with real data.

> RichardBuggs:
>
> However, I also have another possibility that I would like to raise. What if the high number of intermediate frequency alleles in the African 1000 genomes study were due to a more recent bottleneck. I.e. we were still in the phase where the bottleneck had caused positive Tajima's D? How recent would the bottleneck need to be for that to be the case?

I very much doubt you could get both enough variants and enough drift in 250,000 years. As I said above when I showed the 500,000 year scenario, multiple bottlenecks on that timescale might do the trick.[quote="RichardBuggs, post:79, topic:37039"]
I was wondering why you could not include as much variation from the pre-bottleneck population as was needed to cause the simulations to fit the data in the 20-50% range? Why only focus on making them match at the 60-70% frequency range? I didn't quite follow the logic here, with your brief description.
[/quote]
I chose 60-70% because there is very little contribution from post-bottleneck mutation there, so the comparison with data is clean; everything in that range comes from the distribution I needed to scale.

---

glipsnort (Steve Schaffner) 2017-11-22 17:11:36 UTC #90

> Marty:

> If the generation times were faster, perhaps closer to puberty at 15 years:
> How would that affect the mutation rate per generation? Would it be less per generation because they are younger, or are most of the errors copying errors anyway from when the germ cell first forms so the mutation rate is about the same?

It would decrease the mutation rate per generation. Most mutations occur in men, as their germline cells replicate many more times than in females, and the mutation rate increases with age.[quote="Marty, post:83, topic:37039"]
Secondly, if the mutation rate stayed "the same" and the generation time reduced, would that pull the X axis in proportionally? That is, would a 40% reduction in generation times produce a 40% reduction in the X axis?
[/quote]
Just shortening the generation time would scale the x axis, yes. The simulations are done in terms of generations, and the years are just calculated at the end by multiplying.

A short generation time is implausible, though. In modern hunter-gatherer societies, puberty occurs around 15 and first birth about 2 years later, with late weaning and a relatively long time between births. This is the data that makes people think the typical generation time for our recent ancestors was 28 or 29 years. In chimpanzees, the mean generation time is ~25 years. [quote="Marty, post:83, topic:37039"]
George - I can't find it now, but I recall Steve pointing out that the graphs assume fairly constant mutation rates, which is a fair place to try. But, for example, if our solar system goes through regions of space that are higher or lower in various types of radiation or other toxicity, they could vary some. I think the point of **@RichardBuggs** is not to just cast doubt, but to draw legitimate boundaries around what can be said with greater or lesser confidence. Scientists don't want to be guilty of assumptions that could be proven false, but if those assumptions are explicit because there is no better option at this time, well, better to identify those areas. I appreciate Steve stating it up front, and I think it appropriate to recognize it as a fair working assumption which could perhaps be open to revision.
[/quote]
Such possibilities are often quite bounded by other data, though. Radiation contributes a very small fraction of current mutations, with cosmic radiation being a small fraction of that. Very large increases in radiation would increase the mutation rate, but radiation-induced mutations look very different from the genetic variation we actually see in humans.
[quote="Marty, post:83, topic:37039"]
Now for the scientists, is there any way to assess variability in historical mutation rates? And for Steve, if the mutation rate halved, for example, would that double the X axis of your graphs?
[/quote]
The answer to the 2nd question is yes. The answer to the first is yes, but not easily. The mutation rate really isn't likely to change on short timescales, though. Most mutations are the result of internal biochemical processes, processes which are similar in similar species. As I pointed out earlier, different processes produce different mutations, and a change to one process (like radiation-induced mutation) will be evident.

Broad view:
In general, it seems reasonable to conclude that the creature that's quacking, waddling across my lawn, and looking like a duck is in fact a duck. While it is in principle possible that, thanks to a set of circumstances I haven't thought of yet, the creature is actually a turtle, at some point it becomes the responsibility of someone arguing, 'Hey, maybe it's a turtle', to provide some kind of evidence to that effect.

The bottom line is that human genetic variation looks exactly like the result of a long-term largish population plus recent expansion. It does not look at all like the result of a tight bottleneck. Simple pop gen reasoning says that such a bottleneck would leave easily detectable traces for hundreds of thousands of years. Simulations bear this out. Until someone can demonstrate that there actually exists a plausible model that would hide the bottleneck in that time frame, I don't see much point in pursuing the question further.

BTW, my immediate plan is to take at least a few days off from contentious issues on the internet, so I intend not to comment any more for a while. It's going to be nothing but Netflix and puppy videos for me.

DennisVenema (Dennis Venema) 2017-11-22 17:49:25 UTC #91

> glipsnort:
>
> The bottom line is that human genetic variation looks exactly like the result of a long-term largish population plus recent expansion. It does not look at all like the result of a tight bottleneck. Simple pop gen reasoning says that such a bottleneck would leave easily detectable traces for hundreds of thousands of years. Simulations bear this out. Until someone can demonstrate that there actually exists a plausible model that would hide the bottleneck in that time frame, I don't see much point in pursuing the question further.
>
> BTW, my immediate plan is to take at least a few days off from contentious issues on the internet, so I intend not to comment any more for a while. It's going to be nothing but Netflix and puppy videos for me.

Enjoy your rest, Steve. I find real-life puppy therapy (we have a golden retriever) even better.

DennisVenema (Dennis Venema) 2017-11-22 17:54:09 UTC #92

> glipsnort:
>
> In general, it seems reasonable to conclude that the creature that's quacking, waddling across my lawn, and looking like a duck is in fact a duck.

But are you sure it's not a crocoduck?

Sorry, couldn't help myself. 🙂

RichardBuggs (Richard Buggs) 2017-11-22 20:37:45 UTC #93

> DennisVenema:
>
> if the authors can exclude a bottleneck for non-Africans they can exclude one all the more for Africans, which have more diversity

They do not claim to do the latter in the paper, so you can hardly cite the paper to demonstrate it. For the non-Africans they can make a comparison with the Africans, but they have no comparator population for the Africans. Therefore I don't know how they could make a similar exclusion using their data.[quote="DennisVenema, post:87, topic:37039"]
Have a look at Table 5, which shows their data for the distribution of TMRCA values. This is the data and analysis they are basing their conclusions on. Bottlenecks increase the probability of coalescence (this is also how PSMC methods work). We see a distribution of TCMRA values for the alleles in the study. This is basically what a PSMC analysis does sequentially for an entire genome to get a much larger sample size.
[/quote]
Which conclusions are you referring to? **The paper's** calculations of effective population size are in Table 4. Table 5 uses a range of possible ancestral population sizes to estimate times to most recent common ancestors (TMRCA). They use their results shown in Table 4 to pick what they consider to be the most appropriate effective population size for the most reliable estimate of TMRCA in Table 5. As I said earlier their estimates of effective population size are based on present day numbers of segregating sites in the sample sequences, and estimates of mutation rate. They don't use their TMRCA calculations to try to estimate effective population size. They don't make any inferences about bottlenecks or not from the TMRCA results[quote="DennisVenema, post:88, topic:37039"]

I disagree. The methods used are capable of detecting bottlenecks - that's why they are used.
[/quote]
The method this paper is using assumes fairly constant population sizes. Perhaps you are mistaken about what method is actually being used?

RichardBuggs (Richard Buggs) 2017-11-22 22:03:37 UTC #94

Hi Steve, thanks for your reply.

> glipsnort:
>
> First, there is no reason to be calculating a summary statistic like Tajima's D here when we're looking at the actual distribution of allele frequencies; the distribution contains more information.

I was simply using Tajima's D to try to communicate clearly and concisely about what we would expect to see, and to facilitate interaction with the literature. I think that is reasonable – normal even.[quote="glipsnort, post:89, topic:37039"]
Second, Wakeley's paper was looking at a very different scenario than you're proposing. He considered a structured population that had reached a stationary state. You are proposing a population that is very far from stationary, in which allele frequencies are recovering from a tight bottleneck.
[/quote]
But it does make the point that population structure would boost the number of intermediate frequency alleles. The bottleneck hypothesis could have a scenario of rapid population expansion followed by a period with a structured population in a fairly stationary state.

I do think though that sub-division arising a few generations after a bottleneck, accompanied by rapid expansion of sub-populations, would result in higher numbers of alleles at intermediate frequencies in the meta-population as a whole than would be expected in a single expanding panmictic population.

> glipsnort:
>
> Very few alleles will be fixed even in a (reasonably sized) subpopulation in this timeframe. The dominant effect will be to stall the drifting alleles at a frequency limited by the deme size. This is easy to simulate, though, so I did. I simulated a constant-sized population (size = 10,000) for 8000 generations (200,000 years), and then simulated a subpopulation of size 1000 for the same period. To compare the two, I scaled down the frequency bins for the subpop by 10 and scaled up the counts by 100 (10x for ten subpopulations in the big population, another 10x since each frequency bin is now 1/10th the width of my usual bin). Here is the result:

Thanks for doing this! Hmm, this is interesting. Why is there a sudden drop at 0.05 (corresponding to a frequency of 0.5 in the single deme, I guess) for the demes?

Your model certainly suggests that if we only consider new mutations, and no gene flow among demes, constant deme sizes, reasonably large demes, and no convergent mutations among populations, then the effect of population subdivision might not be strong enough to explain the high numbers of intermediate frequency alleles.

I think the number of intermediate frequency alleles would be higher if we included sites that had ancestral polymorphism when the population became subdivided. Then some of the sub-populations would share the same alleles at fixation, giving them higher frequencies in the meta-population as a whole.

> glipsnort:
>
> I very much doubt you could get both enough variants and enough drift in 250,000 years.

But what if the variants were supplied from the ancestral population?

> glipsnort:
>
> As I said above when I showed the 500,000 year scenario, multiple bottlenecks on that timescale might do the trick.

Successive “Adam and Eves” rather than just one couple? Interesting idea.

> glipsnort:
>
> I chose 60-70% because there is very little contribution from post-bottleneck mutation there, so the comparison with data is clean; everything in that range comes from the distribution I needed to scale.

OK, I see. But in your 100kya_component.jpg figure there is very little contribution from post-bottleneck mutation above 20%. Why couldn’t you make the model fit right down to there with more pre-bottleneck variation? What would scenarios look like if you did have a very large and very variable population before the bottleneck?

I really appreciate the time you have put into this, and I do hope you will continue this discussion after your break. I realise I am acting as a defense attorney in a case that seems to you to be a bit hopeless, but I think it is good for us to work this all through in detail as there are so many people out there for whom this is an important issue for their faith - who have very heartfelt beliefs about this - and I think we owe it to them to go through this throughly. Personally, as I said at the end of my **blog**, I am open to this debate going either way. My faith will be unaffected whichever way I end up concluding after this discussion. But for some good people that may not be the case and I think everyone participating meaningfully in this debate is doing them a great service.

---

gbrooks9 (George Brooks) 2017-11-22 22:16:42 UTC #95

> glipsnort:
>
> It’s the same number of variants (slightly less, actually), but bunched at lower frequency. Whatever subpopulation size you pick, the result will be to shift variants to lower frequencies, worsening the fit with real data.

@glipsnort :

Nice demonstration of the math used in simulations!

---

gbrooks9 (George Brooks) 2017-11-22 22:26:03 UTC #96

> glipsnort:
>
> The bottom line is that human genetic variation looks exactly like the result of a long-term largish population plus recent expansion. It does not look at all like the result of a tight bottleneck. Simple pop gen reasoning says that such a bottleneck would leave easily detectable traces for hundreds of thousands of years. Simulations bear this out. Until someone can demonstrate that there actually exists a plausible model that would hide the bottleneck in that time frame, I don’t see much point in pursuing the question further.

@glipsnort

That is one beautiful paragraph! And you have the sample math to demonstrate it.

The various contenders over this position always seem to be arguing that the difference in outcome between:

1 Mating Pair 6000 years ago

and

Thousands of Mating Pairs 100,000 years ago

is a difficult thing to sort through, and that just by using slightly different rates and proportions, either scenario could easily produce the very same results.

If we “called” them on this implied premise from the “get go”, maybe we could reduce the "heat" of the discussion, and shine light where it needs to be shined.

Part of this trend comes from these parties “daring” the scientists to run different scenarios. I think it’s high time that I.D. proponents (if that is who they represent) start learning a little science and run their own scenarios. Then they can spend the endless hours trying to tweak the data to make it do what they think it should.

Once they have accomplished that (if ever) … we will all learn exactly what kind of demographic hand-stands are required to make 1 mating pair (who are really really motivated!) produce the results of thousands of mating pairs who just don’t seem to be trying very much!

Next time they dare, let’s hand them their own kit, and tell them to do it themselves.

DennisVenema (Dennis Venema) 2017-11-22 23:09:08 UTC #97

Hi Richard,

I guess I’m asking you to look at the TMRCA data there and think about your hypothesis (a bottleneck to two in the last few hundred thousand years).

If you don’t think that paper is relevant to your hypothesis, I’m willing to concede the point *arguendo* and direct you to the other papers in the set I supplied that do more explicitly test your particular hypothesis.

I think Steve’s point is also a good one: you have to realize at some point that you’re arguing against the conclusions of an entire field of research. If you want to challenge that consensus - and in science, challenge is always welcome, of course - you’ll have to provide something in the way of evidence to support your challenge. To date, your argument has basically been that your hypothesis has not been tested. It has (as I’ve pointed out in the papers above). Steve has also nicely shown you why the allele frequency spectrum just cannot be squared with your hypothesis. To move on from here, I’d like to see some modelling from you (or someone else) that supports what you are positing.

DennisVenema (Dennis Venema) 2017-11-22 23:14:03 UTC #98

> RichardBuggs:
>
> But what if the variants were supplied from the ancestral population?

You’re positing a bottleneck to two individuals. How is enough variation going to make it through the bottleneck?

DennisVenema (Dennis Venema) 2017-11-22 23:28:39 UTC #99

> gbrooks9:
>
> I think it's high time that I.D. proponents (if that is who they represent)

I know that in the past Dr. Buggs has been reported as an ID advocate, but I don't know if he would claim that identity for himself. Years ago, Richard published a piece claiming that human and chimpanzee genome similarity could be as low as 70%, and this was touted by the Discovery Institute for some time (it was a favourite of Casey Luskin for a while). I'm not sure where Richard stands on ID and or human/chimp common ancestry, or if he might be open to discussing his views.

> Discovery Institute:
>
> A popular Darwinian meme is that humans and chimp genomes are ninety-something percent identical. It varies a bit, but usually hovers close to 99%. The meme hides all sorts of assumptions, of course, but the take home lesson for the headline reader is plain enough: we're almost exactly the same as chimps.
>
> Though the 99% number has received some qualifiers, and has even been referred to as a "myth" in Science, the basic idea remains firmly entrenched in the media collective consciousness.
> But evidence seems to be piling up that the similarities are not nearly what has been advertised. Geneticist Richard Buggs has reflected on this, and has even predicted "that when we have a reliable, complete chimpanzee genome, the overall similarity of the human genome will prove to be close to 70% (and very far from 99%)."
>
> It will be interesting to see how Buggs' prediction holds up over time. If he's right, this will be one more switch from "meme" to "myth" in the Darwinian ledger.
>
> (**source**)

Jonathan_Burke (Jon) 2017-11-23 05:51:01 UTC #100

> RichardBuggs:
>
> I really appreciate the time you have put into this, and I do hope you will continue this discussion after your break. I realise I am acting as a defense attorney in a case that seems to you to be a bit hopeless, but I think it is good for us to work this all through in detail as there are so many people out there for whom this is an important issue for their faith - who have very heartfelt beliefs about this - and I think we owe it to them to go through this throughly. Personally, as I said at the end of my blog, I am open to this debate going either way. My faith will be unaffected whichever way I end up concluding after this discussion. But for some good people that may not be the case and I think everyone participating meaningfully in this debate is doing them a great service.

I apologize for jumping in like this, I only have one question. Does your understanding of the data support the idea of an Adam and Eve who had no ancestors at all (neither human nor pre-human), as the universal progenitors of every human who has ever lived, with no humans descending from any parallel humans or pre-humans, approximately 6,000 years ago? Thanks.

RichardBuggs (Richard Buggs) 2017-11-23 17:22:33 UTC #101

> DennisVenema:

> I guess I'm asking you to look at the TMRCA data there and think about your hypothesis (a bottleneck to two in the last few hundred thousand years).

Please could you explain to me why you think that data excludes a bottleneck of two at some point in the human lineage? I am still puzzled as to why you pointed me to that paper in the first place.

DennisVenema (Dennis Venema) 2017-11-23 17:56:17 UTC #102

That study identified 75 variants in this region that have a minimum coalescence time of over 700,000 years. The mode is 1.2 million years, and 700,000 is the lower bound of the 95% confidence interval for the combined sample.

So, how did all of that variation survive a bottleneck to two? It can't. So, how did all of that variation arise after a proposed bottleneck to two? Through new mutations. How long would that take? Even with a steady-state population of around 10,000, about 1.2 million years.

Even the non-african population under study, with its smaller Ne, still has the lower bound at over 300,000 years ago.

Also notice that as they model lower Ne values for each population, that pushes the lower bound of the TMRCA values further back in time. In other words, in a smaller population, more time is needed to account for the variation we see. Smaller populations require more time for mutations to produce new variants because each generation has less "trials". If you shift that value from 10,000 to a starting population of 2, what do you think might happen?

RichardBuggs (Richard Buggs) 2017-11-23 18:19:52 UTC #103

> RichardBuggs:
>
> But what if the variants were supplied from the ancestral population?

> DennisVenema:
>
> You're positing a bottleneck to two individuals. How is enough variation going to make it through the bottleneck?

Hi Dennis, I think you may be misunderstanding what Steve is modelling. All the variants in his model are SNPs with two alleles. As you have described in your blog, two alleles can get through a bottleneck. What were you thinking that Steve was modelling?

DennisVenema (Dennis Venema) 2017-11-23 18:28:45 UTC #104

I understood what Steve was modelling. I thought you were asking for more alleles to come through the bottleneck as a way to adjust allele frequencies. If you weren't, my bad.

Marty (Marty) 2017-11-23 18:33:29 UTC #105

> glipsnort:
>
> my immediate plan is to take at least a few days off

When you do get back, please accept my appreciation for the detailed answers! Very helpful.

sfmatheson (Stephen Matheson) 2017-11-23 19:05:00 UTC #106

> RichardBuggs:
>
> I realise I am acting as a defense attorney in a case that seems to you to be a bit hopeless

I think that the vast majority of biologists, and especially geneticists, would consider the case to be not merely hopeless but also ridiculous. (That's what I think.) There is only one reason to even consider a recent and dramatic bottleneck in human history, and that is a particular (and dubious) reading of some ancient writings on unrelated topics. Indeed, the rest of your response to Steve effectively concedes this. That is why this conversation is happening on the forum of a religious organization, and not from the platform of a molecular evolution conference or in the pages of a journal.

In my view, it was reasonable to ask Dennis to clarify or even correct his pattern of citation in support of his claim that a recent bottleneck down to two individuals is as credible as geocentrism. Again, just my opinion, but you have not made a credible case against Dennis' claims about an extreme bottleneck—in fact, that proposal is ridiculous outside a window of hundreds of thousands of years. Perhaps you have raised a credible technical objection to the ways that Dennis justified his claim in a book written for laypeople.

You and others on this forum believe it important to talk through the science for the benefit of others who share your view of the value and credibility of those ancient writings. I agree with that, simply because these religious views have import (regrettable, IMO) in our civilization. But I strongly disagree with any claim that the notion of an extreme bottleneck in recent human history is a credible proposition, worthy of any serious consideration in light of what we know about human biology and especially about human genetics. And I strongly disagree with the assertion that the existence of such a bottleneck is an untested hypothesis.

Steve was kind enough to do some nice simulations, but there was no need to do that, at least not scientifically. In fact, I would argue that there is some slight danger in what he did. The simulations and the extensive technical discussion that followed may have given some readers the impression that extreme recent bottlenecks are an open question and that only through extensive technical discussion could some experts carefully rule this out. That picture is unacceptably (to me) misleading. There was no such open question. There is no debate, or dispute, or uncertainty about a recent bottleneck, which is less nonsensical than geocentrism, I'll grant, but only quantitatively.

RichardBuggs (Richard Buggs) 2017-11-23 21:39:13 UTC #107

Dennis, it is fascinating to see how your use of **this paper** is evolving as this discussion continues. You first proposed it to me as a citation to back up the piece in your book about allele counting. Then you described it to **@tallen_1** as follows

> DennisVenema:
>
> For example, this paper looks at a small section of an autosomal chromosome (chromosome 22). They conclude (my emphases):
>
> "The comparable value in non- Africans to that in Africans indicates **no severe bottleneck during the evolution of modern non-Africans**; however, the possibility of a mild bottleneck cannot be excluded because non-Africans showed considerably fewer variants than Africans. The present and two previous large data sets all show a strong excess of low frequency variants in comparison to that expected from an equilibrium population, indicating a relatively recent population expansion. The mutation rate was estimated to be 1.15 10 9 per nucleotide per year. **Estimates of the long-term effective population size Ne by various statistical methods were similar to those in other studies.** "

Now that I have pointed out to you that neither of the parts you highlighted are good evidence against the bottleneck of two hypothesis, you are focusing on the final part of the paper which is not mentioned in the part of the abstract that you copied and pasted for **@tallen_1** . Now you are saying:

> DennisVenema:
>
> That study identified 75 variants in this region that have a minimum coalescence time of over 700,000 years. The mode is 1.2 million years, and 700,000 is the lower bound of the 95% confidence interval for the combined sample.
>
> So, how did all of that variation survive a bottleneck to two? It can't. So, how did all of that variation arise after a proposed bottleneck to two? Through new mutations. How long would that take? Even with a steady-state population of around 10,000, about 1.2 million years.

You are quite wrong to think that 75 variants within a 10,000 base pair region could not pass through a bottleneck of two. The 75 variants are all different sites, each of which has two alleles. All 75 of those variants could, in theory, be contained within a single individual. That individual would be heterozygous at the 75 sites. Thus all 75 variants could easily pass through a bottleneck of two. Indeed, a thousand could.

In your comments above, you are writing as if only one allele could pass through a bottleneck of two. This would be true if a bottleneck of two were maintained for many generations, as the extreme inbreeding would eventually eliminate all genetic variation. Thus all heterozygosity would be lost. But, as we have covered before in our dialogue, only 25% of heterozygosity is lost in a short sharp bottleneck of two followed by a rapid expansion. We seem to be right back at the beginning of our dialogue. This is the first thing I pointed out to you, right back in the spring.

In reality, in the case covered in this paper, not all 75 variants would need to be carried through the bottleneck. 24 of them were mutations that were found in only one sequence in the sample, 22 were found in two sequences, and 32 were found in more than two sequences. The 46 variants that were found in two or less individuals are likely to be fairy recent mutations, leaving only 32 variants that could perhaps have come through the bottleneck. It could have been less, of course, depending on how long ago the bottleneck was - that is not something I am taking a strong position on.

RichardBuggs (Richard Buggs) 2017-11-23 21:42:03 UTC #108

> DennisVenema:
>
> I understood what Steve was modelling. I thought you were asking for more alleles to come through the bottleneck as a way to adjust allele frequencies. If you weren't, my bad.

I don't understand how you could have thought that if you understood what Steve was modelling. I challenge you to explain in your own words (without help from Steve) what Steve was modelling, and how it shows that a bottleneck of two is unlikely to have happened.

DennisVenema (Dennis Venema) 2017-11-23 23:06:18 UTC #109

Richard - are you aware how closely linked those variants are? They're at most 10,000 bases apart. Are you seriously suggesting that they passed through a bottleneck *en masse* in two individuals and then recombined to the forms we see now?

---

gbrooks9 (George Brooks) 2017-11-24 06:50:10 UTC #110

> RichardBuggs:
>
> I don't understand how you could have thought that if you understood what Steve was modelling. I challenge you to explain in your own words (without help from Steve) what Steve was modelling, and how it shows that a bottleneck of two is unlikely to have happened.

@RichardBuggs

Hey, why don't you take a break for a while? All I see you doing is running the scientists ragged, hashing through their work … all to have them defend their work from a dozen different angles - - on a conclusion that you will probably never accept anyway.

A few posts ago, **@DennisVenema** wrote:

> DennisVenema:
>
> To date, your argument has basically been that your hypothesis has not been tested. It has (as I've pointed out in the papers above).
>
> Steve has also nicely shown you why the allele frequency spectrum just cannot be squared with your hypothesis.
>
> **To move on from here, I'd like to see some modelling from you (or someone else) that supports what you are positing.**

I think most everyone would like to see you at least do some mathematical scenarios… Excel is quite capable of representing generational change, where each row of cells can represent each new generation from a single mating pair in your scenario.

Do some benchmarking… make the numbers work the way your mind thinks they should work.

---

tallen_1 (Tim) 2017-11-24 14:48:24 UTC #111

Dennis,

I really appreciate everyone's efforts to work through this topic. However, it's certainly difficult at times to follow along for a non-specialist. For instance, phrases like "Tajima's D" are technical terms familiar only I'd presume to insiders in population genetics. Not the public at large. And points such as you made that 75 allelic variants being at most 10,000 bases apart would fly over most people's heads (it certainly did mine) over why this has relevance to a bottleneck. The rest of us don't have the background knowledge sufficient to determine which arguments are well supported and well reasoned. And which aren't. So someone like me who is inclined to put more weight on the expert consensus will default to thinking you've made the better argument. While those within the ID community who feel the expert consensus is based on faulty presuppositions or some amount of group think, will feel Richard has the better argument. I'd like to see everyone avoid that, since we are dealing with objective data here and not subjective intuitions. So is there a way to make this more digestible to the non-specialists on this thread? Thanks!

Jonathan_Burke (Jon) 2017-11-24 15:13:20 UTC #112

> tallen_1:
>
> The rest of us don't have the background knowledge sufficient to determine which arguments are well supported and well reasoned. And which aren't.

This is why I have asked Richard a single question, the answer to which will explain to me whether or not this discussion is one I need to be following, or whether it's basically irrelevant to what I believe.

DennisVenema (Dennis Venema) 2017-11-24 15:27:40 UTC #113

I hear you!

I wanted to put a shot across Richard's bow, as it were, that his idea of packing a large number of variants into two individuals just doesn't fly, in terms another biologist would understand. I didn't have time then, nor do I now, to unpack that for everyone else. But I will, later today. I was hoping Richard might give some attempt at a justification, but as it is really off the map, I don't see how that is possible. More later.

RichardBuggs (Richard Buggs) 2017-11-24 16:04:29 UTC #114

Dennis, what am I getting wrong here? Please explain why you think I am wrong.

> RichardBuggs:
>
> You [Dennis] are quite wrong to think that 75 variants within a 10,000 base pair region could not pass through a bottleneck of two. The 75 variants are all different sites, each of which has two alleles. All 75 of those variants could, in theory, be contained within a single individual. That individual would be heterozygous at the 75 sites. Thus all 75 variants could easily pass through a bottleneck of two. Indeed, a thousand could.
>
> In your comments above, you are writing as if only one allele could pass through a bottleneck of two. This would be true if a bottleneck of two were maintained for many generations, as the extreme inbreeding would eventually eliminate all genetic variation. Thus all heterozygosity would be lost. But, as we have covered before in our dialogue, only 25% of heterozygosity is lost in a short sharp bottleneck of two followed by a rapid expansion. We seem to be right back at the beginning of our dialogue. This is the first thing I pointed out to you, right back in the spring.
>
> In reality, in the case covered in this paper, not all 75 variants would need to be carried through the bottleneck. 24 of them were mutations that were found in only one sequence in the sample, 22 were found in two sequences, and 32 were found in more than two sequences. The 46 variants that were found in two or less individuals are likely to be fairy recent mutations, leaving only 32 variants that could perhaps have come through the bottleneck. It could have been less, of course, depending on how long ago the bottleneck was - that is not something I am taking a strong position on.

---

cwhenderson (Curtis Henderson) 2017-11-24 16:16:40 UTC #115

If anyone is feeling a little badly due to the conversation going over their head, don't. I have a PhD in biology and much of this is going over my head. This is what I can summarize, though:

1. Scientists that do this for a living have concluded that it is highly unlikely that the human population was ever as low as 2 (or 8, as related to Noah).
2. **@DennisVenema** had some strong words (and possibly too strong) in his book about this observation.
3. **@RichardBuggs** and others objected to the strength of the language, contending that it is not impossible to rule out an ancestral population of 2.

4. **@glipsnort** (a rather notable scientist in this field) was nice enough to take the time to run some time-consuming simulations that supported exactly the strong consensus of the many experts in this field.

5. **@RichardBuggs** had suitable follow-up questions.

My conjecture here:

6. **@glipsnort** satisfactorily answered the questions because **@RichardBuggs** moved back to critique of **@DennisVenema** .

Any of you, feel free to correct anything I have written that is in error.

DennisVenema (Dennis Venema) 2017-11-24 16:27:23 UTC #116

> RichardBuggs:
>
> Dennis, what am I getting wrong here? Please explain why you think I am wrong.

Linkage disequilibrium, in a nutshell. I don't have time to get into it right now though - it will have to come after I teach a class.

AMWolfe (A.M. Wolfe) 2017-11-24 16:58:06 UTC #117

> DennisVenema:
>
> after I teach a class

Canadians. [smh]
If they could just get their holidays right, man…
🙂

DennisVenema (Dennis Venema) 2017-11-24 17:59:09 UTC #118

> AMWolfe:
>
> Canadians. [smh]
> If they could just get their holidays right, man…

Hey, we do share a recent common ancestral population with you Yanks, but we've evolved since then… 😉

DennisVenema (Dennis Venema) 2017-11-24 18:59:42 UTC #119

> cwhenderson:
>
> If anyone is feeling a little badly due to the conversation going over their head, don't. I have a PhD in biology and much of this is going over my head. This is what I can summarize, though:
>
> 1. Scientists that do this for a living have concluded that it is highly unlikely that the human population was ever as low as 2 (or 8, as related to Noah).

> 2. @DennisVenema had some strong words (and possibly too strong) in his book about this observation.
> 3. @RichardBuggs and others objected to the strength of the language, contending that it is not impossible to rule out an ancestral population of 2.
> 4. @glipsnort (a rather notable scientist in this field) was nice enough to take the time to run some time-consuming simulations that supported exactly the strong consensus of the many experts in this field.
> 5. @RichardBuggs had suitable follow-up questions.
>
> My conjecture here:
>
> 6. @glipsnort satisfactorily answered the questions because @RichardBuggs moved back to critique of @DennisVenema .

The only thing I would add is that some of the papers I have directed Richard to, such as the Alu paper and a few others, have not, as of yet, been responded to by Richard. These papers also test Richard's hypothesis of a bottleneck to two, and reject it.

DennisVenema (Dennis Venema) 2017-11-25 07:58:13 UTC #120

Ok, Linkage disequilibrium - here we go. This will probably steal some thunder from my full treatment later, but here's a sampling.

In a bottleneck to 2 people, four versions of any given chromosome pass through the bottleneck (two in each person). Each chromosome has variants on it in a particular pattern. These four chromosomes are now what are called haplotype blocks - groupings of alleles physically linked together.

After the bottleneck, recombination through chromosome breakage and rejoining ("crossing over") will be necessary to start mixing and matching the four sets into new patterns. The closer together two variants are, the less likely a crossing over event will occur between them.

The overall, average recombination (crossing over) rate in humans is around 1% per generation for every million base pairs. This rate can and does vary somewhat across the genome, but the variants we are discussing here are really, really close together - 1000 base pairs apart or less. Crossing over between two such alleles is thus really rare.

You can see the region that Richard and I are discussing here if you want to look at the raw data. (You'll have to play around with the default settings to show all the variants. Click on "tracks" and then "variation" to see the alleles.)

If we were to pack a significant number of alleles into two people, such that the alleles would survive the bottleneck, that would place those alleles into four sets of very tightly linked variants, or haplotype blocks. As the population expands exponentially after the bottleneck - required in order to save as much variation as possible in this scenario - the vast, vast majority of offspring would inherit one of the four blocks without any crossing over. This would continue for generations, with only extremely rare crossing over events eventually breaking up the haplotype blocks.

Once those new, rare, recombinant offspring arise their new haplotype blocks will have to drift up to the intermediate frequencies we see in some cases for such blocks. All of the issues facing drift for individual alleles (as Steve has modelled for us) also apply to new blocks.

The net effect is that the resulting population would be heavily biased towards the starting four haplotype blocks, with all the variants packed together, and there would be fewer haplotype blocks that arose through crossing over.

When we look at this region we don't see what a bottleneck to four would predict. We don't see all the variants grouped together into four different haplotype blocks. We see the variants dispersed in different combinations. What we see just

doesn't fit a two-person bottleneck model.

This sort of analysis was done at a massive, genome-wide scale by **Tenesa et al, 2007**, and they conclude that human population sizes have stayed in the several thousands over the last 200,000 years, as I discuss in the book. This group looks at millions of marker pairs, many of which are much further apart than the ones in this small region of the genome we are discussing here.

No amount of juggling of recombination rates will get these sorts of studies down to 2. To get down to two requires special pleading in the extreme.

Aceofspades25 2017-11-27 16:43:33 UTC #121

What amazes me in all of this is that even with all the time and effort put into this conversation, there hasn't been a single acknowledgement from Richard Buggs that he was wrong or even a mere acknowledgement for that matter of the evidence that has been presented to him.

He hasn't even issued a thank you for all the time that you and Steve have put into answering this.

I'm hoping he doesn't dig in his heels and prove to be immune to evidence, but I fear he has done just that.

---

jpm (Phil) 2017-11-27 16:52:39 UTC #122

I tend to see things a little differently, as there has been a good mutual exchange of ideas and interpretations. We are then capable of looking at the evidence and making our own judgements regarding their validity. In exchanges like this, we seldom see a situation where positions are changed remarkably, but it does help clarify the issues and provides an opportunity for all involved to express their thoughts to our benefit. My thanks to Dr. Buggs and Dr. Venema for their contributions.

Jonathan_Burke (Jon) 2017-11-27 17:06:16 UTC #123

> Aceofspades25:
>
> He hasn't even issued a thank you for all the time that you and Steve have put into answering this.

He certainly has. He has thanked them repeatedly. Here's an example.

> RichardBuggs:
>
> Thanks for doing this!

Here's another example.

> RichardBuggs:
>
> I really appreciate the time you have put into this,

Here's another one.

> RichardBuggs:

> Hi Dennis, just a quick note to thank you for the five papers that you have pointed out in your recent posts.

Two more times in this post.

> RichardBuggs:
>
> Thanks Steve for your patience.

> RichardBuggs:
>
> Thanks again for your patience.

More thanks here.

> RichardBuggs:
>
> Hi Steve, **@glipsnort** , thanks for your responses to the points I raised about your model.

Here also.

> RichardBuggs:
>
> Thank you so much for doing these analyses, Steve.

Richard has been very courteous, grateful, and appreciative. The entire discussion has been complex and difficult, with occasional obvious frustration, but the level of decorum has been extremely high.

---

gbrooks9 (George Brooks) 2017-11-27 20:18:47 UTC #124

Will there ever be a **(Part 2)** ?

If there is to be one, it could be something along the lines:

Adam, Eve and Population Genetics: A Reply to the book: "Theistic Evolution: A Scientific, Philosophical, and Theological Critique"

I see that this book is at the bargain cost of $60.00.

Crossway's "Theistic Evolution" - Edited by J. P. Moreland, Stephen C. Meyer, Christopher Shaw, Ann K. Gauger, Wayne Grudem, Contributions by Douglas D. Axe, C. John Collins, John D. Currid, Guy Prentiss Waters, Gregg R. Allison, Fred G. Zaspel, Matti Leisola, James M. Tour, Winston Ewert, Jonathan Wells, Sheena Tyler, Günter Bechly, Casey Luskin, Paul A. Nelson, Ola Hössjer, Colin R. Reeves, Stephen Dilley, Garret J. DeWeese, Tapio Poulimatka, John G. West, Foreword by Steve Fuller

I've been going through my sofa, trying to pull together the purchase price. I'm up to $3.23, 2 safety pins and three "fun sized" Charleston Chews. I'll trade the pins, the candy, or both (!) for the remaining $56.77.

> **New book explaining why EC is wrong**

> I received a TOC and the first couple of chapters of a new book that promises to explain exactly why BioLogos has gotten everything wrong. It isn't available yet but you can see some information about **Theistic Evolution, A Scientific, Philosophical, and Theological Critique Edited by J. P. Moreland**. A total of 31 chapters covering all of our faults. It is obvious that even though they are aware of the website, "As mentioned in note 6, above, the BioLogos Foundation hosts the primary website …

RichardBuggs (Richard Buggs) 2017-11-27 21:46:17 UTC #125

Hi all,
I have been away over the weekend visiting my parents with my wife and son, and have just got back to this discussion today. I see that **@cwhenderson** has made some comments designed as a summary of where things are at. For my part I would briefly say this.

I came into this discussion with two questions in my mind:

1. Does chapter three of Adam and the Genome make a convincing case that humans have never passed through a bottleneck of two?
2. Is there a better case that can be made?

I came to both of these questions with an open mind. Regarding question (1) I had very serious concerns about Dennis' chapter, which I expressed to him privately in an email in the spring, and then later made public. I did think that Dennis might be able to defend his chapter well when challenged and come up with missing references. So far, however, I have been disappointed with his defence of his chapter (thought grateful that he has made it), and I have growing certainty that even if his conclusion - that there never was such a bottleneck - is correct, it is correct for the wrong reasons. Regarding question (2) Dennis has cited some papers that were not alluded to in his book, which I still need to read. Given my disappointment in the other citations that Dennis has pointed me to in the past through his chapter and in this discussion, I am not optimistic that any of these will really support his case when examined closely. But I will read them in case they do prove his point. In addition, Steve Schaffner has given some evidence from allele frequency distributions that these make a case against a bottleneck of two. This is an intriguing argument, but I have questions that have not been fully dealt with regarding the role in the model of alleles that are derived from before the bottleneck, and also the effect of population structure. I also note that because Steve has presented this analysis that is not in the peer reviewed literature, it seems probable that he does not find what is already in the peer reviewed literature as convincing as Dennis does. I am also getting less optimistic that there is a strong case to be made against a bottleneck of two because I have not had any responses to my blog at Nature Eco Evo - which was aimed at research scientists and has been read many times - saying that I am clearly wrong and have missed a crucial piece of evidence that shows that a bottleneck of two is effectively disproven. I maintain an open mind on this wider issue however.

> cwhenderson:
>
> My conjecture here:
>
> 6. **@glipsnort** satisfactorily answered the questions because **@RichardBuggs** moved back to critique of **@DennisVenema** .

The reason why I stopped asking **@glipsnort** questions was because he was taking some time out over Thanksgiving, and he has not yet responded to the questions I posed just after he left the discussion.[quote="DennisVenema, post:119, topic:37039"]
The only thing I would add is that some of the papers I have directed Richard to, such as the Alu paper and a few others, have not, as of yet, been responded to by Richard. These papers also test Richard's hypothesis of a bottleneck to two, and reject it.

[/quote]
I will come on to those papers in due course, Dennis, as we have not yet completed our discussion of Zhao et al 2000, which is the first one of the batch of papers that you directed me to that I have addressed. As we have discussed, the parts of this paper that you highlighted did not test a hypothesis of a bottleneck of two and do not support your certainty against this hypotheses. I think you have agreed with that critique and we are now in the midst of a discussion as to whether or not the final coalescent analysis of the paper is persuasive evidence against a population bottleneck of two.

I have just had a read through the comments that you made about this since I have been away for the weekend. I am glad to see that you have backed away from your claim that 75 variants could not make it through a bottleneck of two, and that you are now talking about how they are arranged in haplotypes over the 10Kb region. That is much more appropriate and to the point. However, you present no analysis of the haplotype structure of the region we are discussing, nor do the authors Zhao et al write about this in any detail. You are quite out on a limb here, making claims about the data that the authors do not make.

> DennisVenema:
>
> When we look at this region we don't see what a bottleneck to four would predict. We don't see all the variants grouped together into four different haplotype blocks. We see the variants dispersed in different combinations. What we see just doesn't fit a two-person bottleneck model.

Please could you present some analysis of their data and show that there are not four major haplotypes for the higher frequency variants that could have come through a bottleneck? As you know, linkage disequilibrium in the human genome means that very few of the haplotypes that are possible from existing SNVs are present in human populations.

> DennisVenema:
>
> This sort of analysis was done at a massive, genome-wide scale by Tenesa et al, 2007, and they conclude that human population sizes have stayed in the several thousands over the last 200,000 years, as I discuss in the book. This group looks at millions of marker pairs, many of which are much further apart than the ones in this small region of the genome we are discussing here.

Please note that I have already commented on your use to the Tenesa et al paper in my Nature Eco Evo blog, and I am looking forward to your response to my critique.

I would also note, Dennis, that as well as the outstanding task you have given me of reading though four more papers (which I plan to fulfil), I have also suggested a task for you that I believe remains outstanding:[quote="RichardBuggs, post:108, topic:37039"]
to explain in your own words (without help from Steve) what Steve was modelling, and how it shows that a bottleneck of two is unlikely to have happened.
[/quote]
I am sure that many of the readers following this discussion would welcome such a summary.

DennisVenema (Dennis Venema) 2017-11-27 23:23:06 UTC #126

Hi Richard - welcome back to the conversation.

I'll let **@glipsnort** comment on his confidence re: the data as we have it, but don't forget he's also waiting for evidence of a turtle rather than a duck…

I'm also hoping that eventually you'll take this on yourself too - you're a biologist, after all, so this should be possible for you to work on this for yourself. The 1000 genomes data set would be the logical place to start. How about a model that

proposes and explains the linkage disequilibrium data coming from just 2 people? I think if you started working on that angle you would quickly see the problems. It's not without reason that both Steve and I have been asking you to do some modelling for yourself.

Eventually I hope to have a full reply to you done. I've given Part 2 to Brad and Jim, and I'm waiting for their feedback. Pending that I'll draft part 3. I'm also unusually busy this week with a number of events, so, don't hold your breath…

I also don't know why you keep saying things like I don't allude to the papers I've cited to you in the book. Do you really think I would write a book for a popular audience and just make a guess at what the data says? Or is it more likely that I would read the evidence at some depth before writing the book?

I'm also surprised that you haven't already read those papers. If I was in your shoes, I would have familiarized myself with the field as a whole before mounting a public critique.

Jonathan_Burke (Jon) 2017-11-28 01:49:30 UTC #127

> RichardBuggs:
>
> I am sure that many of the readers following this discussion would welcome such a summary.

I am one of the readers who wants to see the evidence for a bottleneck of two. If I have missed it in all the posts, could you please link to it? Are there any scientists who argue for a bottleneck of two any time in the last 100,000 years?

As I said before, I have only one question for this discussion. Does your understanding of the data support the idea of an Adam and Eve who had no ancestors at all (neither human nor pre-human), as the universal progenitors of every human who has ever lived, with no humans descending from any parallel humans or pre-humans, approximately 6,000 years ago? That's all that matters to me.

---

tallen_1 (Tim) 2017-11-28 03:04:08 UTC #128

Richard,

While we're waiting on Dennis' reply, I'm hoping you can bring a little more clarity in your main critique with respect to the studies he referenced for you.

For what it's worth, I can give you my own impression of what may be happening here by way of analogy. Let's say we have a YEC criticize the available peer-reviewed literature for not testing his "hypothesis" of an ice canopy. While the mainstream scientist may provide you with references till they're blue in the face on paleoclimatology, physics, cosmology, etc., you continue to object that your particular "hypothesis" of an ice canopy has not been explicitly tested and rejected and so all this bravado from scientists on their confidence of what the earth looked like in the ancient past is faulty. So, as this mainstream scientist just cannot dig up a laser-focused rebuttal to your particular arbitrary model, they simply run calculations for you demonstrating the implausibility of your claim. Which you then take to be a weakness of the existing literature. Why run the numbers if the available studies already refute it you say?

I think (or hope) we can all see the absurdity of such an approach. And while I'm getting the sense that this MAY be what is happening here with your critique on Dennis, I don't know it. So I'm hoping you can clear this up for me. What are your main issues with how he is or is not engaging the available literature? As succinctly and clearly as you can sum them up? I look forward to your thoughts.

---

cwhenderson (Curtis Henderson) 2017-11-28 03:59:46 UTC #129

> Jonathan_Burke:
>
> I am one of the readers who wants to see the evidence for a bottleneck of two. If I have missed it in all the posts, could you please link to it? Are there any scientists who argue for a bottleneck of two any time in the last 100,000 years?

Agreed, I haven't even seen anything like this at AIG or ICR. Granted, I don't read exhaustively at either site, but such a claim would've likely caught my attention.

Jonathan_Burke (Jon) 2017-11-28 04:10:37 UTC #130

Organizations like AIG and ICR have made a kind of hamfisted attempt to do this with lots of fuzzy talk about **Mitochondrial Eve**, and **AIG has made its own claim** about a genetic bottleneck. This recent genetic bottleneck argument is obviously being promoted by the Discovery Institute. However, **CMI is following** the current discussion at Biologos.

DennisVenema (Dennis Venema) 2017-11-28 04:53:59 UTC #131

> RichardBuggs:
>
> you present no analysis of the haplotype structure of the region we are discussing, nor do the authors Zhao et al write about this in any detail. You are quite out on a limb here, making claims about the data that the authors do not make.

In order to "see" what I'm getting at, you would have to look at the 1000 genomes data and assemble the various haplotypes in their sample from the region in question. There are more in the database now, obviously, than when the paper was published. This is part of what I was saying when I said that some of what you are looking for is just familiarity with published data sets.

This region of the genome is not atypical. It has a haplotype structure like other regions, and scrolling through the data yourself is the best way to convince yourself that it could not descend from just two individuals.

If you want to see how this sort of thing looks, **here's a paper** (PDF) that does this for a limited data set for the entirety of human chromosome 21. Look at figure 2 - those are 20 individual chromosomes from their sample (African, Asian, Caucasian). Note well that this is an early paper with a limited data set, but there are more than four common haplotypes even in this very limited data set. Note also how closely linked these SNP sites are. The problem for a 2-person bottleneck hypothesis only gets worse as you add in the reams of data we've added since.

---

gbrooks9 (George Brooks) 2017-11-28 05:08:05 UTC #132

> cwhenderson:
>
> Agreed, I haven't even seen anything like this at AIG or ICR. Granted, I don't read exhaustively at either site, but such a claim would've likely caught my attention.

@cwhenderson , **@Jonathan_Burke** : All we have seen from Dr. Buggs is a list of assigned tasks for how **@DennisVenema** should run the data differently.

There has been zero effort made to run data the way Dr. Buggs says it should be run, so that we can all see for ourselves.

@RichardBuggs , how long before you do a test run … even with hypothetical data?

DennisVenema (Dennis Venema) 2017-11-28 05:13:40 UTC #133

> cwhenderson:
>
> Agreed, I haven't even seen anything like this at AIG or ICR. Granted, I don't read exhaustively at either site, but such a claim would've likely caught my attention.

Richard's suggestion that all common variation was packed into two founding individuals and then recombined afterwards into the patterns we see today is actually found in the YEC literature. (Yes, I spend too much time on these things - sigh). Robert Carter is an example of a YEC who tries to get around the bottleneck/founding with 2 problem this way. The challenge for YECs (and Richard) is explaining the patterns we see in the present day with reasonable recombination events. There is also the issue of drift to intermediate frequencies, because small haplotype blocks are effectively "alleles" that can increase or decrease in frequency like individual variants. Although I think Carter starts with a population of one, since Eve is a clone of Adam (presumably with a subtracted Y and a doubled X). In this case, you have to deal with only two original chromosomes, not four.

Casper_Hesp (Casper Hesp) 2017-11-28 09:28:49 UTC #134

> RichardBuggs:
>
> to explain in your own words (without help from Steve) what Steve was modelling, and how it shows that a bottleneck of two is unlikely to have happened.

Why would @DennisVenema need to describe separately what @glipsnort was modelling, if Steve himself already explained very clearly what he was modelling? What purpose does that serve, other than "testing" Dennis? It appears to be an unnecessary demand that does not further the conversation.

---

cwhenderson (Curtis Henderson) 2017-11-28 15:38:12 UTC #135

> DennisVenema:
>
> Although I think Carter starts with a population of one, since Eve is a clone of Adam (presumably with a subtracted Y and a doubled X). In this case, you have to deal with only two original chromosomes, not four.

I would suggest that this approach would be more consistent with a literal interpretation of Genesis.

DennisVenema (Dennis Venema) 2017-11-28 15:53:03 UTC #136

> cwhenderson:
>
> I would suggest that this approach would be more consistent with a literal interpretation of Genesis.

I think this is where AIG goes now too, though I can't recall exactly.

---

jpm (Phil) 2017-11-28 15:57:22 UTC #137

And it points out the problems with a very literal interpretation. The genetic makeup of Eve. The origin of Eve's biomass (what does a rib weigh? a pound, depending on which rib?). The genetics of the offspring. The problem of creation of mankind on the 6th day vs Genesis 2 story. To take it as addressing science places you in a strange position if you try to explain it all. I do not mean to sidetrack the conversation, but these issues are what are going on in the background in my mind when these sorts of discussions come up. If further discussion along these lines is desired, we can move to another post to maintain the integrity of this discussion.

DennisVenema (Dennis Venema) 2017-11-28 16:34:01 UTC #138

In some ways it is relevant to the conversation… Richard has been asking about a bottleneck to two individuals, but perhaps a bottleneck to one is what really should be discussed here. In that case we'd be down to only two starting chromosomes.

RHernandez (Roberto L Hernandez) 2017-11-28 18:15:11 UTC #139

> RichardBuggs:
>
> I came into this discussion with two questions in my mind:
>
> 1. Does chapter three of Adam and the Genome make a convincing case that humans have never passed through a bottleneck of two?
> 2. Is there a better case that can be made?

Would not a better start to a good discussion be to analyze the relevant data yourself to see if the data is suggest a bottleneck of two before you enter the public discussion and make many demands of Dennis?

> RichardBuggs:
>
> Given my disappointment in the other citations that Dennis has pointed me to in the past through his chapter and in this discussion, I am not optimistic that any of these will really support his case when examined closely.

I am disappointed in your failure to point anyone to citations that suggest a bottleneck of two. Why does Dennis have so much responsibility, and you seem to have none?

RHernandez (Roberto L Hernandez) 2017-11-28 18:16:07 UTC #140

> Casper_Hesp:
>
> Why would **@DennisVenema** need to describe separately what **@glipsnort** was modelling, if Steve himself already explained very clearly what he was modelling? What purpose does that serve, other than "testing" Dennis? It appears to be an unnecessary demand that does not further the conversation.

I think that you do not need to know any genetics or science to see what is happening here.

---

glipsnort (Steve Schaffner) 2017-11-28 21:35:24 UTC #141

> RichardBuggs:
>
> But it does make the point that population structure would boost the number of intermediate frequency alleles. The bottleneck hypothesis could have a scenario of rapid population expansion followed by a period with a structured population in a fairly stationary state.
>
> I do think though that sub-division arising a few generations after a bottleneck, accompanied by rapid expansion of sub-populations, would result in higher numbers of alleles at intermediate frequencies in the meta-population as a whole than would be expected in a single expanding panmictic population.

Wakeley's results do not apply to your scenario. You do not have enough time to attain a "fairly stationary state". As a result, I don't see how you can draw any relevant conclusions from it.

> RichardBuggs:
>
> Thanks for doing this! Hmm, this is interesting. Why is there a sudden drop at 0.05 (corresponding to a frequency of 0.5 in the single deme, I guess) for the demes?

I don't see a sudden drop at 0.05. I only see the drop at 0.10.

> RichardBuggs:
>
> I think the number of intermediate frequency alleles would be higher if we included sites that had ancestral polymorphism when the population became subdivided. Then some of the sub-populations would share the same alleles at fixation, giving them higher frequencies in the meta-population as a whole.

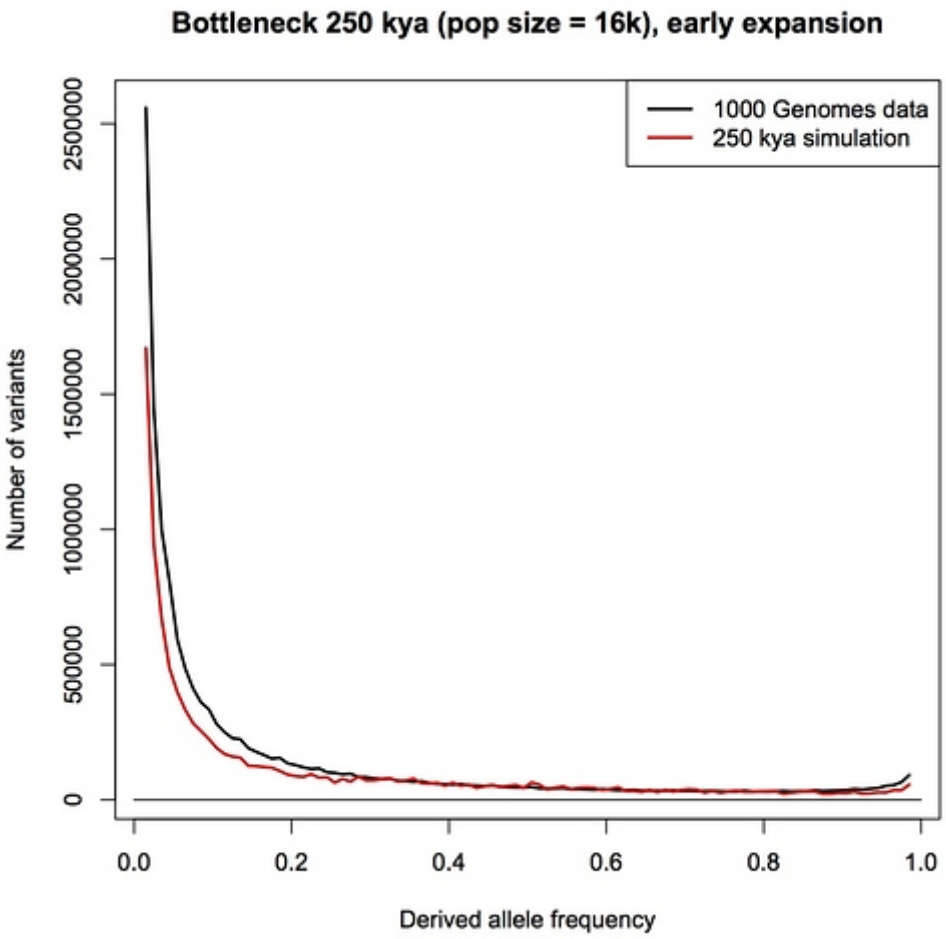
But the problem isn't to find intermediate frequency alleles. You can do that just by increasing the ancestral population size to make it as large as you like. The problem is getting the frequency distribution to look like 1/frequency. How does population structure help? I don't see why that would do anything but give you slower and more granular drift of the ancestral frequencies.

> RichardBuggs:
>
> Successive "Adam and Eves" rather than just one couple? Interesting idea.

A more modest bottleneck that that.

> RichardBuggs:
>
> OK, I see. But in your 100kya_component.jpg figure there is very little contribution from post-bottleneck mutation above 20%. Why couldn't you make the model fit right down to there with more pre-bottleneck variation?

Then it won't fit in the 60% - 70% range. What you can do is have the ancestral population biased toward lower frequency alleles, so that more come through that bottleneck at 25% than under the constant-sized model. I ran one such scenario last week. Here's another, which is the best I can up with; it has a rapidly expanding population prior to the bottleneck:



It does give a better fit above 30% frequency, but it still has two distinct regimes, reflecting a change in population dynamics. It now looks pretty much like a major population expansion happened 250,000 years ago. It also requires an implausibly large ancestral population. I'm still using the trick of scaling up the ancestral size to fit the 60-70 window, (even though it's no longer valid, since the ancestral population wasn't stationary). Doing so yields an effective population size prior to the bottleneck of 1.4 million. Modeling it properly would make it even bigger.

(I've also started modeling incorrect ancestral allele assignments, since we're looking at the higher part of the spectrum now.)

> RichardBuggs:
>
> I really appreciate the time you have put into this, and I do hope you will continue this discussion after your break. I realise I am acting as a defense attorney in a case that seems to you to be a bit hopeless, but I think it is good for us to work this all through in detail as there are so many people out there for whom this is an important issue for their faith - who have very heartfelt beliefs about this - and I think we owe it to them to go through this throughly.

This has been taking up quite a bit of my time, and I really can't afford to keep doing it much longer. In my experience, the number of people who care about this specific scenario – which involves jettisoning a fair bit of the actual Genesis story, after all – and who are likely to care about pop gen simulations is pretty small.

---

glipsnort (Steve Schaffner) 2017-11-28 21:37:23 UTC #142

> RichardBuggs:

> I also note that because Steve has presented this analysis that is not in the peer reviewed literature, it seems probable that he does not find what is already in the peer reviewed literature as convincing as Dennis does.

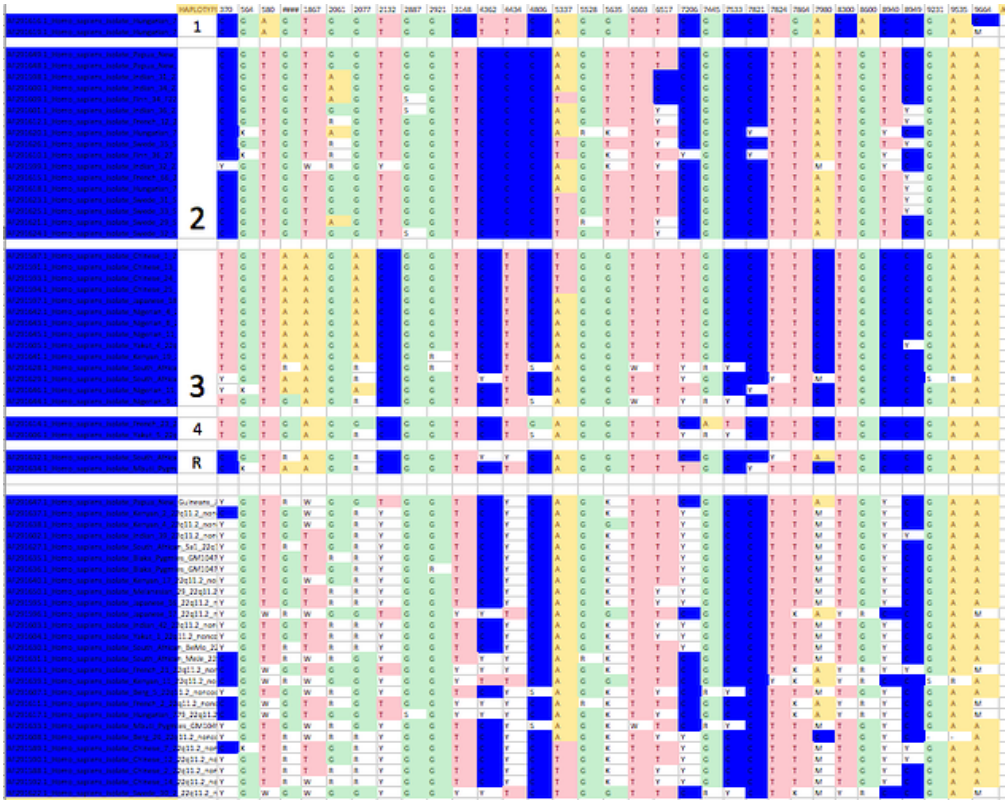
That's quite a shaky inference and I would advise you against making it.

RichardBuggs (Richard Buggs) 2017-11-28 21:55:22 UTC #143

Hi Dennis,
Regarding the 10,000bp region in the Zhao et al paper you say this:

> DennisVenema:
>
> When we look at this region we don't see what a bottleneck to four would predict. We don't see all the variants grouped together into four different haplotype blocks. We see the variants dispersed in different combinations. What we see just doesn't fit a two-person bottleneck model.

To see if you are correct I have downloaded Zhao et al's sequences from Genbank, aligned them, and taken a look at the variation. Here is a very simple portrayal of the variants that are present in more than two individuals.



Each column is a locus with variation (with only the loci where the minor allele is present in more than two individuals being shown). The number at the top of each column is the position within the 10,000bp sequence. Each row is an individual human. I have coloured in calls that are unambiguously A, T, G or C.
Many of the calls in the data are ambiguous, which means that either the individual was heterozygous at that locus, or the sequence data was poor there. Where there are several ambiguous sites in an individual it is not easy to infer the haplotypes (combinations in which the variants are found within the two parental genomes within the individual).
In the figure I have taken the individuals that had few ambiguity codes, and divided their haplotypes into four groups, where each halplotype group contains differences of up to three mutations. I have labelled these in the second column, and put a spacing row between them. I have also labelled a couple of sequences as R in the second column, as these may be recombinants. Then at the bottom I have placed individuals that have lots of ambiguous bases, making their

haplotypes hard to call.
I think it is fairly clear to the eye that the data present can be divided fairly easily into four groups, that could correspond to small variations on four ancestral haplotypes. Given the similarity of them all, the number of ancestral haplotypes could in fact be lower.
This is a very rough and ready analysis that I did partly on the London Underground on my way home from work this evening. I can follow up in more detail if you wish. As a preliminary analysis, I think it supports my point quite nicely.

---

gbrooks9 (George Brooks) 2017-11-28 21:57:32 UTC #144

> RichardBuggs:
>
> I really appreciate the time you have put into this, and I do hope you will continue this discussion after your break.
>
> I realise I am acting as a defense attorney in a case that seems to you to be a bit hopeless, but I think it is good for us to work this all through in detail as there are so many people out there for whom this is an important issue for their faith - who have very heartfelt beliefs about this -
>
> **and I think we owe it to them to go through this throughly.**

@RichardBuggs
cc: **@glipsnort**

I think there is uniform and general agreement that Dr. Schaffner has been **through this thoroughly**. And he has paid his debt to all those people who have rejected, and will continue to reject, his findings no matter what those findings are.

However, if you still feel the keen and heartfelt pain of those who really want someone to pin his or her reputation and credibility to the unfathomable “bottleneck of a mating pair 6000 years ago”, it would seem you are the perfect candidate.

You are an academic.
You really care about their pain.
And you seem to have an endless list of permutations that need testing.

When will you start?

DennisVenema (Dennis Venema) 2017-11-28 22:14:24 UTC #145

Hi Richard - great that you’re looking at data.

Now that you’ve looked at that particular data set and tried to “bin” things into four starting chromosomes, you can start to see that there are some differences between individuals in your bins, and that those differences are shared by other individuals within your bins.

Are those differences the result of de novo mutations, or recombination from the starting four haplotypes, then? And is there time for those variants, once they are produced by rare events, to drift to an intermediate frequency?

For example, in your “bin 2” there are three individuals that share an A where others have a G, and those same three individuals also share a C where no one else does. Why is that not another haplotype in a separate bin in your thinking?

AMWolfe (A.M. Wolfe) 2017-11-28 23:44:43 UTC #146

> jpm:
>
> it points out the problems with a very literal interpretation. The genetic makeup of Eve.

> DennisVenema:
>
> Richard has been asking about a bottleneck to two individuals, but perhaps a bottleneck to one is what really should be discussed here.

Wow, this never occurred to me!

It's worth noting that if God is able to instantaneously organize literal dust particles into the entire human genome in order to make Adam, there's nothing saying that when God took the rib from Adam, he couldn't have miraculously generated a second genome for Eve in the time between the rib removal and Eve's full development.

Of course, this would be an interpolation, but hey, so are most of the details when you try to force a scientific worldview onto a Biblical text. Dino-riding, anyone?

Lastly, it strikes me that if Eve really was a genetic clone of Adam, she would *not* have been judged to be a suitable helper for Adam. To the extent that my wife and I make a good team, it's because our strengths and weaknesses even out. If we were genetically identical (minus a Y, plus an X), Lord help us…

DennisVenema (Dennis Venema) 2017-11-29 05:49:23 UTC #147

> AMWolfe:
>
> Lastly, it strikes me that if Eve really was a genetic clone of Adam, she would not have been judged to be a suitable helper for Adam. To the extent that my wife and I make a good team, it's because our strengths and weaknesses even out. If we were genetically identical (minus a Y, plus an X), Lord help us…

Yes, except most folks who go in for this sort of thing think that A & E were flawless - so they would be - wait for it - *perfect* for each other.

I'll see myself out…

RichardBuggs (Richard Buggs) 2017-11-29 15:59:51 UTC #148

Hi Dennis,
That is absolutely right. As I said in the text accompanying the figure:

> RichardBuggs:
>
> In the figure I have taken the individuals that had few ambiguity codes, and divided their haplotypes into four groups, where each halplotype group contains differences of up to three mutations.

I would attribute these to mutations since a bottleneck, or, in some cases, recombination.
My point is that we can quite credibly trace the different haplotypes currently found in individuals back to four ancestral haplotypes.

best wishes,
Richard

DennisVenema (Dennis Venema) 2017-11-29 20:28:33 UTC #149

Some of your recombination events would require two crossovers in a very short physical space. We would then be left wondering why none of the single crossover events are present in the data set. The single crossover events would have to occur first, and then drift to an appreciable frequency to allow for a reasonable chance of a second crossover event to occur. These haplotypes are not derived from four ancestral types. If they were, why do we not see the single recombinant classes in the data? A far more parsimonious explanation is an ancestral haplotype set greater than 4.

Also, have a look at the data set for chromosome 21 in that paper I posted. How are you going to get that diversity down to 4 starting sets? Your model predicts you should be able to do this for the entire genome.

PDBrown (Paul D. Brown) 2017-11-29 20:37:07 UTC #150

> DennisVenema:
>
> I'm also surprised that you haven't already read those papers. If I was in your shoes, I would have familiarized myself with the field as a whole before mounting a public critique.

As a fly on the wall from time to time, thanks for the interesting discussion. Recently it seems to have lost some of its interesting character. This is an aside to the main content of the debate but I do think a clarification is warranted. In his prefatory remarks to this discussion Dennis also says:

…and a reply to Dr. Buggs was clearly not going to be a note that I could dash off in a spare few minutes. And so I left the email unanswered – sorry Richard, if I may call you that – and after a while I forgot about it. Not surprisingly, and completely understandably, Dr. Buggs assumed I wasn't going to respond, and posted the email on his webpage as an open letter.

One can understand forgetting and certainly can understand not being able to dash off a five minute explanation on a detailed subject. And I'm sure the apology is appreciated. However, as someone who knows both Dennis and Richard, Richard made me aware of his note to Dennis, since there was no reply, shortly after the original note was sent. I would ask Richard if he ever heard from you Dennis, and upon hearing not, reminded you on at least three distinct occasions over the 4+ months passing Richard's correspondence, asking if you were going to reply. Thus it is important to note that Richard had attempted to discourse privately at first. And there was no need for Richard to have assumed anything regarding your future intentions to respond or not. There simply wasn't a response - with ample opportunity to provide at least something. So in that context he went public to stimulate a discussion - "before mounting a public critique" as you put it. And as far as I can see, he has well demonstrated familiarity with the literature, whether one agrees with certain ideas put forward or not.

DennisVenema (Dennis Venema) 2017-11-30 03:46:35 UTC #151

Hi Paul - welcome to BioLogos. Nice to have friends I know in real life on here as well.

Yes, I was remiss in not replying to Richard, despite your reminders. I think I would have eventually got around to something of a reply - at least I hope so - even if Richard hadn't posted his letter as an open letter. I do get a fair number of "you're wrong" - type emails, though not usually from other biologists.

I was correct in that it would not be a quick reply, though! Here we are already several thousand words in already, and more to come… hopefully the fact that the conversation is in the public domain will be useful to some.

PDBrown (Paul D. Brown) 2017-11-30 17:39:21 UTC #152

Thanks for the welcome, Dennis. And yes - it is not a short discussion! I hope it will be useful as well.

RichardBuggs (Richard Buggs) 2017-12-01 09:07:05 UTC #153

Hi Dennis, I am teaching an intensive postgraduate module over the current fortnight so my responses are going to be slower than they were previously, sorry. Which of the variant positions are you suggesting are double recombinants? Why don't you think a mutation or gene conversion would be more parsimonious for these?
Let's keep our focus on this dataset for now. As well as being interesting and a nice illustration that our readers can follow, it is also critical in answering the question of whether the Zhao et al paper supports your case or not.

RichardBuggs (Richard Buggs) 2017-12-01 11:02:49 UTC #154

By the way, I thought of you all as I passed this pub in Westminster yesterday. Dennis, is you're ever in London, we should meet here for a pint!

Argon 2017-12-01 15:45:06 UTC #155

> RichardBuggs:
>
> My point is that we can quite credibly trace the different haplotypes currently found in individuals back to four ancestral haplotypes.

I believe one can trace everything back anywhere from thousands of haplotypes, to a couple dozen, to six, four, two or even a single ancestral haplotype if one is willing to extend the possible lineages ***far enough backwards in time***. For the time spans involved it doesn't seem credible on the basis of characterized mechanisms we observe today.

Dennis Venema is correct when he notes that the notion of a bottleneck of two individuals wasn't discarded out of hand or left untested. It appears the analyses simply don't support it. I wonder if archaeological results could even support it.

---

gbrooks9 (George Brooks) 2017-12-01 16:49:07 UTC #156

> Argon:
>
> Dennis Venema is correct when he notes that the notion of a bottleneck of two individuals wasn't discarded out of hand or left untested. It appears the analyses simply don't support it. I wonder if archaeological results could even support it.

@Argon

Archaeological evidence shows human populations well above 2, 10 or even 100 for thousands and thousands of years … well past the time horizon of Adam & Eve 6000 years ago.

Who do you think built that buried open air temple in Anatolia 10,000 years ago?

Marshall (Marshall Janzen) 2017-12-01 18:30:23 UTC #157

[quote="RichardBuggs, post:143, topic:37039"]
I think it is fairly clear to the eye that the data present can be divided fairly easily into four groups, that could correspond to small variations on four ancestral haplotypes.[/quote]
I'm another non-specialist with some questions. I'm curious what the data would say about the Y chromosome. Would you suggest that there the data would be explainable as a single group? And in the case of the X chromosome, it would divide fairly easily into three groups (one from the male and two from the female at the bottleneck)?

T_aquaticus 2017-12-01 20:14:02 UTC #158

> cwhenderson:
>
> If anyone is feeling a little badly due to the conversation going over their head, don't. I have a PhD in biology and much of this is going over my head. This is what I can summarize, though:

My measly BS in Zoology didn't include much in the way of population genetics, but here is my summary of this discussion using an analogy.

A bunch of scientists are trying to estimate the average weight of a population of elephants. They come up with three different and independent methods of estimating their weight, such as dropping them from airplanes and measuring their terminal velocity, or measuring the weight of water they displace from a tank. They tally their data and find that Method A gives an estimate of 10,500 lbs, Method B gives an estimate of 12,300 lbs., and Method C gives and estimate of 9,600 lbs.

Along comes a scientist who claims that maybe elephants only weigh 2 lbs. He won't say why he thinks that, or even what evidence leads him to suggest such a thing. This skeptical scientist also states that the methods the scientists

used couldn't detect a 2 lb elephant, but doesn't explain why. He even claims that a 2 lb elephant would look identical to a 12,000 lb elephant, but also doesn't explain why this is or back it up with any data.

So we are left with a very, very large group of scientists who have 3 independent methods that all give answers that are close to one another and a single scientist who claims all the other scientists are wrong by a factor of 1,000 for apparently no justifiable reason. Does that seem like it is even a debate?

---

gbrooks9 (George Brooks) 2017-12-01 20:24:04 UTC #159

@T_aquaticus , nice evaluation!

I couldn't put my finger on it … but you did!

RichardBuggs (Richard Buggs) 2017-12-01 21:49:50 UTC #160

Hi Steve **@glipsnort** thanks for re-joining the discussion. I hope you had a good holiday.

> glipsnort:
>
> I don't see a sudden drop at 0.05. I only see the drop at 0.10.

Sorry, my bad. That drop makes perfect sense.

> glipsnort:
>
> How does population structure help? I don't see why that would do anything but give you slower and more granular drift of the ancestral frequencies.

In your original model it seemed that the ancestral frequencies were contributing very little at all to the allele frequencies predicted by the model in the present day, and this is why I assumed that many of them were drifting to zero. Population structure could prevent this drift to zero from happening due to differential fixation of alleles in sub-populations, which could then be supplied back into larger populations when the sub-populations meet again. As for granularity, I was not suggesting a simple or constant sub-structuring of the population. As I said in my original response to your model[quote="RichardBuggs, post:53, topic:37039"]
I am saying that Steve's model (at least in its current preliminary form) is making the approximation that there is one single interbreeding population that has been present in Africa throughout history, and that mating is random within that population. However, the actual history is almost certainly very different to this. The population would have been divided into smaller tribal groups which mainly bred within themselves. Within these small populations, some new mutations would have spread to all individuals and reached an allele frequency of 100%. In other tribes these mutations would not have happened at all. Thus if you treated them all as a large population, you would see an allele frequency spectrum that would depend on how many individuals you sampled from each tribe. It is more complicated than this because every-so-often tribes would meet each other after a long time of separation and interbreed, or one tribe would take over another tribe and subsume it within itself. Such a complex history, over tens or hundreds of thousands of years would be impossible to reconstruct accurately, but would distort the allele frequency spectrum away from what we would expect from a single population with random mating. It gets even more complicated if we start also including monogamy, or polygamy.
[/quote]
On reflection, as I have stated above, I would also extend this argument to the ancestral variants. You have argued convincingly that if we simply divide the population into 10 sub-populations and these do not meet or interbreed, then we cannot fit the data. However I am suggesting that reality is far more complex than this, and a long history of sub-

division, re-meeting, conquest, occasional migrants etc would tend to result in a smooth curve of allele frequencies, rather than granularity.

Also, I mentioned earlier the issue of mating system. Do you have separate sexes in the model, or hermaphrodites? If the latter, could they self-fertilise? If you did have separate sexes and life-long sexual partners, how would that affect the allele frequencies?

Asking this question reminds me of another question I was meaning to ask: how did you determine the ancestral state of the alleles?

> glipsnort:
>
> Here's another, which is the best I can up with; it has a rapidly expanding population prior to the bottleneck: It does give a better fit above 30% frequency, but it still has two distinct regimes, reflecting a change in population dynamics. I

Thank you, that is very interesting. I am glad to see it has a closer fit to the actual data. I wonder if a complex population structure and some admixture from out of Africa could improve the fit further.

> glipsnort:
>
> It also requires an implausibly large ancestral population.

Just a thought: what if you parameterised the ancestral population with the genetic diversity found in present day chimpanzees?

To return to the issue of admixture from our of Africa you previously said[quote="glipsnort, post:67, topic:37039"]
In general, a fragmented population (inside or outside Africa) creates two classes of parts of the genome: those with genetic ancestry entirely within one population, and those with ancestry from a second population. The former will have coalescence times (and therefore diversities) characteristic of the population of the single population, while the latter will have longer coalescence times and higher diversities; their most recent common ancestor has to lie before the time the populations diverged, or at least far enough back for earlier migration to have carried the lineage into the second population. This signature – many regions with low diversity, some with much higher diversity – is also the signature of a bottleneck, in which some regions have variation that made it through the bottleneck and some don't.
[/quote]
But how would this be distinguishable in an allele frequency spectrum?

> glipsnort:
>
> This has been taking up quite a bit of my time, and I really can't afford to keep doing it much longer.

I sympathise - this is taking far longer than I had expected also. One issue we have is that as your model is not published, there are still various details of it that we as readers are unclear about (hence my questions above). Would you consider writing this up as a publication, so that everything can be clearly laid out? Or would you be willing to share the code of your model so others can examine it and perhaps play with more scenarios?

> glipsnort:
>
> In my experience, the number of people who care about this specific scenario – which involves jettisoning a fair bit of the actual Genesis story, after all – and who are likely to care about pop gen simulations is pretty small.

Perhaps so, but it is a fascinating issue and one on which is raised (and I fear is the subject of unsubstantiated claims) in “Adam and the Genome”

> glipsnort:
>
> [RichardBuggs: I also note that because Steve has presented this analysis that is not in the peer reviewed literature, it seems probable that he does not find what is already in the peer reviewed literature as convincing as Dennis does.]
>
> That’s quite a shaky inference and I would advise you against making it.

Could I push you a little on this, please, as it seems quite a faint denial. Are you as certain that a bottleneck of two has not happened as you are that the earth rotates around the sun? Which of the arguments that Dennis makes in the chapter three of “Adam and the Genome” do you find convincing?

Once again, I really appreciate the time you are putting into this discussion, and the expertise that you bring.

Jonathan_Burke (Jon) 2017-12-01 22:03:44 UTC #161

> RichardBuggs:
>
> Are you as certain that a bottleneck of two has not happened as you are that the earth rotates around the sun?

Could I ask if there is any evidence which would suggest these ought not to be in the same category of certainty?

T_aquaticus 2017-12-01 22:05:53 UTC #162

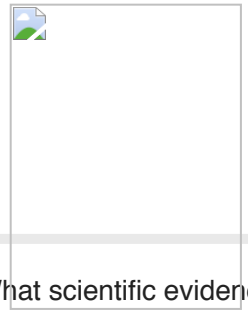
> RichardBuggs:
>
> Are you as certain that a bottleneck of two has not happened as you are that the earth rotates around the sun? Which of the arguments that Dennis makes in the chapter three of “Adam and the Genome” do you find convincing?

Other than your religious beliefs, what makes you doubt the overwhelming consensus among population geneticists that historic human populations have not dipped down to 2 people in the last several hundred thousand years?

From what I have seen, you haven’t been able to point to a single peer reviewed paper that puts any of these conclusions in doubt. Dennis Venema has even cited papers that specifically test the hypothesis of a 2 person bottleneck in historic human populations and the data strongly rejected that hypothesis:

"Genetic variation at most loci examined in human populations indicates that the (effective) population size has been approximately 10(4) (i.e., 10,000) for the past 1 Myr and that individuals have been genetically united rather tightly. Also suggested is that the population size has never dropped to a few individuals, even in a single generation. These impose important requirements for the hypotheses for the origin of modern humans: a relatively large population size and frequent migration if populations were geographically subdivided. Any hypothesis that assumes a small number of founding individuals throughout the late Pleistocene can be rejected."

> **Allelic genealogy and human evolution. I Molecular Biology and Evolution I...**



Genetic variation at most loci examined in human populations indicates that the (effective) population size has been approximately 10(4) for the past 1 Myr and that individuals have been genetically united rather tightly. Also suggested is that the...

What scientific evidence do you find so convincing that it makes you doubt these conclusions?

Jonathan_Burke (Jon) 2017-12-01 22:22:10 UTC #163

> RichardBuggs:
>
> Also, I mentioned earlier the issue of mating system. Do you have separate sexes in the model, or hermaphrodites? If the latter, could they self-fertilise? If you did have separate sexes and life-long sexual partners, how would that affect the allele frequencies?

Someone stop me if I'm wrong (**@glipsnort** **@T_aquaticus**), but this is starting to look like special pleading. If we need to posit the existence of self-fertilizing hermaphrodites for which we have no actual evidence, in order to have a chance at getting the bottleneck down to an original pair, it seems we're drifting well into the zone of apologetics, and further away from actual science.

T_aquaticus 2017-12-01 22:26:44 UTC #164

> Jonathan_Burke:
>
> Someone stop me if I'm wrong (**@glipsnort** **@T_aquaticus**), but this is starting to look like special pleading. If we need to posit the existence of self-fertilizing hermaphrodites for which we have no actual evidence, in order to have a chance at getting the bottleneck down to an original pair, it seems we're drifting well into the zone of apologetics, and further away from actual science.

I think it may be the exact opposite of what you are suggesting. Buggs is making sure that glipsnort's model is using diploid dioecious (i.e. separate sexes) organisms. On the flip side, I don't know if that really matters that much unless we are focusing on the y chromosome.

Jonathan_Burke (Jon) 2017-12-02 00:55:10 UTC #165

> T_aquaticus:
>
> I think it may be the exact opposite of what you are suggesting. Buggs is making sure that glipsnort's model is using diploid dioecious (i.e. separate sexes) organisms.

Since glipsnort was modeling a human population, this question still makes no sense to me.

Chris_Falter (Chris Falter) 2017-12-02 12:51:37 UTC #166

@glipsnort - I hope that everything is going as well for you in New England as it is for the Patriots.

If you could post your code to Github along with a very brief readme of which parameters were used for which posts, I can promise that you will see at least one download. I have recently been studying how to run MCMC simulations in Python, and I would love to see how a master of the craft does it in R.

A Github post would have the additional benefit of allowing those who want further info about your simulations to get it self-service by studying your code. The alternative, as we have seen, is that you do the work of addressing ad-hoc concerns yourself–and that does not seem like a fair or viable solution.

Best,
Chris Falter

Argon 2017-12-02 15:41:34 UTC #167

> RichardBuggs:
>
> Could I push you a little on this, please, as it seems quite a faint denial. Are you as certain that a bottleneck of two has not happened as you are that the earth rotates around the sun? Which of the arguments that Dennis makes in the chapter three of “Adam and the Genome” do you find convincing?
>
> Once again, I really appreciate the time you are putting into this discussion, and the expertise that you bring.

There are two claims involved in this response:

1. Is it true that there seems to be very little support from genetic analyses for the notion of two founder individuals in humanity and is the current consensus justified? Answer: Yes.
2. Are the specific arguments presented in Dennis’ book convincing and strong enough to make the case?

---

glipsnort (Steve Schaffner) 2017-12-05 18:09:25 UTC #168

> Chris_Falter:
>
> If you could post your code to Github along with a very brief readme of which parameters were used for which posts, I can promise that you will see at least one download. I have recently been studying how to run MCMC simulations in Python, and I would love to see how a master of the craft does it in R.

That’s a good idea, but will require a little work, to explain the model and the options. I’ll try to get to it soonish. (If I haven’t done it in a week, I’ve probably forgotten and should be reminded.) My simulation code is actually in C; only the normalization and plotting is done in R.

---

glipsnort (Steve Schaffner) 2017-12-05 20:29:42 UTC #169

> RichardBuggs:
>
> On reflection, as I have stated above, I would also extend this argument to the ancestral variants. You have argued convincingly that if we simply divide the population into 10 sub-populations and these do not meet or interbreed, then we cannot fit the data. However I am suggesting that reality is far more complex than this, and a long history of sub-division, re-meeting, conquest, occasional migrants etc would tend to result in a smooth curve of allele frequencies, rather than granularity.

I don't see how any of those processes increase the number of alleles in the relevant range of frequencies. Combining processes doesn't help when the individual processes don't go in the right direction. Given enough time, a complicated demographic history can produce all kinds of frequency spectra. In this scenario, though, the core problem is recovering diversity in a short time frame; there isn't time for complexity introduced by multiple rounds of anything.

[quote="RichardBuggs, post:160, topic:37039"]
Also, I mentioned earlier the issue of mating system. Do you have separate sexes in the model, or hermaphrodites? If the latter, could they self-fertilise? If you did have separate sexes and life-long sexual partners, how would that affect the allele frequencies?
[/quote]

There is no mating system in my model. The model assumes a pool of 2N genomes consisting of unlinked markers. For allele frequencies averaged over the whole genome, such details should not matter.

> RichardBuggs:
>
> Asking this question reminds me of another question I was meaning to ask: how did you determine the ancestral state of the alleles?

For the simulation, I know the ancestral state, of course. For the 1000 Genomes data, I used the state assigned by the project, which is based on the allele in one or more closely related species. (I think they used some combination of chimpanzee and macaque, but I don't remember off-hand.) The assignment is clearly wrong some of the time.

[quote="RichardBuggs, post:160, topic:37039"]
Just a thought: what if you parameterised the ancestral population with the genetic diversity found in present day chimpanzees?
[/quote]

That would probably look more like the constant-sized population, but I haven't seen many studies of chimpanzee diversity (or if I have, I've forgotten them).

> RichardBuggs:
>
> But how would this be distinguishable in an allele frequency spectrum?

It would correspond to a spectrum with too many low frequency alleles (relative to a constant-sized population) and some much higher frequency ones, with a relative dearth in between.

> RichardBuggs:
>
> Would you consider writing this up as a publication, so that everything can be clearly laid out?

No, for several reasons: (1) I don't think this is currently a viable scientific question, (2) doing publication-worthy demographic inference takes a lot of work, and (3) this isn't what I'm being paid to do. (And it's not just a matter of obligation to my employers – I work on what I do because I think it's important. One of the thing I should be working on is malaria. While I've been writing this comment, twenty-some thousand people have contracted malaria and fifty have died of it, most of them young children. That fact exerts a certain amount of moral pressure.)

> RichardBuggs:
>
> Or would you be willing to share the code of your model so others can examine it and perhaps play with more scenarios?

That's something I intend to do. [quote="RichardBuggs, post:160, topic:37039"]
Could I push you a little on this, please, as it seems quite a faint denial.
[/quote]
My denial was intended to be a polite and fairly neutral way of telling you that your suggestion was both off the mark and presumptuous. I'm doing my own simulations because I want to have a better feel for exactly how long effects of a tight bottleneck persist.[quote="RichardBuggs, post:160, topic:37039"]
Are you as certain that a bottleneck of two has not happened as you are that the earth rotates around the sun?
[/quote]
No. Similarly, I am not as certain that Bigfoot doesn't exist as I am that the earth revolves (not rotates! – I have to look it up myself to be sure) around the sun. That doesn't mean I think the existence of Bigfoot is an open scientific question worth pursuing.

> RichardBuggs:
>
> Which of the arguments that Dennis makes in the chapter three of "Adam and the Genome" do you find convincing?

I don't find any of them convincing since I haven't read the book – which is one reason I've never commented on Dennis's arguments. I think a recent bottleneck of size two is a nonstarter as a hypothesis. If a colleague brought it to me as a grant or paper idea – without any supporting evidence or modeling – I would tell them to stop wasting both our time. Because of the existing data on human genetic variation, the overall state of demographic inference, and my own experience with modeling human bottlenecks, my prior on this hypothesis is too low for it to be worth pursuing. Detailed perusal of the existing studies on the subject is kind of beside the point for me.

---

gbrooks9 (George Brooks) 2017-12-06 00:29:14 UTC #170

> RichardBuggs:
>
> I sympathise - this is taking far longer than I had expected also. One issue we have is that as your model is not published, there are still various details of it that we as readers are unclear about (hence my questions above). Would you consider writing this up as a publication, so that everything can be clearly laid out?

@RichardBuggs ,

Wow… you have lots and lots of chutzpah.

When will you learn enough that you can actually run these scenarios yourself, and learn (the Old Fashioned Way) what works and doesnt work?

However, you then ask this:

"Or would you be willing to share the code of your model so others can examine it and perhaps play with more scenarios?"

Assuming that the code is **not** necessarily proprietary and relevant to **@glipsnort** being able to sustain a viable living, I would support any population geneticist producing a "Kit" for YEC's to use and play with … so that serious scientists can get on with their work!

Jonathan_Burke (Jon) 2017-12-06 04:36:18 UTC #171

> glipsnort:
>
> No, for several reasons: (1) I don't think this is currently a viable scientific question,

> glipsnort:
>
> My denial was intended to be a polite and fairly neutral way of telling you that your suggestion was both off the mark and presumptuous.

> glipsnort:
>
> I think a recent bottleneck of size two is a nonstarter as a hypothesis. If a colleague brought it to me as a grant or paper idea – without any supporting evidence or modeling – I would tell them to stop wasting both our time. Because of the existing data on human genetic variation, the overall state of demographic inference, and my own experience with modeling human bottlenecks, my prior on this hypothesis is too low for it to be worth pursuing.

Thanks for making that abundantly clear for all concerned.

RichardBuggs (Richard Buggs) 2017-12-06 12:55:05 UTC #172

Thanks for your response **@glipsnort** . I will respond as soon as I can. I am teaching a postgraduate module at the moment, and this, together with my PhD students, postdocs and infant son, means I don't have time for this dialogue this week.

@DennisVenema do you plan to respond to my comments on the Zhao et al paper? I see you have posted another blog that does not seem to mention it. Do you no longer see it as supporting your case?

---

cwhenderson (Curtis Henderson) 2017-12-06 13:53:42 UTC #173

> RichardBuggs:
>
> Thanks for your response **@glipsnort** . I will respond as soon as I can. I am teaching a postgraduate module at the moment, and this, together with my PhD students, postdocs and infant son, means I don't have time for this dialogue this week.
>
> **@DennisVenema** do you plan to respond to my comments on the Zhao et al paper? I see you have posted another blog that does not seem to mention it. Do you no longer see it as supporting your case?

Richard, it is clear that you are well-familiar with the fact that life can get very busy. Perhaps you should consider that other people may get busy as well and extend the grace to ask questions in a way that does not border on belligerence.

Jonathan_Burke (Jon) 2017-12-06 15:40:40 UTC #174

Dr Buggs, I realise you're incredibly busy and I do not like to trespass on your time. I'd just like to know if it's convenient or not for you to answer my previously asked question.

> Does your understanding of the data support the idea of an Adam and Eve who had no ancestors at all (neither human nor pre-human), as the universal progenitors of every human who has ever lived, with no humans

> descending from any parallel humans or pre-humans, approximately 6,000 years ago?

If it isn't convenient, then that's fine. I can just let it go.

DennisVenema (Dennis Venema) 2017-12-06 19:36:55 UTC #175

Hi Richard,

Yes, life gets busy. Ditto here.

I'll be honest that I see this discussion as providing ever-diminishing returns. If you want to see your ideas get traction, it's time for you to do some modelling. You also need to deal with the strongest evidence available, not simply pick at what you see as lesser evidence. For example, there **are** regions of the human genome that do have haplotypes that could fit into two people. Those are not the areas you need to deal with (!). The **most variable ones** are the issue.

For that reason it's unclear to me why you want to continue picking at Zhao when there is stronger evidence to deal with, such as the other papers I've pointed you to. For example, the Alu paper, that paper with the haplotype blocks on chromosome 21, and so on. Even if you could shoehorn the data into 4 blocks for Zhao - and even that is not reasonable, as I will discuss briefly below - you just can't shoehorn the variation on chromosome 21 into four blocks.

If you were my colleague approaching me with this as a hypothesis to be tested, I would immediately point you to the challenges - i.e. the haplotype diversity we see across the genome - and tell you that unless you have a reasonable explanation / mechanism for producing that diversity in the timeframe you propose that this is a waste of time. So would any other geneticist.

I'll include a brief discussion of the issues here for the benefit of others, since this sort of thing also applies to any other part of the genome, including those haplotype blocks on chromosome 21.

For Zhao, you have in your second haplotype grouping more variation than reasonably can be attributed to one starting haplotype. For example, three individuals (3, 4 and 5) that share an "A" at the position in column six, and a "C" at the position in column nineteen. That looks like another haplotype to me. At position 15, you have about half in group 2 with either allele (A orT). Again, it would be more reasonable to have these as separate types. Ditto for that same column in your group 3. These are all types that have several people in the data set - these are common types.

If you try to start with four ancestral types and then produce the variant types within each of your groupings, you'll see that you need to invoke too many rare events. For example, in order to produce individuals 3, 4, and 5 in group 2 from one of the other types, here's what would have to happen:

We would need a mutation to an A at position six, followed by drift to make this variant more frequent. Then, one of the variants later would have to mutate to a C at position nineteen, and once again drift would have to occur to make the new variant more common. These two events could be reversed, of course - mutation to C19, drift, and then mutation to 6A, and drift. Once we establish the 6A / C19 variant, we need either (a) a third mutation at 15 to give 15T for some of the 6A / C19 descendants, or (b) a double crossover event in this region to pick up 15T from another type. This would be needed to explain the fifth individual in your group 2. Then, after these events, you would again have to have drift occur to make these new combinations reasonably frequent such that they would be picked up in Zhao's sample size. That's a large number of very rare events, and at least three instances where drift has time to work to take new variants to a reasonable frequency.

You don't have enough time in your model to make this work. Rare events take a long time to appear, and then drift has to act between each rare event, and that takes a long time too. Multiple rare events interspersed with long times for drift = too much time.

It's this sort of thing that would be even more of a problem for the chromosome 21 paper, to say nothing of looking at the scope of haplotype blocks across the entire genome as catalogued by the 1000 genomes database.

It's just not going to squeeze into 4 (or two, which is what it should really be, if Eve was a clone of Adam). If you disagree, feel free to model it and present it for peer review - even the informal peer review that would result from discussing your model here.

RichardBuggs (Richard Buggs) 2017-12-06 21:03:32 UTC #176

I do apologise to anyone who felt hurt by the brevity of my previous post. I had meant to spend longer on it but was interrupted by a PhD student with an urgent request. Once I had spoken to him I had to rush off to lead a class, and decided to sent the post in the minute of my lunch time that I had remaining. Perhaps it was a mistake to send it in such a brief form, but I did want to keep the conversation going. I will respond at greater length to Dennis and Steve soon. It is 9pm my time now, and I have to read three papers for a class tomorrow morning. Apologies.

DennisVenema (Dennis Venema) 2017-12-07 02:06:13 UTC #177

> RichardBuggs:
>
> I do apologise to anyone who felt hurt by the brevity of my previous post.

No worries - I for one did not take it negatively.

Jonathan_Burke (Jon) 2017-12-07 02:20:53 UTC #178

> DennisVenema:
>
> It's just not going to squeeze into 4 (or two, which is what it should really be, if Eve was a clone of Adam).

This may have been raised before, but I'd like to mention the issue of Noah's family, which is another putative bottleneck (down to eight people). I think any case for an Adam and Eve bottleneck of two people should also address whether or not a bottleneck of eight people occurred not too long after.

> RichardBuggs:
>
> I do apologise to anyone who felt hurt by the brevity of my previous post.

I thought it was perfectly reasonable, not a problem at all.

AMWolfe (A.M. Wolfe) 2017-12-07 05:55:07 UTC #179

> Jonathan_Burke:
>
> This may have been raised before, but I'd like to mention the issue of Noah's family, which is another putative bottleneck (down to eight people). I think any case for an Adam and Eve bottleneck of two people should also address whether or not a bottleneck of eight people occurred not too long after.

Well, since someone already did the whole “Since Eve was pulled from Adam’s rib, isn’t it a bottleneck of ONE?” argument, I’ll have fun picking at your “bottleneck of 8”… Wouldn’t it be rather a bottleneck of *five* genetically speaking? It’s Noah & his wife’s genes that were merely recombined in Shem, Ham & Japheth (assuming Noah was monogamous, and the text gives no evidence otherwise), plus three daughters-in-law.

Swamidass (Dr. S Joshua Swamidass) 2017-12-07 07:01:42 UTC #180

FIrst, I want to emphasize the critical importance of taking the questions of the Church seriously. Few have done so, and so that is why there is high value in this conversation.

> AMWolfe:
>
> Well, since someone already did the whole “Since Eve was pulled from Adam’s rib, isn’t it a bottleneck of ONE?” argument, I’ll have fun picking at your “bottleneck of 8”… Wouldn’t it be rather a bottleneck of five genetically speaking? It’s Noah & his wife’s genes that were merely recombined in Shem, Ham & Japheth (assuming Noah was monogamous, and the text gives no evidence otherwise), plus three daughters-in-law.

Though not relevant to this conversation, which is merely about bottlenecks, and not special creation.

Keep in mind that some creationists have proposed that Adam and Eve were genetic mosaics, with different genomes in each of their sperm/eggs. If this is the case, there certainly could have been a bottleneck of two. From a 100% genetic point of view (ignoring archeology), it could have even been a recent bottleneck.

That does not solve the problem of the subsequent 5 genome bottleneck of Noah. And it would also give Adam and Eve a very different sort of biology than us. It would also leave us with an “Appearance of Evolution” problem, because God did not make it clear we did not descend from Apes. It also raises theological problems in inferring incest in the first family. However, it would fit the evidence.

To be clear, however, **@RichardBuggs** been very clear about several things. Also, it appears **@agauger** has taken a similar view.

1. He is not making the case for special creation. So the mosaic solution is off the table, but so is the restriction to one genome by jumping to Eve being a clone of Adam.
2. He is not insisting on a recent bottleneck, and has even been happy to accept a provisional conclusion that "a bottleneck must have been before 500,000 years ago if it happened.”
3. He has granted up front that a single couple bottleneck might not be most likely given the data, but he just wants to know of it is possible; e.g. has it been ruled out, even in the distant past?

This is not to defend his skepticism, but to make sure he is correctly represented. **@RichardBuggs** , as I read him, is asking a reasonable scientific question. I would instead point out that we are actually starting to engage the limits of science. Some of the discussion here seems to circle around trying to prove “what happened without a shadow of doubt.” This is not a reasonable hurdle for human inquiry. Moreover, there are some very subtle and interesting questions about the statistics involved here about rare outliers. However, these details cannot usually be resolved in public debate.

Instead, I emphasizes what **@RichardBuggs** appears to have ***already*** conceded, and what seems to be our common ground. **Regardless of what happened, it really *appears* as if our ancestors never dip down to a single couple.** Whether or not it is ultimately true, the evidence very strongly seems to show that, at least within the last 500,000 years, that our ancestors never dipped down to two.

While some have taken exception to their skepticism and questions, I must disagree. It is the essence of science to ask questions, even of settled answers. **@RichardBuggs** also is not a polemicist, but a practicing scientist who has earned

the right to ask probing questions, even if he is ultimately wrong. I am not skeptical as is he, as I agree with that…

> DennisVenema:
>
> If you want to see your ideas get traction, it's time for you to do some modelling. You also need to deal with the strongest evidence available, not simply pick at what you see as lesser evidence. For example, there are regions of the human genome that do have haplotypes that could fit into two people. Those are not the areas you need to deal with (!). The most variable ones are the issue.

This is the type of inquiry where verbal exchanges have do begin to have limited value. Population genetics in particular is notoriously non-intuitive. Rigorous modeling of the data is the only way forward. Which brings me to what I think is another point of common ground.

While **@RichardBuggs** has an interesting hypothesis, that is not enough.

1. At the moment, the ***only*** mathematical models that fit the full range of data we currently know about are those that show we arise in a population, that never dips down to 2.
2. The ***only*** way to change that is to present a new model, that shows otherwise.
3. Even if a model can be presented that fits the data, it may remain most likely that we arise in a population, not a couple. Consistency with the data is not the same as most likely.

As has been known for a long time, I am a frequent critique of ID. In this case, however, I think **@agauger** and others are taking the right path forward. They are not presuming divine action (directly or indirectly) and they proposing models of their own. They are doing the hard work of building them and plan to test them on data. That is a new and promising development in ID, even though this has nothing to do with recognizing design in nature.

Of course some of us have different beliefs about what the simulations will show. It is my hypothesis that they will end up confirming the consensus. If they do confirm the BioLogos position, and are honest about it, that will do great good for the Church, bringing them into an honest confession of the evidence. If they end up showing a new way forward, that has value on a purely scientific level. I commend them for it. I think the first option (confirming the BioLogos position) is much more likely. They might disagree.

Who cares. Let's see what the data shows. Give them time.

Though I agree, in the meantime…

> DennisVenema:
>
> I'll be honest that I see this discussion as providing ever-diminishing returns.

If Adam and Eve had specially created egg and sperm cells, can we make a bottleneck work?

Chris_Falter (Chris Falter) 2017-12-07 12:56:37 UTC #181

C was actually my first programming language, so I would be happy to see the code whenever you have the time to post it.

Blessings,
Chris

gbrooks9 (George Brooks) 2017-12-07 16:25:24 UTC #182

> Swamidass:
>
> Regardless of what happened, it really appears as if our ancestors never dip down to a single couple. Whether or not it is ultimately true, the evidence very strongly seems to show that, at least within the last 500,000 years, that our ancestors never dipped down to two.

@Swamidass

I'm a little uneasy with how you expressing the target conclusion: "… it really appears as if our ancestors never dip down to a single couple."

Now that you have inserted the "sperm and eggs as a mosaic", we probably should add an additional clause, because all the results discussed so far has actually been **more** than limited to "a couple, yes or no".

The conclusion that **@RichardBuggs** should agree on is not just regarding two (2):

"it appears as if our ancestors never dip down to either a single couple, or even fewer than 1000."

And, further, the good doctor would immediately win support and credibility if he started telling the YEC audience that they have to drop the 6000 year time frame, because none of the evidence supports it.

I'm still waiting for **someone** in the I.D. crowd to step up and start pointing that out… while being a promoter of I.D.

For a while, I thought Dr. Gauger was going to be that person – and what does she do? She writes multiple chapters where she couldn't bring herself to say anything like that… and instead buried her reputation even deeper into the YEC camp.

Jonathan_Burke (Jon) 2017-12-07 16:31:39 UTC #183

> gbrooks9:
>
> The conclusion that **@RichardBuggs** should agree on is not just regarding two (2):
>
> "it appears as if our ancestors never dip down to either a single couple, or even fewer than 1000."
>
> And, further, the good doctor would immediately win support and credibility if he started telling the YEC audience that they have to drop the 6000 year time frame, because none of the evidence supports it.
>
> I'm still waiting for someone in the I.D. crowd to step up and start pointing that out… while being a promoter of I.D.
>
> For a while, I thought Dr. Gauger was going to be that person – and what does she do? She writes multiple chapters where she couldn't bring herself to say anything like that… and instead buried her reputation even deeper into the YEC camp.

As you note, making such a statement would alienate YEC supporters, and there seems to be an unspoken rule that you're not allowed to say anything which might do that.

---

gbrooks9 (George Brooks) 2017-12-07 16:35:55 UTC #184

> Swamidass:

> As has been known for a long time, I am a frequent critique of ID. In this case, however, I think **@agauger** and others are taking the right path forward. They are not presuming divine action (directly or indirectly) and they proposing models of their own. They are doing the hard work of building them and plan to test them on data. That is a new and promising development in ID, even though this has nothing to do with recognizing design in nature.

@Swamidass

They are? Where can I get a summary of their model or models?

What I see is a continued (and baseless) attack on Evolutionary models, with not a wit of or trace of any replacement models.

If you have influence on them in respect to this particular issue, please continue to press them for replacement scenarios… so we can all join in the fun of figuring out what is workable and what is not workable.

Bill_II 2017-12-07 16:52:09 UTC #185

> gbrooks9:
>
> They are? Where can I get a summary of their model or models?

Ann has mentioned here and in the “Everything Wrong With TE” book that work on a model is underway and the results will be available RSN.

From Chapter 16 annotation:

> We argue that a unique origin model, where humanity arose from one single couple, seems to explain data at least as well, if not better. We finally propose an alternative simulation approach that could be used in order to validate such a model.

Bill_II 2017-12-07 16:58:00 UTC #186

> Jonathan_Burke:
>
> As you note, making such a statement would alienate YEC supporters, and there seems to be an unspoken rule that you’re not allowed to say anything which might do that.

Not unspoken. They come right out and say it.

> This book is not about the age of the earth. We are aware that many sincere Christians hold a “young earth” position (the earth is perhaps ten thousand years old), and many others hold an “old earth” position (the earth is 4.5 billion years old). This book does not take a position on that issue, nor do we discuss it at any point in the book.

There is nothing like ignoring the elephant in the room.

Jonathan_Burke (Jon) 2017-12-07 17:02:45 UTC #187

> Bill_II:
>
> There is nothing like ignoring the elephant in the room.

Looks like they actually shot the elephant in the room, then dragged it out of the room, and buried it in the yard behind the house.

---

gbrooks9 (George Brooks) 2017-12-07 17:24:22 UTC #188

> Bill_II:
>
> We argue that a unique origin model, where humanity arose from one single couple, seems to explain data at least as well, if not better. We finally propose an alternative simulation approach that could be used in order to validate such a model.

@Bill_II

Well, they certainly do “argue that”. And the last sentence says they Propose An Alternative Simulation. Yep, I agree. They are proposing it.

This should be amazing if one is ever produced… even a bad one would be amazing at this point !

Argon 2017-12-08 18:14:13 UTC #189

> Swamidass:
>
> Keep in mind that some creationists have proposed that Adam and Eve were genetic mosaics, with different genomes in each of their sperm/eggs. If this is the case, there certainly could have been a bottleneck of two. From a 100% genetic point of view (ignoring archeology), it could have even been a recent bottleneck.

I don’t see the ‘mosaic’ proposal as viable for recent bottlenecks, without also introducing effectively miraculous genetic recombination and segregation events in subsequent generations across various populations. Perhaps if Adam and Eve were hugely polyploid and ‘mosaic’? I also believe that Buggs suggested a mosaic model when he referenced data and suggested that many alleles in one region of the genome could be traced back to four original regions.

In practice, I think that “two human bottleneck” models generally imply a mosaic starting point in which additional variation is added via later mutations. What the current models suggest is that it requires hundreds of thousands of years to reach a point where statistical uncertainty / noise finally overwhelms the ability to distinguish between 2- vs. multi-thousand population bottlenecks.

Swamidass (Dr. S Joshua Swamidass) 2017-12-08 18:18:01 UTC #190

> Argon:
>
> I don’t see the ‘mosaic’ proposal as viable for recent bottlenecks, without also introducing effectively miraculous genetic recombination and segregation events in subsequent generations across various populations. Perhaps if Adam and Eve were hugely polyploid and ‘mosaic’? I also believe that Buggs suggested a mosaic model when he referenced data and suggested that many alleles in one region of the genome could be traced back to four original regions.

That is not what mosaic is. It does not require high recombination or mutation rates or an increased genome size. It just means that Adam and Eve had ***different*** genomes in each of their gamete progenitors. This cannot arise in normal development, but perhaps God created them this way, with a different biology than the rest of us.

> **Mosaic (genetics)**
>
> In genetics, a mosaic, or mosaicism, is the presence of two or more populations of cells with different genotypes in one individual, who has developed from a single fertilized egg. Mosaicism has been reported to be present in as high as 70% of cleavage stage embryos and 90% of blastocyst-stage embryos derived from in vitro fertilization. Genetic mosaicism can result from many different mechanisms including chromosome non-disjunction, anaphase lag and endoreplication. Anaphase lagging is the most ...

Lest there be any doubt, this is **not** my view. I am just explain an proposal put forward by others. Explication is not endorsement.

---

gbrooks9 (George Brooks) 2017-12-08 18:38:17 UTC #191

> Swamidass:
>
> That is not what mosaic is. It does not require high recombination or mutation rates or an increased genome size. It just means that Adam and Eve had different genomes in each of their gamete progenitors. This cannot arise in normal development, but perhaps God created them this way, with a different biology than the rest of us.

@Swamidass

They might as well propose that God miraculously intervened into the population genome, to make people **think** there was no bottleneck!

Argon 2017-12-08 21:28:11 UTC #192

> Swamidass:
>
> That is not what mosaic is. It does not require high recombination or mutation rates or an increased genome size. It just means that Adam and Eve had different genomes in each of their gamete progenitors. This cannot arise in normal development, but perhaps God created them this way, with a different biology than the rest of us.

I thought the mosaic reference was as you referenced in Wikipedia. Thanks to recombination, I think almost every gamete carries a somewhat different ‘genome’ from the fertilized egg that started the parent.

Thanks for the clarification about “Adamic mosaicism” as gamete ‘frontloading’ with individual, unique and extremely diverse genetics . I understand you don’t endorse it. It’s not clear that Adam and Eve had thousands of children (some accounts suggest roughly 50) or that the current diversity reflected in modern day populations are compatible with the notion. I still don’t see how the Adamic mosaic model is a genetically ‘compatible’ view without additional miracles piled on to get around the issue of bottleneck size in a few thousand years.

Swamidass (Dr. S Joshua Swamidass) 2017-12-08 21:34:13 UTC #193

> Argon:
>
> Thanks for the clarification. I understand you don't endorse it. Still, it's not clear that Adam and Eve had thousands of children (some accounts suggest roughly 50) or that the current diversity reflected in modern day populations are compatible with the notion. I don't see how the mosaic model is a genetically 'compatible' view without additional miracles piled further.

Well Eve, I suppose, would have to be a baby making machine. Let's say she lives 900 years (like Adam) and is having a kid every 2 years; perhaps she has 400 kids, each of whom have two distinct genomes. So that would be 800 genomes. We could also wonder if they were in the Garden longer, and perhaps add to their numbers that way.

Fantastical. Yes. That seems implausible to me, stretching into comical. Poor Eve, consigned to be pregnant and nursing her *entire* life.

Argon 2017-12-08 21:48:09 UTC #194

> Swamidass:
>
> Fantastical. Yes. That seems implausible to me, stretching into comical. Poor Eve, consigned to be pregnant and nursing her entire life.

Right? Yet strangely, there are a least a couple major religious organizations that support the notion of frequent childbearing as the desired state. It's one of the reasons why I'm probably related to about half of the people in southern New Jersey.

---

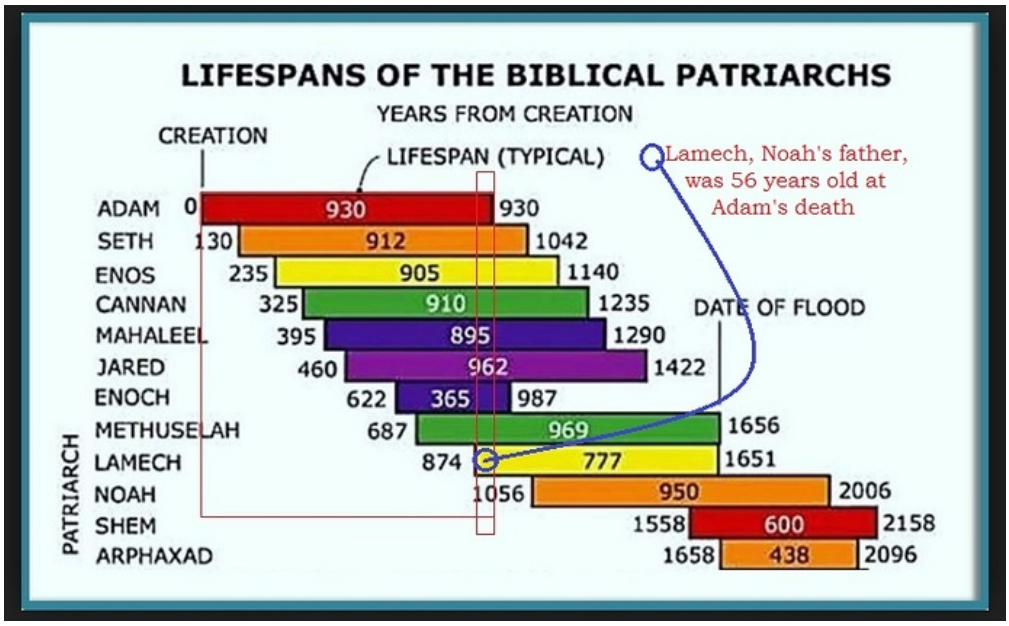
jpm (Phil) 2017-12-08 22:25:55 UTC #195

No matter how long you live, pregnancy is tough on the body. I know several women with large families, and after a dozen pregnancies, you welcome menopause.

---

gbrooks9 (George Brooks) 2017-12-09 00:36:44 UTC #196

I always think it is a little odd, that with such a long life span, and with these key patriarchs, we never hear stories about Adam and Eve in their latter years … or what a rascal their Great Grandchild Cannan was… Heck, Noah's father Lamech was still in his prime of 56 when Adam died at age 930. And we have nothing!



RichardBuggs (Richard Buggs) 2017-12-09 18:24:11 UTC #197

Hi Dennis, [quote="DennisVenema, post:175, topic:37039"]
I'll be honest that I see this discussion as providing ever-diminishing returns. If you want to see your ideas get traction, it's time for you to do some modelling.
[/quote]

I am sorry to hear you say that, as I have invested considerable time in this discussion, and I thought that you were seeing it as valuable peer review of your book. What you call "my ideas" are in fact the hypothesis that you took it upon yourself to raise and refute in chapter three of your book. My point is simply that I think your refutation is mistaken and misleading to your readers. My hope is that you feel sufficient responsibility to your readers to make sure that you can deal with my critiques. Your book chapter places a burden of evidence very heavily upon yourself, especially as you claim such a high level of certainty about your view. I have not written a book telling people what science says about Adam and Eve, but you have. I am simply giving you feedback.

> DennisVenema:
>
> You also need to deal with the strongest evidence available, not simply pick at what you see as lesser evidence. For example, there are regions of the human genome that do have haplotypes that could fit into two people. Those are not the areas you need to deal with (!). The most variable ones are the issue.
>
> For that reason it's unclear to me why you want to continue picking at Zhao when there is stronger evidence to deal with, such as the other papers I've pointed you to.

When you first pointed me to the Zhao et al paper, there was no hint that you saw it as not being strong evidence. Indeed, it seemed one of the most promising papers to back up the claims you made in your chapter, as it was at least close in time to the human genome project. The fact that you are now suggesting it is weak evidence I take as an encouragement that you are at least taking on board the points I have raised about the Zhao et al paper, and agree with some of my critiques of your attempts to use it to support your case. The only reason why I continue to discuss it is that you are continuing to claim that the final part of it supports your case, even though the authors make no hint of this. I am also interested in continuing to discuss it because it is causing us to discuss data (something that you wanted to do!). I have an inkling that perhaps your very high level of certainty in the case you are making is because you may perhaps be misinterpreting the data at quite a fundamental level, and by digging down to primary data I may be able to identify where you are going wrong - if you are. This is why I am keen to complete our discussions of Zhao et al.

> DennisVenema:
>
> If you were my colleague approaching me with this as a hypothesis to be tested.

But I am not. As I say, you have proposed the hypothesis, and have also claimed that it is falsfied with a very high level of certainty. I am just querying your falsification[quote="DennisVenema, post:175, topic:37039"]
you would again have to have drift occur to make these new combinations reasonably frequent such that they would be picked up in Zhao's sample size. That's a large number of very rare events, and at least three instances where drift has time to work to take new variants to a reasonable frequency.

You don't have enough time in your model to make this work. Rare events take a long time to appear, and then drift has to act between each rare event, and that takes a long time too. Multiple rare events interspersed with long times for drift = too much time.
[/quote]
I agree with you that one of my suggested ancestral haploptypes needs three mutations to become reasonably frequent in the population after a bottleneck to explain the data. In fact I said in my initial description of what I had done that I allowed up to three such mutations. [quote="RichardBuggs, post:143, topic:37039"]
each halplotype group contains differences of up to three mutations
[/quote]

So we agree about that. Regarding time, in Zhao et al, the coalescent analysis for this region gave a mean estimate of time to the most recent common ancestor (MRCA) for this region of 1,356,000 years ago; and the 95% confidence interval was between 712,000 and 2,112,000 years ago. This is assuming a constant effective population size of 10,000. To date a bottleneck of two, we do not need to go back to a single MRCA - we need to go back to four haplotypes in two individuals. As you will know, it is the final coalescence events that take longest time in a coalescent analysis - so much of the time to the MRCA can be after (going backwards ie. before in time) the bottleneck. In addition, if we are testing the hypothesis of a bottleneck of two, followed by rapid population expansion, we clearly do not have a constant effective population size of 10,000. The bottleneck will cause coalescence events to occur more rapidly than they would in a constant-sized population. In fact, we would need to use the multiple-merger coalescent to model that coalescence events in the early generations after the bottleneck. All this would reduce the time taken by the coalescence process. As I have said before, I am not putting forward a particular hypothesis about the timing of when a bottleneck could have occurred - I am just querying your assertion that one has never occurred in the human lineage - but it seems to me that a timeframe of low hundreds of thousands of years would be reasonable for this particular region of the genome, and perhaps lower.

If you are happy to agree that the Zhao et al paper does not support the case you are making in chapter 3 of Adam and the Genome, I am very happy to move on from it and discuss the other papers you have cited.

---

gbrooks9 (George Brooks) 2017-12-09 22:50:10 UTC #198

> RichardBuggs:
>
> My point is simply that I think your refutation is mistaken and misleading to your readers.

But which methodology are you using to refute **@DennisVenema** 's refutation?

A. a methdology where you run a plausible set of numbers using plausible assumptions and you get totally different results?

or

B. a methodology where you ask Dennis a hundred questions, and if he ever decides your questions are too farfetched to be entertained, you will portray his lack of response as an indicator that his scenario is flawed?

DennisVenema (Dennis Venema) 2017-12-10 05:02:24 UTC #199

With respect to Zhao, it's part of the evidence that you need to account for, yes - even if there is stronger evidence out there. I'm not sure why you're saying that I think it's weak. It's fine. But there is stronger evidence out there, because there are regions of the genome with more diversity. I still don't think you can shoehorn Zhao's data into 4 haplotypes, but tell me this: in your scenario, are you proposing that the three mutations were recombined together through crossing over, or that they happened sequentially within one lineage without recombination? What mutation rate are you working with? 1.1x10^(-8), or a higher value? If you're using recombination, what recombination rate are you using? How quickly does your proposed population expand after the bottleneck, and what Ne does it reach (and is it stable thereafter)?

Even if I was to grant you Zhao, *arguendo*, just to move the conversation along, how would you handle the haplotype diversity on chromosome 21?

DennisVenema (Dennis Venema) 2017-12-10 07:45:01 UTC #200

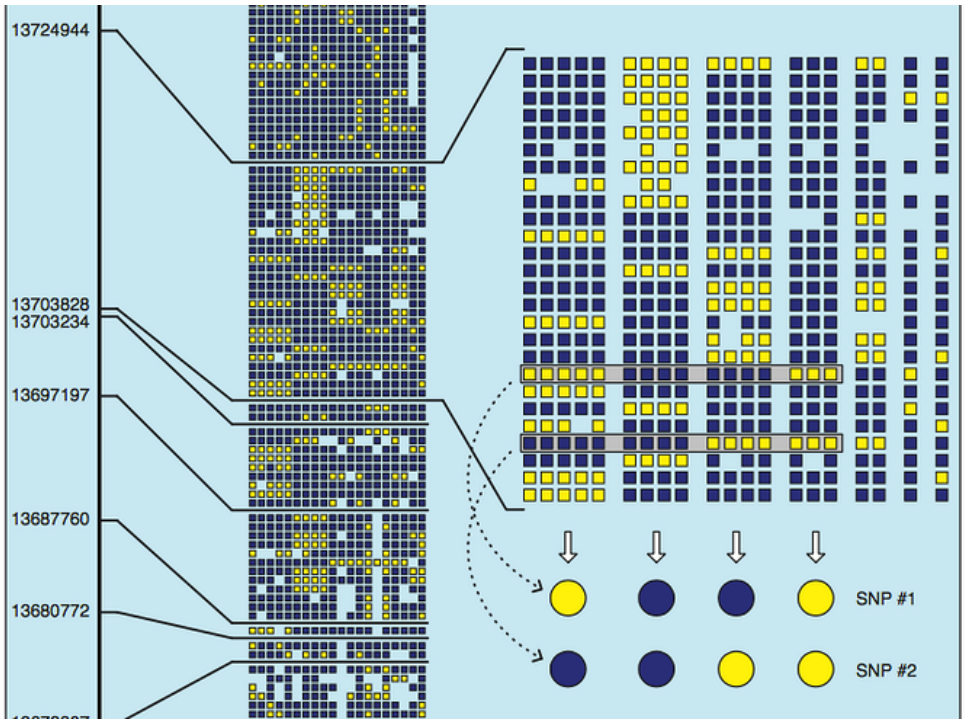
Since I'm (sort of) granting you Zhao (2000), perhaps now is a good time to point out **Zhao (2006)** - which is basically the same approach, by the same team, to a different 10kb genomic region. Here's a summary of the haplotype groups they found (using their numbering for the various types):

```
5     ...G.....G.....................GTG..T.........A.............G..T
11    ...G..........A..............C..GTG..T.........A..C...........G..T
14    ...G.............................GTG..T.........A..C...........G..T
28    ...G.....G......A.................TG..T.........A.............G..T
35    ...G.....G......A.................TG..T.....T...A.............G..T


4     ................................G......G.....................G...
19    ....................T...........G......G.....................G...
21    ....G...............T...A.......G......G.....................G...
27    ....................T...........G......G.....................GT..
33    ....G...............T...........G......G.....................G...
10    ...G......G...........T.........G......G.....................G...


9     ..C.............................G....T.....................A.G...
29    ..C.........................A...G....T.....................A.G...
32    ..C.........G...............A...G....T.....................A.G...
34    ..C.........................A.G.G....T.....................A.G...


20    ...G.....G.....................G.G..T.....................GG...
23    ..CG.....G.....................G.G..T......T..............G..T
26    ...G.....G.....................G.G..T.........A...........G..G..T

17    T..GG....G...C.................G.G.T........G.A.............G..T


24    ...........A....................G....T.........AC.............G.T.
25    ...........A..............G......G......G.......AC.............G...
```

Once you're done with the chromosome 21 paper you can look at this one. Again, there are more than 4 haplotypes to account for.

DennisVenema (Dennis Venema) 2017-12-10 08:09:26 UTC #201

… and just to re-post it so it's easily at hand, **here's the chromosome 21 paper** (PDF). Figure 2 shows the haplotype blocks:



Jonathan_Burke (Jon) 2017-12-10 09:16:35 UTC #202

> RichardBuggs:
>
> My point is simply that I think your refutation is mistaken and misleading to your readers.

Speaking as a reader, I haven't yet seen you provide an evidence based explanation of why it's mistaken and misleading. I've seen a lot of "what if?" and "maybe", and claims that the scientific papers on this issue are all wrong, but I haven't seen you lay out a simple paragraph explanation of your reasons for making this assertion. The longer this continues, the more it looks like Dennis is doing science and you're doing apologetics. It's very frustrating because I thought this discussion was going to be completely the opposite way around.

tallen_1 (Tim) 2017-12-10 14:30:22 UTC #203

Richard,

Since you've put some weight on readers' impressions on this thread, allow me to give mine on how your latest discussion is coming off.

You asked Dennis, and appropriately noted he was obligated, to produce references to back up the claims put forward in his book. He responded to you with a fairly comprehensive list of citations and some commentary on each. I took this to be him laying out the relevant body of literature. Indeed in my own field (not in the life sciences), I'm well accustomed to citing a body of literature where some studies are run better than others or yield stronger or more reliable results than others and fall across a spectrum of moderate to robust support for the scientific claim being advanced. It would seem the Zhao (2000) paper falls more towards the moderate end of the spectrum, whereas the other papers Dennis directed you to fall more to the robust end. And I think Dennis has been indicating as much.

Yet you react to this in a very strange way for a scientist. So much so it makes me question whether you see your role in all this as one of a scientist instead of, say, an apologist. You seem intent on forcing the papers Dennis references into categories of "weak" or "strong." With "weak" apparently matching anything that doesn't pass whatever bar or goal post you're setting for it. And strong apparently matching whatever does (and one would presume such a bar to be

cleared would be truly Herculean in size, if ever even allowing itself to be defined instead of forever ad hoc increasing in height). This forced binary is not scientific. Pushing evidence to extremes to suit one's agenda. It's not the sort of thing a scientist would do. It's the sort of thing apologists do. Quite often in fact.

So I have to tell you Richard, you're starting to force me into concluding you're working as an apologist here rather than a scientist. Perhaps you should either revise your approach (I hope), or rather own up to it.

What is more, some of your actions, whether those of a scientist or apologist, are quite galling. You accuse Dennis of being mistaken and misleading, and pontificate about his burden to back up his claims with evidence, while completely avoiding dealing with the studies he himself claims are the most robust he's put forward thus far. You attempt to critique Steve's simulations with speculations that a certain population substructure and migration & breeding dynamics, etc. may so dramatically alter the numbers to match a bottleneck of 2 on a relevant timeline. Yet when Steve started to address your speculations, whether by running new simulations or referring you to the relevant literature, you continued to insist that the right mix of these factors could get you to your bottleneck of 2. And then put the burden entirely back on Steve, who had already gone above and beyond by any reasonable measure, to then run the simulations as you want them to be run and you even asked him to go through the extensive effort and time to publish them. All the while you have yet to run a single simulation yourself. To test a single model you propose yourself.

I don't know how to tell you this Richard, but there's something very unseemly here. People like Dennis and Steve have been very thorough in their response. And you have not managed to meet their effort. You have studies on your plate you haven't addressed yet. Ones you explicitly demanded be provided to you. And you've sat on them. I suggest before you make a single further demand on Dennis, you read and address these studies. I suggest before you put a single further demand on Steve, you step up and model what you're proposing. I suggest before you say one further word about somebody else's burden, you meet yours.

Jonathan_Burke (Jon) 2017-12-10 14:47:04 UTC #204

> tallen_1:
>
> So I have to tell you Richard, you're starting to force me into concluding you're working as an apologist here rather than a scientist.

So I'm not the only one who thinks this way. Lest this be deemed inappropriate comment, let's remember two facts.

1. The only reason why this "two person bottleneck" question is being raised is theology. Scientists aren't proposing it as an explanation of available data. It is being raised in the context of theology.

2. Dr Buggs has stated explicitly that he considers it theologically useful to see if there is at least a possibility of such a bottleneck, such that it is a matter scientists should investigate (and I agree with that).

I don't object to using science in the service of apologetics, but when we're doing so we should be clear that we're doing so, and not call it something else.

RichardBuggs (Richard Buggs) 2017-12-10 21:57:10 UTC #205

Hi Steve,
Sorry it has taken me a while to respond; my fortnight of teaching has ended now,
I am glad to say and although I now have a backlog with my research group,
I hope I can give this discussion a little more time this week.[quote="glipsnort, post:169, topic:37039"]
Given enough time, a complicated demographic history can produce all kinds of frequency spectra. In this scenario, though, the core problem is recovering diversity in a short time frame; there isn't time for complexity introduced by

multiple rounds of anything.
[/quote]
I agree, and this is the concern with your model that I am pointing to. I am not sure quite what time scale you are alluding to, as in your original models you covered a wide range of time spans. Are you currently referring to a 200,000 year timespan, or a longer one? Also, as we have already discussed, if the founder couple came from a highly variable population themselves, the issue is less about recovering diversity and more about their alleles at 25% and 50% frequencies drifting downwards.[quote="glipsnort, post:169, topic:37039"]
There is no mating system in my model. The model assumes a pool of 2N genomes consisting of unlinked markers. For allele frequencies averaged over the whole genome, such details should not matter.
[/quote]
I am not convinced that such details would not matter. I would think that separate male and female sexes, and the complex breeding patterns that this generates in human populations through monogamy, polygamy, sexual selection etc would be bound to have an effect on allele frequencies.

> glipsnort:
>
> but I haven't seen many studies of chimpanzee diversity (or if I have, I've forgotten them).

I was thinking of **Prado-Martinez et al 2013 Nature**. I mentioned this to Dennis in my original email to him: "The average human has 3.1 million single nucleotide variants (SNVs), but the average chimp has 5.7 million (Prado-Martinez et al 2013 Nature). African humans approximately 1.1 heterozygous SNVs in every 1000bp, whereas central chimpanzees have approximately 1.75 (Prado-Martinez et al 2013 Nature)." If, for the sake of the argument, we assumed that the ancestral couple carried similar levels of diversity to chimpanzees, I imagine that would have an appreciable effect on the model. (Note for readers: please do not mis-read me as suggesting that modern day humans evolved directly from chimpanzees - I am just pointing out that present day great apes have higher levels of genetic diversity than humans (despite much smaller current census population sizes) and that it might not be unreasonable to think that our own ancestors had high levels of genetic diversity).[quote="glipsnort, post:169, topic:37039"]
It would correspond to a spectrum with too many low frequency alleles (relative to a constant-sized population) and some much higher frequency ones, with a relative dearth in between.
[/quote]
But this seems to assume subdivision into just two populations, followed by a merger event. I am suggesting a more complex model which is more likely to reflect the actual population structure: one of multiple sub-populations, multiple migrations – some small, some large – and many mergers and splits. As we have already discussed, this could give smooth allele frequency curve, and the major criticism you have made of this idea is the time available, rather than the ability of complex demographic history to generate "all kinds of frequency spectra".

> glipsnort:
>
> No [to publishing], for several reasons: (1) I don't think this is currently a viable scientific question, (2) doing publication-worthy demographic inference takes a lot of work, and (3) this isn't what I'm being paid to do.

I appreciate that it would be a lot of work, and would distract you from your valuable work on malaria. I respect that. I am also not in a position to give much time to this issue, and have to squeeze it into my evenings and weekends. I am grateful though that you are willing to share your code.

However, I have to admit that although I think that your arguments from allele frequency spectra could potentially make a good test of the Adam and Eve bottleneck hypothesis, I would need to see this worked through in considerably more detail before I was fully persuaded that it was an adequate test. I have been reading a bit more widely about site frequency spectra and the factors that can affect them in a few spare hours. In particular I found these recent papers helpful:

Harpak, A., Bhaskar, A., & Pritchard, J. K. (2016). Mutation Rate Variation is a Primary Determinant of the Distribution of Allele Frequencies in Humans. PLoS genetics, 12(12), e1006489.

Ferretti, L., Ledda, A., Wiehe, T., Achaz, G., & Ramos-Onsins, S. E. (2017). Decomposing the site frequency spectrum: the impact of tree topology on neutrality tests. Genetics, 207(1), 229-240.

Koch, E., & Novembre, J. (2017). A Temporal Perspective on the Interplay of Demography and Selection on Deleterious Variation in Humans. G3: Genes, Genomes, Genetics, 7(3), 1027-1037.

Gao, F., & Keinan, A. (2016). Inference of super-exponential human population growth via efficient computation of the site frequency spectrum for generalized models. Genetics, 202(1), 235-245.

These papers have strengthened my view that a wide range of complex demographic, phylogenetic, selective and mutational processes, together with sampling strategies, can influence site frequency spectra, and that I therefore cannot conclude from the models that you have run that a bottleneck of two in the history of the human lineage is not possible. To be convinced I would need to see more complex models run that try to incorporate these factors. I realise that this is beyond the scope of what you wish to do in the context of the present discussion, but I do hope that in the future others may wish to take up the idea.

> glipsnort:
>
> I'm doing my own simulations because I want to have a better feel for exactly how long effects of a tight bottleneck persist.

OK, that is fair enough. I have to admit, I had thought you were doing them to bolster Dennis's case.

> glipsnort:
>
> No. Similarly, I am not as certain that Bigfoot doesn't exist as I am that the earth revolves (not rotates! – I have to look it up myself to be sure) around the sun. That doesn't mean I think the existence of Bigfoot is an open scientific question worth pursuing.

OK, well it's good to know that you don't quite have the level of confidence against an ancestral bottleneck as Dennis. What about the existence of Littlefoot? 😉

> glipsnort:
>
> I don't find any of them convincing since I haven't read the book – which is one reason I've never commented on Dennis's arguments. I think a recent bottleneck of size two is a nonstarter as a hypothesis. If a colleague brought it to me as a grant or paper idea – without any supporting evidence or modeling – I would tell them to stop wasting both our time. Because of the existing data on human genetic variation, the overall state of demographic inference, and my own experience with modeling human bottlenecks, my prior on this hypothesis is too low for it to be worth pursuing. Detailed perusal of the existing studies on the subject is kind of beside the point for me.

Thank you, this is a very helpful explanation of where you are coming from on this question and in this discussion. I hope that Dennis might perhaps send you a copy of his book, given the time you have invested in this discussion. I think that if you had read chapter three of Dennis' book, and then read my **blog on it** you might have more sympathy with my critique of Dennis' case, even if you agree with his final conclusions. I think you might feel as I did when I was flying to Tenerife from London a few months ago, and across the aisle a man said to his family "You can tell we are getting south, as the cabin is getting warmer". I considered the man to be entirely correct in his conclusion about the location of the plane, but knew that the evidence he had given for it was based on a very partial understanding of

physics, climate and aeronautical engineering. If I had had the time, I might have tried to explain to him that whilst I agreed with his conclusion, the reason he had given his children for it was not going to help their science education.

If you read Dennis' chapter, it would remind you that it is this chapter - and not my blog - that raises the hypothesis of a bottleneck of two, and treats it as a hypothesis that has been raised, tested and disproven with a very high level of certainty.

> glipsnort:
>
> Because of the existing data on human genetic variation, the overall state of demographic inference, and my own experience with modeling human bottlenecks, my prior on this hypothesis is too low for it to be worth pursuing.

I respect your view on this as you have a long track record in the analysis of human genetic variation. However, I know that you would not want me as a scientist to resolve this issue with a simple statement from authority. Until I can see the evidence and appropriate analyses clearly laid out in detail and clearly refuting the hypothesis, I can't see it as decisively disproven.

Given that you do not seem to want to pursue this further due to time constraints, could I finally just ask you these questions (and these can be my final questions to you if you wish): Which published analyses in the literature do you see as most convincingly disproving a bottleneck hypothesis? Do you consider that analyses of the coalescence of different haplotype blocks within the human population could yield decisive tests of the bottleneck hypothesis?

Once again, I would like to say how much I have appreciated your contributions to this discussion. It has certainly moved my understanding of this area forward, and I now have clearer ideas about how the bottleneck of two hypothesis could be tested, which I am very glad about. I am sorry that this has not been as decisive as we might have hoped, but I certainly have learned a great deal. I hope in the future we will see some conclusive testing that can put this issue to rest.

---

gbrooks9 (George Brooks) 2017-12-11 04:46:19 UTC #206

> RichardBuggs:
>
> As I have said before, I am not putting forward a particular hypothesis about the timing of when a bottleneck could have occurred -
>
> I am just querying your assertion that one has never occurred in the human lineage -
>
> but it seems to me that a timeframe of **low hundreds of thousands of years** would be reasonable for this particular region of the genome…

@RichardBuggs

I wonder if we would all concede virtually all your points if you simply declared that even you agree it would take more than 100,000 years in reference to this part of the genome?

T_aquaticus 2017-12-11 20:42:36 UTC #207

> RichardBuggs:
>
> My hope is that you feel sufficient responsibility to your readers to make sure that you can deal with my critiques.

I think the burden is on you to support your criticisms with good science, which I don't think you have done. There is no reason why any author needs to deal with criticisms that lack scientific backing.

Overall, Venema's comparison of a 2 person bottleneck and Geocentrism is dead on. Both have been equally invalidated by evidence in every scientific sense.[quote="RichardBuggs, post:197, topic:37039"]
Your book chapter places a burden of evidence very heavily upon yourself, especially as you claim such a high level of certainty about your view.
[/quote]

That burden has been met. Venema has given at least 3 independent lines of evidence that all support a large historic population for humans over the last 200,000, at a minimum.[quote="RichardBuggs, post:197, topic:37039"]
I have an inkling that perhaps your very high level of certainty in the case you are making is because you may perhaps be misinterpreting the data at quite a fundamental level, and by digging down to primary data I may be able to identify where you are going wrong - if you are.
[/quote]

What you are insinuating is that the entire scientific community is misinterpreting the data, and you have yet to bring anything forward which brings those interpretations into question.

RichardBuggs (Richard Buggs) 2017-12-11 20:59:40 UTC #208

Hi Dennis,

Thanks for being willing to grant me Zhao et al (2000) for the sake of the argument, and for pointing me to other data sets that you think might be harder to explain from a bottleneck of two. However, I would prefer not to be granted Zhao et al (2000) on those terms - I would prefer us to come to a full agreement. I need to know that you are willing to admit that you have been wrong before it is worth us progressing on to other data sets or other papers. If you are not willing to admit you have been wrong, even when there is clear evidence against you, then our discussion is unlikely to make much progress.

I have shown why the two aspects of the Zhao et al (2000) paper that you originally highlighted are not apropos our discussion – and I think that you have accepted my argument on these. More recently, I have sketched out why I think that the Zhao et al (2000) data is explainable from a bottleneck of two within the last few hundred thousand years, taking their own coalescence analysis as a starting point. As you will see from the paper, they used a mutation rate of 1.15x10^(-9). This is an order of magnitude slower than the mutation rate that you have suggested.

I think that what you are ultimately asking me to do in your recent posts is a full coalescence analysis going back to four haplotypes, with a population expansion. I think you are asking me to conduct these on the Zhao et al (2000) data, the Zhao et al (2006) data, and the whole of chromosome 21. I agree with you that this would be interesting to do, and would be a good test for the bottleneck of two hypothesis. Indeed, it would be nice to do this for haplotype blocks over the whole of the human genome, using phased genome sequences for thousands of individuals.

This would be a substantial amount of work, especially as I do not know of an off-the-shelf package that explicitly models coalescence back to two diploid individuals, and includes exponential (or even super-exponential) population growth, with multiple-merger coalescence events allowed. If we could come to an agreement that this would be a good test of the hypothesis (and I would value the view of **@glipsnort** on this) then we would have made some useful progress in this discussion.

I would just point out the elephant in the room, however: this is that every time you suggest to me a dataset to analyse to test the bottleneck of two hypothesis you are implicitly illustrating the major point of my **blog**: that this hypothesis still needs testing and has not been explicitly and reliably tested in an already-published analysis.

In my view the most constructive way ahead would be for you to admit that your chapter expresses far to high a degree of certainty on this matter, and cites a great deal of evidence that is actually not testing the hypothesis. Then we could all collaborate on some analyses that really do explicitly test the hypothesis (which would not be a small amount of work) and really start to come up with some answers. I would be happy to contribute to such a collaboration, in the limited time I have available, and would do so with an open mind as to what the outcome would be.

T_aquaticus 2017-12-11 21:21:48 UTC #209

> RichardBuggs:
>
> If you are not willing to admit you have been wrong, even when there is clear evidence against you, then our discussion is unlikely to make much progress.

Projection is a psychological disorder, not a scientific argument.[quote="RichardBuggs, post:208, topic:37039"]
More recently, I have sketched out why I think that the Zhao et al (2000) data is explainable from a bottleneck of two within the last few hundred thousand years, taking their own coalescence analysis as a starting point.
[/quote]

You need to explain how ALL of the data fits a bottleneck of two, and that includes the entire genome, not just a tiny snippet of it. Remember, there are MULTIPLE and INDEPENDENT lines of evidence. Focusing on just one makes it appear as if you are ignoring the evidence.[quote="RichardBuggs, post:208, topic:37039"]
This would be a substantial amount of work, especially as I do not know of an off-the-shelf package that explicitly models coalescence back to two diploid individuals, and includes exponential (or even super-exponential) population growth, with multiple-merger coalescence events allowed. If we could come to an agreement that this would be a good test of the hypothesis (and I would value the view of **@glipsnort** on this) then we would have made some useful progress in this discussion.
[/quote]

If there really were a bottleneck of two then the data would have reflected that. The methods used in these papers are up to the task, so I don't know why you feel like you need to ignore them. Even estimates of a 100 person bottleneck would lend some credence to your arguments, but that isn't what we see. Instead, the data clearly points to a population that is 4 orders of magnitude larger than the one you are proposing. FOUR ORDERS OF MAGNITUDE.

At what point do you admit you are wrong?[quote="RichardBuggs, post:208, topic:37039"]
I would just point out the elephant in the room, however: this is that every time you suggest to me a dataset to analyse to test the bottleneck of two hypothesis you are implicitly illustrating the major point of my blog: that this hypothesis still needs testing and has not been explicitly and reliably tested in an already-published analysis.
[/quote]

It has been tested.[quote="RichardBuggs, post:208, topic:37039"]
In my view the most constructive way ahead would be for you to admit that your chapter expresses far to high a degree of certainty on this matter, and cites a great deal of evidence that is actually not testing the hypothesis.
[/quote]

The problem is that your views are not supported by scientific evidence, so why should they be taken seriously?

---

gbrooks9 (George Brooks) 2017-12-11 22:11:06 UTC #210

> RichardBuggs:

> I would just point out the elephant in the room, however: this is that every time you suggest to me a dataset to analyse to test the bottleneck of two hypothesis you are implicitly illustrating the major point of my blog: that this hypothesis still needs testing and has not been explicitly and reliably tested in an already-published analysis.

@RichardBuggs

1] All science is subject to testing and re-testing. Your insinuation that Dr. Venema's is especially subject to such testing is not what I would call politie discourse!

2] How do you draw such a conclusion purely on **@DennisVenema** 's willingness to suggest a dataset for **you** to see for yourself? It's exactly what any scientist would do when challenged by someone who appears to be without the fundamental skills to do the analysis himself.

3] If he hadn't suggested datasets, you would say he was tilting at windmills… and that he is conducting his work all by himself with nobody performing comparative work.

4] I certainly can't speak for **@DennisVenema** in terms of confessing - - to your satisfaction !!! - - that his conclusion or conclusions are somehow in error. But how is it that if you are not in a position to conduct these studies yourself that you presume to pressure anyone into admitting error?

Do you engage in this assault on any evolutionist, knowing that if there is ultimately nothing to your assertions, all you have to do is shrug your shoulders and say: "No harm no foul"?

Frankly, I have never seen this kind of approach before. Usually when someone wants to smudge-up someone's reputation, they do the work necessary to prove that his results are in error. Surely you owe Dr. Venema that much of your effort - - instead of "phoning in" accusations that you could make against anyone - - even if purely on the theoretical possibility that someone may have used incorrect grammar in his conclusions.

DennisVenema (Dennis Venema) 2017-12-11 22:13:22 UTC #211

> RichardBuggs:
>
> In my view the most constructive way ahead would be for you to admit that your chapter expresses far to high a degree of certainty on this matter, and cites a great deal of evidence that is actually not testing the hypothesis.

Hi Richard,

I respectfully disagree. The hypothesis has been tested - it's even explicitly stated as such in some of the papers I've provided to you, and that you have not (as of yet) dealt with.

Pointing out other data relevant to the question and asking how this fits with a 2-person bottleneck is not some sort of admission that the hypothesis has not been tested. It's an attempt to get you to see the difficulties.

I remain confident that my conclusion in the book is sound. I have not seen anything in this discussion that remotely suggests otherwise. There simply is no evidence to support the hypothesis of a bottleneck to 2. There are converging lines of evidence that our species has not dipped below several thousand individuals.

I think this exchange has been a good illustration to non-specialists just how far one has to go to try shoehorn the evidence into a 2-person bottleneck.

In part 3 of my reply to you, I'll discuss why PSMC modelling could indeed detect a bottleneck to two, even if followed by rapid expansion. Then, Lord willing, we'll move on to the Tenesa paper on LD. Perhaps you'll have some additional

comments then.

Best,

Dennis

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tallen_1 (Tim) 2017-12-11 22:16:23 UTC #212

Richard,

> RichardBuggs:
>
> However, I would prefer not to be granted Zhao et al (2000) on those terms - I would prefer us to come to a full agreement. I need to know that you are willing to admit that you have been wrong before it is worth us progressing on to other data sets or other papers. If you are not willing to admit you have been wrong, even when there is clear evidence against you, then our discussion is unlikely to make much progress.

If mandating full agreement between each step of a conversation were necessary between persons of an evolutionary and ID/creationist perspective, discussions would simply not happen. The fact that you are insisting Dennis move from his characterization of the Zhao (2000) paper as moderately but not robustly supportive of his claims to instead weak and not at all supportive of his claims, while holding hostage your even looking at and engaging what he put forward as his strongest backing in the literature till then, is extremely disrespectful of Dennis' time and effort honoring your requests to produce such citations and frankly unbecoming of someone of your position. Either deal with Dennis' strongest evidence or don't. But if you choose the latter after all your repeated demands and chastisements for him to produce it, I suspect you will not be leaving with the respect of most readers here.

---

gbrooks9 (George Brooks) 2017-12-11 22:20:19 UTC #213

> RichardBuggs:
>
> I have sketched out why I think that the Zhao et al (2000) data is explainable from a bottleneck of two within the last few hundred thousand years, taking their own coalescence analysis as a starting point.

How does a bottleneck of two in a 200,000 time frame change the impossibility of a bottleneck of two in a 6000 year time frame? This is like the climate denialists who think if they can show climate models are wrong by 10 degrees, then we might as well throw out all the research on global warming !

> T_aquaticus:
>
> If there really were a bottleneck of two then the data would have reflected that. The methods used in these papers are up to the task, so I don't know why you feel like you need to ignore them. Even estimates of a 100 person bottleneck would lend some credence to your arguments, but that isn't what we see. Instead, the data clearly points to a population that is 4 orders of magnitude larger than the one you are proposing. FOUR ORDERS OF MAGNITUDE.
>
> At what point do you admit you are wrong?

Now **that** is a good question. Exactly when does the good Prof. Buggs admit his error?

Jonathan_Burke (Jon) 2017-12-12 00:46:45 UTC #214

> RichardBuggs:
>
> I would just point out the elephant in the room, however: this is that every time you suggest to me a dataset to analyse to test the bottleneck of two hypothesis you are implicitly illustrating the major point of my blog: that this hypothesis still needs testing and has not been explicitly and reliably tested in an already-published analysis.

No he isn't. He has already pointed out that this hypothesis has already been sufficiently tested more than once. As he has told you explicitly, the reason why he has suggested that you analyze the data yourself, is that you keep insisting that the scientific work done thus far has not tested the hypothesis sufficiently, and it seems the only course of action which will persuade you otherwise is to actually use the data and replicate the tests which others have already carried out.

---

cwhenderson (Curtis Henderson) 2017-12-12 04:04:49 UTC #215

> RichardBuggs:
>
> I would just point out the elephant in the room, however: this is that every time you suggest to me a dataset to analyse to test the bottleneck of two hypothesis you are implicitly illustrating the major point of my blog: that this hypothesis still needs testing and has not been explicitly and reliably tested in an already-published analysis.

It sounds as though you are waiting on a peer-reviewed paper before you decide what the data and statistics can truly show us. But from what Steve is saying, it seems a publication in this area is not likely forthcoming, since it would be insufficiently report-worthy. However, it has been demonstrated rather convincingly here and elsewhere that a bottleneck of 2 at a time of 6 kya is highly improbable. The mathematics is pretty clear about this, but of course, it cannot rule out a miracle of God. At this point, this is most tenable defense of the 2-person bottleneck.

I agree that it may be overstatement to conclude that the degree of confidence we have in this is on par with the degree of confidence we have in a sun-centered solar system. But pointing out that this data has not been through peer review and publication and calling it the "elephant in the room" ignores the elephant sitting in your lap whispering into your ear regarding the extreme improbability of a bottleneck of two at a period 6,000 years ago.

DennisVenema (Dennis Venema) 2017-12-12 04:22:20 UTC #216

> cwhenderson:
>
> But pointing out that this data has not been through peer review and publication and calling it the "elephant in the room" ignores the elephant sitting in your lap whispering into your ear regarding the extreme improbability of a bottleneck of two at a period 6,000 years ago.

To be fair to **@RichardBuggs** don't forget that from the get-go he's been open to the idea of a bottleneck much further back than 6KYA.

---

tallen_1 (Tim) 2017-12-12 04:30:38 UTC #217

Yes, but he hasn't said how far back. I'd be curious to know how far back he feels the data excludes a bottleneck of two. And how far back a bottleneck of two may mean something to him.

---

gbrooks9 (George Brooks) 2017-12-12 05:13:52 UTC #218

> cwhenderson:
>
> But pointing out that this data has not been through peer review and publication and calling it the “elephant in the room” ignores the elephant sitting in your lap whispering into your ear regarding the extreme improbability of a bottleneck of two at a period 6,000 years ago.

@cwhenderson ,

And the Elephant sitting on @RichardBuggs ’ lap is wearing a dress! There’s no way to miss it !

---

gbrooks9 (George Brooks) 2017-12-12 05:16:24 UTC #219

> tallen_1:
>
> Yes, but he hasn’t said how far back. I’d be curious to know how far back he feels the data excludes a bottleneck of two. And how far back a bottleneck of two may mean something to him.

@tallen_1 (and **@DennisVenema**):

Sure he has… he wrote it here :

> RichardBuggs:
>
> I have sketched out why I think that the Zhao et al (2000) data is explainable from a bottleneck of two within the last few hundred thousand years, taking their own coalescence analysis as a starting point.

He is willing to go back 200,000 years… but I somehow doubt he’d be willing to write an article that says that …

---

tallen_1 (Tim) 2017-12-12 11:45:42 UTC #220

Thanks. But his earlier statement to which he refers said low hundreds of thousands of years or lower. I’d like to know what Richard considers the lower bound of what the data can reasonably exclude. The reason I ask this is if Richard is willing to concede we can effectively rule out even by his standards a founding pair within the range of when humans became behaviorally modern, then the relevance of any purported “Adam & Eve” from that time would seem called into question. Or conversely, on the upper bound, if Richard would feel he’d garner a “win” by arguing the plausibility of a founding pair say 300,000 years ago, what theological meaning would this have to him for a species that was not just pre-behaviorally modern but not even anatomically modern as well? I’d like him to clearly state his claims here.

---

cwhenderson (Curtis Henderson) 2017-12-12 11:57:35 UTC #221

Thanks for the reminder, Dennis. You have my apologies, **@RichardBuggs** . I should have been more careful.

Jonathan_Burke (Jon) 2017-12-12 13:03:05 UTC #222

> tallen_1:

> But his earlier statement to which he refers said low hundreds of thousands of years or lower. I'd like to know what Richard considers the lower bound of what the data can reasonably exclude.

Yes, and that's why I asked (several times), if he believes the evidence rules out a traditional Adam and Eve pair 6,000 years ago. He has chosen not to answer that, and I am reading that as an apologetic strategy to stay on the side of the YECs and IDers.

---

tallen_1 (Tim) 2017-12-12 13:29:25 UTC #223

I agree. There's something very strange about a man brow-beating others to answer every one of his litany of inquiries while refusing to answer legitimate questions himself.

DennisVenema (Dennis Venema) 2017-12-12 14:21:42 UTC #224

Well, as Jon has noted, he has not answered Jon's repeated question about excluding a pair at 6KYA, so it does lead one to wonder why.

Jonathan_Burke (Jon) 2017-12-12 14:42:33 UTC #225

I don't think he's brow-beating, I think he's asking legitimate questions. But I think he's ignoring a number of the answers, and the fact that he is choosing not to answer certain specific questions is increasingly looking like an apologetic strategy. We have to remember, his entire line of questioning has not been prompted by anything scientific; no scientists have raised this as a legitimate scientific question. The rationale for this line of questioning is entirely theological.

---

tallen_1 (Tim) 2017-12-12 14:52:13 UTC #226

I think he's asking legitimate questions as well. But the brow-beating comes in when he doesn't get the answers he wants in the way he wants them. Look at the latest on his discussion on the Zhao et al. (2000) paper. Dennis has wanted to move on to the stronger studies he provided for some time now, yet Richard continues to press him to admit to something Dennis by all appearances truly has not been convinced of. Until Richard gets not just an answer, but specifically the answer he wants, he's holding the rest of Dennis' more robust papers hostage and not allowing the conversation to progress. In my view, this is brow-beating. Yet notice no one is doing this back to him in kind. He's repeatedly refused to answer questions that don't suit his agenda yet we continue the dialogue. There is a basic issue of fair play here, and I think Richard is not holding up his end.

---

gbrooks9 (George Brooks) 2017-12-12 16:04:26 UTC #227

> tallen_1:
>
> Thanks. But his earlier statement to which he refers said low hundreds of thousands of years or lower. I'd like to know what Richard considers the lower bound of what the data can reasonably exclude.

@tallen_1

I doubt if he has anything substantive on the lower range … that's the way an Apologist frames a sentence so he can later say he "intimated at a time frame even lower than 200,000" … which leaves him plenty of dancing room.

I don't think any of you are going to get anything substantive from Dr. Buggs - - because he won't even publish a blog posting on any of his agreements here that contradict the YEC party line.

He and **@agauger** could be a force for "unity" between the ID and BioLogos camps … but it doesn't look like that is his or her plan!

Despite what any of us write, the only person he will actually direct his thread postings to is **@DennisVenema** - - because he is the "target" to bring down.

Chris_Falter (Chris Falter) 2017-12-12 19:03:33 UTC #228

> RichardBuggs:
>
> I therefore cannot conclude from the models that you have run that a bottleneck of two in the history of the human lineage is not possible. To be convinced I would need to see more complex models run that try to incorporate these factors. I realise that this is beyond the scope of what you wish to do in the context of the present discussion, but I do hope that in the future ***others*** may wish to take up the idea. [emphasis mine]

I pray, Dr. Buggs, you may enjoy this season of the true light entering the world, and the peace the angel promised on earth.

But I have to ask: Why others? Why not you, Dr. Buggs? I understand you don't have the time this weekend, but maybe during the summer?

Best,
Chris Falter

RichardBuggs (Richard Buggs) 2017-12-13 20:46:24 UTC #229

Hi Dennis,

I would very much appreciate it if you would engage with my comments about the coalescence analysis at the end of the Zhao et al (2000) paper, and let me know if you accept my points, and if not, why not? As I have said, I think it is critical that we conclude our discussion of this paper, given that you still seem to hold that it is a citation that you can use to support your case. If you will admit that is not in fact a suitable citation, then I am happy to move on and look at the other citations you have made in this discussion. You were keen for us to discuss data, and now that we are, it would be a pity for you to walk away from our discussion.

> DennisVenema:
>
> Pointing out other data relevant to the question and asking how this fits with a 2-person bottleneck is not some sort of admission that the hypothesis has not been tested. It's an attempt to get you to see the difficulties.

I think I have demonstrated that the Zhao et al (2000) data do not pose me any difficulties. Would you not agree?

> DennisVenema:
>
> There are converging lines of evidence that our species has not dipped below several thousand individuals.

But don't forget I have queried every one of your "converging lines of evidence" in my blog, and you are yet to respond adequately to any of my critiques.

> DennisVenema:
>
> I think this exchange has been a good illustration to non-specialists just how far one has to go to try shoehorn the evidence into a 2-person bottleneck.

Please could you illustrate this claim? Perhaps this appears to be shoehorning to a non-specialist:
[quote="RichardBuggs, post:197, topic:37039"]
Regarding time, in Zhao et al, the coalescent analysis for this region gave a mean estimate of time to the most recent common ancestor (MRCA) for this region of 1,356,000 years ago; and the 95% confidence interval was between 712,000 and 2,112,000 years ago. This is assuming a constant effective population size of 10,000. To date a bottleneck of two, we do not need to go back to a single MRCA - we need to go back to four haplotypes in two individuals. As you will know, it is the final coalescence events that take longest time in a coalescent analysis - so much of the time to the MRCA can be after (going backwards ie. before in time) the bottleneck. In addition, if we are testing the hypothesis of a bottleneck of two, followed by rapid population expansion, we clearly do not have a constant effective population size of 10,000. The bottleneck will cause coalescence events to occur more rapidly than they would in a constant-sized population. In fact, we would need to use the multiple-merger coalescent to model that coalescence events in the early generations after the bottleneck. All this would reduce the time taken by the coalescence process. As I have said before, I am not putting forward a particular hypothesis about the timing of when a bottleneck could have occurred - I am just querying your assertion that one has never occurred in the human lineage - but it seems to me that a timeframe of low hundreds of thousands of years would be reasonable for this particular region of the genome, and perhaps lower.
[/quote]
If you think that is "shoehorning" let me assure you that I am simply referring to well known features of coalescent analysis. You can find them summarised quite nicely in Figure 15.8 of Barton et al's textbook "Evolution" published by CSHL. These are just the basic features of a coalescence analysis involving a bottleneck and rapid expansion.

---

glipsnort (Steve Schaffner) 2017-12-13 21:09:14 UTC #230

> glipsnort:
>
> That's a good idea, but will require a little work, to explain the model and the options. I'll try to get to it soonish. (If I haven't done it in a week, I've probably forgotten and should be reminded.) My simulation code is actually in C; only the normalization and plotting is done in R.

I have slapped together a description of the code and put it on github:

> **glipsnort/bottleneck**
>
> A forward genetic simulator for playing around with demographic bottlenecks

I haven't really proofread the description, so caveat emptor.

DennisVenema (Dennis Venema) 2017-12-13 22:02:35 UTC #231

> RichardBuggs:

> The bottleneck will cause coalescence events to occur more rapidly than they would in a constant-sized population. In fact, we would need to use the multiple-merger coalescent to model that coalescence events in the early generations after the bottleneck. All this would reduce the time taken by the coalescence process. As I have said before, I am not putting forward a particular hypothesis about the timing of when a bottleneck could have occurred - I am just querying your assertion that one has never occurred in the human lineage - but it seems to me that a timeframe of low hundreds of thousands of years would be reasonable for this particular region of the genome, and perhaps lower.

I'm still not seeing how you can fit everything you need into the timeframe you've allowed yourself. If there is a bottleneck to 2, every haplotype in the Zhao (2000) data set has to come from your four ancestral haplotypes. Why did you decide that three mutations was an acceptable deviation from those types? How do you have time for three mutations, each interspersed with drift? Why did some of the intermediates (presumably) drift to an intermediate frequency and then drift down to zero (since we don't see some of the intermediates)? How do you have time for all of this to plausibly happen? Don't forget that if you lower Ne to get a faster coalescence time, you also lower the number of forward mutation events that are plausible.

---

gbrooks9 (George Brooks) 2017-12-13 22:04:38 UTC #232

> RichardBuggs:
>
> Please could you illustrate this claim? Perhaps this appears to be shoehorning to a non-specialist:

@RichardBuggs :

Since I know you aren't going to respond to my post, let me just tell you what I see as "shoehorning":

1. Reverse engineering the numbers from current diversity to the diversity of 1 mating pair,
2. according to some very specific sequence of mutations, drift and rates of change,
3. that would require, at a bare minimum, 200,000 years,
4. and concluding that you have materially changed the parameters of **@DennisVenema** 's analysis.

What you are doing is showing what cherry-picked changes are necessary, at the least, to materially change the conclusions of Dennis' work, without actually making a 6000 year time frame any more possible.

It would seem that you seek the "spoiler" roll, doing whatever you can to throw dust into the air and make **@DennisVenema** somehow less credible. . . while expending none of your own credibility yourself.

I'm not so sure you are being fair to Dennis or to your audience.

---

tallen_1 (Tim) 2017-12-14 04:26:51 UTC #233

Dennis,

Since Richard's made such an effort to hold your feet to the fire over the Zhao et al (2000) paper, I've done my best to try to understand what's being discussed there. I'm hoping you can tell me if I'm on the right track or fill in the gaps.

As far as I can tell, here are the relevant conclusions of the authors discussed on this thread, and how they've arrived there:

1. The conclusion that there was no severe bottleneck during the evolution of non-African humans is surmised off a straight measure of nucleotide diversity (π) equaling 0.082%. Not any coalescent analysis.

2. The conclusion that long-term effective population sizes fell around 10,000 rely upon Watterson's & Tajima's calculations of θ (which are based on coalescent methods), in conjunction with the derived estimated mutation rates. Yet neither of these calculations seem to utilize TMRCA values in any way. Though both are derived through coalescent methods.

3. The TMRCA values provided and the accompanying analysis does not give any explicit descriptions pertaining to bottlenecks or effective populations sizes. Though in your 2nd installation of your response you mention that TMRCA values can be utilized to discern potential bottlenecks. It just looks like the authors didn't leverage that approach in this particular paper.

Also, I'd picked up (if I understand this right) that long-term effective population sizes are harmonic means of a range of idealized population sizes across a period of time, which means that acute minimum population sizes could in theory exist substantially lower than these estimates.

So it looks like if one's to rely on these authors' conclusions, you cannot say that TMRCA values, nor any coalescent methods, were used by them to discern or reject potential bottlenecks. Only that the values for genetic diversity accomplished that. Which may be weaker? And that reasonable coalescent methods were used to estimate long-term effective population sizes, but that as is doesn't map on to exactly Richard's argument unless you do some further work in the way of analysis off the raw data or perhaps further extrapolation off whatever theory or knowledge of how the mechanics of all this works out, such as someone such as yourself might possess?

And now where things sit, you're both analyzing the raw sequence data and coming to differing conclusions off that. Yet thus far neither of you have performed a rigorous analysis?

Anyway, that's what I've been able to gather so far. And maybe goes to some of the confusion or frustration surrounding this paper on this thread. Can you let me know if I'm on track here or clear some things up for me if I'm not? Thanks Dennis!

DennisVenema (Dennis Venema) 2017-12-14 07:55:28 UTC #234

> tallen_1:
>
> Since Richard's made such an effort to hold your feet to the fire over the Zhao et al (2000) paper, I've done my best to try to understand what's being discussed there. I'm hoping you can tell me if I'm on the right track or fill in the gaps.
>
> As far as I can tell, here are the relevant conclusions of the authors discussed on this thread, and how they've arrived there:
>
> 1. The conclusion that there was no severe bottleneck during the evolution of non-African humans is surmised off a straight measure of nucleotide diversity (π) equaling 0.082%. Not any coalescent analysis.

Correct. Note that the measure for African sequences would also preclude a severe bottleneck. In general, I'm trying to figure out from Richard is why he disagrees with this conclusion. This has sent us into the weeds of the data, as it were - but we've mostly been discussing if the haplotypes we see in the data set could be reasonably fit into four ancestral haplotypes within human history. One of the things that's relevant here is what the population size is after the proposed bottleneck to 2 (as well as the mutation frequency). If, as I understand it, Richard wants an exponential population increase after the bottleneck to minimize loss of heterozygosity, then presumably the population would bounce back up to Ne ~ 10,000 in short order - but I'm not sure what Richard is thinking. I'm also not sure if he wants to use 1.1x10-8 or

the lower mutation rate in the paper itself that is estimated based on comparisons to chimpanzees and orang-utans. This actually depends on these species sharing common ancestral populations. It's an issue we haven't yet broached, but I don't know for sure that **@RichardBuggs** accepts common ancestry for humans and other species. Richard was widely quoted some years ago for claiming that the human-chimpanzee genome identity would eventually be recognized as far lower than the accepted value. I suspect - and this is an inference, so **@RichardBuggs** can correct me if I'm off base - that this claim was intended to cast doubt on common ancestry. Perhaps Richard can clarify if he's ok with common ancestry and thus the estimate of the mutation rate for this region of the genome that is in the paper.

> tallen_1:
>
> 2. The conclusion that long-term effective population sizes fell around 10,000 rely upon Watterson's & Tajima's calculations of θ (which are based on coalescent methods), in conjunction with the derived estimated mutation rates. Yet neither of these calculations seem to utilize TMRCA values in any way. Though both are derived through coalescent methods.
>
> 3. The TMRCA values provided and the accompanying analysis does not give any explicit descriptions pertaining to bottlenecks or effective populations sizes. Though in your 2nd installation of your response you mention that TMRCA values can be utilized to discern potential bottlenecks. It just looks like the authors didn't leverage that approach in this particular paper.

Yes - coalescent models can use TMRCA clustering to reveal population size changes. PSMC and related methods are an example. You're right that this paper doesn't use that type of approach. Part 3 - which is nearly ready - will get into PSMC modelling in depth.

> tallen_1:
>
> Also, I'd picked up (if I understand this right) that long-term effective population sizes are harmonic means of a range of idealized population sizes across a period of time, which means that acute minimum population sizes could in theory exist substantially lower than these estimates.

Also correct. This is partially why we're in the weeds of the data. A bottleneck to 2 will throw the entire population into extreme linkage disequilibrium (LD) - all the surviving alleles will be in one of four possible patterns, which will be very common thereafter. (I will discuss LD in part 4). Looking at haplotype data in this paper I see more than 4 types, and Richard sees 4. That's where the conversation has been of late. I'm trying to figure out why Richard set three mutations from a starting haplotype as a cutoff. Three mutations would need to occur in this way: wait for rare mutation; wait for drift to make the first rare mutation reasonably common such that a second rare mutation would be probable on one of the copies of the first; second rare mutation occurs; wait for drift to make this new double mutant variant reasonably common such that a third rare mutation would be probable on one of the copies with two mutations; third rare mutation occurs; wait for drift to make the new triple mutant common enough to be picked up in the limited sample size that the paper uses. Also, some of the intermediate forms would also have to later become lost from the population, even though they were once common enough to allow for a rare second or third mutation to happen on the previously mutated haplotype. Waiting for mutations takes time. Waiting for drift takes time. I don't think there's enough time for all that. Richard disagrees.

Finally, I think the protracted conversation over this paper is a bit pointless. There are other regions of the genome with even more diversity and more haplotypes, which would be harder to explain with a bottleneck of 2 in human history. The chromosome 21 paper, the Alu paper, Zhao 2006, and so on. Then there's the 1000 genomes papers, which use PSMC modelling, which are based on a much larger data set. Why we're beating Zhao 2000 to death when we should be tackling the stronger data is something of a mystery to me. I was willing to grant Zhao for the sake of argument to move

to that stronger data, but here we are. Hopefully once Part 3 goes up we can move on to the PSMC (and related) papers (though I still want Richard to deal with the chromosome 21 paper, the Alu paper, and Zhao 2006 at a minimum).

Hopefully that helps orient things for now.

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gbrooks9 (George Brooks) 2017-12-14 08:18:35 UTC #235

> DennisVenema:
>
> Why we're beating Zhao 2000 to death when we should be tackling the stronger data is something of a mystery to me.

@DennisVenema ,

Why would **@RichardBuggs** want to switch to discuss stronger data ?

Jonathan_Burke (Jon) 2017-12-14 11:42:18 UTC #236

I have just discovered something which makes a lot more sense of Dr Buggs' responses. Up to now I had the idea that Dr Buggs was a secular scientist. However, prompted by Dennis' comments about Dr Bugg's views on chimpanzee DNA, today I looked around a bit and discovered the following facts.

- Dr Buggs is a Christian
- He argues that **Intelligent Design is a science**
- He **says** that "If, as an explanation for organised complexity, Darwinism had a more convincing evidential basis, then many of us would give up on ID"
- He served on the science panel of **Truth In Science**, a creationist organization promoting Intelligent Design and "**Teach the Controversy**", during which time he defended the "information packs" which Truth In Science made for teaching ID in schools, and said ""We're seeking to have intelligent design and criticisms of Darwinism taught in science lessons" (just in case it wasn't clear)

This explains a great deal.

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tallen_1 (Tim) 2017-12-14 12:24:34 UTC #237

Thanks Dennis, that helps a ton!

So do you think some of the initial characterizations of this paper may have fed into some of the frustration over this paper on this thread? Looking back over your early comments, there are a couple statements that may be relevant here: [quote="DennisVenema, post:87, topic:37039"]
Have a look at Table 5, which shows their data for the distribution of TMRCA values. This is the data and analysis they are basing their conclusions on. Bottlenecks increase the probability of coalescence (this is also how PSMC methods work). We see a distribution of TCMRA values for the alleles in the study. This is basically what a PSMC analysis does sequentially for an entire genome to get a much larger sample size.
[/quote] & [quote="DennisVenema, post:88, topic:37039"]
I disagree. The methods used are capable of detecting bottlenecks - that's why they are used.
[/quote]

If you could reword those characterizations now, how would you phrase them? The TMRCA values while listed in the paper weren't used for their analysis regarding effective population size or bottlenecks. And their conclusion on there never having been a severe bottleneck didn't rely on the sort of coalescent methods that might be sensitive to detecting

it such as you'd discussed. But rather just a single measure of genetic diversity. Were you thinking of these coalescent papers as a whole when you made the statements, with perhaps some bleed over to the Zhao et al (2000) paper you didn't intend? Or perhaps unintentionally conflating your analysis of the data on the paper with the analysis the authors performed themselves? I think what you've put out there so far has been pretty compelling, but these two characterizations at least of the Zhao et al (2000) paper seem a little at odds with what was just discussed. If I'm missing something though, please let me know.

As a side note, I'm still trying to wrap my head around how much weight effective population sizes have to bear on acute bottlenecks and why. Just given how frequently those have been mentioned here, they must carry some substantial significance.

BTW, I do agree it's strange that Richard is refusing to move on to your stronger papers. There's been some discussion on that here and it seems most readers are converging on the same conclusion. If Richard would like to preserve any remaining benefit of doubt that he's engaging this conversation in good faith, it may be in his interest to deal with this.

Thanks!

AMWolfe (A.M. Wolfe) 2017-12-14 16:01:49 UTC #238

> tallen_1:
>
> Richard is refusing to move on to your stronger papers.

Not only that, but purposefully mischaracterizing this move as Dennis "walking away from the conversation."

> RichardBuggs:
>
> You were keen for us to discuss data, and now that we are, it would be a pity for you to walk away from our discussion.

DennisVenema (Dennis Venema) 2017-12-14 20:21:30 UTC #239

> tallen_1:
>
> If you could reword those characterizations now, how would you phrase them? The TMRCA values while listed in the paper weren't used for their analysis regarding effective population size or bottlenecks. And their conclusion on there never having been a severe bottleneck didn't rely on the sort of coalescent methods that might be sensitive to detecting it such as you'd discussed. But rather just a single measure of genetic diversity. Were you thinking of these coalescent papers as a whole when you made the statements, with perhaps some bleed over to the Zhao et al (2000) paper you didn't intend? Or perhaps unintentionally conflating your analysis of the data on the paper with the analysis the authors performed themselves? I think what you've put out there so far has been pretty compelling, but these two characterizations at least of the Zhao et al (2000) paper seem a little at odds with what was just discussed. If I'm missing something though, please let me know.

That would require me to remember what was on my mind at the time. 🙂
Pointing out the TMRCA values was shorthand for flagging up the nucleotide diversity issue - seeing a spread of long TMRCA values is a way to "visualize" the nucleotide diversity of the sample that Zhao was working with. So, this is the data set that they based their rejection of a sharp bottleneck on, even if they just used nucleotide diversity to do it. This is what a PSMC analysis does across a whole single genome - here they've done it on one short region in numerous

people. Pointing out the nucleotide diversity then led to the conversation between Richard and I about trying to fit the haplotypes in Zhao into a max of 4 ancestral types . This paper can exclude a severe bottleneck for this small region for non-Africans (and presumably, Africans, but that is left unstated). At least, that's what the authors claim - because nucleotide diversity is too high (it's the same in this paper for Africans and non-Africans). I think they're also suggesting that the TMRCA values supports this conclusion, but you're right, on re-reading the paper I don't see that explicitly stated. Messing about with haplotypes was then my attempt to show the problems with having coalescence back to 4 types within a reasonable timeframe.

This paper, of course, is really only of historical interest at this point. We have way more data, and it's genome-wide. I do see some (possible) value in continuing to hash things out, though - perhaps we can establish why Richard thinks 3 mutations from a haplotype is ok. (We'd need to know mutation rates, population size (Ne) and a proposed time for the bottleneck.) Then, my question would be: is 4 mutations too much? How about 5? and so on. This might be useful to get settled, because then we could port that discussion over to other papers (for example, the Zhao 2006 one or the chromosome 21 one, which have more haplotypes, which would require more mutations from a set of 4).

Of course, eventually Richard will have to deal with the more recent data - papers using PSMC, MSMC (PMSC on multiple genomes), site frequency spectrum (SFS) methods, and methods that blend some of these approaches together in different ways, including some that use LD-type data. If you want to see a recent paper that compares some of these approaches on the same human data sets - humans are actually the best model organism for this sort of thing because we've done so many studies on our demography - **have a look here**. This paper wasn't out when I wrote *Adam and the Genome*, and it's way more technical than I would have wanted to get into anyway even if it was out, but for the purposes of this conversation it's worth a look. I'll give you a spoiler, though: even though the various methods have strengths and weaknesses, all of the methods shown no sign at all of a bottleneck to 2.

T_aquaticus 2017-12-14 21:04:05 UTC #240

> DennisVenema:
>
> . . . even though the various methods have strengths and weaknesses, all of the methods shown no sign at all of a bottleneck to 2.

This point should be brought up whenever possible.

To use an analogy, let's say you are a forensic scientist and you find DNA, fiber, foot print, tire print, and finger print evidence at a murder scene. Of that evidence, the DNA matches the defendant's DNA, the fibers match a bloody shirt in his laundry room, the foot prints match his exact shoes, the tire prints match the tires on his car, and the fingerprints match the defendant's fingerprints. Each piece of evidence has its strengths and weaknesses, and perhaps one single piece of evidence would not lead to a conviction on its own. However, when you have multiple pieces of independent evidence all pointing to the same conclusion the guilt of the defendant is pretty clear.

DennisVenema (Dennis Venema) 2017-12-14 21:24:11 UTC #241

> T_aquaticus:
>
> Each piece of evidence has its strengths and weaknesses, and perhaps one single piece of evidence would not lead to a conviction on its own. However, when you have multiple pieces of independent evidence all pointing to the same conclusion the guilt of the defendant is pretty clear.

Unless you can find a good lawyer who can cause a jury to have doubts about the evidence…

Jonathan_Burke (Jon) 2017-12-14 21:39:12 UTC #242

> T_aquaticus:
>
> Each piece of evidence has its strengths and weaknesses, and perhaps one single piece of evidence would not lead to a conviction on its own. However, when you have multiple pieces of independent evidence all pointing to the same conclusion the guilt of the defendant is pretty clear.

It's just the same as the evidence for the age of the earth.

RichardBuggs (Richard Buggs) 2017-12-16 21:21:15 UTC #243

Hi Dennis,
Thanks for responding to me again on Zhao et al (2000). I think our discussion on this paper continues to hold value because it is helping us both to engage directly with data. For the time being, therefore I would prefer not to move on to other papers (nor other topics, for that matter). I would remind you that when you introduced this paper there was no mention that it was a "weaker" source of evidence for your view. Indeed, it appeared to be one of the strongest contenders for an appropriate reference for your statement about allele counting methods in Adam and the Genome. The fact that you continue to think that their dataset and coalescent analysis does support your case is being very helpful in allowing us to come down to a detailed understanding about what evidence you think supports your case. It seems that you have an intuition that three successive mutations of an ancestral haplotype preclude a bottleneck of two in the human lineage. If this were so, then I can see why you would conclude that a bottleneck of two is impossible (with a high degree of certainty). Thus our discussion of this paper is helping me to understand your thinking better.

> DennisVenema:
>
> I'm still not seeing how you can fit everything you need into the timeframe you've allowed yourself.

You are misreading my posts about the Zhao et al paper if you think I have "allowed myself" a time frame. The time frames I am pointing out are those that arise from their coalescent analysis, and thinking through how a bottleneck followed by a population expansion would affect this.

> DennisVenema:
>
> How do you have time for three mutations, each interspersed with drift? Why did some of the intermediates (presumably) drift to an intermediate frequency and then drift down to zero (since we don't see some of the intermediates)? How do you have time for all of this to plausibly happen? Don't forget that if you lower Ne to get a faster coalescence time, you also lower the number of forward mutation events that are plausible.

Please let me repeat my argument (already outlined above), based on Zhao et al's own analysis. In their own analysis, all the mutations in the 10kb sequence have occurred within the last 712,000 to 2,112,000 years. The different haplotypes currently found in human populations all coalesce back to one haplotype within this timeframe according to their analysis. As I have pointed out, it is well known that in a coalescence analysis, it is the final coalescence events that take the longest time. In other words, the coalescence from two ancestral haplotypes to one ancestral haplotype takes longer than the coalescence from three haplotypes to two haplotypes. And the coalescence from three to two takes longer than the coalescence from four to three. And so on. So within their own analysis, this 10kb sequence would be down to four haplotypes within roughly 300,000-1,000,000 years before present. Thus in their analysis, three cumulative mutations have occurred in this space of time, and indeed, more (remember that there are also mutations that are present in one or two individuals that were not relevant to us when trying to figure our what the ancestral haplotypes could have been).

Their analysis is entirely reasonable. Let's do a quick back-of-the-envelope calculation. If we say that there were four haplotypes 500,000 year ago, and call this 20,000 generations ago, in a 10,000bp region with a mutation rate of 1.1x10-9 mutations per bp per generation, with an effective population size of 10,000 in each generation, then we would expect around 2200 new mutations to occur in total over the 500,000 years. You will recall that the total number of variants that they found in the population was 78. So they can have many many mutations lost via drift, and still see the number of variants that they do.

Now, their analysis assumes a constant effective population size of 10,000. A bottleneck of two, followed by a population expansion to 7 billion individuals will obviously look rather different. The question therefore is: will a bottleneck followed by a rapid expansion increase or decrease the time from a coalescence of four haplotypes to the present? A bottleneck increases the rate of coalescence, as you know, which is why I have said that a bottleneck will decrease the likely timing of coalescence to four haplotypes from the present. I don't make this point because I am restricting myself to a certain time frame, I am making this point because it is a simple fact about coalescence analyses. In other words: If there was a bottleneck in our past, all haplotypes in the present human populations will (on average) coalesce to four ancestral haplotypes in a shorter length of time than they would if the human population had a constant effective population size through history.
I think you agree with this point. However, your counter-argument is that low effective population size after the bottleneck will reduce the number of mutations that can happen.

> DennisVenema:
>
> Don't forget that if you lower Ne to get a faster coalescence time, you also lower the number of forward mutation events that are plausible.

Yes, in a smaller population size, a lower number of new mutations are possible in terms of absolute numbers. But we also have to take into account two things:

(1) a rapid expansion causes a higher proportion of new mutations to be preserved in a population than would be possible in a population of constant size. By virtue of the rapid increase of the population as a whole, new mutations will be held by higher and higher numbers of offspring. If the population expansion is accompanied by a geographical expansion, there is also an effect sometimes called "allele surfing" (**reviewed here**) which can push new alleles up to high frequencies in newly colonised areas.

(2) the low population size will only last a few generations - a rapidly expanding population will soon reach sizes of well over 10,000 individuals. For example, if the population doubles every generation, within 14 generations we will have 16,384 individuals. Thus in the course of human history, the low population size of the human population in the first few generations after the bottleneck will have little impact on the total number of mutations that are possible from the time of the bottleneck until now.

Therefore, it seems to me that your intuition that three cumulative mutations would be impossible (i.e. very very unlikely) after bottleneck of two early in the human lineage is a mistaken intuition. If your intuition were correct, then I would have to agree with you that a bottleneck was more or less an impossibility. But as far as I can see, your intuition is wrong, and Zhao et al's own analyses show this.

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tallen_1 (Tim) 2017-12-17 00:24:59 UTC #244

Richard,

> RichardBuggs:
>
> I don't make this point because I am restricting myself to a certain time frame

I've noticed in your replies you continue to refuse to state what you feel the lower plausible bounds of a timeline for a bottleneck to two is. This has not gone unnoticed by readers, who have (correctly I surmise) inferred that you're not allowing yourself to be held to the same standards of transparency and intellectual honesty to which you're holding Dennis. If the intent of this dialogue is to discredit Dennis (and I believe it is…otherwise why continually avoid his stronger arguments?), you may want to take a look in the mirror and see how your own reputation is coming out through your unapologetic application of these double standards.

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gbrooks9 (George Brooks) 2017-12-17 02:40:42 UTC #245

> RichardBuggs:
>
> Therefore, it seems to me that your intuition that three cumulative mutations would be impossible (i.e. very very unlikely) after bottleneck of two early in the human lineage is a mistaken intuition.

@RichardBuggs doesn't appear to have explained this position very clearly. All of a sudden, it is **@DennisVenema** 's intution that is faulty… not **@RichardBuggs** .

I've read this sentence and the preceding paragraph five times … and I still don't see how he gets to this sentence!

Swamidass (Dr. S Joshua Swamidass) 2017-12-17 20:01:07 UTC #246

I have been cautious about weighing in here because this is such a significant conversation. As things are continuing on, I wanted to make a couple observations from my perspective as scientist in the Church, and how we can better understand and engage what is going on here.

1. **This is a very important conversation**; as is evident, for example, in the large number of views this thread is getting.

2. **@RichardBuggs** is ***entirely*** correct when he explains that **this is a "question that the religious community is asking." He is *appropriately* sensitive to this question.** The insensitivity of many others to this question is a problem that most of us have failed on. The fact that this question arises from theology is not a reason to ignore it, but to take it more seriously. As scientists in the Church, the only correct response is empathy to this question.

3. It has been point out by some that **@RichardBuggs** is associated with the ID movement and skeptical of "Darwinism." Of course Darwinism (atheism) is something of which we are all skeptical here. This also is well known, and ignoring a valid question because of its source is the worst type of *ad hominem*. Of course he cares about this because he is a Christian, and he is willing to publicly question this partly because he has already taken controversial positions (by associating with ID). I am the first to dismantle bad ID arguments, but this is not even about design. It is valid scientific question, and his personal views are not a reason to dismiss his question.

4. **It is very rare to see conversations like this in public.** In science, these conversations happen all the time, but in private. It is rare to see the established science questioned by a scientist of **@RichardBuggs** 's stature in public this way. I have had similar conversations with other scientists regarding evolution, but it has *always* been in private. This is equivalent to having Francis Collins or Richard Dawkins or Jim Tour enter the fray personally, with all the other committments they have. There is real risk here, so this is why it is so rare. Respect what is happening here, and perhaps we can all learn from it.

5. **As many have noted, there is real risks to one's scientific reputation in joining this conversations**. Rather than use that as weapon, it should increase our empathy for those asking valid questions about the mainstream position. Even though I have argued against ID arguments may times, ID advocates have come to me with genuine concern about personal safety as a non-tenured scientist at a secular institution. That is exceedingly kind

and meaningful to me personally. We should be approaching this with the same genuine empathy to @RichardBuggs , who is our brother, even though we might disagree with him.

6. **It is respectful to let @DennisVenema has this out with @RichardBuggs without distracting on side issues and personal assessments of their relative positions.** Material contributions (as those @glipsnort) are helpful and should be offered. However, this is a tendency for non-scientists to weigh "cheering" or "adjudicating" the positions raised. This is, fundamentally, going to be unfair to @RichardBuggs , as this forum is dominated by those who affirm evolutionary science. Nonetheless, he has decided to brave this forum, so we should continue to treat him as a guest. Ultimately, science is not resolved by public debates of any kinds, not even this one. It does not matter what a BioLogos skewed forum feels about the arguments here, but it does matter the observers in the Church see in how you treat @RichardBuggs . If you must comment or attempt to adjudicate this, consider doing it on another thread.

7. @RichardBuggs **has been pretty clear of several things here.** (1) this is not merely about the science, but also ensuring accurate communication to the public in *Adam and the Genome* by @DennisVenema , (2) he is not arguing for *de novo* creation or some special biology in Adam and Eve. (3) he concedes up front that the evidence appears to preclude a bottleneck within the last couple hundred thousand years. (4) he has not proclaimed that he has the answer to this (which he does not have) but wants to ask questions.

8. **In addition to the scientific question, he has also been clear that this is also about @DennisVenema representation of the science.** This explains, for example, why @RichardBuggs has not taken @glipsnort to task, and asked @DennisVenema specifically to explain himself. It is not really about the science, per se, but about whether or not @DennisVenema has honestly represented the science and is competent to be making this case. It might seem rude, but this is fairly standard to do to other scientists (in private usually). I would also add that I share similar concerns (even though I certainly affirm the consensus science here). I do not believe our case is made stronger when we overstate what science does say, and neglect to clarify what it does not say.

9. **The reason why he has focused on the specific reference is because that is what Dennis used in his book; @RichardBuggs is concerned the @DennisVenema overstated the science.** @DennisVenema has pretty much conceded this, saying that in communicating with the public he was not worrying about referencing the most updated and comprehensive science. In @DennisVenema 's defense, he is right on that point. It is very common when communicating established science to the public to give historical or easier to understand references. @DennisVenema 's work here has never been "novel contributions to science" but just trying to explain what others have seen in the data, and the purposes of references are just different in a published scientific study and in commuting to the public. I understand why @RichardBuggs is wanting a larger concession, but I would offer that if he could explain the stronger data against no population bottleneck, this reference would be trivial to explain. @DennisVenema **has already admitted directly that he did not use the best references.**

10. **There is more than enough information in public, right now, to determine if @DennisVenema is a trustworthy voice to the Church.** Given this, I do hope that we can move past the personal referendum on the weak references from *Adam and Genome* to deal with the larger questions. In particular, it is critical for anyone purporting to speak to the Church to engage the question of the Church with empathy, not ambivalence and incuriosity. Let's not loose the bigger questions in the smaller things.

The question on the table is actually quite interesting from a purely scientific point of view. Population genetics is very non-intuitive. Engaging this question can help us all get this straight, even if (as I expect), we will see the mainstream position continue to be supported by the evidence. By taking the questions seriously, it gives us more certainly, and also more credibility to skeptics. Frankly, it is also fun.

WIth that, I expect this conversation can continue, but want to reemphasize how I think this could be most productive:

1. **Let's focus on the strongest evidence**, *unless there is a helpful reason to deal with weaker evidence.* I will say that there is very interesting scientific nuances arising everywhere, some of which are best understood when thinking carefully about simple examples. This will be profoundly educational as this gets deeper, for all of us.

2. **Let's move past the personal referendum** on @DennisVenema . If he is not trustworthy, engaging the substance of the response will make that clear. He has already admitted to having left out the strongest references (which is fairly standard in this case) and to have excluded material information. This, however, is not ultimately about @DennisVenema . It is about the questions of the Church.

3. **Let's hold of on observers "adjudicating" who is right or wrong or behaving well, especially if we are not scientists.** This disagreement is not adjudicated by us, nor is it a fair balance of views here. Let them do their work and respect that we have an amazing opportunity to watch to scientists hash out a scientific disagreement in public; something that rarely happens. I will also say that both @RichardBuggs and @DennisVenema (at least in public) have been engaging in normal ways, as I see happening among scientists all the time. If it seems disrespectful, it is just because science has a different culture than the Church.

Of course, I am just a bystander too. Perhaps everyone will ignore me. However, I really hope that we can see the value of what is happening here, and do what we can to make the most of it. From here, I will largely stay out of this thread, but it seemed important to make these points. In general, will be staying out of this thread, except in a few rare moments to make a critical technical point, or if I am requested by the primaries here.

DennisVenema (Dennis Venema) 2017-12-17 20:47:17 UTC #247

Hi Richard,

Thanks for weighing in again.

A few questions for you - if we take as reasonable your suggestion that Zhao (2000)'s data coalesce to four haplotypes between 300,000 - 1,000,000 years ago, how does that help your case? In *Adam and the Genome* I consistently discuss humans as a species arising ~200,000 years ago. So, by your calculations, Zhao (2000) supports my case - human variation in this all region of the genome cannot be reasonably explained by a bottleneck to 2 individuals within human history, as I argue in *AatG*. Am I missing something here? I want to be sure I'm reading you correctly.

Also, I do think it would be helpful at this point to discuss common ancestry. Zhao (2000) explicitly depends on humans sharing common ancestors with orangutans and chimpanzees. This is how they estimate the forward mutation rate for this region. We're a couple of professional biologists discussing a technical paper, so I was taking for granted that we both accepted that. I'm not so sure now, so I'll ask it again: do you accept that humans share common ancestors with chimpanzees and orangutans? If you don't that is going to substantially affect how you read and interpret Zhao (2000), so I'd like to know.

Swamidass (Dr. S Joshua Swamidass) 2017-12-17 23:33:16 UTC #248

@RichardBuggs ,

You have been appropriately pushed to present specific numbers, and you have. Thanks. I am going to work that out here for others to follow.

I should point out, however, that I think it is already clear that the Zhao 2000 does not demonstrate evidence against (1) a couple bottleneck that was (2) 500,000 years ago, where (3) there was heterozygosity in this couple. The reason why is actually much more straightforward.

In genetics, TMRCA is **always** to 1 allele. However, in your scenario, there was never just 1 allele, because it started with 4. We need to know the **Time to Most Recent 4 Alleles** (TMR4A). This is not a standard computed number in

genetics. Provisionally, I think that on average TMRCA / 4 = TMR4A. So given Zhao's estimate TMRCA of 1 mya, we could estimate that the TMR4A is about 250,000 years ago, matching y-MRCA of about 200,000 years ago and mito-MRCA of about 200 years ago. That is, of course, well within your 500,000 cutoff. So I think we already know (back of the envelope) that the data can be explained by your model.

Someone tell me if I'm wrong in my estimate (TMRCA / 4 approximately equals TMR4A).

This is a pretty classic mistaken regardless. Genetics is not genealogy. Just because genetics has not coalesced, does not mean we are **not** down to one couple. In fact, if the couple is heterozygous, we do not expect TMRCA to equal bottleneck time. That is fairly obvious, but equivocated time and time again.

However, there is value in working out the math for observers. Of course, if I have made an error (which does happen sometimes) please do point it out. I will fix it.

@RichardBuggs Simple Model for Variant Number in Zhao 2002

> RichardBuggs:
>
> Let's do a quick back-of-the-envelope calculation. If we say that there were four haplotypes 500,000 year ago, and call this 20,000 generations ago, in a 10,000bp region with a mutation rate of 1.1x10-9 mutations per bp per generation, with an effective population size of 10,000 in each generation, then we would expect around 2200 new mutations to occur in total over the 500,000 years. You will recall that the total number of variants that they found in the population was 78. So they can have many many mutations lost via drift, and still see the number of variants that they do.

For those who want to see the math, some of it is here: **https://en.wikipedia.org/wiki/Genetic_drift**, but most I'm going to be doing here is from memory. I am using simplified equations at times.

First off, if we are talking of a single couple bottleneck about 500,000 years ago, it will take time to get back up to 10,000 individuals, somewhere between 300 to 1000 generations (depending on growth rates). However, that is just a small effect on your estimate of 20,000 generations, which is actually a bit low any ways. So, let's just say 20,000 generations.

Next, your estimate of 1.1x10-9 mutations / bp is reasonable. We can compute about how many mutations we expect in the *whole* population each generation. 10,000 individuals * 1.1x10-9 mutations / bp * 10,000 bp --> 0.11 mutations per generation in this region.

We can also compute the mutation rate in this region as a whole as 10,000 bp / region * 1.1x10-9 mutations / bp -> 1.1x10-5 mutations in region.

That means every about every 9 generations, one person in a population of 10,000 will have a mutation in this region. So this region would be mutated 0.11 mutations/generation * 20,000 generations -> 2,200 times. This matches **@RichardBuggs** 's number.

How many of these are going to be fixed?

Well, we know that that with random drift, it will take about 10,000 generations (the number of individuals), for a mutation to be fixed. But the variance is high here. Someone who knows better (**@glipsnort** ?) correct me if I am wrong, but the variance is much higher. Regardless, we can expect about 1.1x10-5 mutations / region * 20,000 generations --> 0.22
mutations to fix during this time in this one region.

To be clear, there are few major simplifications in that last number. First, it assumes equilibrium, which is not the case. Remember, in the very first ~500 generations, the population is growing; so there are fewer mutations there. At the same time, when the population is growing, it is much easier for a mutation to be fixed.

And if 0.22 mutations are fixed assuming equilibrium conditions, and it takes 10,000 generations to fix a mutation, it is expected to see several mutations "in transit" during this time, and not fully fixed. As **@RichardBuggs** says, 78 is not a problematic number.

So, **provisionally speaking**, it does seem possible, maybe even likely, that in this scenario we *could* observe this 78 SNP variants (perhaps even at these distributions) in the population today from a primordial pair 500,000 years ago. For observers, it is critical to recognize that a couple at this point in history would ***not*** be a modern Homo sapien. This also ***does not explain all the data*** (if I am right) but just this single region. An effective model would have to explain all the data, not just this area. To be taken seriously, one has to refrain from claiming success in ***one*** area is the same as declaring success ***everywhere***. Moreover, this is merely a qualitative analysis of the sequencing data (as I have not actually verified that only a few variants are required). A better analysis would do a quantitative analysis. Moreover, **this does not take into account the linkage between all the variants.**

Once again, this is consistent with the TMR4A number I computed above, so no real surprise if that can be trusted.

Notably, the *same* math that shows a bottleneck of one couple at 500,000 years ago fits this narrow component of this small part of the data, is **the same math that gives strong evidence that we share common ancestry with the great apes.** It is important to keep this in mind too.

What About Linkage and Recombination?

The analysis above ignores linkage, the adjacency in the chromosomes. We can do a similar analysis for recombination. My intuition here (for what its worth) is that this is not enough to make a definitive statement about a bottleneck of 2 at 500,000 years ago, but it's difficult to know for sure from eyeballing. At issue here is the **distance** between variants (which is *not* included in the image).

The rate of recombination is approximately 1% per million bp, or 10^-4 recomb / individual in this region of 10,000. Eyeballing it, there about 20 variable regions, so we would say that the recombination between variants (assuming equally spaced) is about 5x10^6 / individual between adjacent variants.

Similar calculations as before follow. Expect there to be 10,000 * 5x10^-6, or 0.05 per generation. So every 20 generations, some individual somewhere will recombine betwixt one of the loci here. About 1 individual per generation will show recombination in at one of the 19 regions between variant loci.

How many of these are going to fix?

In the region, we expect 10^-4 recomb in whole region / individual * 20,000 generations --> 2 recombinations to have fixed. **This is 10 times *more* fixed recombinations than the number of fixed SNP variants.** That means we should expect more recombinations "in transit" to fixation than SNP variants themselves.

Notice, that is much faster than the mutation rate, but there is a twist. Not all of these times a recombination is detectable, because there really needs to be heterozygosity here for it to matter. Honestly (help me **@glipsnort** ?) I'm not sure what the correction factor is here. My guess is that it would about 50% less than we observe because of an intuition from Hardy-Weinberg, and then an additional 50% less because of other factors, so 25% of that rate. This, however, is a major fudge factor that should probably reduce the estimates further.

As a simple (and wrong estimate), parameterized by the data itself *may* be possible. if we observe 78 SNP variants, we should also see 780 recombination variants too. With our fudge factor, maybe 200.

Though, really, no one should trust this analysis as anything more than qualitative (because of a lot of assumptions here). More care (as is done in published) work must be given to the **distances** between markers and **considering several places in the genome.** I've only worked this out here to demonstrate how some of the mathe works, and to show that we actually expect to see a lot recombination in this 10kbp region in 500,000 years. And I expect this computation to refined with more information about the data and better formulas, and also recognition of the actual sampling distribution (and past population structure).

Better theoretical analysis of this can be found here: http://www.pnas.org/content/98/24/13757.full For those that want a real treatment, look there, and references within. And ultimatley this is what whole genome wide LD analysis does, and such analysis does not detect any bottlenecks. TMRCA, ultimately, is not as important as effective population size estimates on the whole genome.

Allele Clustering is Unconvincing This Far Back

> RichardBuggs:
>
> To see if you are correct I have downloaded Zhao et al's sequences from Genbank, aligned them, and taken a look at the variation. Here is a very simple portrayal of the variants that are present in more than two individuals.

> RichardBuggs:
>
> I think it is fairly clear to the eye that the data present can be divided fairly easily into four groups, that could correspond to small variations on four ancestral haplotypes. Given the similarity of them all, the number of ancestral haplotypes could in fact be lower.

This argument, from the beginning, was quite weak, because clustering is notoriously subjective. Any data can be clustered, but how many clusters are in the data? That is much more difficult to determine from "eyeballing" the data as we done here.

First off, **given recombination, we do not even expect this to be four allele clusters from a primordial pair.** We would need to look at smaller regions than 10,000 bp (and actually look at them across the genome) to discern 4 alleles in that way. We would need to look at region sizes much smaller to expect 4.

Second off, given drift, even in smaller regions **we expect some of the primordial alleles to have drifted away early on**. So some regions would have to 4 ancestral alleles, some to 3, some to 2, some to 1. The notion that is should be four either (1) assumes no recombination or (2) that this couple had infinite children. In this case (assuming no miracles), we might say they had 10 kids or so (but not 200). That is going to create a *distribution* over 1 to 4 of the number of ancestral alleles, that might in principle be detectable. How far back? I have no idea, but I imagine if done systematically over the whole genome on small regions, we should see that signature quite farther back than 200,000 years ago.

This should be a good reminder that population genetics is not-intuitive. It really does help to work out the math. Eyeballing clusters in data cannot be a substitute for actually modeling the data with simulations and more rigorous treatments…

Move On From Zhao 2000?

From that, can we now move on from Zhao 2000?

I think there is good reason that this single paper's data (in isolation) can be explained by a primordial couple that is heterozygous at 500,000 years ago. Once again, **@DennisVenema** has already admitted this is not the

strongest evidence. **Moreover, he never even considered a couple 500,000 years ago.**

It is not that the 4 allele cluster argument was correct (it was not), but the whole premise that TMRCA in one autosomal location tells you where a single couple bottleneck happens is flawed. It is a category error. Moreover, recombination is happening this area, and we do expect to see it in this region.

Ultimately, I agree that the totality of the evidence shows no bottleneck, but there is also value in delimiting exactly what specific points of data (like Zhao 2000 which only looks at one 10kbp region) do and do not tell us. This data, in particular, seems to allow for **@RichardBuggs** 's hypothesis. Unless, someone can point out the error in my math, perhaps it is time to grant that point and move on.

Of course **@DennisVenema** or **@glipsnort** can correct me if I made an error here (and I may have). If I made an error, it really should be fixed, and I apologize ahead of time.

Swamidass (Dr. S Joshua Swamidass) 2017-12-18 00:06:41 UTC #249

@DennisVenema , in your defense, the question you laid out in Adam and the Genome was answered by your book. If "human" = Homo sapien, and we simplify the problem by ignoring the clear evidence of interbreeding, does that taxonomic category ever go to a single couple within the last 150,000 years? The answer, of course, is "no," unless there was a lot of miracles or interbreeding. No one should be confused by that.

However, that is not the question being ask right now, and it appears it never was, at least not in this exchange.

> DennisVenema:
>
> A few questions for you - if we take as reasonable your suggestion that Zhao (2000)'s data coalesce to four haplotypes between 300,000 - 1,000,000 years ago, how does that help your case? In Adam and the Genome I consistently discuss humans as a species arising ~200,000 years ago. So, by your calculations, Zhao (2000) supports my case - human variation in this all region of the genome cannot be reasonably explained by a bottleneck to 2 individuals within human history, as I argue in AatG. Am I missing something here? I want to be sure I'm reading you correctly.

Your are missing several critical things.

You have assumed without warrant that "humans" = *Homo Sapiens*. This is a minority position in the origins debate. Most YECs now day, for example, would say that *Homo erectus* is "human." As we have seen recently, even OECs like **@agauger** are open to this position too.

Regarding Homo sapiens in particular, there is evidence of a large number of remains as anciently as 300 kya, not 200 kya. It is possible that *Homo sapiens* were around longer than to, say going back as far as 350 kya. So the short timeline of 150 kya is not really justified when considering *Homo sapiens* = "human" anyway. **(This was discovered AFTER *Adam and the Genome* published, so @DennisVenema could not have included it in his book)**

Also, there is very strong evidence that Neanderthals interbred with "humans," as you define them. If that is the case, TMRCA estimates of *Homo sapiens* are going to be pushed back by that interbreeding event. So some sort of correction that excludes these parts of the genome is required. As I understand, no one has done studies like that in the literature.

Also, as I pointed out earlier, TMRCA tells us when things collapse to a single allele, not when they go down to 4 at the TMR4A. So using TMRCA's on autosomal locations embeds the assumption that Adam and Eve were homozygotes and with identical genomes.

Neandertal's Human or Not?

A fairly important question here to make sense of all this is if Neandertal are "human" too. If they are, there is a massive amount of additional variation that must be accounted for (pushing back estimates).

If they are not, some account has to be given for interbreeding. Do we accept it happened or not? How do we make theological sense of this in a way that avoids all the nastiness that so often arises in these conversations?

If we accept Neandertals interbred with "humans" (defined as *Homo sapiens*), then why would we think TMRCA would even give us a good estimate of "humans" in the past? It will always be giving us the sum total of Human plus Neandertal ancestors (and any other hominids *Homo sapiens* interbred with).

This is all to say, given the exceedingly strong evidence (including remains of a hybrid!) of Neanderthal + *Homo sapien* interbreeding, if *Homo sapien* = "human" the argument against a single couple origin of *Homo sapien* seems to weaken substantially. We would **expect** to see no single couple bottleneck, because population estimates are always adding in numbers from our Neanderthal ancestors.

The warrant of saying *Homo sapien* = "human" is very low any ways, so probably that is the part that should be dropped. But this is a big part of what is contributing to confusion about why **@RichardBuggs** and **@agauger** and many in the Church still have question after reading the book.

The case against a single couple origin (without interbreeding) has to be made in a way that does not assume *Homo sapien* = "human." Honestly, the case against interbreeding with other lines is weak Scripturally, that very few people are going to insist on that any way.

Time to Most Recent 4 Alleles (TMR4A) and TMRCA

This last point about TMRCA and TMR4A is most interesting, and most likely to be abused. I've been thinking about this, but we should really see a distribution of TMRCAs of individual autosomal locations if there was a single couple origin.

A key overlooked parameters appears to be the NUMBER of OFFSPRING, that the first couple has. We will get very different distributions if they had 5, 10, 20 or 1000 kids (last on would clearly require miracles). However, in the very first few generations, some locations will very quickly drift to 3, 2, or 1 allele. The exact distribution will depend on precisely what happens in that moment, and even the degree of inbreeding, which will drive it lower. Someone needs to do the modeling here, but there may actually be a detectable variance increases in TMRCA measured in several locations.

The problem however, is that there is already high variance in TMRCA estimates. So if this shift in variance can be seen with any confidence, I am not sure. Regardless, this is a caution of applying my estimate that TMRCA / 4 -> TMR4A when the whole genome is considered (as in the later studies). Those studies would not enable such a facile computation, or at least I do not think so.

However, the really interesting thing is the population structure in the first few generations of a single couple bottleneck. That appears to be an overlooked detail by **@RichardBuggs** and **@agauger** , and I am curious what they are thinking about that. Basically, we expect large linkage domains of the genome to have only ***one*** ancestral sequence, because of drift in the early population. That seems to undercut a major source of variation, and also suggest that this bottleneck should have been detected by now.

Our Common Ground

I do, however, want to emphasize that a very recent common couple ancestor (with no miraculous biology or interbreeding), say within 100,000 years ago, does appear to be ruled out. It is not as if **@DennisVenema** has missed something so large as to call that conclusion into question.

For those that think Adam and Eve are real, in our recent past, and our universal genealogical ancestors, ask if interbreeding with other lines is a problem in your reading of Genesis. If not, a genealogical Adam could have been recent (as recent as 10,000 years ago). To understand how that can be possible, you have to understand the difference between genetics and genealogy.

Christy (Christy Hemphill) 2017-12-18 00:53:11 UTC #250

> Swamidass:
>
> Most YECs now day, for example, would say that Homo erectus is “human.”

Only when they are talking about fossil identification, because they deny any creatures, human or otherwise, were around 150,000 years ago. Every fossil has to be a modern human or a modern ape. So how is the YEC classification of homo erectus relevant to the discussion?

Swamidass (Dr. S Joshua Swamidass) 2017-12-18 01:05:26 UTC #251

> Christy:
>
> Only when they are talking about fossil identification, because they deny any creatures, human or otherwise, were around 150,000 years ago. Every fossil has to be a modern human or a modern ape. So how is the YEC classification of homo erectus relevant to the discussion?

Just pointing out that “human” = *Homo sapien* is a minority position. It seems the scientific community has tipped towards “Homo” = “human” too, but even that is disputed and debated. “human” is ambiguous in the distant past.

Moreover, we see *Homo sapiens* as early as 300 kya ago. So the 200 kya date is not accurate any more.

Clearly, we see no single couple bottlenecks (or Homo erectus) in the last 10,000 years (and I do not think any one here is disputing this). However, the assumption that “human” = *Homo sapien* was central to Dennis’ question:

[taking my own advice and removing a distracting post]

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glipsnort (Steve Schaffner) 2017-12-18 01:47:33 UTC #252

> Swamidass:
>
> Someone tell me if I’m wrong in my estimate (TMRCA / 4 approximately equals TMR4A).

I believe you are correct. The mean TMRCA for 4 chromosomes is 3N and for the entire population is 4N (for the usual constant-sized, blah blah population).

Swamidass (Dr. S Joshua Swamidass) 2017-12-18 01:57:16 UTC #253

Thanks **@glipsnort**

So it is possible that: TMRCA / 4 approximately equals TMR4A. This may be a reasonable estimate where we are looking at (1) a single region and (2) that region is autosomal (not X, mito or Y chromosomes). For Y and Mitochondrial regions, we are still most interested in TMRCA, not TMR4A. And for X we would be interested in TMR3A.

> glipsnort:
>
> I believe you are correct. The mean TMRCA for 4 chromosomes is 3N and for the entire population is 4N (for the usual constant-sized, blah blah population).

I hasten to add that this shortcut does ***not*** work for reducing estimates of Y-Chromosome Adam and Mito-Eve, because we only expect one genome of each in the primordial pair (unless we go to the mosaic hypothesis which is a massive miracle). Moreover, this short cut may not work when considering the whole genome (several places in the genome at once).

Moreover, this is only provision. It needs a lot more careful thought to be sure. There is certainly some assumptions buried here, and I do not have a solid decision on how much I trust this yet.

Swamidass (Dr. S Joshua Swamidass) 2017-12-18 02:18:59 UTC #254

> DennisVenema:
>
> Also, I do think it would be helpful at this point to discuss common ancestry. Zhao (2000) explicitly depends on humans sharing common ancestors with orangutans and chimpanzees. This is how they estimate the forward mutation rate for this region. We're a couple of professional biologists discussing a technical paper, so I was taking for granted that we both accepted that. I'm not so sure now, so I'll ask it again: do you accept that humans share common ancestors with chimpanzees and orangutans? If you don't that is going to substantially affect how you read and interpret Zhao (2000), so I'd like to know.

@RichardBuggs that seems like a fair question. Is this conversation assuming common descent? Are you presuming common ancestry, at least within the context of this conversation?

DennisVenema (Dennis Venema) 2017-12-18 03:50:05 UTC #255

A few comments: the paper that suggests *Homo sapiens* back at ~300,000 years ago came out after *AatG* was published, but I don't see how it really affects things. I don't see any evidence of a bottleneck in our lineage for the last 1 MYA or more. Even Zhao (2000) has a range of TMRCA/4 values (if we want to go with that) that easily pushes back past 300,000.

(Of course, we need to look at the distribution of TMRCA values across the genome as a whole - not just at one 10kb region, as you've noted.)

Also, those fossils are not uniformly accepted as *Homo sapiens*. They have some features that are decidedly different than *Homo sapiens* at 200,000 years ago. This is to be expected. Our species becomes a species as a gradient biologically. With a "perfect" fossil record over the last 2MY, we presumably would have a smooth gradient between early *H. erectus* all the way to modern humans in the present day. As such, it will become more and more difficult to "draw the line on the gradient" - as I discuss in the book- as we get a more complete picture of the fossil record. We're a chronospecies.

I still think pushing an "Adam" back that far is strongly at odds with the scriptural account. Even for the concordists among us, Genesis is clear that one generation after Adam is farming, and a few more generations are doing metal working. How does that work if Adam is at 300,000 or 500,000 years ago? I just don't see the appeal. YMMV.

Swamidass (Dr. S Joshua Swamidass) 2017-12-18 04:14:40 UTC #256

> DennisVenema:
>
> the paper that suggests Homo sapiens back at ~300,000 years ago came out after AatG was published

That is absolutely correct. You should not be held responsible for excluding a new finding that came out after the book was published. That was not an error in your part.

> DennisVenema:
>
> As such, it will become more and more difficult to “draw the line on the gradient” - as I discuss in the book- as we get a more complete picture of the fossil record. We’re a chronospecies.

That is true too. This is a fundamental finding of human origins. No one has an easy time drawing lines. There is disagreement in every camp.

> DennisVenema:
>
> I don’t see any evidence of a bottleneck in our lineage for the last 1 MYA or more. Even Zhao (2000) has a range of TMRCA/4 values (if we want to go with that) that easily pushes back past 300,000.

However, if you take into account interbreeding, you do not expect to see a bottleneck. Given we know that there was interbreeding, that appears to be an important omission.

DennisVenema (Dennis Venema) 2017-12-18 04:25:40 UTC #257

> Swamidass:
>
> However, if you take into account interbreeding, you do not expect to see a bottleneck. Given we know that there was interbreeding, that appears to be an important omission.

I talk about interbreeding in the book. It (as far as know so far) only applies to non sub-Saharan Africans. Yes, it increases the difficulty of “finding Adam” because there are more human ancestors than those within our own species. I don’t avoid this in the book.

Swamidass (Dr. S Joshua Swamidass) 2017-12-18 04:41:57 UTC #258

[taking my own advice and removing a distracting post]

Jonathan_Burke (Jon) 2017-12-18 05:05:24 UTC #259

> Swamidass:
>
> **@RichardBuggs** is entirely correct when he explains that this is a “question that the religious community is asking.” He is appropriately sensitive to this question. The insensitivity of many others to this question is a problem that most of us have failed on. The fact that this question arises from theology is not a reason to ignore it, but to take it more seriously. As scientists in the Church, the only correct response is empathy to this question.

Yes. But my assessment of his sensitivity has been tempered by his practice of consistently ignoring various simple, easily answered, questions from those he is supposedly most concerned about assisting. Several people (including myself), have put very basic questions to him, the answers to which would help us assess the relevance of this complex scientific discussion, to our beliefs or those of others who feel affected by the subject. Those questions have been phrased consistently respectfully and graciously, with full acknowledgment of his time constraints.

However, those questions have been ignored. Note that this is not even a case of Dr Buggs responding to these questions with “I understand your concern and note your questions, but regret I cannot address them within my current time constraints”, it is a question of him completely ignoring them and not acknowledging them in any way at all. Perhaps now you have asked a couple of these same questions, he may feel more inclined to answer them, but at this point it really does look like his main concern is “taking down” Dennis in the name of ID and the Discovery Institute, rather than actually addressing the personal concerns of rank and file Christians.

> Swamidass:
>
> It has been point out by some that **@RichardBuggs** is associated with the ID movement and skeptical of “Darwinism.” Of course Darwinism (atheism) is something of which we are all skeptical here. This also is well known, and ignoring a valid question because of its source is the worst type of ad hominem. Of course he cares about this because he is a Christian, and he is willing to publicly question this partly because he has already taken controversial positions (by associating with ID). I am the first to dismantle bad ID arguments, but this is not even about design. It is valid scientific question, and his personal views are not a reason to dismiss his question.

No one has attempted to dismiss or ignore his question on the basis of its source, or claim that it is invalid on the basis of its source. The point being made is that his question has not arisen on a scientific basis; it has not arisen from a need to find a scientific solution to a scientific problem. It is an apologetic argument which has arisen on a theological basis, and this needs to be both acknowledged and stated explicitly. When someone’s interpretation of the science is affected by their theological constraints, it is important to identify this and examine how it affects their interpretation of the science. When this is swept under the carpet, and discussion of it is discouraged, red flags should fly.

> Swamidass:
>
> **@RichardBuggs** has been pretty clear of several things here. (1) this is not merely about the science, but also ensuring accurate communication to the public in Adam and the Genome by **@DennisVenema** , (2) he is not arguing for de novo creation or some special biology in Adam and Eve. (3) he concedes up front that the evidence appears to preclude a bottleneck within the last couple hundred thousand years. (4) he has not proclaimed that he has the answer to this (which he does not have) but wants to ask questions.

He has also made the claim that there have been no scientific bottleneck studies which have ruled out a bottleneck of only two people. I believe Dennis has already shown that this is simply not true, and has listed a number of them. If Dr Buggs had mentioned these other studies and explained why he thought they didn’t support the conclusions of their authors, that would have been fine, but instead he has given the impression that they don’t even exist. My surprise at this claim of his was matched only by my surprise that Dennis was able to show easily that they do exist.

> Swamidass:
>
> In addition to the scientific question, he has also been clear that this is also about **@DennisVenema** representation of the science. This explains, for example, why **@RichardBuggs** has not taken **@glipsnort** to task, and asked **@DennisVenema** specifically to explain himself. It is not really about the science, per se, but about whether or not **@DennisVenema** has honestly represented the science and is competent to be making this case. It might seem rude, but this is fairly standard to do to other scientists (in private usually). I would also add that I share similar

> concerns (even though I certainly affirm the consensus science here). I do not believe our case is made stronger when we overstate what science does say, and neglect to clarify what it does not say.

There is nothing wrong with Dr Buggs challenging Dennis over Dennis' representation of the science. However, I don't think Dr Buggs has been accurate in his representation of the science, and it is clear to me that he really does believe it is about the science, not simply Dennis' representation of it.

> Swamidass:
>
> The reason why he has focused on the specific reference is because that is what Dennis used in his book; **@RichardBuggs** is concerned the **@DennisVenema** overstated the science. **@DennisVenema** has pretty much conceded this, saying that in communicating with the public he was not worrying about referencing the most updated and comprehensive science.

I don't think that Dennis has conceded this, or that Dennis has overstated the science. I am still wondering why Dr Buggs has not contacted Zhao et a, if he is so concerned that their analysis of the data is wrong.

> Swamidass:
>
> **@DennisVenema** has already admitted directly that he did not use the best references.

I think this wrongly suggests that Dennis is acknowledging some kind of failure on his part which weakens his case.

Swamidass (Dr. S Joshua Swamidass) 2017-12-18 05:29:21 UTC #260

You are missing my point here.

That is actually a defense of **@DennisVenema** .

> Jonathan_Burke:
>
> > The reason why he has focused on the specific reference is because that is what Dennis used in his book; **@RichardBuggs** is concerned the **@DennisVenema** overstated the science. **@DennisVenema** has pretty much conceded this, saying that in communicating with the public he was not worrying about referencing the most updated and comprehensive science.
>
> I don't think that Dennis has conceded this, or that Dennis has overstated the science. I am still wondering why Dr Buggs has not contacted Zhao et a, if he is so concerned that their analysis of the data is wrong.
>
> > Swamidass:
> > **@DennisVenema** has already admitted directly that he did not use the best references.
>
> I think this wrongly suggests that Dennis is acknowledging some kind of failure on his part which weakens his case.

It is NORMAL to quote historical and easier to understand references when engaging the public on established science. Dennis did nothing wrong here. The fact that he used weaker references ends up **strengthening** the case, because there is so much data out there that makes it clearer that our ancestors do not dip down to a single couple (at least within the last several 100,000 years).

Btw, I think the strongest evidence against a bottleneck in the last 6 million years is trans-species variation, which does not even appear to be on the “menu,” as it were. Trans-species does not have the same horizon problems as does allele frequency spectrums and LD estimates. Nor is it subject to as much uncertainty from population structure (though interbreeding can explain it away too).

> DennisVenema:
>
> If you want to see how this sort of thing looks, here’s a paper (PDF) that does this for a limited data set for the entirety of human chromosome 21. Look at figure 2 - those are 20 individual chromosomes from their sample (African, Asian, Caucasian). Note well that this is an early paper with a limited data set, but there are more than four common haplotypes even in this very limited data set. Note also how closely linked these SNP sites are. **The problem for a 2-person bottleneck hypothesis only gets worse as you add in the reams of data we’ve added since.**

To me, that seems to be exactly right. The fact that Zhao 2000 does not make the case with the strongest data is not really a big problem. There is so much more data. Even if a single couple bottleneck at 500,000 years ago, provisionally, can fit Zhao 2000, does not mean the same will work for all the rest of the data. I want to see how far we can go.

It is not really expected to give the best references in a book like *Adam and the Genome*. The field is huge. There is just so many papers out there, I doubt any of us have read absolutely **all** the relevant studies. None of the conclusions Dennis presented are disputed in mainstream science either. So he is not so much “making the case” but explaining what others have found. The evidential standards are just much much lower for that type of activity. He did not thing wrong by quoting a selection of papers.

Taking him to task on that is really beside the point. That is why I think we should move past a referendum on **@DennisVenema** . He has already basically admitted his references are not the best evidence. There is no reason, also, to think his references should include all the relevant evidence, because there is so much here, and historic papers actually make sense in this context.

[taking my own advice and removing a distracting post]

Jonathan_Burke (Jon) 2017-12-18 05:34:18 UTC #261

> Swamidass:
>
> You are missing my point here.
>
> That is actually a defense of **@DennisVenema** .

I know it was, which is why I objected to the word “admission”, since that doesn’t seem congruous with the point you’re making.

> Swamidass:
>
> The fact that he used weaker references ends up strengthening the case, because there is so much data out there that makes it clearer that our ancestors do not dip down to a single couple (at least within the last several 100,000 years).

Yes, which is why I think that “admission” is not the best word to use in this context. It makes it sound like Dennis was caught out in some way, when in actual fact his point was the opposite.

---

gbrooks9 (George Brooks) 2017-12-18 06:14:01 UTC #262

> DennisVenema:
>
> How does that work if Adam is at 300,000 or 500,000 years ago? I just don’t see the appeal. YMMV.

@DennisVenema ,

Absolutely! Your mileage may vary!

If we are going to make any progress with the **@Swamidass** scenario, we have to put Adam at the 6000 year mark… at the very least. And even there, there are problems…

RichardBuggs (Richard Buggs) 2017-12-18 17:13:11 UTC #263

Thanks for sharing this Steve, that is very good of you, given your many other commitments.

RichardBuggs (Richard Buggs) 2017-12-18 21:08:43 UTC #264

Hi **@Swamidass** thank you for contributing some substantial and substantive posts to this discussion in the past few days. Sorry that I have not acknowledged your presence here sooner. Because my time available for this discussion is very limited, I have had to prioritise responding to Dennis as he has invested more in this discussion than anyone else. I have therefore been making a lot of the use of the website function that allows me to only see Dennis’s posts, so many of the other posts I have not even read, let alone had time to engage with (though I would like to have done, were there not so many demands on my time). However, your posts have now come to my attention and I will just make a few comments. I will try to restrict myself to your points most narrowly focused on the points I have raised, as I don’t have time to comment on everything you have said. Many of your comments and observations I agree with, and I appreciate the peaceable nature of your contributions, and your occupation of the middle ground between Dennis and myself.

> Swamidass:
>
> The question on the table is actually quite interesting from a purely scientific point of view. Population genetics is very non-intuitive. Engaging this question can help us all get this straight, even if (as I expect), we will see the mainstream position continue to be supported by the evidence. By taking the questions seriously, it gives us more certainly, and also more credibility to skeptics. Frankly, it is also fun.

Hear, hear!

> Swamidass:
>
> We need to know the Time to Most Recent 4 Alleles (TMR4A). This is not a standard computed number in genetics.

This is exactly my point. Thank you for stating it so concisely. To my mind, the way ahead would be to write a programme that computes the TMR4A for each haplotype block of the human genome, and work out a reasonable time

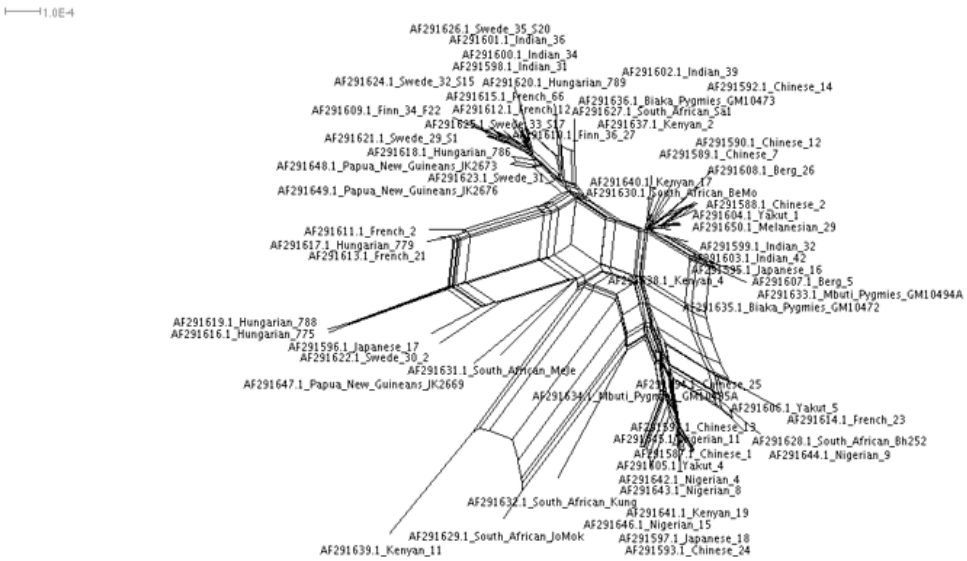
frame using data from all blocks. Until that has been done, I do not think we can say that the bottleneck hypothesis has been rigorously tested.

> Swamidass:
>
> As **@RichardBuggs** says, 78 is not a problematic number.
> So, provisionally speaking, it does seem possible, maybe even likely, that in this scenario we could observe this 78 SNP variants (perhaps even at these distributions) in the population today from a primordial pair 500,000 years ago.

I am glad that you agree with my back-of-the-envelope calculations, and my conclusions from that. I am interested that when you add in recombination you get a potentially shorter time to a primordial pair. I would also be glad to hear what you think of the rest of my post, where I suggest that if the population continued to expand from a single couple up to 7 billion individuals, then the time to a primordial pair could be lower than 500,000 years. All in all, it seems to me that the jury is still out on a minimum bound for a bottleneck.

> Swamidass:
>
> Eyeballing clusters in data cannot be a substitute for actually modeling the data with simulations and more rigorous treatments.

I agree that more rigorous treatment is desirable. However eyeballing the data can be a useful heuristic in illustrating a point and deciding what ideas to follow up. The clustering that I did of the Zhao et al (2000) sequences shows that one can reasonably place them into clusters, and that not every possible combination of the variants are found in that data. If you prefer, here is a haplotype network for the whole Zhao et al (2000) dataset:



Looking at this - “eyeballing” again! - there are clear clusters with fairly recent common ancestors.

> Swamidass:
>
> in the very first few generations, some locations will very quickly drift to 3, 2, or 1 allele.

Agreed. So not every haplotype block in the human population today would have its TMR4A at the bottleneck (if one occurred) - some would have them at a more recent date, due to earlier loss of ancestral haplotypes. Just looking at such blocks in isolation would give a misleadingly young age for a bottleneck.

> Swamidass:
>
> Basically, we expect large linkage domains of the genome to have only one ancestral sequence, because of drift in the early population. That seems to undercut a major source of variation, and also suggest that this bottleneck should have been detected by now.

I think we are planning to come on to linkage disequilibrium in this discussion, one we come to the Tenesa et al paper.
[quote="Swamidass, post:254, topic:37039"]
Is this conversation assuming common descent?
[/quote]
Absolutely[quote="Swamidass, post:260, topic:37039"]
Btw, I think the strongest evidence against a bottleneck in the last 6 million years is trans-species variation,
[/quote]
I agree. I am assuming we would come to this in detail at some point.[quote="Swamidass, post:260, topic:37039"]
None of the conclusions Dennis presented are disputed in mainstream science either. So he is not so much "making the case" but explaining what others have found. The evidential standards are just much much lower for that type of activity. He did not thing wrong by quoting a selection of papers.
[/quote]
Here I disagree with you, sorry! Most mainstream papers have not tested the bottleneck hypothesis. As you have said, the "Time to Most Recent 4 Alleles (TMR4A)… is not a standard computed number in genetics". To test a bottleneck of two hypothesis, this is what is needed. There is quite a lot of interpretation going on by Dennis. Take the Zhao et al paper: Dennis is not making a point that the authors are making. This is to a greater or lesser extent the same for the other papers he cites in Adam and the Genome, as I have shown in my blog. Also, and this is just a minor point, the Zhao et al paper was not cited in Adam and the Genome: Dennis has cited it in this discussion to back up a passage which has no citations in Adam and the Genome. I would also note that thus far, no mainstream scientist has disputed my **blog** which has been read by many scientists.

Thanks again for your input. The time I can give to this discussion today is up. It is 10pm my time and I need to wake my baby son to have his final feed for the day!

Jonathan_Burke (Jon) 2017-12-19 02:54:42 UTC #265

> RichardBuggs:
>
> There is quite a lot of interpretation going on by Dennis. Take the Zhao et al paper: Dennis is not making a point that the authors are making. This is to a greater or lesser extent the same for the other papers he cites in Adam and the Genome, as I have shown in my blog.

I don't see this. Dennis is making the point that there's no evidence for a two person bottleneck in any of the studies he has cited. I don't think that's a matter of interpretation. Your only argument is this.

> None of the studies above set out to explicitly test the hypothesis that humans could have passed through a single-couple bottleneck.

But you haven't demonstrated that this hypothesis needs to be tested in a special way which hasn't already been tested by previous studies. The fact is that previous studies have consistently arrived at the conclusion that a bottleneck of only a very small number of people is just not credible.

Here's one.

> Genetic variation at most loci examined in human populations indicates that the (effective) population size has been approximately 10(4) (i.e., 10,000) for the past 1 Myr and that individuals have been genetically united rather tightly. Also suggested is that **the population size has never dropped to a few individuals, even in a single generation**. These impose important requirements for the hypotheses for the origin of modern humans: a relatively large population size and frequent migration if populations were geographically subdivided. **Any hypothesis that assumes a small number of founding individuals throughout the late Pleistocene can be rejected**.

Here's another.

> **There is no evidence for an exponential expansion out of a bottlenecked founding population**, and an effective population size of approximately 10,000 has been maintained.

Note that this paper states specifically that there's no evidence for "an exponential expansion out of a bottlenecked founding population", which is precisely the model you are proposing. So this study has tested this specific aspect of your hypothesis.

This study likewise specifically denies the severe bottleneck of your hypothesis.

> On the other hand our results also **deny the hypothesis that there was a severe hourglass contraction in the number of our ancestors in the late middle and upper Pleistocene**. If humans were descended from some small group of survivors of a catastrophic loss of population, then the distribution of ascertained Alu polymorphisms would show a pre-ponderance of high frequency insertions (unpublished simulation results). Instead the suggestion is that our ancestors were not part of a world network of gene flow among archaic human populations but were instead effectively a separate species with effective size of 10,000-20,000 throughout the Pleistocene.

This study also specifically tested the hypothesis of a very small bottleneck.

> Moreover, the ancient genetic history of humans **indicates no severe bottleneck during the evolution of humans in the last half million years**; otherwise, much of the ancient genetic history would have been lost during a severe bottleneck

All of these studies are clearly testing exactly what you claim has never been tested. They say there's no evidence for a bottleneck down to a small handful of people, and no evidence for an exponential population expansion after such a severe bottleneck. This is not a matter of Dennis' interpretation, this is what the studies state explicitly. If you want to claim these studies are inadequate, you have to address their contents and explain their deficiencies.

> RichardBuggs:
>
> I would also note that thus far, no mainstream scientist has disputed my blog which has been read by many scientists.

I don't see how this is relevant. Have you attempted to submit this for peer review?

DennisVenema (Dennis Venema) 2017-12-19 05:54:47 UTC #266

> RichardBuggs:

> no mainstream scientist

Did I let my mainstream scientist card expire again? I knew I was forgetting something… 🙂

GJDS (GJDS) 2017-12-19 06:01:58 UTC #267

This “heckling” from the sidelines by amateurs detracts from an otherwise interesting discussion. As I read it, **@RichardBuggs** is questioning the certainty expressed by **@DennisVenema** (that pop gen modelling is as certain as the earth going around the sun), and he is showing that such modelling includes assumptions that may not be testable.

In any event, the notion of two individuals as “starting” human population, instead of a large number, is only relevant to the biblical account, if we discard virtually all meaning in the account in Genesis - I do not think pop gen modelling can do that.

Jay313 (Jay Johnson) 2017-12-19 15:05:12 UTC #268

Yes. Everyone genuflect and remain silent. The scientists are speaking.

RichardBuggs (Richard Buggs) 2017-12-19 17:32:14 UTC #269

Hi Dennis,

I am glad to see that you have taken another look at the Zhao et al (2000) paper now and are willing to say this:

> DennisVenema:
>
> This paper can exclude a severe bottleneck for this small region for non-Africans (and presumably, Africans, but that is left unstated). At least, that’s what the authors claim - because nucleotide diversity is too high (it’s the same in this paper for Africans and non-Africans). I think they’re also suggesting that the TMRCA values supports this conclusion, but you’re right, on re-reading the paper I don’t see that explicitly stated. Messing about with haplotypes was then my attempt to show the problems with having coalescence back to 4 types within a reasonable timeframe.
>
> This paper, of course, is really only of historical interest at this point.

So I think (correct me if I am misunderstanding you here) we agree that the authors are not explicitly supporting your case. If you are happy with the comments that I and **@swamidass** have made on the coalescent analysis at the end of the Zhao et al (2000) paper, suggesting that the data is compatible with a bottleneck in the human lineage, then I am very happy to move on. Please could you tell me which paper you would like me to read next?

I think that to pick up where we were before, it would be helpful if the paper you choose explicitly supports this passage in Adam and the Genome:

“One simple way is to select a few genes and measure how many alleles of that gene are present in present-day humans. Now that the Human Genome Project has been completed and we have sequenced the DNA of thousands of humans, this sort of study can be done simply using a computer. Taking into account the human mutation rate, and the mathematical probability of new mutations spreading in a population or being lost, these methods indicate an ancestral population size for humans right around that 10,000 figure. In fact, to generate the number of alleles we see in the present day from a starting point of just two individuals, one would have to postulate mutation rates far in excess of what we observe for any animal.”

But if you prefer to leave that statement behind now, I would be happy to move onto another method of analysis. If you could tell me which paper you would like me to read next, I will be very happy to give it a close read. I think all of us will be happy to move on to a fresh paper! Thanks again for all the time you are putting into this discussion - I know that all of us have many pressures on our time.

---

tallen_1 (Tim) 2017-12-19 18:19:16 UTC #270

Richard,

I'm encouraged to see you moving on to Dennis' stronger evidence, and am glad to see my dialogue with him was useful to you in that regard. I do believe there is an outstanding question from Dennis for you to address. Since I know you're focusing your efforts in responding to him rather than other readers, I'm confident we'll see a reply from you very shortly on this:

> DennisVenema:
>
> Also, I do think it would be helpful at this point to discuss common ancestry. Zhao (2000) explicitly depends on humans sharing common ancestors with orangutans and chimpanzees. This is how they estimate the forward mutation rate for this region. We're a couple of professional biologists discussing a technical paper, so I was taking for granted that we both accepted that. I'm not so sure now, so I'll ask it again: do you accept that humans share common ancestors with chimpanzees and orangutans?

DennisVenema (Dennis Venema) 2017-12-19 18:47:02 UTC #271

> tallen_1:
>
> I'm encouraged to see you moving on to Dennis' stronger evidence, and am glad to see my dialogue with him was useful to you in that regard. I do believe there is an outstanding question from Dennis for you to address. Since I know you're focusing your efforts in responding to him rather than other readers, I'm confident we'll see a reply from you very shortly on this:
>
> DennisVenema:
> Also, I do think it would be helpful at this point to discuss common ancestry. Zhao (2000) explicitly depends on humans sharing common ancestors with orangutans and chimpanzees. This is how they estimate the forward mutation rate for this region. We're a couple of professional biologists discussing a technical paper, so I was taking for granted that we both accepted that. I'm not so sure now, so I'll ask it again: do you accept that humans share common ancestors with chimpanzees and orangutans?

Since most of the papers in this field use other primates to calibrate mutation rates in specific genome areas, it would be helpful if Richard would answer this straightforward question now before proceeding.

Swamidass (Dr. S Joshua Swamidass) 2017-12-19 18:48:39 UTC #272

> RichardBuggs:
>
> If you are happy with the comments that I and **@swamidass** have made on the coalescent analysis at the end of the Zhao et al (2000) paper, suggesting that the data is compatible with a bottleneck in the human lineage,

Just so my position is not overstated.

In this region alone, not taking LD into account, the number of variants seems consistent with a bottleneck of our ancestors (I would not use the term “human”) at or before 500,000 years ago. It is possible a more careful analysis will show problems, especially if LD is taken into acoount, but we should not mistake TMRCA in a single autosomal region for a limit on bottleneck time. TMRCA also is not an estimate effective population size.

As long as we are here, the data figure of the region clusters shows that samples are clustering strongly with population, which strongly undercuts the notion that any observable clusters correlate with alleles from a primordial couple, which we would expect to be randomly distributed in geography at this point. This does not necessarily mean it does not fit an ancient bottleneck but it does show another view of the data might weaken the case

In the end it doesn’t matter so much because, as Dennis has repeated, the evidence from other sources are much clearer.

DennisVenema (Dennis Venema) 2017-12-19 18:55:27 UTC #273

> Swamidass:
>
> In this region alone, not taking LD into account, the number of variants seems consistent with a bottleneck of our ancestors (I would not use the term “human”) at or before 500,000 years ago.

I agree.

And as such, this paper supports the conclusion I state in *Adam and the Genome*. If one was to squeeze this variation into the last 200,000 years (or even 300,000 years), one would have to increase the mutation rate to do so.

DennisVenema (Dennis Venema) 2017-12-19 18:58:53 UTC #274

> Swamidass:
>
> As long as we are here, the data figure of the region clusters shows that samples are clustering strongly with population, which strongly undercuts the notion that any observable clusters correlate with alleles from a primordial couple, which we would expect to be randomly distributed in geography at this point.

Yep. Where alleles are found in the present day is also important. If everything tracks back to 2 ancestors at 500,000 years ago, why are patterns of alleles in the places they are? Why did some haplotype blocks end up outside Africa only? Why are others only found in Africa?

---

tallen_1 (Tim) 2017-12-19 19:22:06 UTC #275

> DennisVenema:
>
> If everything tracks back to 2 ancestors at 500,000 years ago, why are patterns of alleles in the places they are?

I hope these are only rhetorical questions at this point, otherwise we’re never moving on from this paper 😉

Christy (Christy Hemphill) 2017-12-19 20:11:08 UTC #276

> DennisVenema:

> [Dennis quoting himself] “Also, I do think it would be helpful at this point to discuss common ancestry. Zhao (2000) explicitly depends on humans sharing common ancestors with orangutans and chimpanzees. This is how they estimate the forward mutation rate for this region. We’re a couple of professional biologists discussing a technical paper, so I was taking for granted that we both accepted that. I’m not so sure now, so I’ll ask it again: do you accept that humans share common ancestors with chimpanzees and orangutans?”
>
> Since most of the papers in this field use other primates to calibrate mutation rates in specific genome areas, it would be helpful if Richard would answer this straightforward question now before proceeding.

He has said he is at least assuming it for this discussion, see post 264:

> RichardBuggs:
>
> [Josh] “Is this conversation assuming common descent?”
>
> Absolutely

---

tallen_1 (Tim) 2017-12-19 20:35:59 UTC #277

Christy,

In the same sense Richard was not willing to accept Dennis moving on “ad argumentum” from the Zhao et al (2000) paper but wanted something more real, I think Dennis is also asking for Richard’s actual take on common ancestry. I can think of no legitimate scientific reason to refuse to answer this question. Can you? If Richard does not accept what is universally considered established scientific fact within genetics, it would be informative to the discussion. For instance, he may be more inclined to treat things such as mutation rates as assumptions rather than conclusions. Which may color his intuitions on how much freedom he has to play with the parameters to get to a bottleneck of two. I also believe given all the transparency he’s demanded of Dennis, he owes him an answer.

Christy (Christy Hemphill) 2017-12-19 21:06:17 UTC #278

> tallen_1:
>
> I can think of no legitimate scientific reason to refuse to answer this question.

Not a scientific reason, no. But lots of people commenting here have relationships with various organizations and institutions with certain a-scientific commitments, and so I understand and sympathize with a reticence to be completely upfront with one’s personal beliefs and convictions on points that are considered political or controversial in those arenas. People have lost their jobs over things they have said on BioLogos. It should be enough to clarify what the terms of the discussion are.

---

tallen_1 (Tim) 2017-12-19 21:28:40 UTC #279

Christy,

These aren’t personal beliefs but scientific ones, correct? To my knowledge Dennis is not asking Richard about theological or religious beliefs, but is limiting his questions to scientific ones. Michael Behe has an affiliation with the Discovery Institute, the premier ID association in the US, and he acknowledges his acceptance of common descent

without issue to any relationships or standing there. Nor does it look like the Queen Mary University of London where Richard is employed would impose any negative consequences on him over such an acknowledgement.

But to your point, if Richard feels he cannot be open about where he falls on common descent, then at the minimum I hope he has the wherewithal to say so. And hopefully also address whether he would feel similarly constrained to not be able to openly acknowledge whether a bottleneck to two in the past 500,000…or even 200,000 years for that matter is implausible should Dennis effectively make his case in this exchange. We should at the very minimum have a clear expectation of what can be achieved in this conversation.

DennisVenema (Dennis Venema) 2017-12-19 23:30:15 UTC #280

I can't imagine why **@RichardBuggs** would fear for his job by agreeing with the scientific consensus on this point - but you're correct, there may be other issues at play. I merely want to know if common descent is a given for this discussion. Also, knowing what Richard thinks are reasonable speciation times would also be useful. And yes, there is some irony that I am required to lay out everything in great detail but Richard need not answer even very basic biological questions. I'll just state for the record that I've asked, and if Richard chooses not to reply, then so be it.

> RichardBuggs:
>
> So I think (correct me if I am misunderstanding you here) we agree that the authors are not explicitly supporting your case.

Yes they are. They claim that there is no evidence in their data for a severe population bottleneck in non Africans. Even if we ignore the fact that Africans are by implication even less likely to have had such a bottleneck, the authors rule out a sharp bottleneck for non Africans. Even if non Africans were the only people on earth this paper would still count as support for *Adam and the Genome*.

But, by all means let's move on and let Zhao (2000) rest in peace.

What next? We could do the Alu paper, but given the foregoing conversation and our discussion of TMRCA and TMR4A values, why don't we do **this one** next? I think it follows on nicely from the previous discussion. The authors estimate a TMRCA at over 2MYA, and they also plot out the TMR4A - have a look at figure 3. The TMR4A is over 500,000 years ago. In fact, I count 10 haplotypes at 500,000 years ago in their analysis. This would again support the conclusion I come to in *AatG*, and it's in a format that is easy to see.

---

gbrooks9 (George Brooks) 2017-12-20 00:38:53 UTC #281

> DennisVenema:
>
> I merely want to know if common descent is a given for this discussion. Also, knowing what Richard thinks are reasonable speciation times would also be useful.

I can understand **@RichardBuggs** choice of words: "for the purpose of this discussion" … it knits well on the idea of common descent.

But how does he say "and I think speciation, for the purpose of this discussion, can occur in x years…"

I doubt if you will ever get him to phrase an answer **that** specific!

---

tallen_1 (Tim) 2017-12-20 01:08:55 UTC #282

I think Richard could give some parameters. Such as “I think any bottleneck to two within the last 50,000 years is effectively ruled out by the evidence.” Or 100,000 years, or 200,000 etc. The notion that he cannot (nor can anyone) pinpoint with laser precision a date does not mean you cannot commit to any minimal parameter at all. I would presume Richard could do so if he chooses. If he doesn’t, it’s a safe bet he explicitly chose not to. And transparency and any notion of a free and open discussion on this topic will be the first casualty of such a decision. Ditto if he ducks out of giving an open and transparent answer on common descent. It wouldn’t mean then the conversation isn’t still useful. But we’ll all have to revise downward our expectations for it sadly. As we will have to revise downward the value of any intuitions and judgements of a scientist who can’t be open about what they think scientifically. I hope to avoid that outcome if we can.

---

gbrooks9 (George Brooks) 2017-12-20 02:03:40 UTC #283

> tallen_1:
>
> Such as “I think any bottleneck to two within the last 50,000 years is effectively ruled out by the evidence.”

@tallen_1

Yeah? I think that would be amazing… when will he say that? What I expect he will say is something like that - - but with a few double negatives.

---

tallen_1 (Tim) 2017-12-20 02:08:28 UTC #284

Maybe, though I hope he avoids such obscurantism. Brings to mind the lawyer trick of: “No, those accusations are absolutely false, I didn’t do those things as they they described them.” Which of course can mean (not by accident), that maybe they did do those things just not precisely as described in every detail. Hopefully we can avoid such parlor tricks here.

---

gbrooks9 (George Brooks) 2017-12-20 02:20:18 UTC #285

> tallen_1:
>
> Hopefully we can avoid such parlor tricks here.

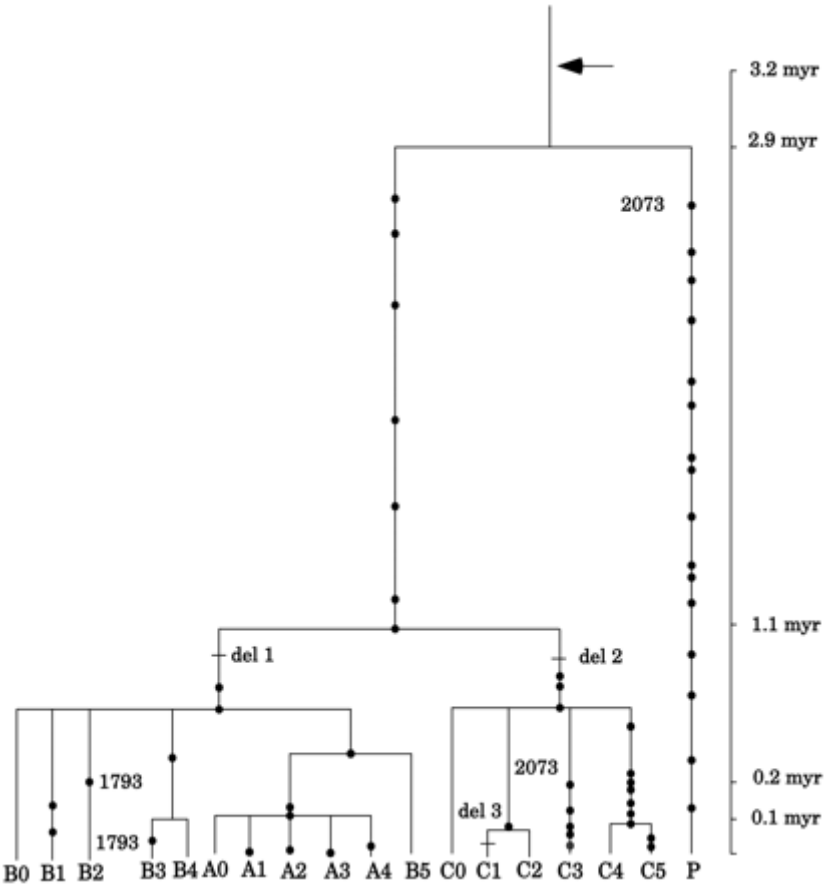
@tallen_1 ,

Then you haven’t been reading some of the threads I’ve been reading the last few days…

Swamidass (Dr. S Joshua Swamidass) 2017-12-20 17:02:42 UTC #286

Interesting paper…

> DennisVenema:
>
> What next? We could do the Alu paper, but given the foregoing conversation and our discussion of TMRCA and TMR4A values, why don’t we do this one next? I think it follows on nicely from the previous discussion. The authors estimate a TMRCA at over 2MYA, and they also plot out the TMR4A - have a look at figure 3. The TMR4A is over 500,000 years ago. In fact, I count 10 haplotypes at 500,000 years ago in their analysis. This would again support the conclusion I come to in AatG, and it’s in a format that is easy to see.



http://www.genetics.org/content/genetics/172/2/1139/F3.medium.gif

So, in this figure, we see a horizontal cut at 0.5 mya shows 10 branches in the phylogenetic tree.
However, this does not seem to make the case very strongly. @DennisVenema and @RichardBuggs , I had some questions and observations…

1. It looks like my estimate of (TMRCA / 4 = TMR4A) is holding up. That is encouraging.

2. At 0.6 mya there is just 3 alleles, and the mutational support for most those splits is low. What do you think is the variance of the date where the transition from 3 to 10 alleles takes place? It seems that a different phylogenetic tree could be easily drawn with the same data that did show 4 or less alleles at 0.5 mya. Even a small variance in mutation rate would do the same thing. @DennisVenema , am I missing something there?

3. However, it would be much harder to see how there were just 4 alleles, say, at 0.2 mya. @RichardBuggs , what is the minimum time to bottleneck you say is plausible with this data (assuming no miracles)? I know your working hypothesis is 0.5 mya, but does this data rule out anything earlier?

4. A couple other interesting features is the 1793 and 2073, which are marked because they do not fall into nested clades (either because of recombination or the birthday problem https://en.wikipedia.org/wiki/Birthday_problem). I'm sure no one disputes these alleles have the same origin (because they are all human!), so that is a good reminder that we do not expect perfect nested clades in evolutionary processes, and that is not what we see.

5. I would also point out that the gene involved here (CMAH) is a **pseudogene**, which means it no longer is producing a functional protien. If we were to say there was a bottleneck here, this would count as some *de facto* evidence for common descent. As the primordial couple's genome would include the history of this gene in its genome; a false history if they had been *de novo* created, and without interbreeding.

6. If we allow for interbreeding, of course, all bets are off. All this diversity could have been injected by interbreeding events. That, as I understand it, is not germane to this conversation. The question is about a single couple bottleneck, not a single couple origin.

7. The distinctions between TMRCA and TMR4A do not apply in considering mitochondrial and Y-chromosomal DNA. Does everyone agree that those dates put a lower bound on bottleneck (assuming no miracles and no interbreeding)? That would be at about 150 kya to 200 kya; do you agree **@RichardBuggs** ?

This dataset, however, has all the same problems as Zhao. It is just one region of the genome, and not even that many samples. A better analysis will look at the whole genome, estimate effective population size, and use a larger number of samples. It is in those studies that the evidence appears clearer. And of course, there is still trans-species variation…

> DennisVenema:
>
> I can't imagine why **@RichardBuggs** would fear for his job by agreeing with the scientific consensus on this point - but you're correct, there may be other issues at play. I merely want to know if common descent is a given for this discussion.

> tallen_1:
>
> Ditto if he ducks out of giving an open and transparent answer on common descent.

He did not duck the question. He answered unequivocally that this conversation presumes common descent. Moreover, as we get deeper into the data, more evidence for common descent is uncovered all the time (e…g the pseudogene).

> tallen_1:
>
> But to your point, if Richard feels he cannot be open about where he falls on common descent, then at the minimum I hope he has the wherewithal to say so.

It seems as if you are asking for him to state what he ***personally*** believes about common descent. That is not a relevant question. As should be clear, if we allow for miracles (e.g. mosaic Adam and Eve) none of this analysis is solid any ways. In science, we do not consider such fantastical things, but in one's personal beliefs we can believe them if we want. As long as that is kept separate from the scientific work, and we are honest about the data, no one cares what we "believe in our heart" about such things.

It just doesn't matter our personal beliefs, if we are honest with what the data shows.

DennisVenema (Dennis Venema) 2017-12-20 18:06:28 UTC #287

I think we're pretty much on the same page with this one, yes.

Is this positive evidence for the claim I make in *Adam and the Genome*? Yes. I can't see how we can squeeze this variation into 2 people at 200,000 years ago (or even 300,000 years ago, if one was to accept *Homo sapiens* at this time). Can you, or can **@RichardBuggs** ?

---

tallen_1 (Tim) 2017-12-20 18:20:41 UTC #288

Swamidass,

I'm sorry, but we're going to have to disagree here. I may not be a biologist or geneticist, but I am scientifically literate and for a time belonged to that community (research-oriented doctoral program I ended with my masters some time ago). What a scientist is or is not convinced of within their field is highly relevant to any discussion within it. You're pretending it isn't. And that's just plain wrong.

Richard is wanting to have this exchange with Dennis take on the appearance of two peers openly debating an issue of scientific merit, both presumably with open minds, both presumably capable of convincing or being convinced to change their minds, and both being being upfront and honest about what the evidence does or does not show.

However, if you have one of these parties absolutely refuse to acknowledge what they believe the science does or doesn't show, and only grant it as an "assumption" for the purposes of debate, then you distance them from that even platform where the capacity to change views and acknowledge good evidence when presented ought reside.

If Richard for personal reasons refuses to acknowledge that, for instance, the genetic evidence clearly shows that a bottleneck to two is implausible within the last 50,000 years, despite himself thinking so, then he's clearly not going to acknowledge that the evidence points to no such bottleneck within 500,000 years no matter how strong a case Dennis may provide. Or, alternatively if he feels that a bottleneck within 50,000 or even 10,000 years is entirely plausible, then he really ought share that with Dennis so he can appreciate just how far apart they are and adjust his conversation appropriately.

If Richard likewise personally accepts that common descent is well and convincingly attested to by the evidence but cannot acknowledge it for personal reasons, we would then have to wonder if he would feel the same reluctance to acknowledge no bottleneck of two within the human lineage for similar reasons. If Richard personally is not convinced of common descent, then Dennis ought know that as even if he "wins" the argument, since it is partially premised on common descent as a dependency, Richard will leave the conversation believing Dennis won a technical but ultimately meaningless victory since he does not accept that dependency and so his position will remain unchanged.

The question is are we going to have a fair and honest conversation between peers, where both sides may be expected to change their views if required by the evidence that comes out here in the discussion? Or aren't we?

Again, I do not think one needs a background in biology or genetics to answer that question.

Swamidass (Dr. S Joshua Swamidass) 2017-12-20 19:40:57 UTC #289

> DennisVenema:
>
> Is this positive evidence for the claim I make in Adam and the Genome? Yes. I can't see how we can squeeze this variation into 2 people at 200,000 years ago (or even 300,000 years ago, if one was to accept Homo sapiens at this time). Can you, or can **@RichardBuggs** ?

It seems like you are limiting your claims to merely *Homo sapiens*, is that correct? I thought we were asking about bottlenecks in our distant past going back to the origin of *Homo* about 2 million years ago. By limiting your claims this way, are you suggesting that you think it is possible for there to have been a single couple bottleneck, say, 2 million years ago?

T_aquaticus 2017-12-20 21:32:28 UTC #290

> Swamidass:
>
> It seems like you are limiting your claims to merely Homo sapiens, is that correct? I thought we were asking about bottlenecks in our distant past going back to the origin of Homo about 2 million years ago. By limiting your claims

> this way, are you suggesting that you think it is possible for there to have been a single couple bottleneck, say, 2 million years ago?

It might be useful to remind everyone that Dennis Venema originally stated that the chances of there being a 2 person bottleneck in the last 200,000 years is the same as the chances of Geocentrism being true. That is the claim which Buggs is challenging. As **@glipsnort** has stated many times, if you go back far enough you can posit a 2 person bottleneck at any time and such a bottleneck will be indistinguishable from a large constant population as determined by modern genetic diversity. This is why Dennis limited the time span so that he could define how certain he was of the conclusion.

DennisVenema (Dennis Venema) 2017-12-20 21:39:07 UTC #291

> Swamidass:
>
> It seems like you are limiting your claims to merely Homo sapiens, is that correct? I thought we were asking about bottlenecks in our distant past going back to the origin of Homo about 2 million years ago. By limiting your claims this way, are you suggesting that you think it is possible for there to have been a single couple bottleneck, say, 2 million years ago?

In the book I make the claim that humans evolve as a population, and I define human as “our species” - *Homo sapiens*. (That’s not to say that other species might not have had the image of God, and so on.) In the book I place *H. sapiens* at 200 KYA, as was the consensus at the time. I think the evidence is solid that there is not a bottleneck to 2 in our ancestry for at least the last 500,000 years, but I don’t defend that in the book per se. From there it gets progressively more challenging to make a strong claim, but I think that even 1,000,000 years is reasonable to exclude a bottleneck. 2MYA? By now we’re at the limit of PSMC and other similar modelling approaches.

Now, is there positive evidence for a bottleneck to 2 (or even 20 or 200 or 2000?) at any time in the last 3,000,000 years or more? Nope. At best one could claim that our present-day methods cannot exclude the possibility between 1-3 MYA.

Homo erectus as Adam? I can’t see how this solves anything.

Swamidass (Dr. S Joshua Swamidass) 2017-12-20 21:48:41 UTC #292

> T_aquaticus:
>
> It might be useful to remind everyone that Dennis Venema originally stated that the chances of there being a 2 person bottleneck in the last 200,000 years is the same as the chances of Geocentrism being true. That is the claim which Buggs is challenging. As **@glipsnort** has stated many times, if you go back far enough you can posit a 2 person bottleneck at any time and such a bottleneck will be indistinguishable from a large constant population as determined by modern genetic diversity. This is why Dennis limited the time span so that he could define how certain he was of the conclusion.

If that is the case, I am confused.

@RichardBuggs seems to have been clear he has been thinking about a bottleneck at around 500 kya. **@agauger** is thinking of one as early as 2 mya. It does not seem that **@RichardBuggs** is challenging claims of a bottleneck before 200 kya, but rather that there was not bottleneck in our ancestors ever. If **@DennisVenema** means to limit his claims to just within the last 200 kya, then perhaps there is not even a disagreement. Perhaps if **@DennisVenema** clarifies that he only intended the limited claim, we are done here.

Though, trans-species variation does seem to make a bottleneck in the last 6 mya unlikely…but if the goal is merely to show that within the last 200 kya a bottleneck is unlikely, I'm not sure how this all fits in. What exactly is the disagreement about?

> DennisVenema:
>
> In the book I make the claim that humans evolve as a population, and I define human as "our species" - Homo sapiens. (That's not to say that other species might not have had the image of God, and so on.) In the book I place H. sapiens at 200 KYA, as was the consensus at the time. I think the evidence is solid that there is not a bottleneck to 2 in our ancestry for at least the last 500,000 years. From there it gets progressively more challenging to make a strong claim, but I think that even 1,000,000 years is reasonable to exclude a bottleneck. 2MYA? By now we're at the limit of PSMC and other similar modelling approaches.

So, it sounds like the "as certain as the earth orbits the sun" claim is merely about *Homo sapiens* (avoiding the term "human" is helpful here) as a taxonomic category and ignoring interbreeding, and only applies to the last 200 kya to 300 kya.

Perhaps **@RichardBuggs** can clarify, but it seems he agrees with that; the issue is more about the distant past, and non-*Homo sapiens*, such as *Homo erectus*. The only evidence that stretches that far back is trans-species variation. In the intermediary zone of 500 kya, it sounds like you still rule out a bottleneck, but with less confidence. *Homo erectus* arises about 2 mya at the limit of PSMC, I'm not sure we have the same confidence here at all. It seems you think that also.

If that is the case, maybe there is no real disagreement here. At least, I am struggling to find it.

> DennisVenema:
>
> Homo erectus as Adam? I can't see how this solves anything.

Some people feel it does solve things. It would be worth understanding why. That is for another thread though.

> DennisVenema:
>
> Now, is there positive evidence for a bottleneck to 2 (or even 20 or 200 or 2000?) at any time in the last 3,000,000 years or more? Nope. At best one could claim that our present-day methods cannot exclude the possibility between 1-3 MYA.

That seems to be the main thing that **@RichardBuggs** and **@agauger** have been arguing for. I still think trans-species variation is the fly in the ointment, but I no longer see the disagreement here. What are we debating exactly?

T_aquaticus 2017-12-20 21:54:36 UTC #293

> Swamidass:
>
> **@RichardBuggs** seems to have been clear he has been thinking about a bottleneck at around 500 kya. **@agauger** is thinking of one as early as 2 mya. It does not seem that **@RichardBuggs** is challenging claims of a bottleneck before 200 kya, but rather that there was not bottleneck in our ancestors ever

Here is the original statement posted by Richard Buggs:

"A few months ago, I was reading a new book by Dennis Venema and Scot McKnight entitled Adam and the Genome. I was surprised to find a claim within the book that the past effective population size of humans has definitely never dropped below 10,000 individuals and that this is a fact of comparable scientific certainty to heliocentrism."
link

In that book, Venema and McKnight stated that the human population has not dipped below 10,000 individuals over the last 200,000 years, and that the confidence they had in that conclusion was equal to their confidence in the accuracy of Heliocentrism. By disagreeing with Venema and McKnight, Buggs is disagreeing with that time frame.

It's a bit like someone saying that a 2 minute mile is nearly impossible for a human, and then changing the argument to a 400 m race and claiming a 2 minute time is completely possible. You can't change the time frame and still be criticizing the same conclusion.

Chris_Falter (Chris Falter) 2017-12-20 22:04:46 UTC #294

@DennisVenema , **@RichardBuggs** , **@Swamidass**

I appreciate the in-depth discussion you are having here. As a tyro in the domain of biology I am only able to listen and learn. However, I do have a pretty good understanding of statistical methods, so I would like to ask that you all *quantify* the certainty of your assertions. If you could say, for example, that a particular study indicates <5% probability of MRCA < 300kya, and some other study indicates <2% probability of MRCA <300kya, the I would conclude the probability of MRCA <300kya is 0.001, assuming the data in the 2 studies are IID.

In addition, the consistency of today's genome with a population of just 2 individuals at a certain point in the past does not mean the scientific community believes that was the actual population at that time, correct? This is important because if we say, e.g., that Zhao 2000 is consistent with a MRCA 50kya, that does ***not*** contradict or overrule 10 other studies that say the MRCA was 500kya. Assuming such studies exist. In that case, we would have to (from the scientific perspective) say the MRCA was no fewer than 500kya, correct?

Thanks!

Swamidass (Dr. S Joshua Swamidass) 2017-12-20 22:16:11 UTC #295

> T_aquaticus:
>
> In that book, Venema and McKnight stated that the human population has not dipped below 10,000 individuals over the last 200,000 years, and that the confidence they had in that conclusion was equal to their confidence in the accuracy of Heliocentrism. By disagreeing with Venema and McKnight, Buggs is disagreeing with that time frame.

We are not going to get into a debate about what "human" should mean, but there is sufficient confusion in its use that it might be the entire reason for the disagreement. In **@DennisVenema** 's mind "human" = Homo sapien, but this not currently the dominant view in science. It appears **@agauger** thinks Homo genus = "human," in agreement with the Museum of Natural History. Without having differences in these meanings clarified, I can see how confusion arose. In general, it is best to avoid the term "human" in making scientific claims for this reason.

It sounds like **@RichardBuggs** and **@agauger** would not have objected to a statement like this; and it also seems this is what **@DennisVenema** thinks:

> *Homo sapiens* arise about 200 kya, and since that time we have ***very high confidence*** that our **ancestors** do not dip down to a single couple. In the deeper past, however, it is harder to know with such certainty, but one would have to accept a very ancient Adam who was not a *Homo sapien*.

And I agree, there is no positive evidence for a bottleneck of 2, but it just might be outside the genetic streetlight.

> Chris_Falter:
>
> In addition, the consistency of today's genome with a population of just 2 individuals at a certain point in the past does not mean the scientific community believes that was the actual population at that time, correct?

Correct. It just means we cannot tell for sure, and have no reason to think that it was a single couple. In fact, if the data is consistent with a single couple, it is probably also consistent with a group of 10.

Also, I'm not sure we concluded that Zhao 2000 is consistent with a MRCA of 50 kya, but that it might be consistent with a MR4A of about 250 kya. You are right too, that this does not contradict the studies that show 500 kya. The issue is that cherry picking locations is always going to be a problem. We have to look at the whole genome, as is done in some of the other papers. There is very high variance in MRCA time for genetics (but not for genealogy!), so we expect there to be different estimates. An average of across several portions of the genome would probably be best.

Also, it is important to keep separate the notion of an ancestor bottleneck and a single couple origin to "human." Part of this gets to the fuzzy definition of species. From a taxonomic point of view, we have very sparse samples of a large population, and cannot really define with clarity any lines. In context of human origins, however, some people do think there was a "line" somehow. Perhaps there was, but we cannot discern it scientifically. There is an open question about what "human" is, but that is a conversation for another day.

DennisVenema (Dennis Venema) 2017-12-20 22:26:46 UTC #296

> T_aquaticus:
>
> In that book, Venema and McKnight stated that the human population has not dipped below 10,000 individuals over the last 200,000 years, and that the confidence they had in that conclusion was equal to their confidence in the accuracy of Heliocentrism. By disagreeing with Venema and McKnight, Buggs is disagreeing with that time frame.

Not quite. The (now infamous) quote says the following:

"As our methodology becomes more sophisticated and more data are examined, we will likely further refine our estimates in the future. That said, we can be confident that finding evidence that we were created independently of other animals or that we descend from only two people just isn't going to happen. Some ideas in science are so well supported that it is highly unlikely new evidence will substantially modify them, and these are among them. The sun is at the center of our solar system, humans evolved, and we evolved as a population."

I also say this in the very next paragraph:

"Put most simply, DNA evidence indicates that humans descend from a large population because we, as a species, are so genetically diverse in the present day that a large ancestral population is needed to transmit that diversity to us. To date, every genetic analysis estimating ancestral population sizes has agreed that we descend from a population of thousands, not a single ancestral couple. Even though many of these methods are independent of each other, all methods employed to date agree that the human lineage has not dipped below several thousand individuals for the last three million years or more—long before our lineage was even remotely close to what we would call "human." Thus the hypothesis that humans descend solely from one ancestral couple in has not yet found any experimental support,— and it is therefore not one that geneticists view as viable."

So, I do discuss studies that go back past humans, and I show that there is not a case to be made from those studies that Adam and Eve are somehow not human and further back in time. The “heliocentrism quote” is more limited in its scope. It’s about humans.

Mervin_Bitikofer (Mervin Bitikofer) 2017-12-20 22:46:27 UTC #297

Had you (in true time-machine style) been able to look ahead to these threads and see all the kerfuffle raised by Dr. Buggs and others around the paragraph(s) above, would you have written anything differently? Is there a single change in any wording you would make were you penning those paragraphs now?

If this is a presumptuous question --feel free to disregard. Just my impertinent curiosity piping up here.

Jonathan_Burke (Jon) 2017-12-21 02:29:00 UTC #298

> Swamidass:
>
> That seems to be the main thing that **@RichardBuggs** and **@agauger** have been arguing for. I still think trans-species variation is the fly in the ointment, but I no longer see the disagreement here. What are we debating exactly?

You’re missing the fact that Dr Buggs is doing a bait and switch.

> Swamidass:
>
> We are not going to get into a debate about what “human” should mean, but there is sufficient confusion in its use that it might be the entire reason for the disagreement. In **@DennisVenema** ’s mind “human” = Homo sapien, but this not currently the dominant view in science. It appears **@agauger** thinks Homo genus = “human,” in agreement with the Museum of Natural History. Without having differences in these meanings clarified, I can see how confusion arose. In general, it is best to avoid the term “human” in making scientific claims for this reason.

But Dennis clarified that he was speaking of homo sapiens.

> Swamidass:
>
> It sounds like **@RichardBuggs** and **@agauger** would not have objected to a statement like this; and it also seems this is what **@DennisVenema** thinks:

If you look at what they’ve posted, they haven’t been contesting the definition of “human”. Their concern has been placed elsewhere.

---

gbrooks9 (George Brooks) 2017-12-21 06:27:51 UTC #299

> Swamidass:
>
> It seems like you are limiting your claims to merely Homo sapiens, is that correct? I thought we were asking about bottlenecks in our distant past going back to the origin of Homo about 2 million years ago. By limiting your claims this way, are you suggesting that you think it is possible for there to have been a single couple bottleneck, say, 2 million years ago?

@Swamidass , what an odd question to ask.

When a scientist rules out a the possibility of something between 2 pm and 10 pm… would you ask him: "… are you suggesting that it could happen between 10 pm and midnight?"

If you got a major eye-roll, would you be surprised?

If the testing is designed to eliminate the possibility of something between 1 and 200,000 years ago … I think it would take a lot more testing to see what happens if you change the time frame **beyond** 200,000 years ago.

But you probably saw this quote from @DennisVenema by now, right?

> DennisVenema:
>
> I also say this in the very next paragraph:
>
> **"Put most simply, DNA evidence indicates that humans descend from a large population because we, as a species, are so genetically diverse in the present day that a large ancestral population is needed to transmit that diversity to us."**
>
> **"To date, every genetic analysis estimating ancestral population sizes has agreed that we descend from a population of thousands, not a single ancestral couple. Even though many of these methods are independent of each other, all methods employed to date agree that the human lineage has not dipped below several thousand individuals for the last three million years or more—long before our lineage was even remotely close to what we would call "human."**
>
> **"Thus the hypothesis that humans descend solely from one ancestral couple … has not yet found any experimental support,— and it is therefore not one that geneticists view as viable."**

RichardBuggs (Richard Buggs) 2017-12-21 09:22:20 UTC #300

Hi Joshua,
Very briefly as I have lots to do before the Christmas break.

> Swamidass:
>
> As long as we are here, the data figure of the region clusters shows that samples are clustering strongly with population, which strongly undercuts the notion that any observable clusters correlate with alleles from a primordial couple, which we would expect to be randomly distributed in geography at this point. This does not necessarily mean it does not fit an ancient bottleneck but it does show another view of the data might weaken the case

I see a good mix of different races in all the major clusters of the network diagram. Indian/Hungarian/Franch/Papua New Guinean in one. Chinese, Kenyan, South African, Melanesian in another. Indian, Japanese, Mbuti pygmies in another. Nigerian, Chinese and French in another. This suggests to me that the clusters come from ancestral haplotypes. Even if they didn't, one could explain it by population structure after a bottleneck with loss of haplotypes by drift in some areas.

I will respond at greater length as time is available.

T_aquaticus 2017-12-21 15:53:57 UTC #301

> Swamidass:
>
> We are not going to get into a debate about what “human” should mean, but there is sufficient confusion in its use that it might be the entire reason for the disagreement.

There is no confusion when a time frame is given. What they are saying is that the population leading to today’s human population did not dip to two people over the last 200,000 years. It doesn’t matter if you define those populations as human or bloppobops, all that matters is the time frame.

---

gbrooks9 (George Brooks) 2017-12-21 16:02:45 UTC #302

> RichardBuggs:
>
> Even if they didn’t, one could explain it by population structure after a bottleneck with loss of haplotypes by drift in some areas.

Yes, yes… **@RichardBuggs** … one **could** explain it … explain it away.

So when will you start lecturing **@DennisVenema** on the idea that no matter what his tests and experimental math shows, God could have just miraculously inserted maximum genetic diversity into the human race - - at any time after the Flood.

When it comes to cherry-picking special circumstances for how to get around the limits of scientific evidence, there’s really nothing like a few miracles of God… or a long series of miracles to create something that looks "just like evolution: … but really isn’t - - because God is quite the prankster (?!).

---

gbrooks9 (George Brooks) 2017-12-21 16:10:43 UTC #303

> T_aquaticus:
>
> There is no confusion when a time frame is given. What they are saying is that the population leading to today’s human population did not dip to two people over the last 200,000 years. It doesn’t matter if you define those populations as human or bloppobops, all that matters is the time frame.

@T_aquaticus , perfect answer.

@Swamidass , it is clear that **@DennisVenema** has been avoiding the “bugaboo” of “Defining what is a Human” by simply ignoring the categories, and working with a single continuity of “common descent”.

While common descent is a maze of riddles if you are going from “older to newer” populations (because you never know when you are going to end up in a genetic cul de sac).

But if we are going backwards, from “newer to older”, there’s only path to follow, right?

Some might want to entertain the idea that one branch “cross-bred” with another branch… but is that in keeping with the Biblical model of human descent? Yes, there are the Nephilim … but is that how you and **@RichardBuggs** are going to solve the diversity problem?: **“we get around the one mating pair bottleneck” by introducing a few hundred additonal breeding pair where one of the genetic contributors are Nephilim"**

Even if we were to allow for that … it doesn't look like you can get down to a single mating pair, or even a few hundred mating pair in just 6000 years.

DennisVenema (Dennis Venema) 2017-12-21 17:15:55 UTC #304

> T_aquaticus:
>
> bloppobops

Oh, I'm quite sure that bloppobops had a unique origin - right here! I guess if I've quoted your post that's now N=2, and writing out the term once more bumps them to N=3. 🙂

In all seriousness, I won't be able to contribute much of anything to this thread for the foreseeable future. Merry Christmas, all.

RichardBuggs (Richard Buggs) 2017-12-21 22:30:22 UTC #305

Hi Dennis,

> DennisVenema:
>
> But, by all means let's move on and let Zhao (2000) rest in peace.

I would love to do this, but my offer of moving on was contingent on us agreeing that it does not provide a suitable citation to support your case in chapter 3 of Adam and the Genome.

Please let me just summarise why this paper does not support your case.

1. The fact that the authors conclude from their data that there was not an out-of-Africa bottleneck is because they have data from both inside and outside Africa and they can compare the two sets of populations. It is the relative levels of diversity in the two populations that allow them to exclude an out-of-Africa bottleneck. They spell this out clearly even in the abstract ("The comparable p value in non-Africans to that in Africans indicates no severe bottleneck during the evolution of modern non-Africans") They cannot exclude an earlier bottleneck using their data because they do not have genetic data for a population from which their African populations were derived. To do this they would, I guess, need to use ancient DNA from bones, and they were working before this was technically possible. Therefore you cannot claim that because they exclude an out-of-Africa bottleneck, they also exclude a bottleneck in the lineage leading to the African populations.

2. The authors estimate a long-term human effective population size of between 8100 and 18800. These estimates are based on present day numbers of segregating sites in the sample sequences, and estimates of mutation rate. This method assumes a fairly constant population size over time. No historical reconstruction of effective population size at different time-points in history is given. Thus this does not exclude a bottleneck.

3. The authors present a coalescent analysis for this region gave a mean estimate of time to the most recent common ancestor (MRCA) for this region of 1,356,000 years ago; and the 95% confidence interval was between 712,000 and 2,112,000 years ago. This is assuming a constant effective population size of 10,000. Using the approximation of **@swamidass** that the time to the coalescent of 4 alleles will be a quarter of this time, this means a bottleneck could have occurred between 178000 and 528000 years ago. And these figures do not include an adjustment in the light the point that I have made about rapid population growth after a bottleneck giving further reductions of these dates.

Therefore it seems to me very clear that this paper does not support your case.

I am puzzled as to why you are not willing to concede this rather minor point. After all, looking back over your previous posts in this discussion, your own understanding of the paper and its methods have clearly deepened during the course of our discussions, and your position has shifted somewhat.

You initially seemed to think that Zhao et al (2000) based their conclusions about effective population size on their coalescent analyses.[quote="DennisVenema, post:87, topic:37039"]
Have a look at Table 5, which shows their data for the distribution of TMRCA values. This is the data and analysis they are basing their conclusions on. Bottlenecks increase the probability of coalescence (this is also how PSMC methods work). We see a distribution of TCMRA values for the alleles in the study. This is basically what a PSMC analysis does sequentially for an entire genome to get a much larger sample size.
[/quote]
I immediately showed that this was wrong, but you continued to believe this through-out most of our discussion until you finally re-read the paper.

> DennisVenema:
>
> I think they're also suggesting that the TMRCA values supports this conclusion, but you're right, on re-reading the paper I don't see that explicitly stated.

You also thought that the method they used to calculate effective population size did not assume a fairly constant population size over time:

> DennisVenema:
>
> I disagree. The methods used are capable of detecting bottlenecks - that's why they are used.

You were wrong on this point, so then you said:[quote="DennisVenema, post:97, topic:37039"]
I guess I'm asking you to look at the TMRCA data there and think about your hypothesis (a bottleneck to two in the last few hundred thousand years).
[/quote]
You then appear to have made the mistake of thinking that a bottleneck could only have happened at the TMRCA. This is clear in the quote below, where you date any potential bottleneck at the TMRCA[quote="DennisVenema, post:102, topic:37039"]
That study identified 75 variants in this region that have a minimum coalescence time of over 700,000 years. The mode is 1.2 million years, and 700,000 is the lower bound of the 95% confidence interval for the combined sample. So, how did all of that variation survive a bottleneck to two? It can't. So, how did all of that variation arise after a proposed bottleneck to two? Through new mutations. How long would that take? Even with a steady-state population of around 10,000, about 1.2 million years.
[/quote]
You then made the mistake of suggesting recombination was unlikely to have occured much in a 10,000kb region[quote="DennisVenema, post:109, topic:37039, full:true"]
Richard - are you aware how closely linked those variants are? They're at most 10,000 bases apart. Are you seriously suggesting that they passed through a bottleneck en masse in two individuals and then recombined to the forms we see now?
[/quote]
I think that Joshua's analysis has shown you to be wrong on this point.

You also suggested that the raw data presented by Zhao et al does not form clusters that could have been derived from four ancestral haplotypes:

> DennisVenema:
>
> When we look at this region we don't see what a bottleneck to four would predict. We don't see all the variants grouped together into four different haplotype blocks.

By "eye-balling" in Excel and by drawing a haplotype network in Splitstree, I have shown this to be wrong.

You later expressed skepticism that three mutations could occur within a timeframe of a few hundred thousand years[quote="DennisVenema, post:231, topic:37039"]
I'm still not seeing how you can fit everything you need into the timeframe you've allowed yourself. If there is a bottleneck to 2, every haplotype in the Zhao (2000) data set has to come from your four ancestral haplotypes. Why did you decide that three mutations was an acceptable deviation from those types? How do you have time for three mutations, each interspersed with drift?
[/quote]

However, the coalescent analysis of Zhao et al clearly shows that many cumulative mutations have occurred in this region in such a time-frame.

You also suggested that the low Ne after a bottleneck would reduce the numbers of mutations available[quote="DennisVenema, post:231, topic:37039"]
Don't forget that if you lower Ne to get a faster coalescence time, you also lower the number of forward mutation events that are plausible.
[/quote]
But I argued that if the population revered quickly, this effect would be small, and expansion to an Ne of over 10,000 would quickly allow far more mutations.

Thus, I am struggling to see how you can still think that this paper supports your case.

As we have been discussing the paper, you appear to have changed your position on when in history you believe a bottleneck has been shown to be almost certainly impossible. On page 55 of Adam and the Genome, you wrote:

"It seems our smallest effective population size over the last 18 million years was when we were already human, at around the time our ancestors left Africa…
All methods employed to date agree that the human lineage has not dipped below several thousand individuals for the last 3 million years or more – long before our lineage was even remotely called "human".

You now seem to be saying in the current discussion that in fact you only think a bottleneck is excluded by the data in the last 200,000 years:[quote="DennisVenema, post:247, topic:37039"]
A few questions for you - if we take as reasonable your suggestion that Zhao (2000)'s data coalesce to four haplotypes between 300,000 - 1,000,000 years ago, how does that help your case? In Adam and the Genome I consistently discuss humans as a species arising ~200,000 years ago. So, by your calculations, Zhao (2000) supports my case - human variation in this all region of the genome cannot be reasonably explained by a bottleneck to 2 individuals within human history, as I argue in AatG. Am I missing something here?
[/quote]
Yes, you do discuss humans as a species arising ~200,000 years ago, but you also say that "the human lineage has not dipped below several thousand individuals for the last 3 million years or more – long before our lineage was even remotely called "human"". Thus, it seems to me that a bottleneck between 300,000 and a million years ago would be a direct contradiction of the claim you make on page 55 of Adam and the Genome.

All in all, it seems to me that we have made considerable progress in our discussion of Zhao et al over the past weeks. It has helped us clear up several misunderstandings of the paper and of its methods. It has helped us all to think through how to think about a bottleneck in terms of a coalescent analysis. It also appears to have helped you to change

your position expressed in Adam and the Genome – that a bottleneck could not have occurred in the last 18 or 3 million years – to a position that one could not have occurred in the last 200,000 years.

Given all this progress, it baffles me that you are not willing to now concede that Zhao et al does not support you case in Adam and the Genome, and is not therefore an appropriate citation. I honestly don't think you have much to lose by making this admission. It is not as if you actually cited Zhao et al in your book. It is not mentioned there. Why not just admit that you were mistaken to cite it?

I also will struggle to contribute much to this discussion over the Christmas period. I will be reflecting on it though from time to time. I wish you and all other contributors and readers a very happy Christmas. Thanks for an interesting discussion so far, and helping me to try to answer my questions about bottlenecks.

---

tallen_1 (Tim) 2017-12-21 22:56:14 UTC #306

> RichardBuggs:
>
> I would love to do this, but my offer of moving on was contingent on us…

Richard, while I think it's very magnanimous of you to "offer" to review the stronger papers you demanded of Dennis 300 comments in on this thread, all for the meager price of his admitting something you're demanding of him, I cannot help but notice you remain free of offering your own such admissions of whether the body of evidence compellingly attests to common descent, or if the body of evidence compellingly excludes a bottleneck of two in the human lineage within the past 10,000; 50,000; 100,000; 200,000; etc. years. Obviously basic questions of science highly relevant to this conversation.

I merely point this out as you're drawing a link between what a scientist is willing to admit to what the evidence does or does not support, and ostensibly their credibility as well as how productive a conversation with them may or may not be. All the while you continue to refuse to admit to what the evidence does or does not support. On topics Dennis and others have repeatedly asked you to address.

> DennisVenema:
>
> Also, I do think it would be helpful at this point to discuss common ancestry…I was taking for granted that we both accepted that. I'm not so sure now, so I'll ask it again: do you accept that humans share common ancestors with chimpanzees and orangutans?

> DennisVenema:
>
> knowing what Richard thinks are reasonable speciation times would also be useful.

> DennisVenema:
>
> I can't see how we can squeeze this variation into 2 people at 200,000 years ago (or even 300,000 years ago, if one was to accept Homo sapiens at this time). Can you, or can **@RichardBuggs** ?

I just thought I'd point this out. Since I believe in the golden rule. So please don't do unto Dennis what you yourself are not prepared to have done to you. Or perhaps more aptly put:

> DennisVenema:

> And yes, there is some irony that I am required to lay out everything in great detail but Richard need not answer even very basic biological questions.

Yet, as only a simple reader on this thread who only captures your interest whenever I elicit information from Dennis you find useful, I breathlessly await your ignoring what I've brought to your attention (or lack thereof) while you continue on your merry way of pushing the envelope on what double standards may achieve.

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gbrooks9 (George Brooks) 2017-12-21 23:45:01 UTC #307

@RichardBuggs , introduces his charge that **@DennisVenema** contradicts himself with this reference to page 55 of "Adam and the Genome":

> RichardBuggs:
>
> As we have been discussing the paper, you appear to have changed your position on when in history you believe a bottleneck has been shown to be almost certainly impossible. On page 55 of Adam and the Genome, you wrote:
>
> "It seems our smallest effective population size over the last 18 million years was when we were already human, at around the time our ancestors left Africa…
>
> All methods employed to date agree that the human lineage has not dipped below several thousand individuals for the last 3 million years or more – long before our lineage was even remotely called "human".

He then proceeds down a long-winded narrative, where he quotes **@DennisVenema** on the following:

DennisVenema:
"A few questions for you - if we take as reasonable your suggestion that Zhao (2000)'s data coalesce to four haplotypes **between 300,000 - 1,000,000 years ago**, how does that help your case? In Adam and the Genome I consistently discuss humans as a species arising ~200,000 years ago. So, by your calculations, Zhao (2000) supports my case - human variation in this all region of the genome cannot be reasonably explained by a bottleneck to 2 individuals within human history, as I argue in AatG. Am I missing something here?"

As we can readily see, Dennis asks the rhetorical question: "if we take as reasonable your suggestion that Zhao's … data coalesce to four haplotypes between 300,000 [to] 1,000,000 years ago, how does that help your case?"

This is where **@RichardBuggs** attempts the coup de grace: "… Thus, it seems to me that a bottleneck **between 300,000 and a million years ago [aka 1,000,000 years]** would be a direct contradiction of the claim you make on page 55."

Waaaaiiiiiiittttttttt a minute here … You are quoting Dennis as contradicting himself by using his sentence "… if we take as reasonable **your** suggestion that Zhao (2000)'s data coalesce to four haplotypes **between 300,000 - 1,000,000 years ago,** how does that help your case?"

I think everyone in the room should nonchalantly check the continued presence of their wallets in their back pockets or in their purses. I think we're watching one of those classic movie plots in real time … where wallets go missing and and someone almost always gets an ice pick in the throat…

DennisVenema (Dennis Venema) 2017-12-22 00:52:15 UTC #308

> RichardBuggs:

> As we have been discussing the paper, you appear to have changed your position on when in history you believe a bottleneck has been shown to be almost certainly impossible. On page 55 of Adam and the Genome, you wrote:
>
> "It seems our smallest effective population size over the last 18 million years was when we were already human, at around the time our ancestors left Africa…
> All methods employed to date agree that the human lineage has not dipped below several thousand individuals for the last 3 million years or more – long before our lineage was even remotely called “human”.
>
> You now seem to be saying in the current discussion that in fact you only think a bottleneck is excluded by the data in the last 200,000 years:

The heliocentric quote, which I thought was the object of your concern, is about humans (Homo sapiens). When I’m speaking about our lineage leading up to humans at 200KYA I use “lineage” or similar.

The other two quotes remain valid. Does “it seems” sound like I’m saying this is as certain as heliocentrism? That would be quite the understatement. That is a summary statement of all the lines of evidence in the literature to date that do not provide support for a bottleneck below ~10,000 at any time in the last 18MY (which remains the case).

"All methods employed to date agree that the human lineage has not dipped below several thousand individuals for the last 3 million years or more – long before our lineage was even remotely called “human”.

This quote also remains valid. There are no studies in the literature that support a lower bottleneck, and several that support large Ne values over this timeframe (PSMC and LD studies, for example). If there were (perhaps if I had missed one somewhere?) I’m sure you would point it out if you were aware of it.

So: “heliocentric certain”: humans. Pretty darn certain: lineage leading to humans over the last several hundred thousand years (say back to ~500,000 years ago). Confident but not as definitive: lineage over the last few million years. Survey of literature to date: no evidence of a bottleneck greater than thousands anywhere, regardless of time.

You suggest that perhaps the data in Zhao could go back to 4 haplotypes in 178,000 years. How certain are you about that value? You have to (a) pick the very lowest value within the 95% CI and then (b) assume that 1/4 of that is reasonable in this case. One quarter of the mean value is 339,000 years ago, which pretty much any scientist on the planet would say is more accurate than cherry-picking the lowest value. The upper bound (528,000 years ago) is just as probable as the lower bound. I could pick that value with the same confidence which which you pick the lowest one.

If that’s what counts as a “win” that’s a pretty thin “win”, don’t you think?

Ok, so that we can move this conversation forward to the stronger data: I agree that Zhao (2000) does not support the case I make in *Adam and the Genome*, in that it might be statistically possible to have the variation in their dataset come from 4 haplotypes less than 200,000 years ago.

Done and dusted. Shall we move on?

Are you ever going to answer my questions about common ancestry and what you think are reasonable speciation times? They are directly relevant to determining mutation rates.

Jonathan_Burke (Jon) 2017-12-22 16:46:18 UTC #309

> RichardBuggs:
>
> I realise I am acting as a defense attorney in a case that seems to you to be a bit hopeless, but I think it is good for us to work this all through in detail as there are so many people out there for whom this is an important issue for

> their faith - who have very heartfelt beliefs about this - and I think we owe it to them to go through this throughly.

I am still wondering exactly who out there thinks its important to their faith that there's a bottleneck of two in the homo sapiens lineage somewhere in the last 500,000 years, where this bottleneck is part of a lineage which includes common descent and homo sapiens evolving from pre-homo sapiens ancestors. Who are these people?

AMWolfe (A.M. Wolfe) 2017-12-22 17:00:36 UTC #310

> Jonathan_Burke:
>
> I am still wondering exactly who out there thinks its important to their faith that there's a bottleneck of two in the homo sapiens lineage somewhere in the last 500,000 years, where this bottleneck is part of a lineage which includes common descent and homo sapiens evolving from pre-homo sapiens ancestors. Who are these people?

I actually think there could be quite a few such people.

What I don't understand is who it is that thinks it's so important to pin Dennis into admitting fault in his published work. I would expect people are more interested in using this amazing meeting of the minds to discuss the actual science at hand. But what do I know?

DennisVenema (Dennis Venema) 2017-12-22 17:30:07 UTC #311

> Jonathan_Burke:
>
> I am still wondering exactly who out there thinks its important to their faith that there's a bottleneck of two in the homo sapiens lineage somewhere in the last 500,000 years, where this bottleneck is part of a lineage which includes common descent and homo sapiens evolving from pre-homo sapiens ancestors. Who are these people?

This is speculation - so it's worth what you paid for it - but I think the people most interested in this idea are people who reject common ancestry to begin with. There is already a move to make *H. erectus* "fully human" and ignore all the problems with that approach. In the big new anti-TE book this is clearly the strategy: they state that the cranial capacity of erectus falls within the sapiens range, and selectively quote the literature to make it sound like erectus is just like us. There is also no mention of the difficulties with such an approach.

---

tallen_1 (Tim) 2017-12-22 17:40:50 UTC #312

I'd agree. It seems Richard has purposefully evaded any acknowledgement that he sees humans sharing common ancestry, any acknowledgment that humans speciated some hundreds of thousands of years ago, and any acknowledgment that a bottleneck to two within any timeframe that exceeds young earth boundaries, whether 10K, 50K, 100K, 200K, etc. years is implausible.

If this is a truth finding mission Richard is engaged in, he's done an excellent job avoiding stating what he thinks is scientifically true on these highly relevant issues. All for ostensibly the purpose of sowing doubt that perhaps if Dennis is wrong about a greater than 500,000 year timeframe on his bottleneck, maybe he's also wrong on a bottleneck of less than 500,000 years including maybe only 6,000 years. A conclusion he may not state but would be more than happy to have his readers infer. And of course in such a model other hominids are just considered other humans and descendants of Adam.

This is what I suspect may be going on. Given Richard's evasiveness on answering these very basic questions of biological science.

Jonathan_Burke (Jon) 2017-12-22 18:20:48 UTC #313

> DennisVenema:
>
> This is speculation - so it's worth what you paid for it - but I think the people most interested in this idea are people who reject common ancestry to begin with. There is already a move to make H. erectus "fully human" and ignore all the problems with that approach. In the big new anti-TE book this is clearly the strategy: they state that the cranial capacity of erectus falls within the sapiens range, and selectively quote the literature to make it sound like erectus is just like us. There is also no mention of the difficulties with such an approach.

That's what I think, and that's where the bait and switch comes in. These people want a literal "Adam and Eve". I believe in a literal Adam and Eve, but they want all humans to have descended from this Adam and Eve, and it seems to me that they're going to be told "Science cannot rule out an Adam and Eve who were the ancestors of all humans", while quietly leaving out the part about no such bottleneck being found within the history of actual homo sapiens, and the fact that all models which might even allow for such a bottleneck are still predicated on common ancestry of humans from pre-human ancestors.

Swamidass (Dr. S Joshua Swamidass) 2017-12-22 18:28:42 UTC #314

> Jonathan_Burke:
>
> I am still wondering exactly who out there thinks its important to their faith that there's a bottleneck of two in the homo sapiens lineage somewhere in the last 500,000 years, where this bottleneck is part of a lineage which includes common descent and homo sapiens evolving from pre-homo sapiens ancestors. Who are these people?

> AMWolfe:
>
> I actually think there could be quite a few such people.

There are quite a few such people. Just yesterday a theologian commented to me on how he saw this conversation progressing. Right now, many are asking:

1. Who is empathetic to the questions in the Church?
2. Are those empathetic to their questions treated with respect?
3. What are the certainty, limits, and extents of these findings?
4. Who can we trust to be honest with us about the scientific evidence?

So yes, this is an immensely important conversation. **@RichardBuggs** , even if he is ultimately wrong, is coming off pretty good. Whatever one's disagreement is with him, he is empathetic to the questions in the Church. That counts for a lot.

It is also surprising the resistance to #3, as that is a fundamental question in scientific work. Scientists are always questioning the mainstream consensus this way. This is not a rejection science, but how it proceeds. Clarity here has real value.

> DennisVenema:

> This is speculation - so it's worth what you paid for it - but I think the people most interested in this idea are people who reject common ancestry to begin with. There is already a move to make H. erectus "fully human" and ignore all the problems with that approach. In the big new anti-TE book this is clearly the strategy: they state that the cranial capacity of erectus falls within the sapiens range, and selectively quote the literature to make it sound like erectus is just like us. There is also no mention of the difficulties with such an approach.

Other than the standard challenges with the "antiquity" of humans, what exactly are the difficulties with such an approach? And is this approach even really new?

Claiming that Homo erectus = "human" is a fairly standard claim in creationist circles. I've been reading AiG, for example, and was just given a copy of *Contested Bones* to review, which follows this age old pattern. Ironically, most scientists actually agree with them now. There was a major shift in thought on this over the last several years (decades?). This is why, for example, that Homo Erectus is considered "human" in the Natural History Museum. At the very least, we have to acknowledge that there is not yet consensus on the degree to which Homo erectus was "human."

Moreover, their may never been consensus.I think the challenge everyone faces is in drawing a line somewhere in the distant past. There is no clear dividing point, so there is disagreement and consensus is ellusive.

---

tallen_1 (Tim) 2017-12-22 18:31:51 UTC #315

And Richard could clear up all that confusion by answering a few basic scientific questions Dennis and others have requested of him. Let us hope he has it within him to do so.

DennisVenema (Dennis Venema) 2017-12-22 18:57:34 UTC #316

> Swamidass:
>
> Other than the standard challenges with the "antiquity" of humans, what exactly are the difficulties with such an approach? And is this approach even really new?

Yes, it's common in the YEC literature, but they have all of this variation arising in less than 10,000 years, so they've got bigger problems that they are not dealing with.

It's a relatively new approach in the OEC literature. RTB, for example, would strongly disagree with *erectus* as human.

The basic issues are that cranial capacity in *erectus* is quite different from *sapiens*, and behaviourally *erectus* lacks things we consider definitive of *sapiens*. Add to that the challenges of squaring the Genesis context with 2MYA.

And then there's the challenge of carving a line between *erectus* and earlier hominins. If erectus is fully human, then the "gap" between "humans" and australopithecines and *habilis* gets that much smaller. Which doesn't stop **@agauger** from trying - a big section in the TE book is devoted to trying to draw a firm line between *erectus* and other hominins.

AMWolfe (A.M. Wolfe) 2017-12-22 19:47:53 UTC #317

> Swamidass:
>
> It is also surprising the resistance to #3, as that is a fundamental question in scientific work. Scientists are always questioning the mainstream consensus this way. This is not a rejection science, but how it proceeds. Clarity here has real value.

I couldn't agree more. But it seems to me that there is a particular fervor here not primarily to determine "certainty, limits, and extents" but more than anything to force Dennis's hand to recant something in his published work.

> Swamidass:
>
> There are quite a few such people.

That's right; the Tim Kellers and Henri Blochers of the world (who wrote *In the Beginning*) are keen on preserving a literal first couple who fell from grace, even if common descent has to be maintained. At least this modicum of literalness helps, for some, to preserve a certain fidelity to Pauline (Pauline/Augustinian) theology. We can agree or disagree and debate that, but this is how some will see it. And we do well to respect that.

Lastly, a general comment…

> Swamidass:
>
> However, this is a tendency for non-scientists to weigh "cheering" or "adjudicating" the positions raised. This is, fundamentally, going to be unfair to **@RichardBuggs** , as this forum is dominated by those who affirm evolutionary science. Nonetheless, he has decided to brave this forum, so we should continue to treat him as a guest.

May I request that you divide participants here into "specialists" and "non-specialists" rather than "scientists" and "non-scientists"? Otherwise one gets the distinct impression that non-geneticist scientists are second-class citizens around here.

But in general, I agree: my comments (among others') are not particularly helpful here. Let me add that while I've not said it, I honestly do respect and greatly appreciate the work that all the primary participants here — you, Steve, Dennis & Richard — are donating to this discussion. It is vitally important to the Church, and we (I) would do well to step aside and let it take its course with as little interference as possible, rather like a good golf tournament with its silent crowds. 🙂

Jonathan_Burke (Jon) 2017-12-22 19:56:27 UTC #318

> Swamidass:
>
> There are quite a few such people. Just yesterday a theologian commented to me on how he saw this conversation progressing. Right now, many are asking:

But none of those questions are actually what I am referring to. So I am still looking for the people described in my questions. Remember, my question only includes Christians who accept evolution, obviously. It excludes the vast majority of people who don't accept evolution, because they could not possibly accept an "Adam and Eve" who were not homo sapiens, or who were the descendants of non-homo sapiens ancestors. It also excludes anyone who doesn't accept the earth could be over 10,000 years old. So who really are the people to whom Dr Buggs is referring?

> Swamidass:
>
> Whatever one's disagreement is with him, he is empathetic to the questions in the Church. That counts for a lot.

But he has not shown the least empathy for, or even interest in, the exceptionally polite questions put to him right here, on this forum, by people who want to know the theological implications of his proposal. That also counts for a lot, but in

a rather different way.

---

gbrooks9 (George Brooks) 2017-12-22 23:10:25 UTC #319

> Swamidass:
>
> 1.Who is empathetic to the questions in the Church?
> 2.Are those empathetic to their questions treated with respect?
> 3.What are the certainty, limits, and extents of these findings?
> 4.Who can we trust to be honest with us about the scientific evidence?
>
> So yes, this is an immensely important conversation. **@RichardBuggs** , even if he is ultimately wrong, is coming off pretty good.

Right… **@Swamidass** , his role as Champion Apologist is certainly assured.

But on the other side, I think it's pretty clear that he is also coming across as a bully.

---

tallen_1 (Tim) 2017-12-22 23:33:00 UTC #320

> Swamidass:
>
> Who can we trust to be honest with us about the scientific evidence?

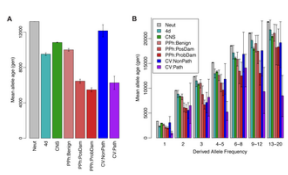
Certainly not someone who refuses to say what they think the scientific evidence does or does not support, for apologetic reasons presumably. Those people I do not trust to give an honest picture of the evidence. Nor should anyone. Though let their arguments proceed forward fairly all the same.

DennisVenema (Dennis Venema) 2017-12-23 05:45:37 UTC #321

Here's another two papers for **@RichardBuggs** 's reading list. I was chasing another rabbit trail and came across these, and thought they were relevant to the conversation.

First one is here (PDF). This one looks at polymorphisms that were present in the common ancestral population of humans and chimpanzees and which do *not* coalesce in either lineage. This means that both humans and chimpanzees (and in one case in their data set gorillas) have the same variants. The TMRCA values for these would thus be over ~4MYA (the lower bound of the human-chimp divergence). This would put an estimate of TMR4A at around 1MYA (or higher). Note: some of their examples are called into question by the next paper, but others are supported.

The next one references the one above, and also does a genome-wide scan for regions with limited and elevated TMRCA values. They identify several regions with TMRCA scores that predate the human-chimp divergence (including some identified in the above paper). Some of the TMRCA values are above 8 million years, which would place our estimate of TMR4A at around 2 MYA or more.



Genome-Wide Inference of Ancestral Recombination Graphs

Author Summary The unusual and complex correlation structure of population samples of genetic sequences presents a fundamental statistical challenge that pervades nearly all areas of population genetics. Historical recombination events produce an...

Just in case Richard, Josh and I needed more reading material… and **@RichardBuggs** , we really do need to know if you accept common ancestry if we're going to profitably discuss these two papers.

Swamidass (Dr. S Joshua Swamidass) 2017-12-23 15:34:07 UTC #322

Dennis,

Very interesting papers. I've read the first one already, but not the second. However, I am not sure how they help your case. As I understand it, you are trying to demonstrate…

1. *Homo sapiens* specifically do not dip down to a single couple in 300 kya to the confidence we have in heliocentrism.
2. Our ancestors as a whole do not dip down to a single couple between 300 kya and 3 mya with very high confidence, but maybe not as high.

As you put it…

> DennisVenema:
>
> The heliocentric quote, which I thought was the object of your concern, is about humans (Homo sapiens). When I'm speaking about our lineage leading up to humans at 200KYA I use "lineage" or similar.

> DennisVenema:
>
> So: "heliocentric certain": humans. Pretty darn certain: lineage leading to humans over the last several hundred thousand years (say back to ~500,000 years ago). Confident but not as definitive: lineage over the last few million years.

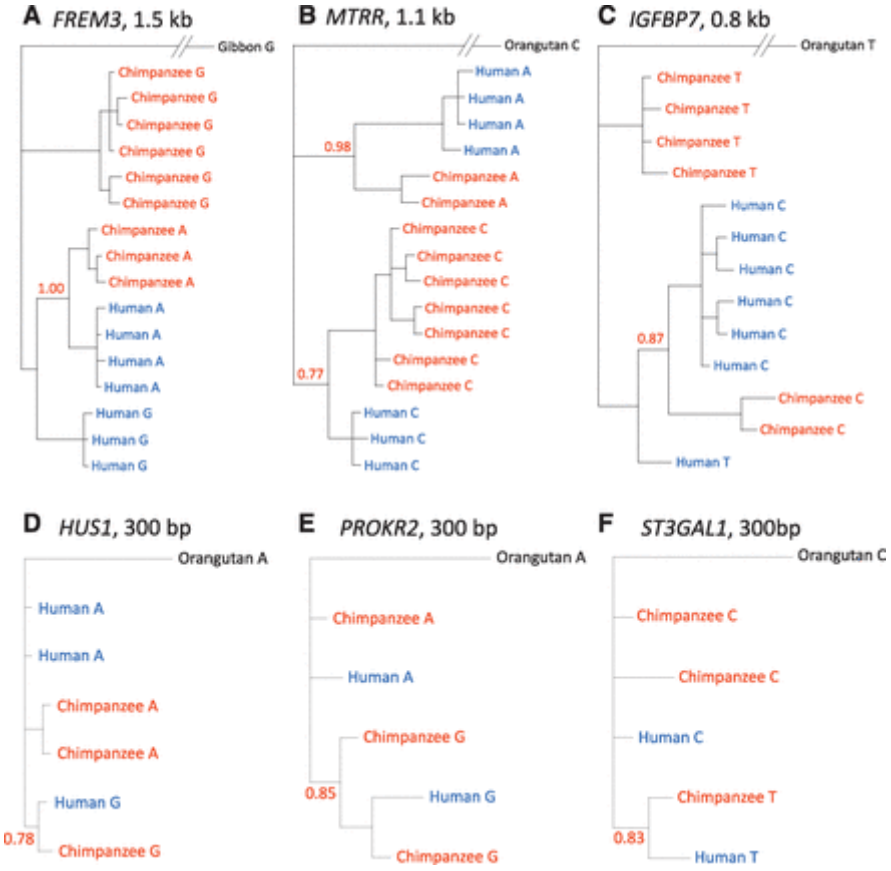
As I understand it, the first claim appears to be novel, and I cannot find it in the literature anywhere. It would be help to see a paper that estimates population size of Homo sapiens specifically. I have not been able to find one. Have you?

The second one is only supported by the Ayala paper on MHCs, which is strong evidence in my view. The vast majority of studies are not even looking at population structure past 2 mya. So I am not sure how you get to high confidence at 2 mya to 3 mya.

As I read the papers you , the first paper…

> DennisVenema:
>
> First one is here (PDF). This one looks at polymorphisms that were present in the common ancestral population of humans and chimpanzees and which do not coalesce in either lineage. This means that both humans and chimpanzees (and in one case in their data set gorillas) have the same variants. The TMRCA values for these would thus be over ~4MYA (the lower bound of the human-chimp divergence). This would put an estimate of TMR4A at around 1MYA (or higher). Note: some of their examples are called into question by the next paper, but others are supported.

This paper does not give a TMRCA > 4 mya for more than 4 alleles at any locus. They find 125 non MHC regions with ancestral variation, However, at none of these locations is there more than two or three haplotype clades shared by chimp and human. You can see some of them below; Figure 3…



The second paper is really an important paper, and I am glad you raised it. However, I am not sure how it helps your case. Table 2 and 3 give the TMRCAs the calculate in their method, which is notable for doing a much better job with recombination that most analysis:

#	Chr[a]	Start	End	TMRCA[b]	Poly/kb[c]	Npoly[d]	CNV[e]	Comments
1	chr4	190590001	190600000	615775	16.6	32.8	√	Part of large intergenic region near telomere of long arm of chr 4 (see [76])
2	chr5	21560001	21570000	503311	16.2	5.1	√	Intron of *GUSBP1*
3	chr3	97930001	97940000	479803	16.4	5.3		Intergenic region in cluster of olfactory receptor genes
4	chr6	57270001	57280000	479504	13.7	28.0	√	Intron of *PRIM2*
5	chr2	223940001	223950000	449728	19.8	4.3		Intergenic region downstream of *KCNE4*
6	chr5	21550001	21560000	412679	14.2	4.4	√	Intron of *GUSBP1*
7	chr6	57220001	57230000	399887	16.2	12.8	√	Intron of *PRIM2*
8	chr6	29680001	29690000	380228	15.3	10.0		Intergenic region upstream of *HLA-F*
9	chr1	94220001	94230000	377017	8.0	4.2		Intron of *BCAR3*
10	chr8	123070001	123080000	375128	15.3	4.2		Intron of *BC052578*
11	chr11	55670001	55680000	374537	12.0	4.3		Intergenic region between *TRIM51* and *OR5W2*
12	chr6	29950001	29960000	371110	17.6	7.6		Intergenic region between *HLA-A* and *HLA-J*
13	chr17	64010001	64020000	367842	8.6	5.5		Intron of *CEP112*
14	chr6	29670001	29680000	365313	15.8	10.1		Intergenic region upstream of *HLA-F*
15	chr11	55690001	55700000	361088	11.5	4.1		Intergenic region between *OR5W2* and *OR5I1*
16	chr6	158680001	158690000	345382	10.4	4.8		Intergenic region upstream of *TULP4*
17	chr6	29720001	29730000	341797	12.4	8.0		Intergenic region between *HLA-F* and *HLA-G*
18	chr17	43790001	43800000	335647	11.2	5.0		Intron of *CRHR1*
19	chr6	8470001	8480000	325656	10.1	4.5		Intron of noncoding RNA *LOC100506207*
20	chr4	141920001	141930000	325570	12.1	3.2		Intron of *RNF150*

[a]Genomic coordinates in hg19 assembly. The genome was simply partitioned into nonoverlapping 10 kb intervals in hg19 coordinates.
[b]Posterior expected TMRCA in generations, averaged across unfiltered genomic positions in region.
[c]Number of polymorphisms in Complete Genomics dataset in region per kilobase of unfiltered sequence.
[d]Normalized polymorphism rate: number of polymorphisms per unfiltered kilobase divided first by the local mutation rate (as estimated from divergence to nonhuman primate outgroup genomes) then by the average of the same polymorphism/divergence ratio in designated neutral regions. The resulting value can be interpreted as a fold increase in the mutation-normalized polymorphism rate compared with the expectation under neutrality. The same measure was computed from the much larger 1000 Genomes Project Phase 1 data set, and was significantly elevated in these 20 high-TMRCA regions (Supplementary Figure S13).
[e]Possible copy number variant (CNV), based on Complete Genomics "hypervariable" or "invariant" labels (see Methods). Polymorphism rates in these regions may be over-estimated.
doi:10.1371/journal.pgen.1004342.t002

This tables show the MAXIMUM estimates for TMRCA across the whole genome. Taking recombination into account, therefore, seems to REDUCED the estimates for TMRCA from 2 mya (as in your last study) to at most 600 kya. That measurement, however, appears to be an outlier. More consistently, we see TMRCA's around 400 kya. **[An error was made here. The TMRCA is by generation, not year. See my response below.]**

Using our estimate that TMR4A approximately equals TMRCA / 4, that allows for a bottleneck after 100 kya (or 150 kya if want to use largest coalescence). This is consistent with TMRCAs from Y-chromosomes and mitochondria, and undermines your last paper too. I trust the TMRCAs here more than the 2 mya MRCA from the prior paper (which used

a simplified analysis), because this is across the whole genome and uses a much more sophisticated method for detecting recombination. **[An error was made here. The TMRCA is by generation, not year. See my response below.]**

Now, it is possible when more data is used (rather than just the 69 genomes here) that a higher bound is placed. This is all strong evidence for common descent too. I am not sure, however, what this shows about your two claims. If anything, these two papers appear to undermine claim #1 and limit the amount of data we can expect to find for #2. **[An error was made here. The TMRCA is by generation, not year. See my response below.]**

Can you clarify how these papers help you?

Also, it seems odd to remind us all that absence of evidence is not evidence of absence.

[quote="DennisVenema, post:308, topic:37039"]the literature to date that do not provide support for a bottleneck below ~10,000 at any time in the last 18MY (which remains the case).
[/quote]

This quote is helpful and accurate…

> If someone were to assert that there is an elephant on the quad, then the failure to observe an elephant there would be good reason to think that there is no elephant there. But if someone were to assert that there is a flea on the quad, then one's failure to observe it there would not constitute good evidence that there is no flea on the quad. **The salient difference between these two cases is that in the one, but not the other, we should expect to see some evidence of the entity if in fact it existed.**
> — J.P. Moreland and W.L. Craig,

I'm not sure we expect to see any evidence against a brief bottleneck in the very distant past (before TMRCA4). We do find the strongest evidence in transpecies variation of MHC, but that is remarkable. As far as I know, that is the strongest evidence there is (and I have always pointed to it).

However, appealing to lack of evidence is only meaningful if we expect to see evidence. It certainly does not get us to "heliocentrism level certainty".

---

tallen_1 (Tim) 2017-12-23 15:39:45 UTC #323

Swamidass,

Was it not a bottleneck to two within 200KYA Dennis was trying to demonstrate was implausible at "heliocentric" levels of certainty? Not 300KYA? I may have missed something here, but I want to make sure we're not stacking the deck unfairly.

DennisVenema (Dennis Venema) 2017-12-23 15:43:55 UTC #324

> Swamidass:
>
> Can you clarify how these papers help you?

Hi Josh **@Swamidass** ,

Those TMRCA values (in the second paper) are not in years - they are in generations. Multiply them by 25 to get TMRCA in years. That tripped me up at the first as well.

---

tallen_1 (Tim) 2017-12-23 16:11:16 UTC #325

> tallen_1:
>
> Was it not a bottleneck to two within 200KYA Dennis was trying to demonstrate was implausible at “heliocentric” levels of certainty? Not 300KYA? I may have missed something here, but I want to make sure we’re not stacking the deck unfairly.

Dennis, it’d probably be more appropriate to ask this question of you. Which bar were you setting here?

DennisVenema (Dennis Venema) 2017-12-23 16:21:26 UTC #326

It’s up the thread ^ . “Heliocentrism certain” = humans. 200KYA in the book. I’m ok with stretching that to 300KYA if needed.

Swamidass (Dr. S Joshua Swamidass) 2017-12-23 16:21:53 UTC #327

> DennisVenema:
>
> Those TMRCA values (in the second paper) are not in years - they are in generations. Multiply them by 25 to get TMRCA in years. That tripped me up at the first as well.

That is certainly helpful. Thanks! I did make that mistake. I’d use a generation time of about 15 (at minimum) to 25. So that brings the TMR4C from that table up past 2 mya. Now I see why it helps your case.

However, they are MAX values of samples from a distribution with a very high variance. This is an extreme-value distribution. We need to see the whole distribution. Know any papers with that? Perhaps they can send us their values if we ask them? Perhaps send them an email.

Because of how these numbers are selected, we cannot draw a strong inference from them yet. It is not sound to cherry pick regions with low TMRCA’s, but this study is just cherry picking the ones with high TMRCAs, if it is used this way.

> tallen_1:
>
> Was it not a bottleneck to two within 200KYA Dennis was trying to demonstrate was implausible at “heliocentric” levels of certainty? Not 300KYA? I may have missed something here, but I want to make sure we’re not stacking the deck unfairly.

The claim was that **Homo sapiens do not dip down to a single couple**, and we know this with **certainty approaching heliocentrism.**

At the time, everyone thought Homo sapiens arose 200 kya, but now there is strong enough evidence that this is no longer the consensus. Some think Homo sapiens arose 300 kya or even as early as 350 kya. If that new finding unsettles Dennis’ claim, then that claim should never have been presented as heliocentrism level certainty. There is no similar sort of evidence we can imagine that would unsettle our view of heliocentrism. The fact that Dennis did not take into account uncertainty in determine the origin date of Homo sapien is part of what is at question here.

To be clear, he certainly is not responsible for excluding evidence published after his book was published. However, that evidence does call into question his heliocentrism certainty, if in fact population bottlenecks between 300 kya and 200 kya are plausible (which we have not yet determined). If that is the case, then part of his certainty rested on false confidence in when humans arise. Of course, if we cannot see plausibility for a bottleneck till say, before, 1 mya, that is not really relevant any ways.

Setting that issue aside, none of the studies I have seen correct for interbreeding. The scientific consensus is that our **ancestors** never dip to a single couple, not that **Homo sapiens** never dip to a single couple. It would be really interesting to see the studies that raises Dennis' confidence so high on this one. He has read the literature more, so he might have seen something I missed.

Just as he corrected me on that TMRCA table, I'd love to have him correct me here too. However, this really does to seem to be a novel claim he is making. I am not even sure I can envision the study that could demonstrate this claim.

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tallen_1 (Tim) 2017-12-23 16:22:46 UTC #328

That's what I'd thought ;). Thanks! Is it your sense Richard is disputing an exclusion of a bottleneck within 200KYA then? Or just your upper ranges with less than such a high level of confidence?

DennisVenema (Dennis Venema) 2017-12-23 16:24:48 UTC #329

> Swamidass:
>
> Because of how these numbers are selected, we cannot draw a strong inference from them yet. It is not sound to cherry pick regions with low TMRCA's, but this study is just cherry picking the ones with high TMRCAs, if it is used this way.

The paper is a whole-genome study, and these are the largest TMRCA values that they found. Why is this "cherry picking"? Shouldn't we be interested in the range of TMRCA values in the genome if we're interested in the range of estimated TMR4A values?

Put another way: finding more recent TMRCA values is not an issue for Richard. The issue is how far back the range of TMRCA values we see in the genome goes.

I was actually surprised to see some regions with TMRCA values higher than the MHC complex. I expected that to be near the top (and it is) but there are several regions with similar TMRCA values.

DennisVenema (Dennis Venema) 2017-12-23 16:25:47 UTC #330

> tallen_1:
>
> That's what I'd thought 😉. Thanks! Is it your sense Richard is disputing an exclusion of a bottleneck within 200KYA then? Or just your upper ranges with less than such a high level of confidence?

I have no idea. Richard has not clarified what timeframe he is interested in.

Swamidass (Dr. S Joshua Swamidass) 2017-12-23 16:30:21 UTC #331

> DennisVenema:

> The paper is a whole-genome study, and these are the largest TMRCA values that they found. Why is this “cherry picking”? Shouldn’t we be interested in the range of TMRCA values in the genome if we’re interested in the range of estimated TMR4A values?

We need to see the whole distribution. Just looking at the tail of the distribution does not tell you about the mean or the mode. Using these TMRCA values is like using an estimate well outside the 95% confidence interval (on the high side). We could have just as well used the minimum TMRCA values as valid estimates. Both approaches are not valid for similar (though not identical) reasons.

As you know, the sampling distribution for TMRCAs have ***very*** high variance. As I understand it, the signal to noise ratio actually increases as you go farther back. For that reason, looking at extremal values (maxs and mins) is always going to be flat out wrong. We need to see the full distribution, to see if it is unimodal, bimodal, and what the means/modes are. That’s just basic statistics, right?

The good news is that these authors actually have the data we need. I’m going to send them a note asking for data.

---

tallen_1 (Tim) 2017-12-23 16:31:28 UTC #332

> DennisVenema:
>
> I have no idea. Richard has not clarified what timeframe he is interested in.

I think that’s my frustration as well. It’d be very helpful for him to do so. He’s been asked by yourself and others. Hopefully when he returns to this thread he will be more forthcoming with his answers to these questions, especially since you’ve held up your end of the bargain in meeting all of his.

In the meantime, what do you think of Swamidass‘ point that humans may have speciated at 300 or even 350KYA? Do you find this relevant? For me, given that distances us so far from behaviorally as well as anatomically modern humans, it doesn’t mean much to me. But I’m curious as to your thoughts and whether Swamidass‘ point means a revision of your claim is warranted.

DennisVenema (Dennis Venema) 2017-12-23 16:36:50 UTC #333

> Swamidass:
>
> We need to see the whole distribution. Just looking at the tail of the distribution does not tell you about the mean or the mode. Using these TMRCA values is like using an estimate well outside the 95% confidence interval (on the high side). We could have just as well used the minimum TMRCA values as valid estimates. Both approaches are not valid for similar (though not identical) reasons.

I’m not quite following you here (maybe I need another cup of coffee). I agree if we’re interested in the TMRCA for the genome as a whole then the whole distribution is important. In this case, we’re interested in the TMRCA value of specific genome regions. Why would the oldest measures be intrinsically less accurate?

Also, we’re looking at TMRCA values in excess of 10 million years in some cases. Are we saying that this isn’t good evidence for a TMR4A > 400KYA?

Swamidass (Dr. S Joshua Swamidass) 2017-12-23 16:39:38 UTC #334

> tallen_1:
>
> In the meantime, what do you think of Swamidass' point that humans may have speciated at 300 or even 350KYA? Do you find this relevant? For me, given that distances us so far from behaviorally as well as anatomically modern humans, it doesn't mean much to me. But I'm curious as to your thoughts and whether Swamidass' point means a revision of your claim is warranted.

I'm not making any revisions.

There is immense debate about what "human" and Homo sapiens is. If we are trying to communicate the scientific consensus to the public, to make claims of heliocentrism level certainty, we need to be taking that lack of consensus into account.

The real problem, however, is not with the date of 300 kya vs 200 kya, but in making a claim about Homo sapiens, when population genetics seems only to be making claims about "our ancestors", our total "lineage", which includes non-Homo sapiens.

> DennisVenema:
>
> I'm not quite following you here (maybe I need another cup of coffee). I agree if we're interested in the TMRCA for the genome as a whole then the whole distribution is important. In this case, we're interested in the TMRCA value of specific genome regions. Why would the oldest measures be intrinsically less accurate?

You can try this yourself with a gaussian distribution and python code. If you want, I can even write up a piece of code. Sample numbers from a distribution ten thousand times. Take the maximum of those samples. How close is that to the mean? Not very close. Same problem here.

We cannot really estimate the average height of people by just looking at the heights of people in the NBA. Its just not statistically sound. Same thing here.

DennisVenema (Dennis Venema) 2017-12-23 16:39:48 UTC #335

> tallen_1:
>
> In the meantime, what do you think of Swamidass' point that humans may have speciated at 300 or even 350KYA? Do you find this relevant? For me, given that distances us so far from behaviorally as well as anatomically modern humans, it doesn't mean much to me. But I'm curious as to your thoughts and whether Swamidass' point means a revision of your claim is warranted.

One of the things I try to communicate in the book is that delineating "species" is an attempt to draw a line on a gradient. As we learn more and more about our ancestors, it's going to get harder and harder to draw a line - a point I make in the book. I think we see with the remains at 300KYA exactly that issue - some say they are *sapiens*, others aren't so sure. It's exactly what we would expect.

DennisVenema (Dennis Venema) 2017-12-23 16:41:03 UTC #336

> Swamidass:

> We cannot really estimate the average height of people by just looking at the heights of people in the NBA. Its just not statistically sound. Same thing here.

We're not interested in the genome average, though. We're interested in the range.

---

tallen_1 (Tim) 2017-12-23 16:50:31 UTC #337

> Swamidass:
>
> The real problem, however, is not with the date of 300 kya vs 200 kya, but in making a claim about Homo sapiens

Since the only real reason we're examining the claim as to whether a bottleneck down to two humans could ever be plausible is driven by theological concerns, it would be helpful to examine what sort of human then would be relevant to those concerns. For me, a non-behaviorally modern human, or any other hominid for that matter, that can accomplish perhaps merely the construction of rudimentary stone tools does not map well onto the sort of Adam & Eve referenced in scripture. Curious as to your thoughts though.

Swamidass (Dr. S Joshua Swamidass) 2017-12-23 17:05:22 UTC #338

> DennisVenema:
>
> We're not interested in the genome average, though. We're interested in the range.

We are interested in the ***distribution***. The distribution includes the range, the mean, mode, min, max, and much much more information.

DennisVenema (Dennis Venema) 2017-12-23 17:17:47 UTC #339

Don't forget that in several cases here we're talking about polymorphisms shared between humans and chimpanzees. That places the TMRCA for those regions prior to the human-chimp divergence, which is over 3.5MYA (using a very conservative value). Thus TMR4A would be over 875,000 years ago.

DennisVenema (Dennis Venema) 2017-12-23 17:20:03 UTC #340

I also agree that if we were talking about one or two genome regions I might be more skeptical - but we're talking about several independent regions with very high TMRCA values. Not sure how looking at a distribution is going to change the conclusions of the authors of that paper.

---

tallen_1 (Tim) 2017-12-23 17:30:51 UTC #341

Dennis, since the conversation is happening on this thread rather than the 2nd part to this series, what of your argument presented there that a bottleneck down to two would cause a discernible spike in the TMRCA at the time of such an event? Would that be pertinent to the analysis of these papers?

DennisVenema (Dennis Venema) 2017-12-23 17:38:59 UTC #342

> tallen_1:
>
> Dennis, since the conversation is happening on this thread rather than the 2nd part to this series, what of your argument presented there that a bottleneck down to two would cause a discernible spike in the TMRCA at the time of such an event? Would that be pertinent to the analysis of these papers?

For that we need the distribution of the TMRCA values across the genome. This is actually what PSMC modelling does - it's really a distribution of TMRCA values that is then used to infer Ne at the various times. So, it would show up as a dip in a PSMC plot. Richard thinks it would not be detected, but I disagree.

---

tallen_1 (Tim) 2017-12-23 17:39:48 UTC #343

Got you, thanks!

DennisVenema (Dennis Venema) 2017-12-23 17:41:47 UTC #344

The trick is PSMC papers only use one genome at a time. These two papers look at many individuals. So, we can find deeper TMRCA values than a typical PSMC study might find.

---

tallen_1 (Tim) 2017-12-23 17:48:19 UTC #345

Understood. Is there anyway to visualize a distribution of whole genome TMRCA data outside a PSMC analysis then? Or is noticing such a dip (or its lack) our only option?

DennisVenema (Dennis Venema) 2017-12-23 18:01:10 UTC #346

> tallen_1:
>
> Understood. Is there anyway to visualize a distribution of whole genome TMRCA data outside a PSMC analysis then?

I think Josh has asked the authors of the paper for their dataset, so that would be another way. In published papers? Not that I'm aware of, though they might be out there. Of course the MSMC papers (Durbin group) are also a representation of the distribution, but that's a modified PSMC on several genomes at once.

DennisVenema (Dennis Venema) 2017-12-23 18:04:15 UTC #347

The other thing is that PSMC models seem to lose power once you're past TMRCA values of over 3MYA. There are fewer coalescence events back there, so the method has a harder time. That in itself is an indication that the distribution of TMRCA values is thin out that far.

---

tallen_1 (Tim) 2017-12-23 18:16:20 UTC #349

Thanks! It seems then, rereading this back into your part 2 on this topic, that the coalescent analyses presented there… since they weren't PSMC…dealt primarily with effective population sizes as a means for indicating a lack of a severe bottleneck in relevant timescales. The telltale mark of a spike in TMRCA distributions wouldn't have been picked up in those studies. I'm still unclear though on the relationship of effective population sizes and even very severe bottlenecks as those figures only represent harmonic means of an effective population, not minimal values. Thoughts?

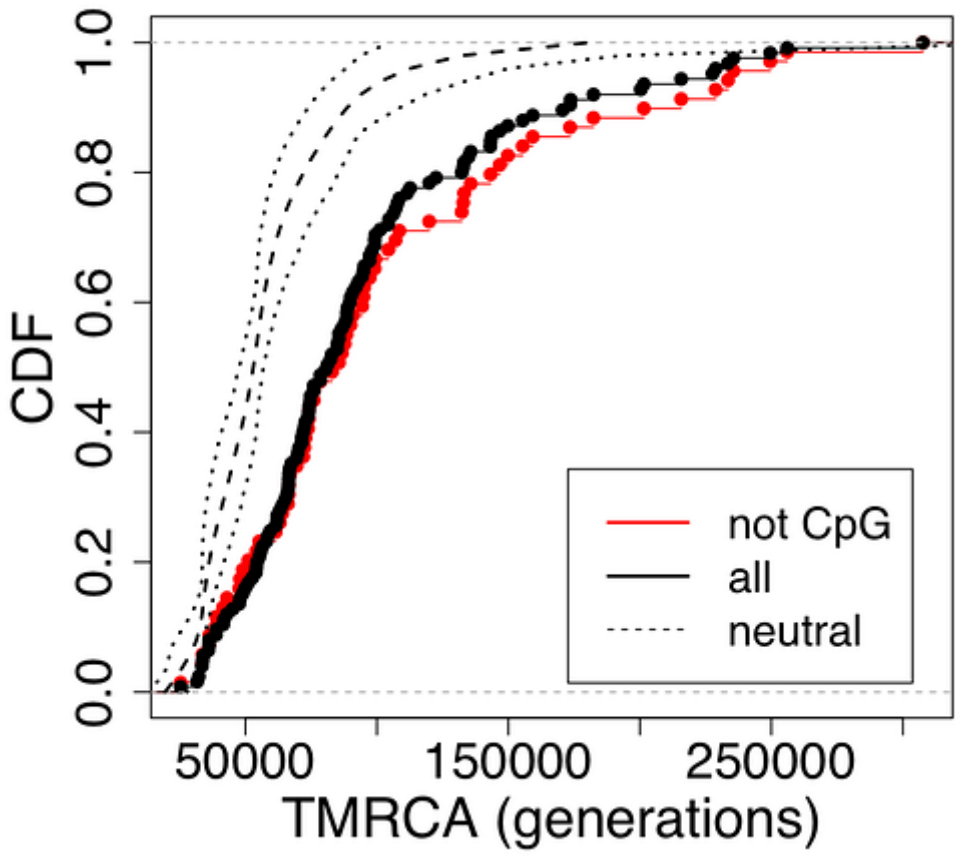
Swamidass (Dr. S Joshua Swamidass) 2017-12-23 18:21:51 UTC #350

So this new data is really helpful. Got some results to show.

Also, I was able to clarify that they are using a generation time of 25 years / generation. That becomes helpful in converting to years.

> Swamidass:
>
> We are interested in the distribution. The distribution includes the range, the mean, mode, min, max, and much much more information.

Okay, some good news, they include enough to reconstruct the distribution in Figure S17. **http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1004342#s5** This data includes a random sample of 69 neutral regions (dashed line), compared with 69 regions undergoing balancing selection and containing no CpGs (black). The red line is the 56 regions undergoing balancing selection by with shared CpGs. **Though not the entire genome, the dashed line is going to be a good estimate of the neutral genome-wide distribution.**



Distribution of TMRCAs in regions predicted to be under balancing selection. Cumulative distribution functions (CDFs) are shown for the 125 regions identified by Leffler et al. [77] based on segregating haplotypes shared between humans and chimpanzees (black circles), the subset of 69 loci containing no shared polymorphisms in CpG dinucleotides (black circles) and a collection of 69 putatively neutral regions having the same length

> distribution. Neutral regions consisted of noncoding regions from which known genes, binding sites, and conserved elements had been removed (see [109]). Notice the pronounced shift toward larger TMRCAs in the regions predicted to be under balancing selection, and a slightly more pronounced shift for the subset not containing CpGs (which are more likely to have undergone parallel mutations on both lineages). TMRCAs are measured in generations, as in all other figures and tables.

For the statistically untrained, this going to be a hard graph to read. It is a CDF, not a PDF (**https://en.wikipedia.org/wiki/Cumulative_distribution_function**).

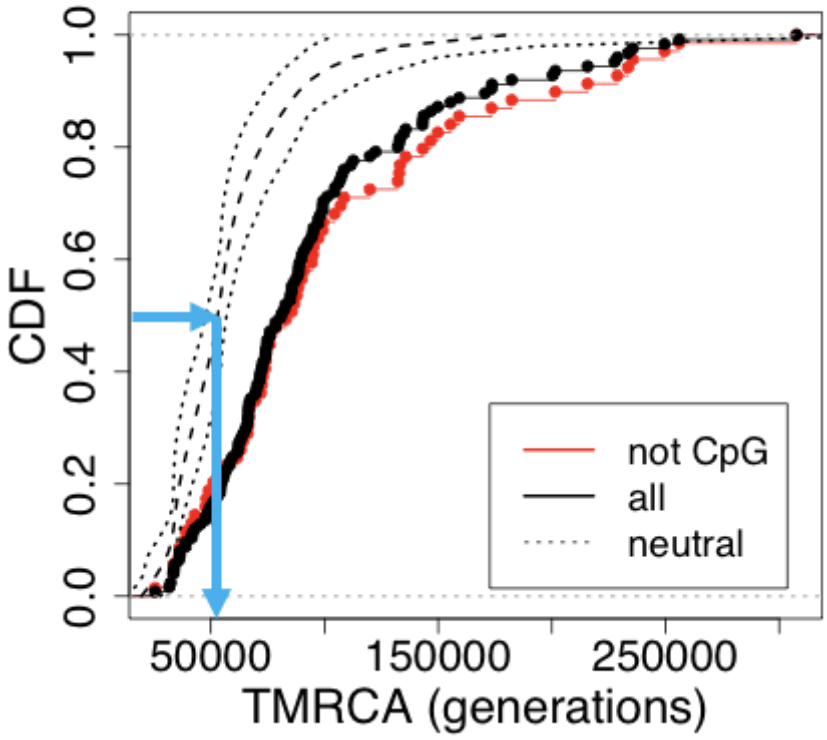
> DennisVenema:
>
> I also agree that if we were talking about one or two genome regions I might be more skeptical - but we're talking about several independent regions with very high TMRCA values. Not sure how looking at a distribution is going to change the conclusions of the authors of that paper.

This distribution changes things quite a bit. We do not see multiple modes. We also see that there is a very high positive skew to the data, and that balancing selection (black and red lines) increases TMRCA estimates quite a bit (no surprise), as much as by 2 fold (the magnitude of that effect is a surprise to me, but in retrospect is not so surprising). This means that estimates of TMRCA that do not take balancing selection into account are going to overestimate the value substantially. The CpG sites, which have a higher mutation rates but these mutations are more likely to be shared, so these regions can decrease TMRCA by about 10%.

Several factors can conspire to increase or reduce TMRCA. Molecular clocks only work when these factors are not interfering. That is why whole genome distributions are so important. We can test the effect of different regions. For example, if we wanted, we could start to untangle how identifiably neanderthal interbreeding biases results upwards, by seeing the results on those regions separately. We can also see how positive selection (which violates the assumptions required for dating). Some regions of the genome, also have lower mutation rates (and therefore will overestimate TMRCA).

From this, we want the best estimate of TMRCA in *neutral* regions of the genome (the dashed line) in a way that reduces these sources of error. This is a fairly important point as dates, can can only be reliably inferred in places that are not under selection. These are the only places where a molecular clock is expected to hold. Even then, some regions will still get "lucky" and coalesce more quickly to or much more slowly. So to a first approximation, we want the the *median* of these values. The median has another helpful feature. It should exclude the effect of regions we know for a fact include evidence of interbreeding with neanderthals and denisovans in the last 100 kya or so. Unfortunately, it cannot exclude regions affected by more ancient interbreeding (which could be the entire genome).

Nonetheless, we can make our estimate. In the regions not under selection, we see a mode for the TMRCA at *about* 50,000 generations. You can see it yourself tracing the blue line in the graph:



Multiplying by 25 years / generation, and dividing by four, this gives us a TMR4A of about 300 kya. By the way, I've grown more convinced in the TMR4A estimate, based on a brush up on the mathematics of phylogenies and coalescents.

This is a TMR4A about 2 times greater than y-MRCA and m-MRCA (which are about 150 kya to 200 kya); how do we make sense of this? Remember, Y and mito DNA does not recombine. So it is essentially a lot of data about single "block" of the genome. To some extent, is a single sample from this distribution. When we look at a whole genome, however, we are looking at about 100,000 "blocks". We have less information per block, but there are just so many more of them. With that in mind, the y-MRCA and m-MRCA are entirely consistent with this distribution, but the mode of this distribution is a better estimate.

I should add that TMR4A in autosomal regions outside this range are suspicious. We need an explanation of why we should trust values inconsistent with the y-MRCA and m-MRCA. I've given one here for this data, but based on this data I'd be skeptical of data that put TMR4A outside this range.

So this does plausibly make the case stronger, pushing the TMR4A back from 150K to 200K (from y-MRCA to m-MRCA) to a non-cherry picked number of about 300 kya (probably plus or minus 20 kya). This number is corrected for bias due to positive selection and recent interbreeding, and is consistent with the y-MRCA and m-MRCA data.

That does support Dennis's claim if *Homo sapiens* arise 200 kya ago and there was no interbreeding. However, there was interbreeding, and we found out this year that Homo sapiens might have arisen earlier than 300 kya. To be clear, the correspondence between 300 kya between the mode TMR4A and the origin of Homo sapiens can not be interpreted as evidence *for* a bottleneck at this specific point in time. Rather, this view of the data data does not specifically dispute the bottleneck hypothesis. To the point, I think we have much more confidence in heliocentrism than this data's ability to demonstrate Dennis's claim.

> Swamidass:

> 1. Homo sapiens specifically do not dip down to a single couple in 300 kya to the confidence we have in heliocentrism.

Though this has been immensely interesting and informative.

There is, of course, other data. I still point to trans-species variation. Speaking of which…

> DennisVenema:
>
> Don't forget that in several cases here we're talking about polymorphisms shared between humans and chimpanzees. That places the TMRCA for those regions prior to the human-chimp divergence, which is over 3.5MYA (using a very conservative value). Thus TMR4A would be over 875,000 years ago.

The only way there can be trans-species variation between us and chimps is for there to be balancing selection (or perhaps inconceivably recent interbreeding). Coalescence times for neutral regions are more than one order of magnitude smaller than divergence (as we have just seen). We just do not expect any trans species variation in neutral regions of the genome. Evidence of trans-species variation are very strong evidence that TMRCA's in this region are not valid.

Regions under balancing selection need to be handled with seperate reasoning. For example, the TMRCA / 4 = TMR4A estimate certainly does not apply here. TMR4A can be arbitrarily smaller than TMRCA if the trans species variation is 4 or less alleles (coalesced). The paper being referenced here appears to show only five regions with only 1 to 3 ancestral alleles in each region. That would push the TMRCA back, but not the TMR4A.

To be sure, this is evidence for common descent, but unless we see more than four alleles in a single locus (in an autosomal region), as it appears we do in MHC antigens (the Ayala), it does not make the case against a bottleneck. The alternative explanation for Ayala's MHC data is convergent evolution (which is where I'm sure **@RichardBuggs** will go). I'm much less convinced by this; and it is also testable by comparing with orangutan and gorilla data (though admittedly not yet tested).

DennisVenema (Dennis Venema) 2017-12-23 18:34:47 UTC #351

> Swamidass:
>
> but unless we see more than four alleles in a single locus (in an autosomal region), as it appears we do in MHC antigens (the Ayala), it does not make the case against a bottleneck. The alternative explanation for Ayala's MHC data is convergent evolution (which is where I'm sure **@RichardBuggs** will go). I'm much less convinced by this; and it is also testable by comparing with orangutan and gorilla data (though admittedly not yet tested).

I don't have time to go through all of you analysis at the moment - but thanks, I will look at it later - but I do agree with you on this point. I'm certain **@RichardBuggs** will appeal to convergent evolution for this as well. I guess he would have to appeal to the same for any trans-species polymorphism.

I haven't had time to look at this in detail, but in the Science paper they discuss neutral hitchhiking along with the selected SNPs (i.e. neutral loci in LD with selected ones).

DennisVenema (Dennis Venema) 2017-12-23 18:45:00 UTC #352

Another quick comment, because I might be missing something here. From that CDF graph, it looks like about 50% of the dataset is above TMRCA = 50,000 generations. Am I reading that correctly? 50% is above, 50% is below?

Edit: I mean for the neutral stuff.

Swamidass (Dr. S Joshua Swamidass) 2017-12-23 18:49:05 UTC #353

That's correct. I accidentally called that the mode. I should have said median.

DennisVenema (Dennis Venema) 2017-12-23 18:54:51 UTC #354

No worries. Thanks for pointing out that graph.

I'm eyeballing it, but it looks like the 0.5 to about 0.9 sits between 50,000 and 100,000 generations. If I'm reading this correctly, that would mean a substantial portion of the neutral dataset would have a TMR4A above 300KYA (the range would be 300 - 600 KYA). Am I missing anything here?

Jonathan_Burke (Jon) 2017-12-23 20:06:12 UTC #355

I think it's clear who Dr Bugg's actual audience is; people who don't accept evolution, who don't accept common descent, and who believe in a historical Adam and Eve who were a specially created pair of homo sapiens from whom all homo sapiens who ever lived, have descended.

First the article "**Geneticist: Adam and Eve could have existed**". The title alone is pretty clear. The follow up articles are even clearer. The article "**Adam, Eve, Richard Buggs, and Dennis Venema: Could Adam and Eve have existed?**" makes it abundantly clear what the aim of the exercise is; to establish the historicity of Adam and Eve as a special creation who were the sole ancestors of every homo sapiens who has ever lived, in accordance with standard conservative Christian theology (and YECs).

The article gets right to the point, explaining exactly what the issue is really about.

> Dennis Venema replies to Buggs, insisting that Adam and Eve could not likely exist. **Geneticist Richard Buggs thinks that they could have**.

It's worth noting of course that Dr Buggs has actually said nothing about Adam and Eve, and has in fact avoided mentioning them entirely. But that won't stop the author of this article.

In case we didn't get the point, it's repeated at the end of the article.

> **Geneticist defends possible Adam and Eve** in Nature: Ecology and Evolution

> and

> Geneticist: **Adam and Eve could have existed**

The comments are another excellent indicator of Dr Bugg's audience.

> J-Mac November 10, 2017 at 4:38 pm

> *I am a Christian and I disagree with the claim that mankind descended from a single breeding pair.*

> Then you not a Christian…You are a pseudo-christian like all theistic-evolutionists resembling Ken Miller, Dennis Venema and the rest of the so-called christians who sold Christianity for the sake of being called a scientist…

> Dean_from_Ohio November 10, 2017 at 5:33 pm

> Four Faces @ 1,

> *I am a Christian and I disagree with the claim that mankind descended from a single breeding pair.*

> Be careful; Christian theology, and the forgiveness of your sin, require an actual Adam. Romans chapter 5 irrefutably makes this claim. Believe it or not.

DennisVenema (Dennis Venema) 2017-12-23 20:13:47 UTC #356

> Swamidass:
>
> So this does plausibly make the case stronger, pushing the TMR4A back from 150K to 200K (from y-MRCA to m-MRCA) to a non-cherry picked number of about 300 kya (probably plus or minus 20 kya). This number is corrected for bias due to positive selection and recent interbreeding, and is consistent with the y-MRCA and m-MRCA data.

I agree, but I would say this places the *median* TMR4A at ~300 KYA. The distribution has a substantial amount of the neutral data above this value. If we're interested in the maximum range of TMR4A that we can have confidence in, it would seem to me that we could look at the error lines on the CFP. The upper error line for the neutral set hits 1.0 right around 100,000 generations. So, worst case scenario, about 50% of the neutral TMRCA distribution sits between 50,000 and 100,000 generations. This would mean that about 50% of the neutral dataset has a TMR4A between ~300 KYA and 625 KYA. That seems pretty relevant to the question at hand. Thoughts?

---

tallen_1 (Tim) 2017-12-23 20:35:28 UTC #357

Dennis…trying to follow along here, what is the significance of what you and Josh are discussing relating to the TMRCA distributions?

Swamidass (Dr. S Joshua Swamidass) 2017-12-23 20:45:18 UTC #358

> Jonathan_Burke:
>
> I think it's clear who Dr Bugg's actual audience is; people who don't accept evolution, who don't accept common descent, and who believe in a historical Adam and Eve who were a specially created pair of homo sapiens from whom all homo sapiens who ever lived, have descended.

Isn't that our audience too? We also already know that belief, as you stated, is consistent with the evidence any ways. So I am not sure what it has to do with this conversation.

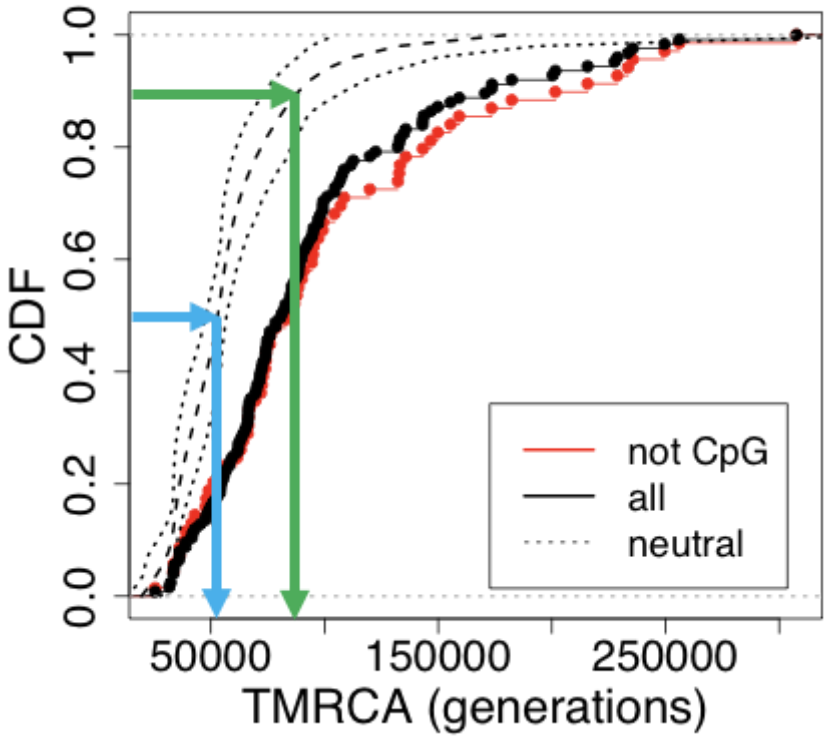
The other quotes are interesting on theology, and would be great to discuss on another thread. Especially if you can provide references (i.e. links). If that is what **@RichardBuggs** has ever written, he is wrong. Those are by random commenters on the internet though. Seriously. Even the recent critique of Theistic Evolution goes out of its way to clarify that they see theistic evolutionists as brothers and sisters. Fully Christian, even if they are wrong.

I'd love to see that conversation continue. Elsewhere. It is not relevant to the scientific question at hand.

Lest anyone doubt it, Scripture is 100% clear that doctrine of Adam is not how we determine who is a true and pseudo-Christian. **@DennisVenema** affirms the BioLogos belief statement, and that puts him solidly within the Christian community.

> DennisVenema:
>
> I'm eyeballing it, but it looks like the 0.5 to about 0.9 sits between 50,000 and 100,000 generations. If I'm reading this correctly, that would mean a substantial portion of the neutral dataset would have a TMR4A above 300KYA (the range would be 300 - 600 KYA). Am I missing anything here?

That is about right, if you follow the green line you can see this. However, this does not really give us any additional information that helps your case. We can't use these to legitimately skew our estimate upwards.



> DennisVenema:
>
> I agree, but I would say this places the median TMR4A at ~300 KYA. The distribution has a substantial amount of the neutral data above this value. If we're interested in the maximum range of TMR4A that we can have confidence

> in, it would seem to me that we could look at the error lines on the CFP. The upper error line for the neutral set hits 1.0 right around 100,000 generations. So, worst case scenario, about 50% of the neutral TMRCA distribution sits between 50,000 and 100,000 generations. This would mean that about 50% of the neutral dataset has a TMR4A between ~300 KYA and 625 KYA. That seems pretty relevant to the question at hand. Thoughts?

This is not sound statistical reasoning.

Keep in mind that these are not TMRCAs but TMRCA **estimates**. There is very high variance to all these estimates that *increases* as the true TMRCA increases. We ***expect*** a spread much like this if there was a bottleneck. If the goal is to rule out a bottleneck hypothesis, data we ***do not expect*** under the hypothesis is needed instead. That is not what this is.

Remember, the Zhao 2000 paper (which I am now glad we covered in depth) gave a ***very*** large range.

> DennisVenema:
>
> You suggest that perhaps the data in Zhao could go back to 4 haplotypes in 178,000 years. How certain are you about that value? You have to (a) pick the very lowest value within the 95% CI and then (b) assume that 1/4 of that is reasonable in this case. One quarter of the mean value is 339,000 years ago, which pretty much any scientist on the planet would say is more accurate than cherry-picking the lowest value. The upper bound (528,000 years ago) is just as probable as the lower bound. I could pick that value with the same confidence which which you pick the lowest one.

Notably, the region size here is 10,000 bp, matching the block size in this study. That means the confidence interval estimate here is going to somewhat match the confidence intervals we expect for individual blocks near the median in this study. However, for blocks giving larger TMRCAs the variance will be even ***higher***. Really, we have no confidence that any individual blocks did in fact actually colesce after the median estimate of 4*300 kya.

Remember, in a bottleneck hypothesis, all their errors would be correlated. We cannot just aggregate them after selection like that to reduce their confidence intervals. That is the definition of cherry picking.

There is another problem too. Mutation rates.

You can probably clarify from a deeper reading, but it appears that this study assumes a constant mutation rate across the whole genome. We know from both genome wide comparison **and** direct measurement now, that de novo mutation rates vary by 2 to 3 fold across the genome. Using the average mutation rate instead of the region specific rate, essentially, will **double** the TMRCA estimated at fast mutating sites (e.g. high CpG regions that are recombination hotspots). The effect this would have, if in fact a constant mutation rate was used, is that the spread of this distribution would increase, with biggest effect on the high TMRCAs.

This means, therefore, that we cannot really get a high confidence ancient TMRCA from your observation. It just isn't there. All that this graph tells us is that there is opportunity for cherry picking data. At both ends of the spectrum. I suppose I oppose cherry picking on both ends. I'm sure you do to.

> tallen_1:
>
> Dennis…trying to follow along here, what is the significance of what you and Josh are discussing relating to the TMRCA distributions?

The significance of this is high.

It strongly undercuts the claim that genome wide TMRCAs provide strong evidence against a bottleneck in Homo sapiens since they arose. Moreover, we have not even corrected yet for ancient interbreeding.

Perhaps there is strong evidence against a Homo sapien bottleneck, but I have yet to see it. As far as a I know, there is no way to correct for ancient interbreeding. Without that correction, I'm not sure how we get to heliocentrism level certainty. Though maybe Dennis can show us.

Regarding an ancestral bottleneck (not a Homo sapien bottleneck), as I've repeated the strongest evidence is trans species variation, as far as I know.

Lynn_Munter (Lynn Munter) 2017-12-23 21:10:09 UTC #359

> Swamidass:
>
> It strongly undercuts the claim that genome wide TMRCAs provide strong evidence against a bottleneck in Homo sapiens since they arose. Moreover, we have not even corrected yet for ancient interbreeding.

Would the definition of a bottleneck be that all subsequent population is descended from a limited number of individuals? So if there's later interbreeding with a neighboring population (Neanderthals et al) then does it really count as a bottleneck in the first place?

And theologically speaking, just to clarify, would an argument that there was a bottleneck to two in very ancient homo sapiens, only it's genetically undetectable due to later interbreeding with Neanderthals etc, rely heavily on reinterpretation of the sons of God/daughters of men in Genesis 6:2 to be referring to this interbreeding?

DennisVenema (Dennis Venema) 2017-12-23 21:34:14 UTC #360

> Swamidass:
>
> We expect a spread much like this if there was a bottleneck.

At what time? I'm not following you here.

Jonathan_Burke (Jon) 2017-12-23 21:54:53 UTC #361

> Swamidass:
>
> Isn't that our audience too?

I don't know about you, but I don't think my audience is people who want to be convinced that there's good genetic evidence that they can retain credible belief in a literal, specially created Adam and Eve (who had no ancestors), less than 10,000 years ago as the ancestors of all homo sapiens, while rejecting evolution. I don't think that argument can be made.

> Swamidass:
>
> We also already know that belief, as you stated, is consistent with the evidence any ways.

Consistent with what evidence?

Jonathan_Burke (Jon) 2017-12-23 21:55:45 UTC #362

> Swamidass:
>
> The other quotes are interesting on theology, and would be great to discuss on another thread. Especially if you can provide references (i.e. links).

I linked to the page with the comments, and said I was quoting comments from that page.

Swamidass (Dr. S Joshua Swamidass) 2017-12-24 02:28:34 UTC #363

Putting this on pause till new years. Post saved. Will return it later =).

Christy (Christy Hemphill) 2017-12-24 02:48:23 UTC #364

Christy (Christy Hemphill) 2017-12-24 02:51:20 UTC #365

Okay, you BioLogos junkies…I'm insisting that you take that break you have all been promising your loved ones and get off this thread for at least the next two days. Because none of the moderators want to read esoteric calculations over the next couple days. Have a lovely Christmas everyone, I'll open the thread on the 26th.

Christy (Christy Hemphill) 2017-12-26 16:25:34 UTC #366

Lynn_Munter (Lynn Munter) 2017-12-26 17:47:11 UTC #367

> Swamidass:
>
> As far as a I know, there is no way to correct for ancient interbreeding. Without that correction, I'm not sure how we get to heliocentrism level certainty. Though maybe Dennis can show us.

I went back to look, and I don't think the way he phrased his heliocentrism quote in the book allows for a bottleneck of two followed by interbreeding. Here it is:

> DennisVenema:
>
> That said, we can be confident that finding evidence that we were created independently of other animals or that we descend from only two people just isn't going to happen. Some ideas in science are so well supported that it is highly unlikely new evidence will substantially modify them, and these are among them. The sun is at the center of our solar system, humans evolved, and we evolved as a population.

So the implication is clearly of "we descend from only two people," not of interbreeding, although the last bit does give you perhaps a bit more wiggle room as far as how far back to stretch it: not just Homo Sapiens but whatever intermediate directly preceded it, i.e. the 300kya Homo Sapiens with evolutionary differences would clearly be included by this statement. Which Dennis has already agreed to include, so that's all right.

It's probable he's phrased it other ways in the course of this conversation, but this was the published statement.

Chris_Falter (Chris Falter) 2017-12-26 18:06:50 UTC #368

Question: Why is this an accurate simulation for haplotype distributions? A Gaussian distribution is essentially pure noise except for the mean and the variance. **@DennisVenema** is claiming that the existence of TMRCA values > mya is a legitimate signal of ancestry, not just noise. ***If*** the observed PDF across the genome is the result of a stochastic process that makes some regions *seem* younger than the ground truth (as measured by TMRCA), ***then*** the noise should not be interpreted as nullifying the signal from regions at extrema that point to a very ancient TMRCA.

Does that make sense?

---

glipsnort (Steve Schaffner) 2017-12-26 18:15:41 UTC #369

> Swamidass:
>
> Perhaps there is strong evidence against a Homo sapien bottleneck, but I have yet to see it. As far as a I know, there is no way to correct for ancient interbreeding. Without that correction, I'm not sure how we get to heliocentrism level certainty.

I don't know what you mean by correcting for interbreeding here. If many of us are descendants of ancient interbreeding between lineages that diverged at least half a million years ago (which we are), then we are not a product of a bottleneck of size two within the last half million years. To take seriously a recent tight bottleneck, you don't have to correct for introgression – you have to ignore it.

Swamidass (Dr. S Joshua Swamidass) 2017-12-27 21:59:57 UTC #370

> glipsnort:
>
> I don't know what you mean by correcting for interbreeding here. If many of us are descendants of ancient interbreeding between lineages that diverged at least half a million years ago (which we are), then we are not a product of a bottleneck of size two within the last half million years. To take seriously a recent tight bottleneck, you don't have to correct for introgression – you have to ignore it.

I'll post more later. This is just regarding **@DennisVenema** 's claim re: Homo sapiens. If we care about measuring Homo sapien population size, we have to correct for interbreeding.

> RichardBuggs:
>
> This is exactly my point. Thank you for stating it so concisely. To my mind, the way ahead would be to write a programme that computes the TMR4A for each haplotype block of the human genome, and work out a reasonable time frame using data from all blocks. Until that has been done, I do not think we can say that the bottleneck hypothesis has been rigorously tested.

The good news is that I found exactly the data we need to do this study. It includes a scan of phylogenies constructed across the entire autosomal genome. Each phylogeny is computed for non-recombining blocks, which corrects for recombination introduced artifacts. From this we can compute TMRCA and T4MRCA across the whole genome, by looking at the times of the first and third coalescent nodes. Once we rescale to years with the mutation rates, we will have the distribution across the whole genome.

1. We can test to see how well TMRCA / 4 = TMR4A.
2. We can see the distribution of TMR4A across the genome.

3. We can identify the outlier areas, or subset on any region of the genome.

The bad news is that the source data is **424 GB of compressed data**. I got a plan to handle it though. If that is a good analysis to do?

What is everyone's thoughts? **(especially @glipsnort , @DennisVenema , and @RichardBuggs)** Not expecting a response till Jan of course.

---

glipsnort (Steve Schaffner) 2017-12-28 13:38:09 UTC #371

> Swamidass:
>
> I'll post more later. This is just regarding @DennisVenema 's claim re: Homo sapiens. If we care about measuring Homo sapien population size, we have to correct for interbreeding.

I have to admit that I haven't looked at the precise wording of Dennis's statements lately, but my impression was that his claims were not about "organisms arbitrarily labelled as Homo sapiens" but about "us", which would correspond to contemporary Homo sapiens. Contemporary Homo sapiens did not go through a bottleneck of size two 200,000 years ago. *My ancestors* did not go through a tight bottleneck 200,000 years ago. At that time, some of them were living in Africa and some of them were living in Europe. I still don't see why the demographic history of one branch of the structured population I descend from has anything other than purely academic interest to anyone. The fact that many (but not all) biologists have slapped different names on the different branches doesn't strike me as relevant at all.

---

tallen_1 (Tim) 2017-12-28 15:02:32 UTC #372

Josh, would you agree with this statement based on your understanding of the evidence?

> glipsnort:
>
> My ancestors did not go through a tight bottleneck 200,000 years ago.

Jon_Garvey (Jon Garvey) 2017-12-28 15:18:44 UTC #373

"Sir, Is it on your grandfather's or your grandmother's side that you claim descent from a tight bottleneck 200,000 years ago?"🙂

---

gbrooks9 (George Brooks) 2017-12-28 16:59:04 UTC #374

I once pointed out in another group that if we go back far enough, both sides of all human lineage is African!

I thought that was a pretty clever turn of the phrase. But wouldn't you know I was soon confronted by a Texan, amateur anthropologist and white supremacist, who insisted that some human races have no ancestors from Africa.

I turned him off and it was blissfully quiet.

---

glipsnort (Steve Schaffner) 2017-12-28 17:35:29 UTC #375

> Jon_Garvey:

> “Sir, Is it on your grandfather’s or your grandmother’s side that you claim descent from a tight bottleneck 200,000 years ago?”🙂

Excuse me, but in my family we prefer not to talk about “those” relatives.

Lynn_Munter (Lynn Munter) 2017-12-28 18:12:35 UTC #376

> glipsnort:
>
> I have to admit that I haven’t looked at the precise wording of Dennis’s statements lately

Are you implying, sir, that it has become onerous to scroll the length of this thread?

I recently shared the fruits of such scrolling to answer this same question in comment 361, to save others the trouble.

---

glipsnort (Steve Schaffner) 2017-12-28 18:32:32 UTC #377

> Lynn_Munter:
>
> Are you implying, sir, that it has become onerous to scroll the length of this thread?
>
> I recently shared the fruits of such scrolling to answer this same question in comment 361, to save others the trouble.

Yeah, that was the quotation I was basing my response on; I exploited your effort without citing it (or even liking it – bad glipsnort). What I don’t know is whether Dennis wrote other things that phrased the claim in different ways, and to which this discussion would actually be relevant.

Lynn_Munter (Lynn Munter) 2017-12-28 20:57:31 UTC #378

I went through the first 290 posts looking for any relevant statements by **@DennisVenema** . I don’t see any that can be construed as saying that a bottleneck to two in Homo Sapiens (as opposed to “our lineage” including interbreeding) is ruled out with certainty comparable to heliocentrism. This is getting pretty nitpicky, but if it aids the discussion then good.

> DennisVenema:
>
> I remain confident that my conclusion in the book is sound. I have not seen anything in this discussion that remotely suggests otherwise. There simply is no evidence to support the hypothesis of a bottleneck to 2. There are converging lines of evidence that our species has not dipped below several thousand individuals.

> DennisVenema:
>
> In Adam and the Genome I consistently discuss humans as a species arising ~200,000 years ago. So, by your calculations, Zhao (2000) supports my case - human variation in this all region of the genome cannot be reasonably explained by a bottleneck to 2 individuals within human history, as I argue in AatG.

> DennisVenema:
>
> A few comments: the paper that suggests Homo sapiens back at ~300,000 years ago came out after AatG was published, but I don't see how it really affects things. I don't see any evidence of a bottleneck in our lineage for the last 1 MYA or more. Even Zhao (2000) has a range of TMRCA/4 values (if we want to go with that) that easily pushes back past 300,000.
>
> (Of course, we need to look at the distribution of TMRCA values across the genome as a whole - not just at one 10kb region, as you've noted.)
>
> Also, those fossils are not uniformly accepted as Homo sapiens. They have some features that are decidedly different than Homo sapiens at 200,000 years ago. This is to be expected. Our species becomes a species as a gradient biologically. With a "perfect" fossil record over the last 2MY, we presumably would have a smooth gradient between early H. erectus all the way to modern humans in the present day. As such, it will become more and more difficult to "draw the line on the gradient" - as I discuss in the book- as we get a more complete picture of the fossil record. We're a chronospecies.

> DennisVenema:
>
> And as such, this paper supports the conclusion I state in Adam and the Genome. If one was to squeeze this variation into the last 200,000 years (or even 300,000 years), one would have to increase the mutation rate to do so.

> DennisVenema:
>
> > Swamidass:
> >
> > > DennisVenema:
> > >
> > > Is this positive evidence for the claim I make in Adam and the Genome? Yes. I can't see how we can squeeze this variation into 2 people at 200,000 years ago (or even 300,000 years ago, if one was to accept Homo sapiens at this time). Can you, or can **@RichardBuggs** ?
> > > [/quote]It seems like you are limiting your claims to merely Homo sapiens, is that correct? I thought we were asking about bottlenecks in our distant past going back to the origin of Homo about 2 million years ago. By limiting your claims this way, are you suggesting that you think it is possible for there to have been a single couple bottleneck, say, 2 million years ago?
>
> In the book I make the claim that humans evolve as a population, and I define human as "our species" - Homo sapiens. (That's not to say that other species might not have had the image of God, and so on.) In the book I place H. sapiens at 200 KYA, as was the consensus at the time. I think the evidence is solid that there is not a bottleneck to 2 in our ancestry for at least the last 500,000 years, but I don't defend that in the book per se. From there it gets progressively more challenging to make a strong claim, but I think that even 1,000,000 years is reasonable to exclude a bottleneck. 2MYA? By now we're at the limit of PSMC and other similar modelling approaches.
>
> Now, is there positive evidence for a bottleneck to 2 (or even 20 or 200 or 2000?) at any time in the last 3,000,000 years or more? Nope. At best one could claim that our present-day methods cannot exclude the possibility between 1-3 MYA.

ETA: Adding some more past 290:

> DennisVenema:
>
> The heliocentric quote, which I thought was the object of your concern, is about humans (Homo sapiens). When I'm speaking about our lineage leading up to humans at 200KYA I use "lineage" or similar.
>
> The other two quotes remain valid. Does "it seems" sound like I'm saying this is as certain as heliocentrism? That would be quite the understatement. That is a summary statement of all the lines of evidence in the literature to date that do not provide support for a bottleneck below ~10,000 at any time in the last 18MY (which remains the case).
>
> "All methods employed to date agree that the human lineage has not dipped below several thousand individuals for the last 3 million years or more – long before our lineage was even remotely called "human".
>
> This quote also remains valid. There are no studies in the literature that support a lower bottleneck, and several that support large Ne values over this timeframe (PSMC and LD studies, for example). If there were (perhaps if I had missed one somewhere?) I'm sure you would point it out if you were aware of it.
>
> So: "heliocentric certain": humans. Pretty darn certain: lineage leading to humans over the last several hundred thousand years (say back to ~500,000 years ago). Confident but not as definitive: lineage over the last few million years. Survey of literature to date: no evidence of a bottleneck greater than thousands anywhere, regardless of time.

> DennisVenema:
>
> It's up the thread ^ . "Heliocentrism certain" = humans. 200KYA in the book. I'm ok with stretching that to 300KYA if needed.

Also including **@Swamidass** ' restatement which has become the jumping-off point for much subsequent discussion:[quote="Swamidass, post:322, topic:37039"]
Dennis,

Very interesting papers. I've read the first one already, but not the second. However, I am not sure how they help your case. As I understand it, you are trying to demonstrate…

1. Homo sapiens specifically do not dip down to a single couple in 300 kya to the confidence we have in heliocentrism.
2. Our ancestors as a whole do not dip down to a single couple between 300 kya and 3 mya with very high confidence, but maybe not as high.

As you put it…

DennisVenema: The heliocentric quote, which I thought was the object of your concern, is about humans (Homo sapiens). When I'm speaking about our lineage leading up to humans at 200KYA I use "lineage" or similar.

DennisVenema: So: "heliocentric certain": humans. Pretty darn certain: lineage leading to humans over the last several hundred thousand years (say back to ~500,000 years ago). Confident but not as definitive: lineage over the last few million years.

Swamidass: As I understand it, the first claim appears to be novel, and I cannot find it in the literature anywhere. It would be help to see a paper that estimates population size of Homo sapiens specifically. I have not been able to find one. Have you?

Charles_Alexandre (Charles Alexandre Roy) 2017-12-29 14:36:14 UTC #379

I fully agree with you and I've raised similar points about people's tone in other threads, only to be told otherwise by moderators. Obviously, it's nearly impossible to police for tone leaving only overtly hostile or crude comments as objectively inappropriate. However, my guess is that moderators who frequently see and censor that sort of dialogue end up with overly low expectations of what civil dialogue looks like. Unfortunately, to non-experts reading these sorts of exchanges, tone plays a large role because it's one of the few elements that they can actually assess. So while it's not really realistic to moderate, I think that we could at least admit that it could often be better and that as Christian brothers and sisters, we should strive for the most gracious dialogue possible. I think that Dennis (and all Biologos writers, really), are completely above board on this and I honestly think that that is one of the most persuasive aspects of their position.

jpm (Phil) 2017-12-29 15:56:11 UTC #380

While I have trouble what post of tallen_1 you are referring to, agree with your comments on tone. As a suggestion, if you comment on a post that is way back in the thread, highlight and quote it to allow others to easily see what you are referring to.
Part of the problem is that some seem to see these discussions as competitions to be won by the knights carrying their colors, when they are more an effort to reach understanding of the relative positions.

tallen_1 (Tim) 2017-12-30 15:32:23 UTC #381

It's a bit odd to see this dug back up, but my concern now is simply one of basic fairness rather than tone. By now we're all accustomed to Richard's inquisitorial conversation style. It is what it is. What I do want to see happen, and what I think Richard owes his conversational partners on this thread, is to abide by his same standards of accountability in openly and honestly answering questions posed to one about what the evidence does or does not support. As long as he plays by the same rules as he holds others to, then I think we're good. But if he thinks the only important questions to answer are the ones he pushes, then I don't think we are. He has some unanswered pertinent questions put to him by Dennis and others. Let's see what he does with them.

GJDS (GJDS) 2017-12-31 00:12:42 UTC #382

I have not read every single post, but I have read with interest the various expert opinions, and for what it is worth, I give my impression.

The certainty that is displayed by one side seems to be the absence of modelling that would support a "bottleneck" of two (I find it hard to believe two creatures are a bottleneck? but this is the terminology).

The questions that are asked however point to a "lack of similar certainty" regarding what I think are important parameters in the modelling.

I (as a non-participant) am at a loss as to the physical evidence that is supposed regarding this bottleneck of a few hundred or whatever number is discussed. Am I missing something? Has someone discovered remains at a particular location to show such a group existed at some point in time? If not, is this not an inference derived from the modelling. If there is direct physical evidence, why is this not discussed at length, as it would be relevant to the certainty/uncertainty aspect of the discussion?

Jon_Garvey (Jon Garvey) 2017-12-31 09:21:56 UTC #383

Yes - one can use considerable expertise and ingenuity to argue whether the population genetics model supports a particular contention or not. That's the nature of this thread.

But the question of whether the model *itself* is adequately valid over such timescales, given its known limitations and the state of flux of theories of large-scale evolution, is a significant one.

"All models are wrong - some are useful". But their utility is only measurable by the ability to validate them by independent observation under the situation for which they are being used - in this case the origin of humanity defined, at least, as our species or even across hominin species by some protagonists. That's very different from studying the evolution of Y-chromosomes in the living population.

In this case, validation would seem to require counting fossils that are as rare as hens' teeth - in the absence of physical evidence, the population genetics model seems to validate itself in a circular manner.

Chris_Falter (Chris Falter) 2017-12-31 13:49:59 UTC #384

> Jon_Garvey:
>
> But their utility is only measurable by the ability to validate them by independent observation under the situation for which they are being used - in this case the origin of humanity defined, at least, as our species or even across hominin species by some protagonists. [/quote]
>
> The models are estimating the minimum size of an ancestral population at various points on the past. The models can be validated by examining their predictions for the current state of the genome(s). Also, their assumptions regarding the initial state and regarding rates of various kinds of mutations can be supported or disproven by experimental evidence regarding current states and rates.
>
> That said, if this modeling were easy, we non-biologists would not have had the opportunity to grab some popcorn and enjoy the show.
>
> [quote="Jon_Garvey, post:383, topic:37039"]That's very different from studying the evolution of Y-chromosomes in the living population.

AFAIK, it's basically the same thing, but on a longer time scale and across more of the genome than typical Y-chromosome studies.

Perhaps one of our biologist friends like **@Swamidass** , **@glipsnort** , **@DennisVenema** or **@RichardBuggs** would be able to shed more light.

GJDS (GJDS) 2017-12-31 23:06:09 UTC #385

> Chris_Falter:
>
> The models can be validated by examining their predictions for the current state of the genome(s).

Perhaps you would elaborate; what predictions can any model make on what seems to be current data used to set up the model itself?

Chris_Falter (Chris Falter) 2018-01-01 01:31:48 UTC #386

Good question, George. Assuming I have understood this thread, the data being predicted/compared with current state and the data used in rate calculations are not the same. The predictions/observations of current state focus on the distribution of genomic features, whereas the assumptions of rates of change are based on known history.

GJDS (GJDS) 2018-01-01 08:40:00 UTC #387

Hi Chris,

Validation of models, as I have practiced (and is commonly understood) requires a result from the model to be similar to an observation/measurement of a system independent of the model data base. Within this I have a difficult time noting such validation of the models discussed here. Since a major point is the size and time of a bottleneck, for example, validation would be considered by using physical data of a real bottleneck. There may be other ways, and if you can identify them I would be interested to know.

This is not a question on the technicalities of the modelling proceure.

Swamidass (Dr. S Joshua Swamidass) 2018-01-01 08:57:35 UTC #388

> Chris_Falter:
>
> Perhaps one of our biologist friends like **@Swamidass** , **@glipsnort** , **@DennisVenema** or **@RichardBuggs** would be able to shed more light.

Thanks for the invitation.

> Chris_Falter:
>
> The models are estimating the **minimum size** of an ancestral population at various points on the past. T

This is not accurate. They are estimating the ***average*** population size ***in a sliding window*** (that is quite large). They are not estimating the minimum. Just the average. The really interesting question is whether or not there is a way to determine the minimum.

Population size estimate studies, to be clear, are ***not*** testing for a brief bottleneck followed by an exponential expansion. The only paper I know that did this is the Ayala paper on MHC (**http://www.pnas.org/content/91/15/6787.abstract**) from 1994. Eventually we will get around to it, but this is the only published study I know that actually tests the idea. That was 25 years ago though, so the follow up studies are going to be interesting to look at.

The point that **@RichardBuggs** is making is that the power of population studies past about 500 kya to detect brief bottlenecks are not well studied. The fact that they do not find them, therefore, cannot be taken as evidence they do not exist. At least not yet. This is a question about ***detectability*** and ***statistical power***.

> Lynn_Munter:
>
> And theologically speaking, just to clarify, would an argument that there was a bottleneck to two in very ancient homo sapiens, only it's genetically undetectable due to later interbreeding with Neanderthals etc, rely heavily on reinterpretation of the sons of God/daughters of men in Genesis 6:2 to be referring to this interbreeding?

We are not speaking theologically at all. This is about the science.

I imagine those that take this position might take it not for Genesis, but because of Paul's statements in Acts, Romans, and I Cor. I suspect New Testament theology drives this more than Genesis hermeneutics. Whatever the case, the impact on theology should be sorted out later. Perhaps we start a thread for that?

> Chris_Falter:
>
> Question: Why is this an accurate simulation for haplotype distributions? A Gaussian distribution is essentially pure noise except for the mean and the variance. **@DennisVenema** is claiming that the existence of TMRCA values > mya is a legitimate signal of ancestry, not just noise. If the observed PDF across the genome is the result of a stochastic process that makes some regions seem younger than the ground truth (as measured by TMRCA), then the noise should not be interpreted as nullifying the signal from regions at extrema that point to a very ancient TMRCA.
>
> Does that make sense?

I'm not sure I understand the question. For one, I agree that that TMRCA > 1mya are legitimate signal of ancestry, ***for DNA***. We are not talking about segments of DNA though, but a couple with four genome copies between them both. Its an equivocation to place them at an autosomal TMRCA. Right?

> glipsnort:
>
> I still don't see why the demographic history of one branch of the structured population I descend from has anything other than purely academic interest to anyone. The fact that many (but not all) biologists have slapped different names on the different branches doesn't strike me as relevant at all.

Well, for one, I am an academic! =)

Also, we were brought here by the claim that "Homo sapiens" never dip below a few thousand. Though, we all know, they eventually go to zero in the past. How can we know then that they do not stop at 2 on the way to zero? Yes, this is all about definitions. No scientific study goes here, because there is not enough traction to get clarity here. Which is why heliocentric certainty is not likely.

As I understand it (and it seems was confirmed by others, there are two claims at question here.

> Swamidass:
>
> 1. Homo sapiens specifically do not dip down to a single couple in 300 kya to the confidence we have in heliocentrism.
> 2. Our ancestors as a whole do not dip down to a single couple between 300 kya and 3 mya with very high confidence, but maybe not as high.

> Chris_Falter:
>
> AFAIK, it's basically the same thing, but on a longer time scale and across more of the genome than typical Y-chromosome studies.

That's right. I'd say this higher confidence than the Y-chromosomal studies too.

> GJDS:

> Validation of models, as I have practiced (and is commonly understood) requires a result from the model to be similar to an observation/measurement of a system independent of the model data base

That is exactly what these studies do. There is real quality work here.

> GJDS:
>
> Perhaps you would elaborate; what predictions can any model make on what seems to be current data used to set up the model itself?

If you read the papers, you will see that quite a bit of validation is going on. There is really good work being done by scientists here. It is a mistake to dismiss it this way. There is a great deal of independent validation. Often they find that specific parameters do not affect the results much (e.g. mutation rate and generation time), except to scale the time. That leaves the debate on exact dates open (and does expand the confidence intervals), but it does not invalidate the whole effort.

The question here is actually far more interesting on a scientific level. We are getting into understanding exactly what these approaches can and cannot tell us.

Swamidass (Dr. S Joshua Swamidass) 2018-01-01 09:14:15 UTC #389

If this is what **@DennisVenema** means by his first claim, I'm not sure its defensible:

> **1. Homo sapiens specifically do not dip down to a single couple in 300 kya to the confidence we have in heliocentrism.**

Population size estimates are always of Homo sapiens + all of our other ancestors at the time. The finding that our ancestors do not go to a single couple tells us nothing about Homo sapiens specifically, because Homo sapiens are not our only ancestors past about 50 kya.

The Ecological Fallacy.: *Homo sapiens* go to zero, so why couldn't they go to two?

Regarding the second claim, things are more interesting.

> **2. Our ancestors as a whole do not dip down to a single couple between 300 kya and 3 mya with very high confidence, but maybe not as high.**

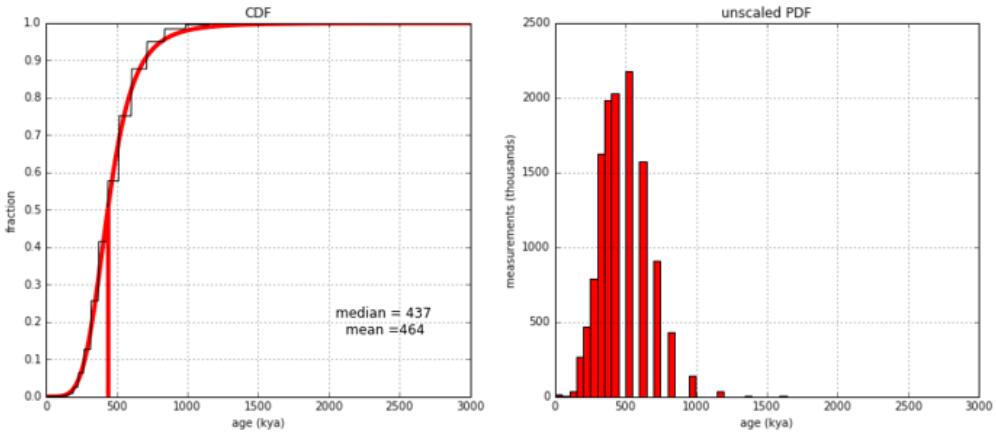
I had some fun spelunking the data. **@RichardBuggs** suggested…

> RichardBuggs:
>
> > We need to know the Time to Most Recent 4 Alleles (TMR4A). This is not a standard computed number in genetics.
>
> This is exactly my point. Thank you for stating it so concisely. To my mind, **the way ahead would be to write a programme that computes the TMR4A for each haplotype block of the human genome, and work out a**

> **reasonable time frame using data from all blocks.** Until that has been done, I do not think we can say that the bottleneck hypothesis has been rigorously tested.

I took him up on the challenge and computed it across the whole genome.

That puts a fair estimate of the TMR4A at 430 kya. I'd estimate that there is about 20% error one way or another, at least. That, could, perhaps be even extended down to 340 kya, when some think first Homo sapiens arise (though I would not bank on it). It would ***certainly*** work for the common ancestors of Neanderthals, Denisovans and *Homo sapiens*.



I explain the details here. **https://discourse.peacefulscience.org/t/heliocentric-certainty-against-a-bottleneck-of-two/** And **@DennisVenema** , the authors of the ArgWeaver paper were really helpful. So kudos to you for sending me that way. The linked discourse is pretty long.

The exact path here is fairly technical, and I wanted to document it so that others could replicate these results. There is a lot in that thread, so this might be a helpful guide:

Claims of Heliocentric Certainty. What are the scientific claims in question?

TMRCA or Time to Most Recent 4 Alleles? TMR4A (not TMRCA) puts the bounds on a couple bottleneck.

Estimate with Median or Max? The statistically sound approach is the median.

TMR4A from Genome-Wide TMRCA. An initial estimate of TMR4A, which we improve on later.

The ArgWeaver Genome Wide Phylogenies **424 GB of data with genome-wide answers.**

Genome-Wide TMR4A. **A better estimate of TMR4A, based on the ArgWeaver data.**

The last two may be most interesting if you have time to take a look. So have fun, I'll look forward to seeing the conversation continue. I've been learning a lot.

Not All the Evidence

To be clear, we have still yet to deal with the stronger evidence, such as Ayalas work where the bottleneck hypothesis was tested, and he put a minimum bound on bottlenecks.

---

tallen_1 (Tim) 2018-01-01 15:16:17 UTC #390

Josh,

In your part (1) above, focusing on taxonomically classified homo sapiens narrowly rather than our hominid ancestors to modern day homo sapiens (obviously so very close genetically to interbreed), you would not even require an “Adam & Eve,” but merely an Adam or Eve in proximity to our other genetically compatible ancestors. A bottleneck of one if you will, a bit of a silly proposition that exposes the arbitrariness of such an endeavor.

In your part (2), should I take this as an affirmation of agreement with Steve’s claim below…extending this even further to 300KYA, which I believe echos Dennis’ framing of this issue as well?

> glipsnort:
>
> my impression was that his claims were not about “organisms arbitrarily labelled as Homo sapiens” but about “us”, which would correspond to contemporary Homo sapiens. Contemporary Homo sapiens did not go through a bottleneck of size two 200,000 years ago. My ancestors did not go through a tight bottleneck 200,000 years ago.

---

glipsnort (Steve Schaffner) 2018-01-01 16:50:07 UTC #391

> Swamidass:
>
> This is not accurate. They are estimating the average population size in a sliding window (that is quite large). They are not estimating the minimum. Just the average

To be more precise, they’re estimating the effective population size in time windows. The effective population size may or may not correspond well to the actual population size.[quote=“Swamidass, post:388, topic:37039”]
The point that **@RichardBuggs** is making is that population studies past about 500 kya are not powered to detect brief bottlenecks.
[/quote]
I would say rather that their power to detect brief bottlenecks has not been well explored. [quote=“Swamidass, post:388, topic:37039”]
Also, we were brought here by the claim that “Homo sapiens” never dip below a few thousand.
[/quote]
You may have been, but I certainly wasn’t brought here by that question. I think that question (even as you hashed it out with Dennis) is subject to multiple interpretations that lead to very different answers, and different people seem to be assuming different things about what question is actually being asked or answered. Here are at least some of the possible questions we might be addressing:

1. Could our ancestors have passed through a bottleneck of size two within some time frame? This is one possible interpretation of asking whether Homo sapiens could have passed through such a bottleneck, since “we” are Homo sapiens and Homo sapiens is us. It is a question that may be of scientific, theological and broad human interest.

If the time frame is the last 500,000 years, it is a question whose answer is unambiguously “no”, thanks to the ancestry many of us have in Neanderthals and Denisovans.

2. Can we answer question (1) based only on genetic variation data from the current human population (i.e. ignoring Neanderthals). This is effectively the question that is addressed by looking at haplotypes and coalescent methods (e.g. PSMC).

3. Did the African branch of our ancestry go through the same kind of tight bottleneck? In practice, this is the same question as (2), but with datasets restricted to individuals of African ancestry. It is the question I was actually addressing in my simulations (mostly because I wasn’t even thinking about Neanderthals). Both (2) and (3) are of technical interest to population geneticists, and might be of broader interest as well.

4. Did organisms that we would classify as Homo sapiens ever go through a tight bottleneck? This addresses not just modern H. sapiens, many of whom have Neanderthal ancestry, but also H. sapiens population prior to ~75,000 years ago, who (probably) didn't. As I have previously pointed out, this is a very different question from (1). I view it as essentially unanswerable and nearly meaningless. Classification as H. sapiens as you look back in time is largely arbitrary and subjective. More importantly, there could well have been interbreeding within Africa between groups that we would classify as H. sapiens and group that we would not, but we have no way of ascertaining whether or when such events happened. Looking at modern genetic variation, therefore, cannot answer this question.

Swamidass (Dr. S Joshua Swamidass) 2018-01-01 18:50:04 UTC #392

> glipsnort:
>
> To be more precise, they're estimating the effective population size in time windows. The effective population size may or may not correspond well to the actual population size.

Agreed.

> glipsnort:
>
> I would say rather that their power to detect brief bottlenecks has not been well explored.

Agreed. Edited the original text.

> glipsnort:
>
> You may have been, but I certainly wasn't brought here by that question. I think that question (even as you hashed it out with Dennis) is subject to multiple interpretations that lead to very different answers, and different people seem to be assuming different things about what question is actually being asked or answered. Here are at least some of the possible questions we might be addressing:

> glipsnort:
>
> You may have been, but I certainly wasn't brought here by that question. I think that question (even as you hashed it out with Dennis) is subject to multiple interpretations that lead to very different answers, and different people seem to be assuming different things about what question is actually being asked or answered. Here are at least some of the possible questions we might be addressing:

I agree with you that the terms are ambiguous. However, they were clarified. Dennis clarified that he mean *Homo sapiens* specifically and NOT Neanderthals, and pegged his claim on the time at which Homo sapiens arise. I'm sure he was mistaken, bit that is what he claimed.

> glipsnort:
>
> If the time frame is the last 500,000 years, it is a question whose answer is unambiguously "no", thanks to the ancestry many of us have in Neanderthals and Denisovans.

I thought Neanderthals and Denisovans and Homo sapiens could share common ancestry at 500 kya, or even earlier. Did I miss something there?

> glipsnort:
>
> Could **our ancestors** have passed through a bottleneck of size two within some time frame?

That is how I understand the question as normally posed. Restricting it to Homo sapiens specifically seemed novel.

> glipsnort:
>
> As I have previously pointed out, this is a very different question from (1). I view it as essentially unanswerable and nearly meaningless. Classification as H. sapiens as you look back in time is largely arbitrary and subjective. More importantly, there could well have been interbreeding within Africa between groups that we would classify as H. sapiens and group that we would not, but we have no way of ascertaining whether or when such events happened. Looking at modern genetic variation, therefore, cannot answer this question.

Exactly my point. Which is why I was genuinely surprised to see **@DennisVenema** make the claim. I did not realize that this is what he mean when he was making his heliocentric certainty claim.

Though, I'm not sure this is meaningless. Some may find this meaningful.

---

tallen_1 (Tim) 2018-01-01 20:30:14 UTC #393

> Swamidass:
>
> Though, I'm not sure this is meaningless. Some may find this meaningful.

Then we may as well drop the "bottleneck" language pretending to have found some way to preserve genetic diversity in a founding original pair. We could just as easily say at some point that a lone homo sapien survivor, not even a mating couple, bred with a population of genetically compatible ancestors of ours. Those ancestors themselves could of course posses a mosaic of various proportions of Neanderthal, Denisovan, Homo Sapien, etc. DNA. Just as we do today. So in what scenario does this even remotely mean anything theologically?

Lynn_Munter (Lynn Munter) 2018-01-02 18:07:09 UTC #394

> Swamidass:
>
> I agree with you that the terms are ambiguous. However, they were clarified. Dennis clarified that he mean Homo sapiens specifically and NOT Neanderthals, and pegged his claim on the time at which Homo sapiens arise. I'm sure he was mistaken, bit that is what he claimed.

You are ignoring an important point. What he was clarifying was the statement "we evolved as a population," and he was indicating that by "we" he meant humans, Homo sapiens. He engaged in this clarification strictly to limit the time scales he was referring to, as can be seen in most of the quotes above.

What you are arguing is that since he clarified he meant Homo sapiens, the statement no longer has the meaning "we:"

> Swamidass:
>
> The scientific consensus is that our **ancestors** never dip to a single couple, not that **Homo sapiens** never dip to a single couple.

I think when a statement is *clarified*, you keep “we” and add “humans” and “Homo sapiens;” I don’t see the justification for leaning all of our weight on “Homo sapiens” and jettisoning the other two to make your point.

I don’t think you are deliberately misinterpreting here. The conversation was long, involved and complex. Statements were made without the original text being quoted for reference. The conversation has continued quite some time additionally without anyone pinpointing the error, which always makes it difficult. However, at the end of the day, I do not think you have enough basis to say **@DennisVenema** made a mistake.

Swamidass (Dr. S Joshua Swamidass) 2018-01-02 18:57:05 UTC #395

> Lynn_Munter:
>
> You are ignoring an important point. What he was clarifying was the statement “we evolved as a population,” and he was indicating that by “we” he meant humans, Homo sapiens. He engaged in this clarification strictly to limit the time scales he was referring to, as can be seen in most of the quotes above.

Exactly as i understood too, which is why it is an error. Restricted to the time scale in question (300 or 200 kya to present) we do not know if Homo sapiens dip to a single couple. That is why the claim seems to be in error. I that is not what Dennis meant, then his statements specifically excluding neanderthal’s don’t make any sense.

Of course if Dennis meant something else, he should speak up. I’m happy to be corrected by him, as i myself have been corrected by him in the past. Though that would make the string of statements he made about his definition of “human” incoherent. Eg how do we explicitly exclude Neanderthals and then mean Homo sapiens exclusively when discussing a “human” bottleneck? Especially when pop genetics only talks about ancestral bottlenecks, not homo sapien bottlenecks?

My honest opinion is that he, in good faith, misstated the science. That is common. I do the same and quickly correct myself; i’ve even done so more than once on this thread. Identifying and correcting errors is a good thing, right?

[quote=“Lynn_Munter, post:394, topic:37039”]
I don’t think you are deliberately misinterpreting here.
[/quote]Thanks also for clarifying that. This is just a well intentioned and good faith pushback. I’m sure **@DennisVenema** will clarify shortly.

Mark_Moore (Mark Moore) 2018-01-07 23:40:03 UTC #396

> John_Rood:
>
> I think the meaning of Eve being the “mother of all the living” deserves some explanation…maybe that’s been addressed somewhere else on this site

The bible does not really teach that Adam is the sole progenitor of the human race. Gen. 2:1 says that “hosts” were created in heaven and on earth, and the word for host means an army. The instructions to mankind in chapter one sound martial, and nothing like the interactions with Adam and Eve in chapter 2.

The Christ-centered model of early Genesis explains Adam's naming of Eve very elegantly. It was a funny thing for him to do because she had actually just gotten them both "killed". But just prior to him calling her the "Mother of All the Living" we understand that the LORD God gave them a talk about "the seed" that would crush the serpent's head. IOW, they were told that Christ would be born of a woman, and in Christ men can beat the curse and live eternally. So this passage makes perfect sense- if Genesis is viewed through the lens of Christ.

Swamidass (Dr. S Joshua Swamidass) 2018-01-12 21:11:33 UTC #397

Thoughtful response at the DI:

https://evolutionnews.org/2018/01/on-prejudiced-models-and-human-origins/

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gbrooks9 (George Brooks) 2018-01-13 05:47:53 UTC #398

@Swamidass

Somehow I think the author is twisting things a little too tightly …

"Having said that, I think Swamidass's new work further illustrates the difficulty of answering far-out questions using mainstream methods. The tool used, ARGweaver, is fantastic in that it combines an enormous amount of real genetic information to model the past genetic history of humans. For this reason it gives the impression of being truly objective, **and so when I first read it, I thought he had proved that there could be no bottleneck earlier than 300,000 years."**

"However, a little digging into how ARGweaver works reveals that it too assumes a constant population, and uses this assumption to assign probabilities to ancestry trees. Therefore, again, it is not clear if it is really appropriate for asking questions about Adam and Eve. The particular reason why it is a problem is a bit technical: coalescence (branching but backwards in time) happens much more slowly in a large population. In a large population, the last few coalescents could take thousands of generations. **But what if you have a small number of generations, drawing to a smaller and smaller population and terminating in a single couple? All the lineages will coalesce (down to at most four as explained above) but at a faster rate."**

I think we beat this one to death long ago!

Jonathan_Burke (Jon) 2018-01-13 05:59:52 UTC #399

> Swamidass:
>
> Thoughtful response at the DI:

They aren't thoughtful comments, it's just the usual apologetic spin.

- Science is based on assumptions
- Assumptions may nor may not be true
- We can't trust what scientists say because of these assumptions
- You have proved that it's possible all humanity derived from a single couple

---

Swamidass (Dr. S Joshua Swamidass) 2018-01-13 06:24:22 UTC #400

> Jonathan_Burke:

> They aren't thoughtful comments, it's just the usual apologetic spin.
>
> Science is based on assumptions
> Assumptions may nor may not be true
> We can't trust what scientists say because of these assumptions
> You have proved that it's possible all humanity derived from a single couple

Its a bit more complex in this case. I think they misunderstood how argweaver works. I'll explain later. I can't say if they will publicly acknowledge it, but I can show what the misunderstanding was.

> gbrooks9:
>
> QUOTING ENV:
> For this reason it gives the impression of being truly objective, and so when I first read it, I thought he had proved that there could be no bottleneck earlier than 300,000 years."

That is what this data shows. It is ***not*** consistent with a bottleneck before 300 kya.

> gbrooks9:
>
> QUOTING ENV:
> "However, a little digging into how ARGweaver works reveals that it too assumes a constant population, and uses this assumption to assign probabilities to ancestry trees.

This is not exactly correct. Rather, there is a weak prior placed on the coalescence times, that pulls the TMRCA and TMR4A estimates more recent (not more ancient) than would best fit the data. Once again, I'll explain later in detail.

At this point, before I add anything more substantial, I'm curious the response from **@RichardBuggs** and **@DennisVenema** and **@glipsnort** .

Jay313 (Jay Johnson) 2018-01-13 14:50:59 UTC #401

> Swamidass:
>
> That is what this data shows. It is not consistent with a bottleneck before 300 kya.

Aren't you talking about a bottleneck of two? There are numerous studies that show bottlenecks in the human population associated with the "Out of Africa" event. I think it's confusing to keep saying "no bottleneck" when what you really mean is "no bottleneck to two individuals," unless you are arguing that you have disproved all previous papers on the subject.

RichardBuggs (Richard Buggs) 2018-01-13 15:29:01 UTC #402

Hi all, I hope you had a good Christmas and New Year. Sorry it has taken me a while to come back online since the break: I was away at a population genetics conference, and then have come back to a lot of urgent tasks, and a stack of marking. I have just taken the time to read through the posts that have been made since I last posted in this discussion, and I am delighted with the progress that has been made, and impressed with the time and effort that Joshua and Dennis in particular have been putting into this while I have been away.

As I come back into the discussion, I would like to reiterate (in response to some posts above) that I am assuming that we share common ancestry with apes and that chimpanzees are our closest living relatives from whom we diverged at least 6 million years ago. I am also assuming that no miracles have occurred in our past. I am also assuming that the earth revolves around the sun (sorry for wrongly saying “rotates” at one point, **@glipsnort**). I thought that I had been clear on these assumptions, and that it was obvious that much of what I am saying would not make sense if it were otherwise.

I would also reiterate that I do not come into this discussion with any assumption about whether or not there has been a bottleneck of two in the human lineage since the split from chimpanzees. I just come in asking the question of whether or not this hypothesis has been tested. I am not taking a position about the possible timing of such a bottleneck if there were one. If anyone is frustrated that I am not taking a position on these matters, I apologise, but I simply have not explored this issue and the relevant evidence enough to feel able to take a position. This is why I am engaging in this discussion. I am here to learn and to weigh the evidence. I hope that at some point in the future I will know enough to be able to take a position, or to be able to conclude that we simply can’t know for sure from the current evidence.

I see that some references have been made to other blogs that claim that I am taking a stronger position on these issues. Such blogs are mistaken. I tried to correct the author of one such blog a few weeks ago, and asked for it to be changed, but my request was not granted.

I am very glad that **@DennisVenema** now agrees with me that Zhao et al (2000) does not support the case he makes in Adam and the Genome and I would assure Dennis that I do not view this as “win” for me. I have never seen this discussion in terms of a competition. Indeed, the fact that Dennis is willing to make this admission in the light of evidence and explanation has won him respect as a scientist, in my eyes. I am glad that we examined this paper, and Dennis’ earlier claims about it, in such detail, as it helped us all to think more clearly about the nature of evidence that could be used to test a bottleneck hypothesis. In particular, it has led on to the very interesting work by **@swamidass** in TMR4As.

I have learned a lot by reading the posts by **@swamidass** on TMR4As, and the comments about his analyses by **@DennisVenema** **@glipsnort** and others. Joshua has brought a great deal of expertise and time to this discussion and I am very grateful for that. This is highly interesting and informative. I think this is getting close to a test of the bottleneck hypothesis. I am still taking in some of the details of what Joshua has done and may have more comments in due course. I do think that the coalescent models used in a test of the bottleneck hypothesis would need to include the effective population size decreasing down to two as we go back in time. I realise that this would be a lot of work, but I do think that this would be necessary. Do correct me if I am missing something, Joshua. I am grateful for the many excellent points that you have made over the past few weeks.

Christy (Christy Hemphill) 2018-01-13 16:30:55 UTC #403

From the EN&V blog linked in post 391:

“Swamidass stresses that he does not actually believe all humanity derived from a single couple but he has shown that it is *possible*, if the couple lived more than 300,000 years ago.”

@Swamidass In your mind, is there a difference between saying “science has shown it is possible” and “science cannot rule out the possibility”? Don’t you usually say the latter not the former?

---

tallen_1 (Tim) 2018-01-14 15:39:53 UTC #404

Richard,

> RichardBuggs:

> I am assuming that we share common ancestry with apes and that chimpanzees are our closest living relatives from whom we diverged at least 6 million years ago…

> RichardBuggs:
>
> I am not taking a position about the possible timing of such a bottleneck if there were one.

> RichardBuggs:
>
> If anyone is frustrated that I am not taking a position on these matters, I apologise, but I simply have not explored this issue and the relevant evidence enough to feel able to take a position.

So, drawing from your above statements, you seem to be asking us to believe that in your experience as a geneticist you're completely unconvinced one way or the other on common ancestry. Or that humans didn't exclusively descend from an ancestral pair say 6,000-10,000 years ago. You just have no idea. It's a toss up. If only you may have sufficiently explored those topics in your relevant field of expertise, maybe you might have reached a conclusion one way or the other. But alas it's not to be.

Based on your statements this is what you would have us believe. Which I have to tell you does put a strain on our credulity. One I personally may be unable to bear. But putting that aside, it's very difficult to imagine what sort of case you would find convincing enough to have satisfactorily tested the "hypothesis" that humans did not descend from an exclusive ancestral pair in the last hundreds of thousands of years if you still have yet to be convinced that the "hypotheses" of common ancestry or, presumably, whole human populations persisting past 10K years ago have been adequately tested. In fact, we have no idea what you think has been adequately tested. So there's a credibility issue here Richard. If you want us to have confidence you would recognize and acknowledge adequate evidence to affirm such a hypothesis as we've been discussing here, you're giving us every reason to doubt your ability or will in this regard.

Swamidass (Dr. S Joshua Swamidass) 2018-01-14 22:21:11 UTC #406

Good point.

> Jay313:
>
> Aren't you talking about a bottleneck of two? There are numerous studies that show bottlenecks in the human population associated with the "Out of Africa" event. I think it's confusing to keep saying "no bottleneck" when what you really mean is "no bottleneck to two individuals," unless you are arguing that you have disproved all previous papers on the subject.

Here, we are discussing a bottleneck of 2 for a single generation, followed by rapid expansion. In this case, we are not considering miracles, and we entirely expect this couple to be a heterozygous, and not clones of one another. We are most curious about a "bottleneck" earlier than 300 kya and as far back as 2 mya.

> Christy:
>
> > "Swamidass stresses that he does not actually believe all humanity derived from a single couple but he has shown that it is possible, if the couple lived more than 300,000 years ago."

> @Swamidass In your mind, is there a difference between saying “science has shown it is possible” and “science cannot rule out the possibility”? Don’t you usually say the latter not the former?

Good point too @Christy . I do not think we are going to find positive evidence for a bottleneck. However, there might be enough ambiguity in the evidence we cannot rule it out in the deep enough past. This is really a question about what the evidence does and does not tell us, and the strength with which it speaks.

I would also add that there is a categorical difference between this question and the regular arguments from Intelligent Design. Here, there is no indirect invocation of divine action (we’ve ruled out special creation), and @aguager (and others) engaging evidence in a manner largely consistent with what we see with mainstream scientists. At times the rhetoric goes places I think ultimately undercuts their case (e.g. when that article connects this effort to ID), but the actual inquiry is recognizably scientific. We are using the rules of mainstream science, asking a valid question of the data.

It is for this reason that I feel this question needs to be taken seriously.

> RichardBuggs:
>
> As I come back into the discussion, I would like to reiterate (in response to some posts above) that I am assuming that we share common ancestry with apes and that chimpanzees are our closest living relatives from whom we diverged at least 6 million years ago. I am also assuming that no miracles have occurred in our past. I am also assuming that the earth revolves around the sun (sorry for wrongly saying “rotates” at one point, @glipsnort). I thought that I had been clear on these assumptions, and that it was obvious that much of what I am saying would not make sense if it were otherwise.

You have been clear on this.

> RichardBuggs:
>
> I see that some references have been made to other blogs that claim that I am taking a stronger position on these issues. Such blogs are mistaken. I tried to correct the author of one such blog a few weeks ago, and asked for it to be changed, but my request was not granted.

This is very unfortunate @RichardBuggs . I’m very sorry to hear this. I request that you clarify either publicly or in a private message to me how you have been misrepresented. I do not want to accidently ascribe a view to you that is not yours.

I should also emphasize that when I address the ID movement, that does not necessarily include you. Though they have take some delight in your public effort, I’m not sure I’ve seen any public evidence that you are associated with them. My references to ID are not meant to connect you to them, unless you so wish to be connected to them.

> RichardBuggs:
>
> I have learned a lot by reading the posts by @swamidass on TMR4As, and the comments about his analyses by @DennisVenema @glipsnort and others.

In truth, I’ve learned a lot too. This has been an interesting and informative direction.

ArgWeaver Does Not Assume Large Population

> RichardBuggs:
>
> I do think that the coalescent models used in a test of the bottleneck hypothesis would need to include the effective population size decreasing down to two as we go back in time. I realise that this would be a lot of work, but I do think that this would be necessary. Do correct me if I am missing something, Joshua.

It appears you are drawing upon an observation by Andrew Jones at the DI, who writes:

> **However, a little digging into how ARGweaver works reveals that it too assumes a constant population, and uses this assumption to assign probabilities to ancestry trees. Therefore, again, it is not clear if it is really appropriate for asking questions about Adam and Eve.** The particular reason why it is a problem is a bit technical: coalescence (branching but backwards in time) happens much more slowly in a large population. In a large population, the last few coalescents could take thousands of generations. But what if you have a small number of generations, drawing to a smaller and smaller population and terminating in a single couple? All the lineages will coalesce (down to at most four as explained above) but at a faster rate.
> **https://evolutionnews.org/2018/01/on-prejudiced-models-and-human-origins/**

This turns out, in my opinion, not to be the correct assessment. I'm going to do a more detailed post on this in the future, but can explain a little bit more now.

ArgWeaver is using a **prior** on trees, that is parameterized by population size (N = 10,000). The language of "assumes a large population size" is just correct. It is more accurate to say that is starts with a weak prior belief of a population size of 10,000. It is a weak prior belief, because it is designed to be quickly overcome by data. Let me give you two reasons why it does not impact the results I've put out on TMR4A. These will be expanded later on some posts that I'll link here when done:

1. As a prior, this is not an assumption, but a starting belief that is meant to be overridden by the data. The only way that the ArgWeaver program uses the population size is in computing this prior. Population size is neither simulated nor modeled in the program except for placing this weak prior on population size. **Remember, priors are not assumptions or constraints.**

2. The ArgWeaver output files tell us the strength of the prior vs. the data, and it is just about 5%. That means the model output is dominated 95% by the data, and not by the prior (as it is designed).

3. The prior distribution for TMR4A is at about 200 kya (which I will show later), but we measured the TMR4A at about 420 kya. That means the data is pulling the estimate upwards from the prior, not downwards.

This last point should end any confusion. To draw analogy, it's like we measured the weight of widgets, with the weak starting belief that the average weight of these widgets is 200 lb. After weighing several of them, and taking the prior into account, we compute the average weight is 420 lb. The fact we used a prior could be an argument that the real average is greater than 420 lb, but that is not a plausible argument that the true average is less than 420 lb. The prior, in our case is biasing the results downwards, not upwards.

With that in mind Dr. Jones was just mistaken when he writes:

> The tool used, ARGweaver, is fantastic in that it combines an enormous amount of real genetic information to model the past genetic history of humans. For this reason it gives the impression of being truly objective, and so when I first read it, I thought he had proved that there could be no bottleneck earlier than 300,000 years…However, a little digging into how ARGweaver works reveals that it too assumes a constant population, and uses this assumption to assign probabilities to ancestry trees.

I would submit that, given what I have just explained, that this is not a reason to doubt the results that I put forward. I do believe this data shows there could be no bottleneck earlier than 300,000 years without either miracles or our ancestors have vastly different mutation rates than us. Both those possibilities, howver, are off the table right now.

There are three ways that could prove me wrong here:

1. Do an experiment with simulated data, showing that the prior is strong enough to override detecting a bottleneck before 300 kya in the argweaver code. **(not likely)**
2. Modify argweaver to no longer use the prior (which is fairly easy), and run it on the same dataset, demonstrating that the estimated TMR4A goes down, not up. **(not likely)**
3. Find another way that population size is used by argweaver that I missed, and show it has a stronger effect that I imagine. **(not likely)**

Of all these #3 is most likely way to show me wrong here. Until that happens though, I think that 420 kya +/- 100 kya is a reasonable bound on when we think a couple bottleneck could have occured. **Do you agree @RichardBuggs ?** I'm being fairly generous in how I set the confidence interval there too.

My Next Steps

My next steps, when I get around to it, are:

1. To test the ability of PSMC, MCMS and/or ArgWeaver to detect bottlenecks on simulated data. Have the simulation code working, and it's really a matter of running the code. My instinct tells me this will increase the bound to about 500 kya, but I won't know till I run it.

2. Recompute TMR4A while weighting coalescents by the segment length. Failure to do this before, I think, is the biggest source of error in the prior analysis. I think it might shift things around a small amount…

3. Using the argweaver data to estimate population size. If this works correctly, ti should increase our confidence that this is a good proxy for understanding the success and failure of PSMC and MCMS. Incidentally, MCMS uses a ***very*** similar model as ArgWeaver (but a different representation).

@DennisVenema and **@glipsnort** correct me if I'm wrong, but it seems that the LD data is really not worth getting into in detail, as PSMC, MCMS and Argweaver are (essentially) modeling the LD data with much higher accuracy than other approaches. The key thing is understand how these methods model the DNA, which by extension is the best way to understand all the LD data. Do you agree?

Do You Agree?

For the reasons outlined above, I'm not sure this is a valid critique. Though I do agree, this has been highly informative for all of us, including me. I had no idea what the data would show till I did this analysis.

> RichardBuggs:
>
> am still taking in some of the details of what Joshua has done and may have more comments in due course. I do think that the coalescent models used in a test of the bottleneck hypothesis would need to include the effective population size decreasing down to two as we go back in time. I realise that this would be a lot of work, but I do think that this would be necessary.

In Argweaver, the size of tree is determined primarily by (1) mutation rate (2) allelic diversity, and (3) only to a small amount by the prior. There is no sensible way to "include the effect of population size decreasing." I would endorse running the model again without a prior, but as I've shown there is no good reason to think that will reduce the TMR4A time. I think that should settle this concern. Right?

@RichardBuggs , you pushed @DennisVenema to concede your point on Zhoa 2002. That ended up being valuable, as it clarified some key strengths and weaknesses of the evidence. Respectfully, would you reciprocate? Do you acknowledge the ArgWeaver evidence seems to rule out a single couple bottleneck before 300 kya? **Can you agree to that?** If that is not something you agree with, please clarify why not. Of course, if you see a solid technical problem that I missed, that is all the more reason to clarify. Let's get to the bottom of it.

---

tallen_1 (Tim) 2018-01-14 22:44:24 UTC #407

> Swamidass:
>
> Do you acknowledge the ArgWeaver evidence seems to rule out a single couple bottleneck before 300 kya? Can you agree to that? If that is not something you agree with, please clarify why not.

Josh, I do not believe Richard would agree to this. I also do not believe he would agree to this evidence ruling out a bottleneck to 2 within the past 10K years in fact. Go ahead and ask him as a follow up. But I think he's been pretty clear that nothing he's seen so far has lead him to the view of any kind of minimum bound on when a bottleneck may have happened. Or if there is something that has lead him to such a view, he's declining to say so. And of course his position on this lower bound within the YEC timeframe has been asked of him repeatedly, and so it would follow this timeframe is included in his statement below:

> RichardBuggs:
>
> I am not taking a position about the possible timing of such a bottleneck if there were one

---

Swamidass (Dr. S Joshua Swamidass) 2018-01-15 00:10:13 UTC #408

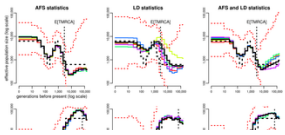
I also want to agree with and emphasize this.

> RichardBuggs:
>
> I am very glad that @DennisVenema now agrees with me that Zhao et al (2000) does not support the case he makes in Adam and the Genome and I would assure Dennis that I do not view this as "win" for me. I have never seen this discussion in terms of a competition. Indeed, the fact that Dennis is willing to make this admission in the light of evidence and explanation has won him respect as a scientist, in my eyes

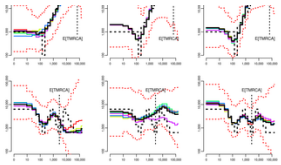
This is very counterintuitive, but exactly how things work out in a scientific community. We end up respecting those who concede mistakes. We trust those that retract mistakes. So admitting mistakes certainly does win people respect among scientists.

Swamidass (Dr. S Joshua Swamidass) 2018-01-15 02:25:43 UTC #409

Technical note relevant to this conversation is this paper I came across. It is a much more easy to follow approach than MSMC and others. It is based on Bayesian analysis and machine learning, and has some advantages over the other approaches we have discussed.



Inferring Population Size History from Large Samples of Genome-Wide Molecular...



Author Summary Molecular data sampled from extant individuals contains considerable information about their demographic history. In particular, one classical question in population genetics is to reconstruct past population size changes from such...

The underlying data is LD blocks and allele frequency spectrum (as **@glipsnort** used). One of the nice things about this approach is that it should (I think) run much more quickly, and allow for direct testing of the bottleneck hypothesis (with modification). I also trust the confidence intervals on this method. Among its disadvantages, it does not actually reconstruct the phylogenetic trees. So it is going to be a bit more opaque in other sense.

Jonathan_Burke (Jon) 2018-01-15 02:33:52 UTC #410

> Swamidass:
>
> **@RichardBuggs** , you pushed **@DennisVenema** to concede your point on Zhoa 2002. That ended up being valuable, as it clarified some key strengths and weaknesses of the evidence. Respectfully, would you reciprocate? Do you acknowledge the ArgWeaver evidence seems to rule out a single couple bottleneck before 300 kya? Can you agree to that?

So it appears the evidence does actually support Dennis' position, as summarized by you (summary approved by Dennis).

> Homo sapiens specifically do not dip down to a single couple in 300 kya to the confidence we have in heliocentrism.

If the only quibble is over what level of confidence in this conclusion is legitimate, I'd say the main argument is already over.

Swamidass (Dr. S Joshua Swamidass) 2018-01-15 02:38:13 UTC #411

The recent posts are not talking about bottlenecks of Homo sapiens, but bottlenecks of our ancestors as a whole.

Therefore…

> Jonathan_Burke:
>
> So it appears the evidence does actually support Dennis' position, as summarized by you (summary approved by Dennis).

That is ***not*** correct.

As we have discussed. **@DennisVenema** clarified that he meant *Homo sapiens* exclusively, not our ancestors a whole. As you quoted me summarizing him:

> **Homo sapiens** specifically do not dip down to a single couple in 300 kya to the confidence we have in heliocentrism.

Without belaboring the point, that claim seems to be unsubstantiated by evidence. We already *know* that Homo sapiens dip down to zero, so positing they dip down to two is certainly not a problem. Perhaps Homo sapiens do arise as a single couple, subsequently interbreed with other hominids, thereby giving rise to us.

---

tallen_1 (Tim) 2018-01-15 02:41:21 UTC #412

Agreed, our ancestors who were either properly homo sapien or so very close enough to be genetically reproductively compatible. To me, that pretty much feels like a taxonomical distinction without a meaningful difference but agreed all the same.

Now after Richard tells you that he doesn't see the evidence falsifying the 'hypothesis' that our ancestors dipped down to 2 within the past 300K years, you can ask him if it falsifies the 'hypothesis' that our ancestors dipped down to 2 within the past 10K years.

Jonathan_Burke (Jon) 2018-01-15 02:59:31 UTC #413

> Swamidass:
>
> The recent posts are not talking about bottlenecks of Homo sapiens, but bottlenecks of our ancestors as a whole.

This distinction doesn't look meaningful in the context of the original debate. If homo sapiens had non-homo sapiens ancestors, how can homo sapiens have emerged **solely** from a bottleneck of two homo sapiens who had **no** ancestors? I just don't get how you're going to make the evidence fit YEC.

> Swamidass:
>
> Without belaboring the point, that claim seems to be unsubstantiated by evidence. We already know that Homo sapiens dip down to zero, so positing they dip down to two is certainly not a problem.

Saying the population of homo sapiens dips to two is not the same as saying homo sapiens emerged from a single pair. This is why I view the "population of homo sapiens may have dipped down to two" argument as extremely misleading. It looks a lot like a bait and switch.

---

tallen_1 (Tim) 2018-01-15 03:08:55 UTC #414

Jonathan,

What Josh is saying is that our ancestors if you go back far enough wouldn't be classified as homo sapien any longer. They'd be other species (e.g., homo erectus). That would be your population of zero. Of course gradual changes wouldn't ever result in a pre-homo sapien to homo sapien transition where you say, ah hah! Here are the first two humans. The differences at that point in time would be negligible and largely invisible within a generation. As Dennis has noted previously, if you go back far enough taxonomical distinctions break down. What I think Josh is proposing is that our ancestors which would have constituted breeding populations preserving our genetic diversity could not have dipped to 2 within the past 300K years. If only that what we classify as homo sapien could have dipped down to 2 while other "homo" classed species so very genetically and behaviorally similar to ours maintained larger population sizes. Like I said, a taxonomical difference without a meaningful distinction.

Jonathan_Burke (Jon) 2018-01-15 03:12:33 UTC #415

> tallen_1:
>
> What Josh is saying is that our ancestors if you go back far enough wouldn't be classified as homo sapien any longer. They'd be other species (e.g., homo erectus). That would be your population of zero.

Yes I understand that. My question remains; how does this fit the idea of homo sapiens emerging exclusively from a pair of homo sapiens with no ancestors?

> tallen_1:
>
> What I think Josh is proposing is that our ancestors which would have constituted breeding populations preserving our genetic diversity could not have dipped to 2 within the past 300K years. If only that what we classify as homo sapien could have dipped down to 2 while other "homo" classed species so very genetically and behaviorally similar to ours maintained larger population sizes.

Yes I understand he is saying that. As I said, I don't see how it's relevant to the idea that homo sapiens emerged from a population of two people with no ancestors. Additionally, I see the emphasis on "homo sapiens could have dipped down to two individuals" as a loaded statement intended to imply that homo sapiens could have emerged from a single couple without ancestors.

---

tallen_1 (Tim) 2018-01-15 03:13:32 UTC #416

> Jonathan_Burke:
>
> Yes I understand that. My question remains; how does this fit the idea of homo sapiens emerging exclusively from a pair of homo sapiens with no ancestors?

It doesn't. I don't believe Josh is proposing that.

---

tallen_1 (Tim) 2018-01-15 03:27:06 UTC #417

> Jonathan_Burke:
>
> Additionally, I see the emphasis on "homo sapiens could have dipped down to two individuals" as a loaded statement intended to imply that homo sapiens could have emerged from a single couple without ancestors.

I don't believe that is how Josh is using the bottleneck language. Apparently there's some fraction of a percent of Christians who feel if you could argue that it's possible there were two homo sapien (on a technicality) survivors to regrow a population of humans within the larger breeding population of human ancestors so very similar genetically and behaviorally, that you could rescue some sliver of the Adam & Eve story. If you were so inclined.

I'd contrast this with Richard's approach. Which appears to be one of extended agnosticism on anything that might contradict the YEC narrative, and who crafts his statements in such a way to be 100% compatible with that 'doctrine.'

---

gbrooks9 (George Brooks) 2018-01-15 03:49:43 UTC #418

> Swamidass:

> Its a bit more complex in this case. I think they misunderstood how argweaver works. I'll explain later. I can't say if they will publicly acknowledge it, but I can show what the misunderstanding was.
>
> **Author states:**
> "For this reason it gives the impression of being truly objective, and so when I first read it, I thought he had proved that there could be no bottleneck earlier than 300,000 years."
>
> That is what this data shows. It is not consistent with a bottleneck before 300 kya.
>
> Author states:
> "However, a little digging into how ARGweaver works reveals that it too assumes a constant population, and uses this assumption to assign probabilities to ancestry trees."
>
> This is not exactly correct. Rather, there is a weak prior placed on the coalescence times, that pulls the TMRCA and TMR4A estimates more recent (not more ancient) than would best fit the data. Once again, I'll explain later in detail.

@Swamidass ,

Just reminding you that these quotes are me quoting from the author who was trying to dismiss **@DennisVenema** 's conclusions…

> gbrooks9:
>
> **@Swamidass** Somehow I think the author is twisting things a little too tightly … "Having said that, I think Swamidass's new work further illustrates the difficulty of answering far-out questions using mainstream methods. The tool used, ARGweaver, is fantastic in that it combines an enormous amount of real genetic information to model the past genetic history of humans. For this reason it gives the impression of being truly objective, and so when I first read it, I thought he had proved that the…

Jonathan_Burke (Jon) 2018-01-15 04:10:59 UTC #419

> tallen_1:
>
> I don't believe that is how Josh is using the bottleneck language. Apparently there's some fraction of a percent of Christians who feel if you could argue that it's possible there were two homo sapien (on a technicality) survivors to regrow a population of humans within the larger breeding population of human ancestors so very similar genetically and behaviorally, that you could rescue some sliver of the Adam & Eve story. If you were so inclined.

You mean like this.

> And that is exactly the hypothesis that YECs and OECs have been working with over the last decade. Anyone who does know this has just not been listening.
>
> **What if Their Scenario Could Work?**
>
> Wouldn't that be great? Would it not be really exciting to demonstrate such an non-intuitive finding? I certainly think that would be newsworthy.

> Honestly, I think it would be really great if we could find a way for YEC time scale to work with the evidence without abusing. I'm rooting for them.

Swamidass (Dr. S Joshua Swamidass) 2018-01-15 04:57:59 UTC #420

@Jonathan_Burke , let's put this in context…

> Jonathan_Burke:
>
> Wouldn't that be great? Would it not be really exciting to demonstrate such an non-intuitive finding? I certainly think that would be newsworthy.
>
> Honestly, I think it would be really great if we could find a way for YEC time scale to work with the evidence without abusing. I'm rooting for them.

What is written here is an honest gesture of good will coming from a curious scientist in the Church. I have also been clear that I do not think the YEC data fits the data, and am happy to explain why, and have explained why several times. The fact that I am glad to acknowledge when the data does fit their model does not make me suspect. It makes me honest.

Jonathan_Burke (Jon) 2018-01-15 05:01:48 UTC #421

> Swamidass:
>
> What is written here is an honest gesture of good will coming from a curious scientist in the Church.

Yes I understand that.

> Swamidass:
>
> I have also been clear that I do not think the YEC data fits the data, and am happy to explain why, and have explained why several times. The fact that I am glad to acknowledge when the data does fit their model does not make me suspect. It makes me honest.

Yes, but I am not talking about that. I'm talking about the fact that you want to "find a way for YEC time scale to work with the evidence without abusing" indicates that your motivation for involvement in this subject is apologetic and theological, rather than scientific.

Swamidass (Dr. S Joshua Swamidass) 2018-01-15 05:05:52 UTC #422

> Jonathan_Burke:
>
> Yes, but I am not talking about that. I'm talking about the fact that you want to "find a way for YEC time scale to work with the evidence without abusing" indicates that your motivation for involvement in this subject is apologetic and theological, rather than scientific.

Not true **@Jonathan_Burke** . Seriously, that is not a valid read. It honestly comes off as an ad hominem. If you have a problme with the data I've presented, feel free to point it out.

I'm honestly curious how you are going to square my statements about the evidence with being a YEC apologists. That is totally absurd. Remember, I've said:

> Swamidass:
>
> I do believe this data shows there could be no bottleneck earlier than 300,000 years without either miracles or our ancestors have vastly different mutation rates than us.

Jonathan_Burke (Jon) 2018-01-15 05:22:49 UTC #423

> Swamidass:
>
> Not true **@Jonathan_Burke** . Seriously, that is not a valid read. It honestly comes off as an ad hominem.

It is not ad hominem. An ad hominem argument takes the form "Person X has character flaws Y, therefore their argument is false". I have not said anything like that. I have not said that any of your arguments about the data are false, and I have certainly not said "Swamidass has character flaws X, therefore his arguments about the genetic data are wrong". Nor have I said "Swamidass is a YEC apologist, therefore his arguments about the genetic data are wrong". Nor have I called you a YEC apologist, which is a phrase implying you believe in YEC (which you obviously don't).

> Swamidass:
>
> If you have a problme with the data I've presented, feel free to point it out.

As you know, I have not contested the data you have presented.

> Swamidass:
>
> I'm honestly curious how you are going to square my statements about the evidence with being a YEC apologists.

I have not said you are a YEC apologist. I have said that your statement that you think it would be great to "find a way for YEC time scale to work with the evidence without abusing" indicates that your motivation for involvement in this subject is apologetic and theological, rather than scientific. If your only interest in the topic was scientific, then I don't understand the need for such a statement. I don't see why you would say it would be great to "find a way for YEC time scale to work with the evidence without abusing" if that is not actually something you would like to see happen.

I should not need to remind you that this entire topic was raised by Dr Buggs specifically as a Christian apologetic for Christians who believe in a literal Adam and Eve (as in fact I do). **This** is the post in question.

- "Does genomic evidence make it scientifically impossible that the human lineage could have ever passed through a population bottleneck of just two individuals? This is a question I am asked semi-frequently by religious friends."
- "The issue is this. Believers in Abrahamic religions who accept evolution often combine it with belief that all humans have descended from a single couple. Until now, many have assumed that this belief is compatible with evolution and mainstream science."
- "Venema declares that a bottleneck of two is impossible, and this is a fact of comparable scientific certainty to heliocentrism. He gives his Christian readers a stark choice between embracing mainstream science, or sticking with untenable beliefs about an ancestral couple."

- “Whilst this issue may seem trivial to many readers, for large numbers of religious believers in the world, this is a critical issue. Do they really face a binary choice between accepting mainstream science and believing that humans have, at some point in their history, all descended from a single couple?”

> Swamidass:
>
> Remember, I’ve said:

Yes I know what you’ve said. You’ve said this.

> Swamidass:
>
> I do believe this data shows there could be no bottleneck earlier than 300,000 years without either miracles or our ancestors have vastly different mutation rates than us.

YECs wouldn’t have an issue with that, since you’ve deliberately said “without either miracles”. Naturally they would be happy with the idea of fixing the data with miracles. You’ve also said this.

> Jonathan_Burke:
>
> Honestly, I think it would be really great if we could find a way for YEC time scale to work with the evidence without abusing. I’m rooting for them.

I don’t see those as mutually exclusive statements, and clearly you don’t believe you’ve contradicted yourself either.

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tallen_1 (Tim) 2018-01-15 15:33:25 UTC #424

Jonathan,

It took some digging to find the original quote, but what I gather Josh is getting at is not attacking strawmen. Something I very much agree with as well. There’s enough absurdity within the YEC movement that there’s no need for us to manufacture it. That’s why when Dennis and others started talking about Eve as essentially a clone of Adam, my eyes rolled. Virtually all of my family are YEC, and I don’t know a single one who would ascribe to that view. They’d rather think that God worked some magic genetically to pack in as much diversity as possible into their genomes. Also silly, but let’s talk about the silliness that exists rather than forcing on others that which doesn’t.

Josh also points out that if you can get in the habit of avoiding strawmen, your rebuttals of YEC’s actual arguments will carry much more weight. Again, I completely agree. He also makes clear the aspect of the YEC timeline he’s interested in is Adam. Not all of creation or all of humanity or human ancestors. If “what’s important” to the YEC community is an Adam at 6,000 years ago, well if Josh can give them a sliver of a straw to grasp onto on some technicality, and that works for them, then maybe that might open the doors to a few to accept what we know to be scientific fact about the history of our planet and life on it. I personally think that’s a stretch too far and require, even by YEC standards, too much in the way of mental gymnastics. But that’s where Josh’s head seems to be at. I do think you’re misunderstanding him on this. He seems to be trying to play the role of “missionary” to the YEC community.

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jpm (Phil) 2018-01-16 17:44:21 UTC #425

A post was merged into an existing topic: **Reaching out through Adam**

Jonathan_Burke (Jon) 2018-01-15 18:10:15 UTC #426

> tallen_1:
>
> It took some digging to find the original quote, but what I gather Josh is getting at is not attacking strawmen.

I raised no objection to his statement that strawmen should not be attacked. I fully support him on that point. The quotation I provided was on a completely different subject.

> tallen_1:
>
> That's why when Dennis and others started talking about Eve as essentially a clone of Adam, my eyes rolled. Virtually all of my family are YEC, and I don't know a single one who would ascribe to that view.

In about ten minutes I found and posted two YEC organizations which discussed the idea that Eve was a clone of Adam. One presented it as one of two possible ways God had created Eve, the other said it was the way God had created Eve. Creation Ministries said **this**.

> "**There is an intriguing possibility that Eve was a clone of Adam**. The science of cloning involves taking DNA from an organism and using it to manufacture an almost perfect copy of the original. Here, God is taking a piece of flesh, with cells, organelles, and, importantly, Adam's DNA, and using it to manufacture a woman. Of course, she could not be a perfect clone, because she was a girl! But what if God had taken Adam's genome and used it to manufacture Eve? All he would have had to do was to **leave out Adam's Y chromosome and double his X chromosome** and, voilá, instant woman!"

They go on to say this later.

> "There are indications, however, that Eve may not have been a clone."

But they still say the cloning idea is one of two available possibilities. Meanwhile, another YEC organization says **this**.

> "Since Eve was made from one of Adam's ribs [Genesis 2:21-22], **she would have been a clone of Adam** and, had there been any genetic mutation in Adam, this would have been reproduced in Eve and expressed in their offspring."

So there are definitely YECs who argue this.

> tallen_1:
>
> Josh also points out that if you can get in the habit of avoiding strawmen, your rebuttals of YEC's actual arguments will carry much more weight. Again, I completely agree.

I agree in part. It's a nice idea which might work in some cases, but the fact is that most of us avoid strawmen when it comes to YECs and it makes not a scrap of difference whatsoever.

> tallen_1:

> He also makes clear the aspect of the YEC timeline he's interested in is Adam. Not all of creation or all of humanity or human ancestors. If "what's important" to the YEC community is an Adam at 6,000 years ago, well if Josh can give them a sliver of a straw to grasp onto on some technicality, and that works for them, then maybe that might open the doors to a few to accept what we know to be scientific fact about the history of our planet and life on it.

Yes he is definitely trying to offer them a sliver of hope, but I don't see that his motivation for helping them believe they are right, is to move them to a position where they accept they are wrong. I really don't see how that is going to work. We're talking about people who think that the "soft tissues" found by Schweitzer proves that dinosaurs only died out recently. I cannot see how giving them the impression (wittingly or unwittingly), that their views on Adam and Eve and a 6,000 year old earth are not in conflict with science, is going to help them change their minds.

Consequently I can't see this is as a missionary endeavour. Trying to give them reasons to hold onto their 6,000 year old earth and 6,000 year ago Adam and Eve, isn't going to lead to them abandoning their 6,000 year old earth and 6,000 year ago Adam and Eve, especially when that 6,000 year timeframe is there precisely as their only bulwark against evolution.

[quote="tallen_1, post:424, topic:37039"]
I do think you're misunderstanding him on this. He seems to be trying to play the role of "missionary" to the YEC community.[/quote]

I see him as mediator rather than missionary. If he was playing the role of missionary he would be aiming to change their views, not suggesting people come up with concordist interpretations of the evidence which could agree with what YECs believe.

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tallen_1 (Tim) 2018-01-15 18:35:20 UTC #427

Jonathan,

I was providing the background context for Josh's sympathizing with the YEC community. The quote you lifted out of that context can create the wrong impression.

Also, I don't think what I provided was off topic given you included this in your quote: "And that is exactly the hypothesis that YECs and OECs have been working with over the last decade. Anyone who does [not] know this has just not been listening." To know what Josh is referring to you have to attend to what he was saying about misrepresentations and straw men, which is what I explained. Maybe you didn't mean to include that section in your quote, but there it is.

Anyway, Josh does not appear to be facilitating any sort of hope to the YEC community for their 6K year earth or creation de novo of all living species within that time. He's only extending them that hope for a 6K year old Adam. As their greatest theological hold up always seems to go back to Adam.

Josh - do I have this about right?

---

jpm (Phil) 2018-01-15 19:45:23 UTC #428

> Jonathan_Burke:
>
> I see him as mediator rather than missionary.

Certainly they are combined roles. As fellow Christians, I would not see a YEC adherent as in need of a missionary, but there are many in that mindset who have fallen away from Christ due to the dichotomy presented in that culture (of

course, that is another kettle of fish but AIG seems to agree with that loss from what I have read) and that becomes a place where a missionary field is present.

---

tallen_1 (Tim) 2018-01-15 20:32:07 UTC #429

Phil,

I was using the term “missionary” metaphorically of course ;). That said, I think the YEC community does an amazing amount of harm. They spread a distrust of science and established scientific fact, and a pernicious tribalism that glorifies everything within their echo chamber while seeding suspicion and dismissal without. So, in the metaphorical sense, I’d value all the missionaries we can send their way.

Swamidass (Dr. S Joshua Swamidass) 2018-01-15 22:39:47 UTC #430

> tallen_1:
>
> Josh - do I have this about right?

Yes, you do. There are enough challenges that science brings to theology that we do not need to force them where they do not exist. Certainly some Christians see need for Adam. Many do. Let’s just be honest about the science with them and see how it shakes out from there. Perhaps the will end up just a different type of Christian than us in the end. That is okay, as long as they are in Christ.

> Jonathan_Burke:
>
> I see him as mediator rather than missionary.

I think mediator is a better term than missionary. But I am aiming to change their views so that we all might adopt a more Christ centered faith. With Jesus as the foundation, we adopt a more orthodox faith and these questions are not so concerning.

My biggest problem with scientific YEC creationism is not its scientific problems but its theological emphases. Our faith is not grounded in a specific understanding of creation and the human effort to study nature (creation science or evolutionary science). Rather, our faith is grounded in Jesus, the one who rose from the dead. By Him, we can find a confident faith, unthreatened by evolution.

As for Adam? There are reasons why the common solutions offered by TE / EC Christians are unsatisfying to many Christians. My point is just that we should be empathetic to the questions of the Church, and not force conflict where it need not be. Instead, lets be honest about how the theological values we bring to the table could work in light of mainstream science.

Regarding Adam and Eve as homologous clones.

> Jonathan_Burke:
>
> In about ten minutes I found and posted two YEC organizations which discussed the idea that Eve was a clone of Adam. One presented it as one of two possible ways God had created Eve, the other said it was the way God had created Eve. Creation Ministries said this.

Yes of course some people thing that. However. that is not what **@agauger** and **@RichardBuggs** has argued, nor is it what John Sanford or most knowledgeable YECs I know have argued. If one model of Adam is falsified by the data, does not mean the other is falsified too. If we are going to make strong claims about what the evidence rules out, it behooves us to take seriously the all the alternate hypotheses we can. To the point, for at least 5 years now, most YECs in this area have been trying to work out a model of created diversity. We cannot claim to rule this model out, unless we actually examine it in light of the evidence.

Of course, as should be clear from my prior posts, baring miracles this seems to be ruled out in the recent past. However, in the more distant past, maybe not. It seem false to say we have certainty there was no single couple bottleneck over the last several million years (as has been put forward). The evidence does not seem substantiate that claim. except perhaps in trans-species variation (but we haven't even discussed that yet).

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jpm (Phil) 2018-01-16 17:33:41 UTC #431

15 posts were split to a new topic: **Reaching out through Adam**

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jpm (Phil) 2018-01-16 17:38:10 UTC #432

Replies moved to new post to clean things up a bit, tough to find a good cut off so may have to modify a bit but bear with me: "Reaching out through Adam"

RichardBuggs (Richard Buggs) 2018-01-16 21:43:16 UTC #433

Hi Joshua,

This is just going to be a rather brief holding response as I have only got part way through my first read of the ARGweaver paper, and a series of mini-crises in my lab are taking up much of my time now, so it may be a while before I can give you a fully considered response. I don't want to leave you waiting for too long, so here is a quick reply, with all the shortcomings that this necessitates.

I agree with you that the ARGweaver results, given the assumptions and simplifications behind its analyses, does appear, on your further analyses of its graphs, to give a reasonable bound of a bottleneck of 420 kya +/- 100 Kya. I don't say this as someone who has worked through all of the analyses for a second time: I just say this as what you have described seems to me to be reasonable. To be perfectly honest, I am quite surprised at how low this figure is. If you had asked me to guess beforehand I would have probably suggested a higher figure.

Having said that, on my rather shallow reading of the work so far, I would be slightly cautious, in that just having 4 lineages left in a population does not mean that those 4 lineages are all found in just two individuals, as I think you have already pointed out. Demonstrating that only four alleles are left in a population is a necessary pre-requisite of a bottleneck of two, but is not in itself evidence that a bottleneck of two actually occurred. For the four alleles to coalesce to the point of being in the same human bodies may take quite some while and could add a bit to to the timing (This depends on effective population size, of course, as has been frequently noted in the discussion above). I think I would therefore have more confidence in your lower bound than your upper bound.

My point "I do think that the coalescent models used in a test of the bottleneck hypothesis would need to include the effective population size decreasing down to two as we go back in time. " Was a reiteration of a point that I have made several times before in the discussion above when discussing coalescent analyses in the Zhao et al paper.

In the ARGweaver paper, in a footnote to Table 1 the author's write "Model allows for a separate Ni for each time interval I but all analyses in this paper assume a constant N across time intervals." It sounds to me as if they use a constant Ne. I have to admit that I find the paper rather confusing on the point of effective population sizes, but you have spent longer than I have working out exactly what they did, so I look to you for enlightenment.

[By the way, I was reflecting on my point “I do think that the coalescent models used in a test of the bottleneck hypothesis would need to include the effective population size decreasing down to two as we go back in time” after I had posted it, and I have a caveat about this. No method of estimating Ne based on genetic diversity (that I am aware of) is capable to identifying a short sharp bottleneck of two as an Ne of two. That is because every method (that I know of) would need the population size to remain constant for at least a few generations before it could estimate an Ne of 2. Thus, I think we can safely say that when effective population size is defined by an equation based on genetic data, **a single generation of census size two does not have an Ne of 2, but of a higher number** (exactly what I don’t know - I guess it would depend on the size of the pre-population bottleneck and the rate of population expansion afterwards). I have - in effect - made this point before, but have never quite formulated it in my mind in these terms, so thought it might be worth sharing for discussion/correction.]

I think the most important take home message for me from your ARGweaver analyses is that (as far as I can see) you have shown nicely that **genome-wide allele counts do not provide evidence that a bottleneck of two has not happened in the human lineage**. That is a real step forward in our understanding of this area. Thank you!

Swamidass (Dr. S Joshua Swamidass) 2018-01-16 23:20:08 UTC #434

> RichardBuggs:
>
> This is just going to be a rather brief holding response as I have only got part way through my first read of the ARGweaver paper, and a series of mini-crises in my lab are taking up much of my time now, so it may be a while before I can give you a fully considered response. I don’t want to leave you waiting for too long, so here is a quick reply, with all the shortcomings that this necessitates.

No problem. Believe it or not, I have my own fires I’m putting out in my lab this week. I also have 4 public events I’m doing next week, including one with Hugh Ross. So a lot is going on here too.

Take your time in responding, but there is a lot you’ve written here I want to echo.

> RichardBuggs:
>
> I agree with you that the ARGweaver results, given the assumptions and simplifications behind its analyses, does appear, on your further analyses of its graphs, to give a reasonable bound of a bottleneck of 420 kya +/- 100 Kya.

Thanks for offering your public thoughts on that too, as hopefully that should put some criticism to rest.

> RichardBuggs:
>
> To be perfectly honest, I am quite surprised at how low this figure is. If you had asked me to guess beforehand I would have probably suggested a higher figure.

I agree. This was surprising for me too. I would have guessed a different number. It is still important to caveat that this is just a subset of the data, and subject to revision to a more ancient data with more evidence. It is hard, however, to imagine it being revised more recent than 300 kya.

In particular, I would point to two pieces of evidence that are not considered here:

1. Genetic evidence of interbreeding with Neanderthals/Densiovans seems to put a bound on a single couple bottleneck back to the Homo sapien common ancestor with them, perhaps 400 kya to 700 kya ago. This analysis

of TMR4A used the median, and would underestimate that date because interbreeding with them only affects the minority of the gnome (it seems).

2. Interspecies variation will always put an asterix on these results. Though on re-looking at the literature, it is very sparse. In contrast with population genetics estimates of population size, there are only a handful of papers that address this. I have not been able to find definitive evidence of >4 alleles at a single locus with interspecies counterparts. However, that maybe just because no one has looked at enough of the Chimp data (which very sparse). Nonetheless, I'm less convinced now than when I started that this will be (at least in current form) definitive evidence against a couple bottleneck. Still, we have not taken it into account here.

> RichardBuggs:
>
> Having said that, on my rather shallow reading of the work so far, I would be slightly cautious,

> RichardBuggs:
>
> I think I would therefore have more confidence in your lower bound than your upper bound.

The phrasing here is difficult, but it sounds like you are saying you have more confidence in bound on single-couple bottlenecks of 520 kya than 320 kya. I'd agree with you here too.

> RichardBuggs:
>
> That is because every method (that I know of) would need the population size to remain constant for at least a few generations before it could estimate an Ne of 2. Thus, I think we can safely say that when effective population size is defined by an equation based on genetic data, a single generation of census size two does not have an Ne of 2, but of a higher number (exactly what I don't know - I guess it would depend on the size of the pre-population bottleneck and the rate of population expansion afterwards

That is correct, and I have been working out the math on this, and planning some experiments. It looks like the key variables for Ne is (1) how many generations are at a single couple (just one in our case), (2) the number of offspring they have and degree of exponential growth in the few subsequent generations (which we can assume here is very high), and (3) how distant this is in the past (as the averaging window for Ne increases in the past). Keeping mind that #2 is essential a free parameter, #1 and #3 are such that the farther back we go in time the much less a single couple generation affects Ne. So, therefore, a single couple bottleneck can be entirely consistent with a very high Ne in the distant past (say at 500 kya)

Once again, this is just an informal description, but there are some interesting details in the math. Sufficiently interesting, I'm nearly convinced its worth turning into a publication in its own right. Interesting stuff.

> RichardBuggs:
>
> just having 4 lineages left in a population does not mean that those 4 lineages are all found in just two individuals, as I think you have already pointed out. Demonstrating that only four alleles are left in a population is a necessary pre-requisite of a bottleneck of two, but is not in itself evidence that a bottleneck of two actually occurred. For the four alleles to coalesce to the point of being in the same human bodies may take quite some while and could add a bit to to the timing (This depends on effective population size, of course, as has been frequently noted in the discussion above).

This is an important caveat to emphasize.

This is not evidence ***for*** a single couple bottleneck but evidence that population genetics will be unable to detect a bottleneck in the distant past. It is an argument that such a bottleneck would be hidden in the shadows, and not clearly seen in the data.

Moreover, median TMR4A, as you suggest, may be too generous a cutoff. My instinct is that we should probably use a CDF cutoff of about 70 to 80% instead of 50%, which would put TMR4A at about 525 kya. Though, I cannot be certain on instinct. The right way forward is to determine this cutoff from simulations, which I am nearly convinced are worth the effort to embark on. There seems to be good theoretical reason to think that detection power will correspond relatively tightly with some cutoff on the TMR4A CDF. Once I get around to doing those experiments, we'll have a much better bound.

> RichardBuggs:
>
> In the ARGweaver paper, in a footnote to Table 1 the author's write "Model allows for a separate Ni for each time interval I but all analyses in this paper assume a constant N across time intervals." It sounds to me as if they use a constant Ne. I have to admit that I find the paper rather confusing on the point of effective population sizes, but you have spent longer than I have working out exactly what they did, so I look to you for enlightenment.

They are not clear in the paper. But the code itself is clear. The only way they seem to use Ne is to set the prior, and the prior (if anything) pulls TMR4A downwards. However, the influence of the prior on the joint likelihood (just 5%) is very low, so I'm not really concerned about this. There is no plausible reason I see to doubt the results of this study because of their use of the prior. As I have explained, the prior thinks mediant TMR4A is at about 200 kya, but we compute it at about 420 kya. So the data is pulling the estimate upwards, and there is sufficient data to totally overwhelm the prior.

> RichardBuggs:
>
> I think the most important take home message for me from your ARGweaver analyses is that (as far as I can see) you have shown nicely that genome-wide allele counts do not provide evidence that a bottleneck of two has not happened in the human lineage.

To be clear, I agree that "genome-wide allele counts" alone are not very good evidence. Moreover, their overall diversity do **not** provide evidence against a single couple bottleneck **after about 400 kya**_ (subject to revision). They **do,** however, provide evidence against a more recent bottleneck, as you have already affirmed.

As many people have noted, for most people, this is a fairly disturbing challenge to theology. Perhaps some will find solace in an ancient Adam that was not *Homo sapien*. At the moment, that seems to be an outlier position, though perhaps it will grow, especially as it seems we are beginning to come to a consensus here.

RichardBuggs (Richard Buggs) 2018-01-17 21:56:32 UTC #435

Hi Joshua,

I am glad we have reached such a level of agreement.

Regarding ARGweaver:

> Swamidass:
>
> They are not clear in the paper. But the code itself is clear. The only way they seem to use Ne is to set the prior, and the prior (if anything) pulls TMR4A downwards.

I wonder if the code itself is pointing in a slightly different direction to the paper. Their footnote under table 1 suggest that the code does allow for separate Ne estimates at each time interval, but for all the analyses in the paper itself they assumed that Ne did not vary among time intervals. Perhaps they did this to speed up the analysis as they had such a large dataset? I still have more reading to do of this paper.

I am not sure how much different this would make anyway, as (as we both agree) any method they used to estimate Ne would likely not detect a bottleneck anyway, if one had in fact occurred.

> Swamidass:
>
> That is correct, and I have been working out the math on this, and planning some experiments.

That is brilliant. Do keep me updated!

> Swamidass:
>
> Perhaps some will find solace in an ancient Adam that was not Homo sapien. At the moment, that seems to be an outlier position, though perhaps it will grow, especially as it seems we are beginning to come to a consensus here.

Interestingly, I believe that this has been the position of **@agauger** all along.

RichardBuggs (Richard Buggs) 2018-01-20 22:14:23 UTC #436

Hi all,

I have been doing a bit more reading about the theoretical background of some of the methods we have been discussing here. I am not a mathematician, so much of this is outside of my area of expertise. However, I have come across three papers that suggest that seem to suggest that site frequency spectra (as presented earlier in this discussion) have severe limitations as a source of evidence about past population sizes. The second of these papers specifically examines scenarios of a bottleneck followed by exponential population growth.

Simon Myers, Charles Fefferman, Nick Patterson **Can one learn history from the allelic spectrum?** Theoretical Population Biology, Volume 73, Issue 3, 2008, pp. 342-348
https://www.sciencedirect.com/science/article/pii/S0040580908000038
Abstract: It is well known that the neutral allelic frequency spectrum of a population is affected by the history of population size. A number of authors have used this fact to infer history given observed allele frequency data. We ask whether perfect information concerning the spectrum allows precise recovery of the history, and with an explicit example show that the answer is in the negative. This implies some limitations on how informative allelic spectra can be.

Terhorst, Jonathan, and Yun S. Song. **Fundamental limits on the accuracy of demographic inference based on the sample frequency spectrum**. Proceedings of the National Academy of Sciences 112.25 (2015): 7677-7682.

> **Fundamental limits on the accuracy of demographic inference based on the sample...**
>
> National Academy of Sciences

Abstract: The sample frequency spectrum (SFS) of DNA sequences from a collection of individuals is a summary statistic that is commonly used for parametric inference in population genetics. Despite the popularity of SFS-based

inference methods, little is currently known about the information theoretic limit on the estimation accuracy as a function of sample size. Here, we show that using the SFS to estimate the size history of a population has a minimax error of at least O(1/log s), where s is the number of independent segregating sites used in the analysis. This rate is exponentially worse than known convergence rates for many classical estimation problems in statistics. Another surprising aspect of our theoretical bound is that it does not depend on the dimension of the SFS, which is related to the number of sampled individuals. This means that, for a fixed number s of segregating sites considered, using more individuals does not help to reduce the minimax error bound. Our result pertains to populations that have experienced a bottleneck, and we argue that it can be expected to apply to many populations in nature.

Baharian, Soheil, and Simon Gravel. **"On the decidability of population size histories from finite allele frequency spectra."** Theoretical population biology (2018).
https://www.sciencedirect.com/science/article/pii/S004058091730148X
Abstract: Understanding the historical events that shaped current genomic diversity has applications in historical, biological, and medical research. However, the amount of historical information that can be inferred from genetic data is finite, which leads to an identifiability problem. For example, different historical processes can lead to identical distribution of allele frequencies. This identifiability issue casts a shadow of uncertainty over the results of any study which uses the frequency spectrum to infer past demography. It has been argued that imposing mild 'reasonableness' constraints on demographic histories can enable unique reconstruction, at least in an idealized setting where the length of the genome is nearly infinite. Here, we discuss this problem for finite sample size and genome length. Using the diffusion approximation, we obtain bounds on likelihood differences between similar demographic histories, and use them to construct pairs of very different reasonable histories that produce almost-identical frequency distributions. The finite-genome problem therefore remains poorly determined even among reasonable histories, where fits to few-parameter models produce narrow parameter confidence intervals, large uncertainties lurk hidden by model assumption."

So I think I should add these to the criticism I made earlier of this approach to **@glipsnort** here:

> RichardBuggs:
>
> However, I have to admit that although I think that your arguments from allele frequency spectra could potentially make a good test of the Adam and Eve bottleneck hypothesis, I would need to see this worked through in considerably more detail before I was fully persuaded that it was an adequate test. I have been reading a bit more widely about site frequency spectra and the factors that can affect them in a few spare hours. In particular I found these recent papers helpful:
>
> Harpak, A., Bhaskar, A., & Pritchard, J. K. (2016). Mutation Rate Variation is a Primary Determinant of the Distribution of Allele Frequencies in Humans. PLoS genetics, 12(12), e1006489.
>
> Ferretti, L., Ledda, A., Wiehe, T., Achaz, G., & Ramos-Onsins, S. E. (2017). Decomposing the site frequency spectrum: the impact of tree topology on neutrality tests. Genetics, 207(1), 229-240.
>
> Koch, E., & Novembre, J. (2017). A Temporal Perspective on the Interplay of Demography and Selection on Deleterious Variation in Humans. G3: Genes, Genomes, Genetics, 7(3), 1027-1037.
>
> Gao, F., & Keinan, A. (2016). Inference of super-exponential human population growth via efficient computation of the site frequency spectrum for generalized models. Genetics, 202(1), 235-245.
>
> These papers have strengthened my view that a wide range of complex demographic, phylogenetic, selective and mutational processes, together with sampling strategies, can influence site frequency spectra, and that I therefore cannot conclude from the models that you have run that a bottleneck of two in the history of the human lineage is not possible. To be convinced I would need to see more complex models run that try to incorporate these factors.

In addition, I came across this paper which @DennisVenema may find interesting as he writes his blog about the PSMC method

Kim, J., Mossel, E., Rácz, M. Z., & Ross, N. (2015). **Can one hear the shape of a population history?**. Theoretical population biology, 100, 26-38.
http://www.sciencedirect.com/science/article/pii/S0040580914000987?via%3Dihub

I have also been reading up more on ARGweaver and intend to post again on this soon @Swamidass .

Swamidass (Dr. S Joshua Swamidass) 2018-01-21 01:07:53 UTC #437

> TedDavis:
>
> Dennis,
>
> I appreciate the great clarity of your reply to Dr. Buggs–not that an absence of clarity has ever been something I would associate with your work. 🙂
>
> I hope that Discovery also tweets your reply to Dr. Buggs. They owe it to fair discourse to do exactly that much, since they are responsible for bringing Buggs' concerns out of the academic tent and into their own, much larger tent. Otherwise, they might be skirting with the same danger that Buggs is worried about: that "of alienating Christians from science on the basis of a wrong interpretation of the current literature."
>
> I resonate with that concern. That's one of the main reasons why I decided to devote my professional life to helping Christians (and others too) understand the history better. Thank you for helping us understand the science better.

Hello @TedDavis , I hope you are well my friend. Things have come a long substantially since you first posted on this thread, back about 2 months ago. I summarized the scientific highlights of this conversation here.

Heliocentric Certainty Against a Bottleneck of Two?

Do "Humans" arise from a single couple? It is a deceptively simple question, with a great deal of subtlety. Some claim "no," with certainty approach that of our certainty that the sun is the center of the solar system: "heliocentric certainty." ...

Surprisingly, at lease to me, @RichardBuggs was on to something. Our certainty about a bottleneck in the distant past (e.g. before 500 kya) may not be as high as we imagined. As I write here…

> Swamidass:
>
> This is not evidence for a single couple bottleneck but evidence that population genetics will be unable to detect a bottleneck in the distant past. It is an argument that such a bottleneck would be hidden in the shadows, and not clearly seen in the data.

And the implications for theology…

> Swamidass:
>
> As many people have noted, for most people, this is a fairly disturbing challenge to theology. Perhaps some will find solace in an ancient Adam that was not Homo sapien. At the moment, that seems to be an outlier position,

> though perhaps it will grow

Now, **@TedDavis** , I agree with you that a recent genealogical Adam (**peacefulscience.org/genealogical-rapprochement/**) is probably more significant in the long run that an ancient single-couple bottleneck. This, nonetheless, is a surprising finding. Assuming, of course, that it pans out. We are still early in the game, and might find a mistake. This reminds, many ways, of a similar point we were almost exactly 12 months ago on the genealogical Adam work.

Nonetheless, this really could pan out, and some Christians mich join **@agauger** in taking this view. At the very least, much of the claims on the science have been overstated if it takes this much effort to disprove an ancient bottleneck, and we have yet to do so.

I'm curious, therefore, your thoughts on a few levels as a historian many of us trust in this conversation:

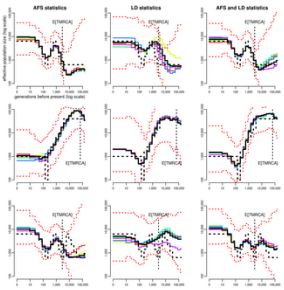
1. How do you think an ancient bottleneck couple will influence the conversation?
2. How do you think a recent genealogical Adam will influence the conversation?
3. If TE / EC's have overstated or been overconfident on the evidence, how should this correction rework our voice?
4. Do you know any good historical analogies to these two corrections, if they end up being correct.
5. I am planning for the ASA Workshop in June in Boston on "Reworking the Science of Adam." What do you think are the key things for the ASA community to know about these exchanges?

Thanks for your thoughtfulness here. I'm wondering how your perspective could guide us here. Many of us are doing what we can to serve the Church, and the science of Adam appears to be a place where the ball was fumbled.

Swamidass (Dr. S Joshua Swamidass) 2018-01-21 01:23:06 UTC #438

> RichardBuggs:
>
> So I think I should add these to the criticism I made earlier of this approach to **@glipsnort** here:

Allele frequency spectrums (AFS) do not give a solid view of ancient bottlenecks, but they do of recent population structure. Ironically, very recent bottlenecks are not well ascertained by MSMC and PSMC and LD-Blocks, but they are clear in AFS. This is covered pretty well here:



Inferring Population Size History from Large Samples of Genome-Wide Molecular...

Author Summary Molecular data sampled from extant individuals contains considerable information about their demographic history. In particular, one classical question in population genetics is to reconstruct past population size changes from such...

So yes, in the ancient past you cannot really infer much from AFS, but that has never been **@glipsnort** 's claim. His claims are consistent with what I showed with argweaver.

1. **@glipsnort** has not made any claims of heliocentric certainty.

2. He would agree that past about 500 kya, we do not expect allele frequency spectrums to detect a bottleneck of a single couple. That is where he places a tentative cutoff. So his results are essentially the same as argweaver, though the evidence form argweaver is much stronger.

3. His original reason for delving into AFS was to respond to some young earth creationists that claimed the AFS was inconsistent with a large ancient population and ***required*** a single couple origin just 6,000 years ago: (**Can someone explain like I'm 5 yo, what's wrong with this refutation of Biologos?**).

4. His response to Ola Hossjer (colleague of **@agauger**) has been very well measured, and entirely correct. (**Glipsnort responds to a critical article**) Notice that he does not prese a case against ancient bottlenecks, but only for common ancestry with great apes and huamns, and against a recent bottleneck. Both those claims are very well supported by the evidence, and he produces analysis of his own all the time.

I know you are not attacking **@glipsnort** personally, or even leveling an unfair scientific critique. I do think, however, it is important to clarify that he has been a measured and careful voice. In my opinion, he has not drawn incorrect conclusions from the AFS work, nor has he overstated his certainty of those results.

Swamidass (Dr. S Joshua Swamidass) 2018-01-21 10:28:34 UTC #439

A couple technical updates:

ArgWeaver Does Not Assume Large Population. The computed TMR4A is biased downwards, not upwards, by the prior.

The Correct Mutation Rate. ArgWeager is using an experimentally confirmed mutation rate.

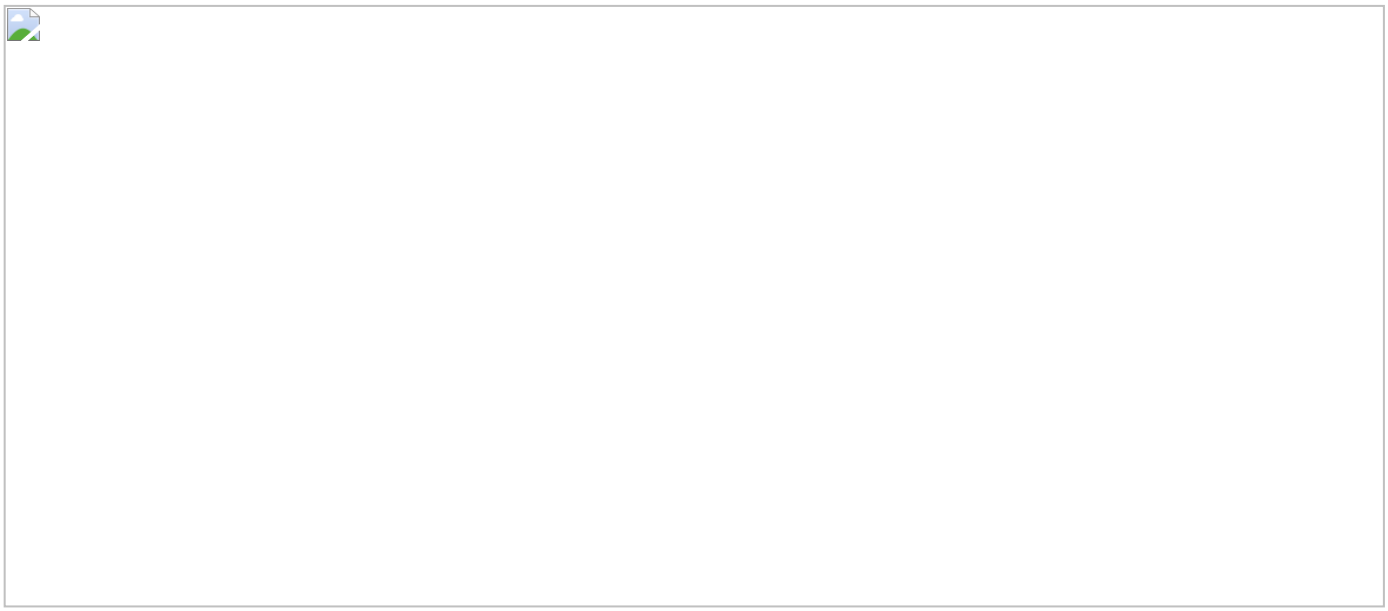
Swamidass (Dr. S Joshua Swamidass) 2018-01-21 11:06:45 UTC #440

And, more importantly, this improvement of the estimate…

Correctly Weighting Coalescents. An improve esitmate of TMRCA is about 500 kya.

> At the moment, all coalescents are weighted equally. This biases the averages to high recombination areas, which might be biased towards upward errors in TMRCA estimates. It would be wiser to average weighting by the length of the DNA segment to which the phylogeny applies.

I finally got around to correcting this part of the code, and recomputing the TMR4A. Here is what we arrive at, a TMR4A of 495 kya, nearly 500 kya. This is a better estimate.



Acts 17:26 and Adam

Jay313 (Jay Johnson) 2018-01-21 18:48:38 UTC #441

> Swamidass:
>
> Our certainty about a bottleneck in the distant past (e.g. before 500 kya) may not be as high as we imagined.

An actual *H. erectus* (or *heidelbergensis*) named “Adam” might have been capable of naming “Eve” and the animals, but not much more. Of that much, we **are** certain …

RichardBuggs (Richard Buggs) 2018-01-22 21:08:19 UTC #442

Hi Joshua,

I’m just catching up with this dialogue on a train. I should be marking essays, but will just take a moment to quickly repond to a couple of points.

> Swamidass:
>
> His response to Ola Hossjer (colleague of **@agauger**) has been very well measured, and entirely correct. (Glipsnort responds to a critical article) Notice that he does not prese a case against ancient bottlenecks, but only for common ancestry with great apes and huamns, and against a recent bottleneck. Both those claims are very well supported by the evidence, and he produces analysis of his own all the time.
>
> I know you are not attacking **@glipsnort** personally, or even leveling an unfair scientific critique. I do think, however, it is important to clarify that he has been a measured and careful voice. In my opinion, he has not drawn incorrect conclusions from the AFS work, nor has he overstated his certainty of those results.

Thanks, I had not seen that exchange before between Ola Hossjer and **@glipsnort** . Very interesting. However, it does pre-date the current discussion, and I am keen to hear Steve’s own response to the papers I have referenced on the AFS method. I agree with you that he has been a measured and careful voice in this discussion and I have great respect for his expertise.

> Swamidass:
>
> A couple technical updates:
>
> ArgWeaver Does Not Assume Large Population. The computed TMR4A is biased downwards, not upwards, by the prior.

But would you agree than in their analyses reported in the paper they have assumed a constant effective population size? If not, how do you understand the footnote to the table that I referenced above.

My train has just arrived at King’s Cross Station - sorry to have sign off. I greatly appreciate your work on this thread, and the honesty and open-mindedness that you have shown.

gbrooks9 (George Brooks) 2018-01-23 16:51:51 UTC #443

> Swamidass:
>
> 1] How do you think an ancient bottleneck couple will influence the conversation?
>
> 2] How do you think a recent genealogical Adam will influence the conversation?
>
> 3] If TE / EC's have overstated or been overconfident on the evidence, how should this correction rework our voice?
>
> 4] Do you know any good historical analogies to these two corrections, if they end up being correct.
>
> 5] I am planning for the ASA Workshop in June in Boston on "Reworking the Science of Adam." What do you think are the key things for the ASA community to know about these exchanges?

@Swamidass :

Once you go back beyond 6,000 years, and especially 10,000 years, what's the point of trying to prove a bottleneck "older than 10,000 years, and hidden in a shadow"?

If it creates a motivation for YEC's to preserve their position in an Old Earth Scenario… good… .let them work for that.

Our job has been to show that the "Young Earth" part of any Christian's world view is untenable. The more YEC's work to legitimize an Old Earth Scenario, the better it will be for everyone!

---

glipsnort (Steve Schaffner) 2018-01-23 21:16:55 UTC #444

> RichardBuggs:
>
> am keen to hear Steve's own response to the papers I have referenced on the AFS method.

I hope to get back to this thread within a few days.

RichardBuggs (Richard Buggs) 2018-01-25 20:47:05 UTC #445

Hi Joshua **@Swamidass**
I am taking a look at the ARGweaver paper more throughly. It is very clear that the ratio of mutation rate to recombination rate is critical to the accuracy of the method, as the authors comment in the paper, and as several of their supplementary figures (S4-S8) show. When the mutation rate is high relative to the recombination rate, they have much more power than when it is low. However, I am struggling to see what recombination rate they used or estimated when analysing the 54 human genome sequences. Do you know what recombination rate was used? I notice that on page 8 they comment that ARGweaver has "a slight tendency to underestimate the number of recombinations, particularly at low values of mu/rho" and also that they say that other sources give a low value of mu/rho for human populations. This suggests that in their analysis of the 54 human genomes they may well have estimated a lower rate of recombination than the correct rate. However, I can't find the figure. Is this something that you have looked at, please? If they have underestimated the recombination rate, how do you think that would affect the TMR4A?
best wishes
Richard

RichardBuggs (Richard Buggs) 2018-01-25 20:48:33 UTC #446

> glipsnort:
>
> I hope to get back to this thread within a few days.

Steve, that's great news. I would also be really glad to hear your view on Joshua's analyses of the ARGWeaver data, if you have time.

Swamidass (Dr. S Joshua Swamidass) 2018-01-27 01:21:42 UTC #447

@RichardBuggs please exuse the delay in responding to you. I'd normally put a high priority on it, but my father unexpected passed away this last Saturday. I will return with haste, but have more pressing matters at the moment. Peace.

---

gbrooks9 (George Brooks) 2018-01-29 02:35:42 UTC #448

> Swamidass:
>
> my father unexpected passed away this last Saturday.

@Swamidass ,

My deepest sadness to hear this news. Prayers for you and your family! George Brooks

---

RichardBuggs (Richard Buggs) 2018-01-29 21:39:51 UTC #449

Joshua, I am so sorry to hear this. You and your family are in my thoughts and prayers.

DennisVenema (Dennis Venema) 2018-01-31 04:30:11 UTC #450

Josh, so sorry to hear this. I will be praying for you and your family.

RichardBuggs (Richard Buggs) 2018-01-31 19:33:22 UTC #451

Just to come back to points raised by @GJDS and @Jon_Garvey that I did not get a chance to respond to earlier:

> GJDS:
>
> Validation of models, as I have practiced (and is commonly understood) requires a result from the model to be similar to an observation/measurement of a system independent of the model data base. Within this I have a difficult time noting such validation of the models discussed here. Since a major point is the size and time of a bottleneck, for example, validation would be considered by using physical data of a real bottleneck. There may be other ways, and if you can identify them I would be interested to know.

> Jon_Garvey:
>
> in the absence of physical evidence, the population genetics model seems to validate itself in a circular manner.

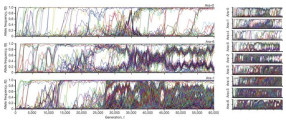
I am not sure if this is relevant to your question, and you probably are well aware of this already, but just in case it is useful to the discussion, here are some comments.

There is quite a large literature modelling the population genetic effects of severe bottlenecks on genetic diversity in populations, by, amongst others, Alan Templeton, Brian Charlesworth, Nick Barton and Masatoshi Nei. This was partly motivated by a debate about whether or not founder event bottlenecks can cause speciation (note, the debate was not about whether or not severe bottlenecks can happen - it was about whether they drive evolutionary change). This led to quite a lot of empirical studies on natural populations that were known to have passed through bottlenecks (evidenced by past human observation and records) and on experimental populations. For example, here is a recent paper that experimentally shows that populations do much better after a bottleneck if the founding couple are outbred rather than inbred previous to the bottleneck: Szűcs, M., Melbourne, B. A., Tuff, T., Weiss-Lehman, C., & Hufbauer, R. A. (2017). Genetic and demographic founder effects have long-term fitness consequences for colonising populations. Ecology letters, 20(4), 436-444.

I think it is fair to say that models of the effects of bottlenecks on genetic diversity are well developed and well tested. Of course, there are inherent limits to how well we can test the long term effects of bottlenecks in natural populations or experiments, as we are limited in the number of generations that we can study. I guess this is the major problem that you were both pointing out.

Perhaps the best empirical study available to us on the effects of bottlenecks is the Lenski long-term evolution experiment. Though this has the disadvantage of being on an asexual organism, it has the advantage of having run for 60000 generations. This experiment started with an extreme bottleneck, as each of the 12 parallel populations came from the same bacterial colony. Lenski et al (1991) wrote: “over all the founding populations, there was essentially no genetic variation either within or between populations, excepting only the neutral marker.”

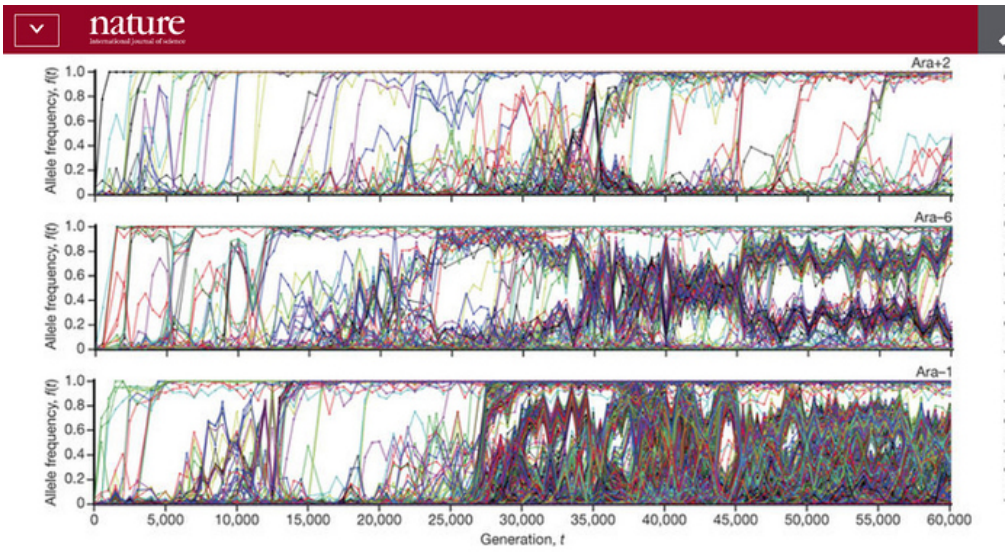
Recently a fantastic study was done by Lenski and his collaborators tracking the genetic changes that have occurred in each of the 12 populations that all originated at the same time with the same bottleneck.



The dynamics of molecular evolution over 60,000 generations

The Escherichia coli long-term evolution experiment (LTEE) is the longest running bacterial evolution experiment, including 12 replicate populations of E. coli serially propagated for more than 60,000 generations. Michael Desai,...

The results are quite startling, in that very different dynamics have occured in each population. Here are the allele frequency trajectories for just three of the populations, from Figure 1 of the paper:



Allele frequency trajectories of all *de novo* mutations detected in the twelve LTEE populations.

The authors found that the different dynamics were for several reasons, including: changes in mutation rates, periodic selection, and negative frequency dependent selection. The final paragraph of the paper reads:

“Together, our results demonstrate that long-term adaptation to a fixed environment can be characterized by a rich and dynamic set of population genetic processes, in stark contrast to the evolutionary desert expected near a fitness optimum. Rather than relying only on standard models of neutral mutation accumulation and mutation–selection balance in well-adapted populations, these more complex dynamical processes should also be considered and included more broadly when interpreting natural genetic variation.”

I think this perhaps supports the point you were making. It is a very very different system to human populations, but in many ways it should be a simpler system, and therefore easier to model. It underlines the difficulty of going from models to real evolution.

If we were presented with the twelve different Lenski LTEE populations that exist today and asked to reconstruct their past, I very much doubt we would be able to detect the fact that they all went through the same bottleneck 60000 generations ago.

Jon_Garvey (Jon Garvey) 2018-01-31 19:55:48 UTC #452

@RichardBuggs Thanks for the reply, Richard.

That’s a truly astonishing graphic, given the tight constraints in the Lenski experiment.

---

gbrooks9 (George Brooks) 2018-01-31 22:45:58 UTC #453

> RichardBuggs:
>
> If we were presented with the twelve different Lenski LTEE populations that exist today and asked to reconstruct their past, I very much doubt we would be able to detect the fact that they all went through the same bottleneck 60000 generations ago.

@RichardBuggs ,

Those are impressive numbers! And now we actually have a baseline for more fulsome future discussions when someone inevitably asks “Have we tried to demonstrate evolution in a laboratory.”

But there are those amongst us who are interested in how this labor demonstration applies to a 6,000 year time frame.

So I thought I would take the scale of the three sample results, and “zoom in” as required.

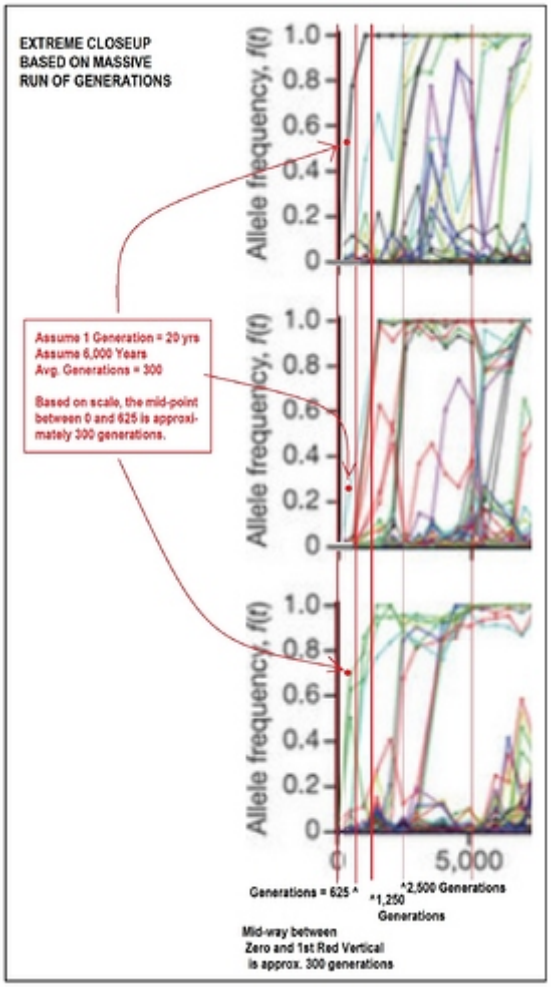
Taking the first 5000 generations as my starting point (and to provide context), I then made an approximate division of the 5000 generations in two, indicating where 2,500 generations would end.

I then divided 2,500 in half, to show where 1,250 generations would end. This was followed by another division in half, showing the end of 625 generations.

If we use the aggressive number of 20 years to a generation, 6,000 years would translate into about 300 generations. So rather than insert yet another confusing red line, I placed a bold red dot “in the middle” of the Zero-to-625 generations area of each chart.

I wonder if anyone would care to comment what these three samples can tell us about a proxy for 6,000 years, or 300 generations, as the time scale of the genetic experiment?

Readers, be sure to click on the image to see it at it’s largest magnification!



GJDS (GJDS) 2018-02-01 00:18:01 UTC #454

Thanks Richard; you have provided a great deal of information and it will take me some time to digest it.

I will respond in a general way at this time (note I am not questioning any technical aspect, or making any criticism of the modelling approache (s)). My interest is in “imagining” how a population of species that appear to be dispersed in a large area would somehow come together to form a relatively stable population, and then from there undergo further

modification to form a bottleneck that may indicate a shrinking number. (at least that is how I envisage the modelling - a population that causes a mixing leading to genetic diversity) and followed by a bottleneck that leads to new genetically relevant species. I wish I can make the comment clear, but I cannot.

Is the proposed bottleneck (whatever its size) a result of hunters forming communities of thousands, to be followed by some type of shrinking? Is a bottleneck a devise required by models of one sort or another? Or am I asking the wrong questions?

Jon_Garvey (Jon Garvey) 2018-02-01 11:13:23 UTC #455

“All models are wrong, but some are useful.”

My original point was about how accurate population genetics is over prolonged periods (and how it could be verified). Approximations or neglected factors in models can tend (one hopes) to be self correcting over time, or to lead to increasing divergence (as in uncalibrated Carbon dates), which one may have to live with if no calibration can be found. That was what I mainly had in mind.

But Lenski’s results are astonishing because they appear to show that the neglected factors *“including: changes in mutation rates, periodic selection, and negative frequency dependent selection factors”* seem (to me, at least) to result in a *chaotic* type of divergence over 60K generations.

Would that not suggest that such things *cannot* be factored in successfully, in order to correct the model over such timeframes, any more than additional factors would enable one to describe the weather a year ago from calculations based on the last three days weather?

I would add that this chaotic divergence is seen in Lenski’s *model* system, where the environment is entirely stable, reproduction asexual and the original population genetically uniform. To apply it to humans (or anything else) in the wild, one must also consider sexual (and non-random) reproduction, migration that’s far more uncertain after recent deiscoveries than this time last year (with the separation and rejoining of multiple breeding populations), known (and unknown) hybridization events, and an environment changing in entirely unknown ways.

“Certainty” seems a little hard to come by in all that. Can one even produce useful *ranges* of possibilities?

Chris_Falter (Chris Falter) 2018-02-01 14:19:22 UTC #456

Hi Jon,

I would point out that **@Swamidass** often provides his conclusions in terms of a range, such as 300 - 400kya. This tells me that he is taking stochastic factors into account, such as the ones Lenski mentions, in communicating his results. Trsnslating his phrasing into a number, I eould guess that the error in his estimates might be on the order of ±15%.

To acknowledge some uncertainty in the estimate does not open the door to speculation from the peanut gallery that the numbers might be off by orders of magnitude.

Moreover, if the error were substantial enough to get us from 500kya to 7kya, I am sure that a well-informed skeptic of the modeling such as **@RichardBuggs** would have brought that to our attention.

Your fellow member of the peanut gallery,
Chris

Swamidass (Dr. S Joshua Swamidass) 2018-02-01 21:10:32 UTC #457

Hello All,

Going to try work through some of this in the coming days.

> RichardBuggs:
>
> But would you agree than in their analyses reported in the paper they have assumed a constant effective population size? If not, how do you understand the footnote to the table that I referenced above.

I do not think they assumed constant population size, but I do agree they used that word “assume” imprecisely. What they did was compute an estimate of the trees ***using a weak prior***, which was overwhelmed by the data, by design. This is a standard approach in statistical modeling and is not correctly called an assumption.

This is important because there is no modeling of the population taking place in argweaver; its just computing trees. Contrast this with, for example, the ABC method. In the ABC method (e.g. **http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1005877**) populations are explicitely modeled and assuming Ne > 10,000 would make detection of lower Ne impossible.

As I explain here: **https://discourse.peacefulscience.org/t/heliocentric-certainty-against-a-bottleneck-of-two/61/10?u=swamidass**

> 1. As a prior, this is not an assumption, but a starting belief that is meant to be overridden by the data. The only way that the ArgWeaver program uses the population size is in computing this prior. Population size is neither simulated nor modeled in the program except for placing this weak prior on population size. Remember, priors are not assumptions or constraints. That is why the measured
> 2. The ArgWeaver output files tell us the strength of the prior vs. the data, and it is just about 5%. That means the model output is dominated 95% by the data, and not by the prior (as it is designed).
> 3. The prior distribution for TMR4A is at about 100 kya, but we measured the TMR4A at about 420 kya. That means the data is pulling the estimate upwards from the prior, not downwards.
>
> This last point should end any confusion. To draw analogy, it’s like we measured the weight of widgets, with the weak starting belief that the average weight of these widgets is 200 lb. After weighing several of them, and taking the prior into account, we compute the average weight is 420 lb. The fact we used a prior could be an argument that the real average is greater than 420 lb, but that is not a plausible argument that the true average is less than 420 lb. The prior, in our case is biasing the results downwards, not upwards.

The paper is imprecise in its use of the word “assume,” but the way it is actually used in the code, it is a weak prior, not an assumption.

That means the TMR4A (and all TMRCAs) are determined primarily using the formula: D = T * R, where D is mutational distance, T is time, and R is the mutation rate. That is the key determinants of the TMR4A. The prior has only a tiny impact on this, pushing the estimated T *lower* (not higher) than that which the data indicates.

Of course, we could try and redo the analysis without a prior, or a weaker prior. We would not expect much to change except for the TMR4A estimate to increase.

Remember, also, as you pointed out…

> RichardBuggs:

> That is because every method (that I know of) would need the population size to remain constant for at least a few generations before it could estimate an Ne of 2. Thus, I think we can safely say that when effective population size is defined by an equation based on genetic data, a single generation of census size two does not have an Ne of 2, but of a higher number (exactly what I don't know - I guess it would depend on the size of the pre-population bottleneck and the rate of population expansion afterwards).

So we expect high Ne, even if there was a bottleneck. This is a pretty important point. Even if the method assumed Ne is high, there is no reason to doubt the TMR4A we compute from the data. Because Ne is largely decoupled from a single generation bottleneck in the distant past.

> RichardBuggs:
>
> My train has just arrived at King's Cross Station - sorry to have sign off. I greatly appreciate your work on this thread, and the honesty and open-mindedness that you have shown.

And I appreciate you bringing the question forward. It has been fun to get to the bottom of this.

More to come when I can.

Swamidass (Dr. S Joshua Swamidass) 2018-02-01 21:46:25 UTC #458

About recombination,

> RichardBuggs:
>
> Hi Joshua **@Swamidass**
>
> I am taking a look at the ARGweaver paper more throughly. It is very clear that the ratio of mutation rate to recombination rate is critical to the accuracy of the method, as the authors comment in the paper, and as several of their supplementary figures (S4-S8) show. When the mutation rate is high relative to the recombination rate, they have much more power than when it is low. However, I am struggling to see what recombination rate they used or estimated when analysing the 54 human genome sequences. Do you know what recombination rate was used? I notice that on page 8 they comment that ARGweaver has "a slight tendency to underestimate the number of recombinations, particularly at low values of mu/rho" and also that they say that other sources give a low value of mu/rho for human populations. This suggests that in their analysis of the 54 human genomes they may well have estimated a lower rate of recombination than the correct rate. However, I can't find the figure. Is this something that you have looked at, please? If they have underestimated the recombination rate, how do you think that would affect the TMR4A?

There are several issues tied up in this question.

1. The simulated ratio of mutation rate to recombination rate has to be high to accurate **in estimating ARGs**, not TMRCA. That is what fig S4-S8 are showing. They find works well at u/p = 2 to 6, but not as well at u/p=1.
2. They point to references that show in human data (on average) the u/p is 1 to 2, but for most of the genome (away from recombination hotspots) it is greater than 2.
3. It appears they used a recombination rate of 1.15e-8 and a mutational map of ~1.25e-8 per generation. So a u/p of 1.13.
4. It appears that if u/p is low, the model misses some of the recombinations.

The first point to make here is that the they determining the accuracy of the method in detecting single/individual recombination events, not in estimating TMRCA. They are not testing the accuracy in measuring global statistics (like median TMR4A).

The second point to make is that recombination events that are difficult to detect are difficult because the data fits the model pretty well one way or another. There is just not enough signal in the data to determine if the event happened, because it would look identical either way. This is a problem if we really want to know the full recombination history, however its just fine if this is not what we are after.

As an aside, a seminal paper was published in 2016 that showed many recombinations are *not* detectable, even in principle, from extant genetic data. So their report that detection of the recombination events is difficult is consistent with this result.

Efficient Coalescent Simulation and Genealogical Analysis for Large Sample Sizes

Author Summary Our understanding of the distribution of genetic variation in natural populations has been driven by mathematical models of the underlying biological and demographic processes. A key strength of such coalescent models is that they...

The third point is that this should not affect the TMRCA times very much, if at all. It is true that recombination events are not easy to detect. That is because in some cases the data is entirely consistent with recombination and no-recombination (if, for example, no mutations happen at a leg in the tree). There is just no evidential way to discriminate these cases, but the TMRCAs of the tree are not affected.

The clarify this last point, the recombinations that ***are*** detectable are those that will reduce the TMRCA substantially. Those that do not reduce the TMRCA are much more difficult to detect, so they are missed.

Finally, we are not relying on a single TMR4A estimate but the whole distribution. That does protect us from the problem areas (like recombination hotspots). If a relatively high portion of the TMR4A's are off, that will not affect our median estimate very much at all. That is why we chose it that way; so it will be a robust estimate to problems like this.

Does that help make sense a bit? There are ways to improve the estimate, but this is a good estimate.

I do want to emphasize that this is just the "first word" on TMR4A. Better estimates are possible, and I expect the number will be refined, perhaps up or down. The fact that some might be able imagine refinements should not diminish our confidence in these results. We can be sure it will be something around 350 kya to 650 kya. Certainly not plausible for a bottleneck 100 kya or 6 kya, but maybe farther back.

> Chris_Falter:
>
> I would point out that **@Swamidass** often provides his conclusions in terms of a range, such as 300 - 400kya. This tells me that he is taking stochastic factors into account,

That is right, though I am giving an expert opinion there. Some people might have more or less confidence. The key thing is that it does push the TMR4A back past 200 kya, easily. Anyone who has a problem with that would be served by producing better estimates with at least as much transparency as have I.

RichardBuggs (Richard Buggs) 2018-02-01 22:14:03 UTC #459

> GJDS:
>
> My interest is in “imagining” how a population of species that appear to be dispersed in a large area would somehow come together to form a relatively stable population, and then from there undergo further modification to form a bottleneck that may indicate a shrinking number.

Hi **@GJDS** I am struggling to follow, and don’t know if the following is helpful or not.

Possible bottleneck hypotheses in a sexual organism are:

(1) Near extinction: a pandemic or natural disaster wipes out a population, and only one male and one female from the survivors reproduce successfully

(2) Founder event: a single couple successfully colonise a new geographical region and form a new population. Their new population does not meet the descendents of the original population again until both populations have diverged to the point that reproduction between them is impossible or very rare, or the original population has gone extinct.

(3) Sexual selection: a change in sexual preference occurs in a single family such that they find the offspring of their own parents more attractive as mates than the rest of the population, and isolation is maintained by sexual selection.

There are more variations, but I think these are the main scenarios I have seen discussed in the literature.

GJDS (GJDS) 2018-02-01 22:40:53 UTC #460

Hi **@RichardBuggs** ,

Thanks, as this brings some clarity to me - from your response, I gather the modeller assumes one or more of these events has taken place, and is not claiming a specific set of data are providing the basis for his model.

Yet another assumption seems to me is made, and that is a population of a particular species has formed and interbred, and fortuitously an event or events occurs to cause a small number, or a couple, to be separate and begin to populate (ugg, I feel as if I am writing a tongue twister). These comments of mine are an attempt to find out what specific physical evidence/data is used when constructing a model or simulation.

I wish I can make my comments clear, but with my background in molecular modelling, I find it a struggle to comprehend the difference between assumptions and data in your modelling exercise.

Lynn_Munter (Lynn Munter) 2018-02-02 14:56:36 UTC #461

Hello **@GJDS** , I am not sure what exactly you are trying to ask, but I want to humbly try to cover a few basics in hopes that something I say may spark or clarify your thoughts in a helpful manner.

> GJDS:
>
> The certainty that is displayed by one side seems to be the absence of modelling that would support a “bottleneck” of two (I find it hard to believe two creatures are a bottleneck? but this is the terminology).

A “bottleneck” is any significant reduction of a population followed by expansion. This discussion has focused specifically on the severest bottleneck possible (barring self-fertilization or asexual reproduction) of two individuals.

When speaking of a bottleneck of hundreds or thousands, it is not necessary that they all know each other or live in the same group or area: it is simply a statement that the genetic material does not have the diversity of a larger group of

ancestors. Bottlenecks happen all the time and they are one of the easiest things to “see” in the data of a genome or group of genomes. We can tell that cheetahs don’t have the genetic diversity of many other species, and we infer that that must be because their population historically was reduced to a small number. This is a solid and unquestioned conclusion, even if scientists may quibble the exact numbers involved.

> GJDS:
>
> I (as a non-participant) am at a loss as to the physical evidence that is supposed regarding this bottleneck of a few hundred or whatever number is discussed. Am I missing something? Has someone discovered remains at a particular location to show such a group existed at some point in time? If not, is this not an inference derived from the modelling.

What you are asking for is literally evidence of absence. The bottleneck is not a group of (pre)humans so much as the absence of greater numbers of (pre)humans. As such I can’t really imagine what sort of archeological evidence would indicate anything. The physical evidence is what we can tell from the genome itself.

> GJDS:
>
> Perhaps you would elaborate; what predictions can any model make on what seems to be current data used to set up the model itself?

The distant past of humanity is far from the only question being examined through genetics. Current and recent known population histories are extensively compared with the genetic information gathered. This information is so vast that predictions need not be of future events, but as-yet-unexamined present data can be predicted, successfully and unsuccessfully.

Hope a little of this is helpful, and of course feel free to correct me if I’m getting anything wrong!

Swamidass (Dr. S Joshua Swamidass) 2018-02-02 16:57:36 UTC #462

> Lynn_Munter:
>
> A “bottleneck” is any significant reduction of a population followed by expansion. This discussion has focused specifically on the severest bottleneck possible (barring self-fertilization or asexual reproduction) of two individuals.

Bottlenecks are defined by the size of the bottleneck and the number of generations. A pair of individuals is severe, but it is only being posited for a single generation. So it is not nearly the “severest possible” bottleneck, which would be a single couple for several generations.

That is the puzzle actually. If it is just a single couple for merely one generation, would it be detectable? In one sense it is severe, in another sense it is not.

Bill_II 2018-02-02 17:36:19 UTC #463

> Swamidass:
>
> So it is not nearly the “severest possible” bottleneck, which would be a single couple for several generations.

I have to ask. How could you have several generations in which each generation was a single couple? Wouldn't the second generation be brother/sister who then have another brother/sister pair, and so on.

---

gbrooks9 (George Brooks) 2018-02-02 21:26:33 UTC #464

> Swamidass:
>
> Bottlenecks are defined by the size of the bottleneck and the number of generations. A pair of individuals is severe, but it is only being posited for a single generation. So it is not nearly the "severest possible" bottleneck, which would be a single couple for several generations.
>
> That is the puzzle actually. If it is just a single couple for merely one generation, would it be detectable? In one sense it is severe, in another sense it is not.

@Swamidass

If I understand your point correctly, a single couple for just one generation, is 10,000 couples going down to 1 couple, and then a return to "normal reproduction" and expansion.

Compared To:

A single couple for multiple generations … which is the "real world equivalent" of a population that starts, out of nowhere, with just one couple, and no further bottleneck.

Would you agree with that?

RichardBuggs (Richard Buggs) 2018-02-02 21:41:30 UTC #465

Hi Chris, I think it would be fair to say that the ranges that Joshua **@Swamidass** is calculating from the TMR4A analysis do not include the uncertainty that would come from some of the more exotic effects that are evidenced in the Lenski experiment. It would be extremely difficult to do so. There is no way (that I am aware of) that we could trace the 12 Lenski populations back to one simultaneous bottleneck based only on their current diversity. This is especially true for the populations in which mutation rates have accelerated in the past, and then slowed down again. There are limits to what is knowable from present day genetic diversity, and there are some questions we will never be able to give a certain answer to. That does not mean that Joshua's calculations are not useful – they are very useful in that they tell us that, given a fairly standard set of simplifying assumptions, a bottleneck of two in the human lineage is a scientific possibility over 500,000 years ago. It is very interesting to know that, and it helps us to discount the idea that a bottleneck of two in the human lineage in the last 7 million years is impossible. However, despite it's usefulness, the analysis does not tell us the true history, which may include effects that have not been accounted for. The Lenski experiment is a salutary reminder of this. I am sure that what I am saying here complements, rather than contradicts, the posts by Joshua.

RichardBuggs (Richard Buggs) 2018-02-02 21:44:42 UTC #466

Hi Bill, that is correct. This is done quite commonly in genetics labs. See **https://en.wikipedia.org/wiki/Inbred_strain**

RichardBuggs (Richard Buggs) 2018-02-02 22:25:00 UTC #467

Hi Joshua, it is great to have you back in the conversation so soon, and I know this reflects the importance and interest that you attach to this discussion, and your servant-hearted attitude towards all those who are interested in this topic.

> Swamidass:
>
> Even if the method assumed Ne is high, there is no reason to doubt the TMR4A we compute from the data. Because Ne is largely decoupled from a single generation bottleneck in the distant past.

This is a very interesting point, and I can see that in some ways it may seem contradictory that I am saying that a single generation bottleneck would not give a detectable Ne of 2, but also saying that a bottleneck of two followed by exponential population growth would have a profound affect on TMR4A. Thank you for pointing that out.
I think I can hold these two points together but I am going to have to pause a bit to work out how to explain this.
I am still rather unclear on how (and indeed whether) Ramussen et al estimated Ne going back in time in their paper, and this makes it harder to think through this issue in this context.

> Swamidass:
>
> The clarify this last point, the recombinations that are detectable are those that will reduce the TMRCA substantially. Those that do not reduce the TMRCA are much more difficult to detect, so they are missed.

Thank you - this is a very helpful point. My concern was that undetected recombinations would lead to higher TMRCA estimates, but your point here is a good one. I just want to take a bit of time looking at the supplementary figures again before I say more on this, but this will have to wait until tomorrow as it is getting late.

GJDS (GJDS) 2018-02-03 00:40:05 UTC #468

> Lynn_Munter:
>
> When speaking of a bottleneck of hundreds or thousands, it is not necessary that they all know each other or live in the same group or area: it is simply a statement that the genetic material does not have the diversity of a larger group of ancestors.

Thanks **@Lynn_Munter** for taking the time to clarify some points - as you state, I am looking at basic matters to obtain an idea of what the modelling may show. My interest in this discussion is to try and “imagine” the way species eventually are thought to have become the present day humanity. By this, I mean this: for example, if some event(s) caused a rapid reduction of human-like species X to form a bottleneck, did this also caused the extinction of other “human-type” species Y, Z, etc, so that we may infer the present human population arose from this bottleneck. If so, why would other species be extinct and how would this modelling account for that. If not, why not? I understand your point on “absence of evidence”, but your modelling needs some context regarding human lineage, so if there is no-evidence for various (pre)humans, and the narrative states there must be various (pre)humans, than I suggest this may be a weakness in the model - remember, the point of all of this has been to throw doubt on Adam and Eve.

Again, if you and other are patient in considering my questions: unless we can see something relevant to our understanding of the composition of the present human population, I fail to comprehend the relevance of these matters to the debate on BioLogos regarding Adam and Eve. The alternate modelling that uses recorded data of population growth, deaths and births, migration etc., which provides a recent common ancestor of about 10,000 years appears to me to be more realistic. However, I can accept correction if you and others can demonstrate how dealing with genetic diversity would be a more powerful technique regarding the basis for the discussion.

Swamidass (Dr. S Joshua Swamidass) 2018-02-03 01:30:46 UTC #469

@RichardBuggs thanks for the kind words.

> RichardBuggs:
>
> Hi Joshua, it is great to have you back in the conversation so soon, and I know this reflects the importance and interest that you attach to this discussion

This is important conversation for a lot of people. It also has been useful.

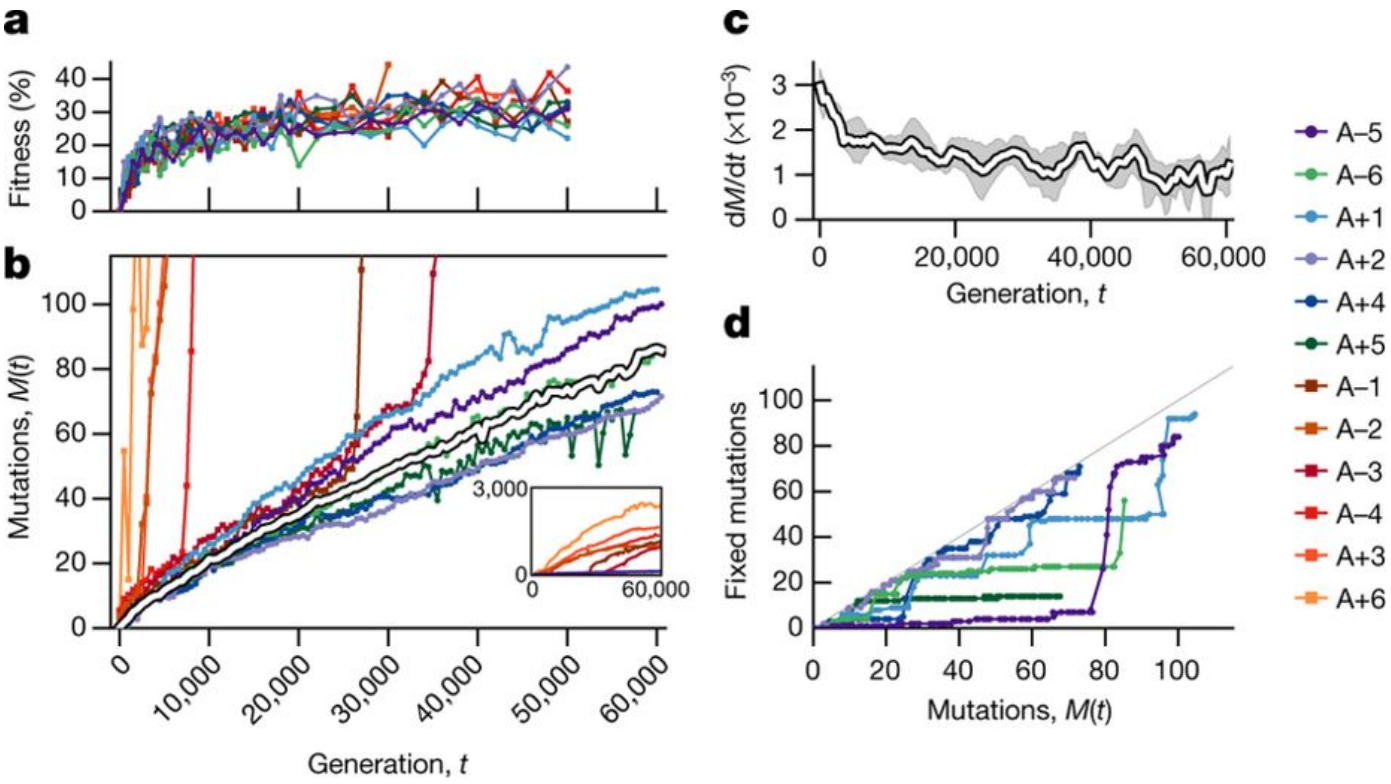
Can you clarify what you are getting at here?

> RichardBuggs:
>
> Hi Chris, I think it would be fair to say that the ranges that Joshua **@Swamidass** is calculating from the TMR4A analysis do not include the uncertainty that would come from some of the more exotic effects that are evidenced in the Lenski experiment.

What exactly are the exotic effects from the Lenski experiment that (1) apply to large mammals like humans, and (2) are capable of dramatically affecting TMRCA estimates?

The key formula we are relying upon to compute times is D = R * T, or the number of differences equals the product of mutation rate with time. This formula is expected to hold best in non-coding regions of the genome, when there is not balancing selection.

Look at figure 2 from the Lenski paper, which shows how mutation rate varies in each experiment. Look at panel B.



Here we can see there are two groups. One group (red and orange) are **mutators**, that at some point start rapidly mutating much more than the normal rate. One group (blue - purple) are **non-mutators** which are just mutating a a more normal rate. The key point is that there is a wild difference between these two groups.

However, this wild of variation in mutation rates is not relevant to mammalian populations. There is much much more constraints on mammalian germline mutation rates, and we do not see such wild swings between populations. So this is

an example of an effect in the Lenski experiment that we do not need to account for when studying human DNA. Adding to that pattern, we know that much more of the human genome is non-coding than in bacteria, so it will be more clock like too.

Yes, we do expect some variation, but it's hard to imagine that variation being more than just 10 to 20% when averaged over 10s of thousands of years.

Also, we are using a **median** estimate TMR4A, so even if some regions of the genome behave weird (e.g. because of balancing selection) they have no effect on the results. So can you clarify what specific effects you think will substantially reduce our confidence in the TMR4A estimate I gave? As I understand it, the confidence intervals I've put forward are gestimates, but they do take into account everything relevant from the Lenski experiment. Let me know what I am missing.

> RichardBuggs:
>
> I am still rather unclear on how (and indeed whether) Ramussen et al estimated Ne going back in time in their paper, and this makes it harder to think through this issue in this context.

I'm not sure what is unclear. I've already explained that they are not estimating Ne, but have a weak prior on the trees computed using Ne. They do not estimate Ne in the past, nor do they assume specific value.

> RichardBuggs:
>
> However, despite it's usefulness, the analysis does not tell us the true history, which may include effects that have not been accounted for.

Let's not be too dismissive.

I think this analysis seems to be pretty strong evidence against a single couple before, say, 300 kya. It does not tell us if a bottleneck happened after 500 kya, but it seems to indicated one did not happen after. It is just a simple formula that is relevant here: D = R * T. We can directly measure D and R (number of differences and mutation rate). So no real leaps are being made.

You'd have to specify more carefully what effects need to be better modeled, and give good reason to believe this would substantially alter the results. I'm all for questioning the data, but I cannot imagine plausible model with a couple at (say) 100 kya. I trust you agree with me on that, right?

> GJDS:
>
> The alternate modelling that uses recorded data of population growth, deaths and births, migration etc., which provides a recent common ancestor of about 10,000 years appears to me to be more realistic.

If you are referring to the value of a recent genealogical Adam to the theological debate, I agree with you. That option seems like it will have a bigger impact on the conversation. That model has a great deal of consilience with the Biblical record and is 100% consistent with the genetic data.

However this question about a single couple bottleneck is important too, because it seems we are coming to a consensus that a single couple bottleneck before about 300 kya (taking into account the uncertainties in a TMR4A of 500 kya) is very unlikely. **@RichardBuggs** is pressure testing it now, but I trust he will eventually acknowledge this point. The way we constructed that estimate (as a median across the genome), it will not be susceptible to most of the concerns that have been raised. The evidence here is pretty strong (though I do not make any "heliocentric"

statements). Nonetheless, this opens up the possibility of an ancient bottleneck (say at 600 kya or 2 mya), for those who feel it's necessary.

Rather than prosecuting that TMR4A value I computed *ad nasueum*, I think a better idea would be to turn to trans-species variation. Of course, there will be better estimates of TMR4A in the future, but the conversation might be better served by looking at another class of evidence.

Lynn_Munter (Lynn Munter) 2018-02-03 11:45:51 UTC #470

> GJDS:
>
> your modelling needs some context regarding human lineage, so if there is no-evidence for various (pre)humans, and the narrative states there must be various (pre)humans, than I suggest this may be a weakness in the model - remember, the point of all of this has been to throw doubt on Adam and Eve.

Woah, I was taking for granted that of course we have **evidence of various pre-humans!** Perhaps I shouldn't have assumed though. Do you want to talk about any in particular?

> GJDS:
>
> if some event(s) caused a rapid reduction of human-like species X to form a bottleneck, did this also caused the extinction of other "human-type" species Y, Z, etc, so that we may infer the present human population arose from this bottleneck. If so, why would other species be extinct and how would this modelling account for that. If not, why not?

The scenario of a bottleneck in one species, followed by interbreeding with a related species would not be nearly as obvious genetically because the genetic diversity would be lowered by the bottleneck and higher due to inbreeding. We would have to be able to pick out which genetic material came from the interbreeding somehow. Not impossible, but complicated.

Luckily usually when we speak of a bottleneck we simply mean a bottleneck of all ancestors of a given organism, whether they are one species or not.

> GJDS:
>
> The alternate modelling that uses recorded data of population growth, deaths and births, migration etc., which provides a recent common ancestor of about 10,000 years appears to me to be more realistic.

I'm unfamiliar with this modeling, do you have a link?

Lynn_Munter (Lynn Munter) 2018-02-03 12:04:56 UTC #471

> RichardBuggs:
>
> they tell us that, given a fairly standard set of simplifying assumptions, a bottleneck of two in the human lineage is a scientific possibility over 500,000 years ago.

Doesn't this need a qualifier, *according to this particular line of evidence*? I know there are other topics than TMR4A which have yet to be discussed in detail.

> gbrooks9:
>
> A single couple for multiple generations … which is the “real world equivalent” of a population that starts, out of nowhere, with just one couple, and no further bottleneck.

@gbrooks9 ,
No, a single couple for multiple generations would be losing genetic diversity fast with each generation, very unhealthily. I think we’re assuming Adam and Eve could’ve had different genes from each other.

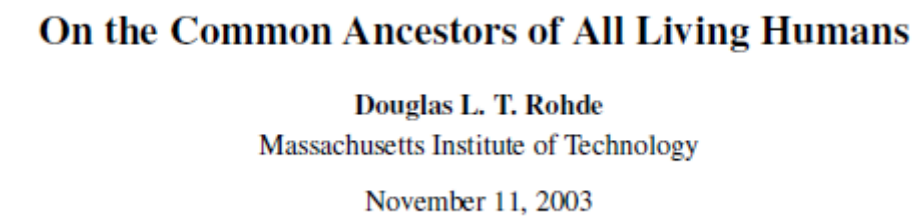
> Swamidass:
>
> So it is not nearly the “severest possible” bottleneck, which would be a single couple for several generations.

@Swamidass ,
Thanks for the correction! I am very sorry to hear about your father. I appreciate the time you are taking for this thread!

GJDS (GJDS) 2018-02-03 12:17:22 UTC #472

> Lynn_Munter:
>
> I’m unfamiliar with this modeling, do you have a link?

A search of my folder on this blog provided the following:



On the Common Ancestors of All Living Humans

Douglas L. T. Rohde
Massachusetts Institute of Technology

November 11, 2003

Let me know if this is sufficient.

The difficulty I am experiencing when I try to follow the discussion is to imagine a bottleneck for the model of one species, when it may be that a number of (pre)humans may need to be modelled with individual bottlenecks - I assume the various species would not mingle - however I hasten to add that I will not pretend to comprehend the basis of this modelling, as it seems to be vastly different to computer modelling/simulations I have carried out.

Perhaps the various (pre)humans did mingle, but again, should the model take some sort of physical data that would show if such existed at the same time, or various times; or are we assuming the human species we presently examine wrt genetic diversity just emerged from a mixture in the distant past.

I again emphasise that my interest is in linking the strange modelling of genetic diversity with the point of this discussion of what catholic Christianity terms truly humans, and of course Adam and Eve. My impression is of a complicate past, a lot of which cannot be verified within these models (but obviously of interest to workers on population genetics).

Lynn_Munter (Lynn Munter) 2018-02-03 13:29:17 UTC #473

> GJDS:
>
> Let me know if this is sufficient.

Found it!

To be clear, this is about our common ancestor, but not our *sole* common ancestor: it would be Adam and Eve within a population of other humans that their children married into.

> GJDS:
>
> when it may be that a number of (pre)humans may need to be modelled with individual bottlenecks - I assume the various species would not mingle

I don't quite understand. We would need DNA with which to do this modeling, yes? And the only living descendants of any post-chimpanzee-split hominins are us, modern humans. We have also managed to retrieve a little Neanderthal/Denisovan DNA, but we can't genetically model lines we don't have DNA from.

> GJDS:
>
> Perhaps the various (pre)humans did mingle, but again, should the model take some sort of physical data that would show if such existed at the same time, or various times; or are we assuming the human species we presently examine wrt genetic diversity just emerged from a mixture in the distant past.

Like I said above, it is complicated but possible to pick out DNA which seems to have come from interbreeding events, and we do find such evidence of interbreeding with Neanderthals and other older populations which we have not yet matched with fossil evidence. These findings are still pretty recent.

I'm still not sure I'm getting at what you're asking, but I'll agree with you that it's complicated!

Jay313 (Jay Johnson) 2018-02-03 14:24:08 UTC #474

> Swamidass:
>
> My next steps, when I get around to it, are:
>
> To test the ability of PSMC, MCMS and/or ArgWeaver to detect bottlenecks on simulated data. Have the simulation code working, and it's really a matter of running the code. My instinct tells me this will increase the bound to about 500 kya, but I won't know till I run it.
>
> Recompute TMR4A while weighting coalescents by the segment length. Failure to do this before, I think, is the biggest source of error in the prior analysis. I think it might shift things around a small amount…
>
> Using the argweaver data to estimate population size. If this works correctly, ti should increase our confidence that this is a good proxy for understanding the success and failure of PSMC and MCMS. Incidentally, MCMS uses a very similar model as ArgWeaver (but a different representation).

Sorry to reach all the way back to this old post, but it seems to me that the following paper is pertinent, since they present a new method of calculating past population sizes.

Inferring Past Effective Population Size from Distributions of Coalescent Times

Inferring and understanding changes in effective population size over time is a major challenge for population genetics. Here we investigate some theoretical properties of random-mating populations with varying size over time. In particular, we...

The abstract:
Inferring and understanding changes in effective population size over time is a major challenge for population genetics. Here we investigate some theoretical properties of random-mating populations with varying size over time. In particular, we present an exact solution to compute the population size as a function of time, Ne(t), based on distributions of coalescent times of samples of any size. This result reduces the problem of population size inference to a problem of estimating coalescent time distributions. To illustrate the analytic results, we design a heuristic method using a tree-inference algorithm and investigate simulated and empirical population-genetic data. We investigate the effects of a range of conditions associated with empirical data, for instance number of loci, sample size, mutation rate, and cryptic recombination. We show that our approach performs well with genomic data (≥ 10,000 loci) and that increasing the sample size from 2 to 10 greatly improves the inference of Ne(t) whereas further increase in sample size results in modest improvements, even under a scenario of exponential growth. We also investigate the impact of recombination and characterize the potential biases in inference of Ne(t). The approach can handle large sample sizes and the computations are fast. We apply our method to human genomes from four populations and reconstruct population size profiles that are coherent with previous finds, including the Out-of-Africa bottleneck. Additionally, we uncover a potential difference in population size between African and non-African populations as early as 400 KYA. In summary, we provide an analytic relationship between distributions of coalescent times and Ne(t), which can be incorporated into powerful approaches for inferring past population sizes from population-genomic data.

They call their method POPSICLE and describe it as such:
There are two important steps for most of these types of approaches: the inference of the underlying gene genealogies and the inference of population size as a function of time from the inferred genealogies. In this article we introduce the Population Size Coalescent-times-based Estimator (Popsicle), an analytic method for solving the second part of the problem. We derive the relationship between the population size as a function of time, Ne(t), and the coalescent time distributions by inverting the relationship of the coalescent time distributions and population size that was derived by Polanski et al. (2003), where they expressed the distribution of coalescent times as linear combinations of a family of functions that we describe below. The theoretical correspondence between the distributions of coalescent times and the population size over time implies a reduction of the full inference problem of population size from sequence data to an inference problem of inferring gene genealogies from sequence data. This result represents a theoretical advancement that can dramatically simplify the computation of Ne(t) for many existing and future approaches to infer past population sizes from empirical population-genetic data.

Data and code availability are given in the paper:

*Simulated data can be regenerated using the commands given in File S1. Data from the 1000 Genomes Project are available on the ftp server **ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/**. Code for the computations is available at: **jakobssonlab.iob.uu.se/popsicle/**.*

Don't know if any of this is helpful, but it seemed pertinent, at least.

RichardBuggs (Richard Buggs) 2018-02-03 15:20:14 UTC #475

Hi Joshua,

Thanks for your thoughtful responses. I will try to repond to you on the three issues we are now discussing about Ramussen et al 2014: (1) estimation of Ne (2) estimation of recombination rate (3) “exotic effects”. This may be quite a long post, or may have to end up broken in to a series of three!

(1) Estimation of Ne
Here, I am responding to your post #457 **Adam, Eve and Population Genetics: A Reply to Dr. Richard Buggs (Part 1)** Your post discusses two issues, the prior on time (T) and the prior on Ne. Here I am only concerned with Ne. I still think that the footnote in the paper under Table 1 shows that even though ARGweaver can allow for changes in Ne, they did not use this ability in their analyses of the human dataset. They say “Model allows for a separate Ni for each time interval I but all analyses in this paper assume a constant N across time intervals.” I think that you have examined the code, and are rightly saying that the code can allow for changes in Ne, but you also need to take this footnote into account that says that Ne was kept constant in their analyses. I think that the effect of this will be to push back the TMR4A. If they had assumed that the human population had increased from a single couple to 7 billion individuals, I think the median TMR4A would be lower.

> Swamidass:
>
> So we expect high Ne, even if there was a bottleneck. This is a pretty important point. Even if the method assumed Ne is high, there is no reason to doubt the TMR4A we compute from the data. Because Ne is largely decoupled from a single generation bottleneck in the distant past.

My original point here was that all our methods (that I know of) that calculate Ne from genetic diversity will give a high value of Ne over the time period of a short, sharp bottleneck. However, this does not mean that if there were such a bottleneck it would not have profound population genetic effects even if it were undetected by our methods. It would cause sharp increase in the number of coalescence. I think (though I am not completely sure) that **@DennisVenema** may be correct in his Part 2 blog in response to me that 25% of polymorphic genes will have coalescence events at a bottleneck of two. However, I think that these will be hard to detect, as the inaccuracy of our estimates of TMRCAs will mean that the coalescence events will appear to us with our estimates to be smeared out over a longer period of time and we will detect a small drop in Ne, rather than a bottleneck (BTW, this is one reason why PSMC struggles to detect bottlenecks).

So I think what I am saying is that even if in the real history of a population there is a short sharp bottleneck that causes a burst of coalescence, we will struggle to pick that up, and thus will thus miss the bottlenecks and the effects we might expect it to have on rates of coalescence. This argument is assuming a method that allows estimation of coalescence times and Ne, with feedback between the two, but this is not what ARGweaver does, so this is a slightly academic conversation in this context. As you say, ABC methods are better at modelling Ne and TMRCA at the same time, but my experience of this is that the two variables are so dependent on each other that it is hard to know for sure what is the effect of time and what is the effect of population size – but this is a separate discussion that is not really relevant to the Ramussen et al paper, which is not modelling Ne.

I will discuss recombination in a new post.

Swamidass (Dr. S Joshua Swamidass) 2018-02-03 17:50:36 UTC #476

The purpose of argweaver is not to estimate Ne, so they do not estimate it. They instead are estimating phylogenetic trees. The times on trees is determined not by population modeling but by the formula:

D = R * T

The only way Ne affects things is by putting a weak prior on T, but this prior is lower than that which is measured. So we know that the prior only reduces the TMR4A estimate.

> RichardBuggs:
>
> I think that you have examined the code, and are rightly saying that the code can allow for changes in Ne, but you also need to take this footnote into account that says that Ne was kept constant in their analyses. I think that the effect of this will be to push back the TMR4A.

@RichardBuggs I have taken that into account and said exactly the same. Moreover, I have shown that their choice of Ne ***reduces*** the estimate of TMR4A, not increases it. One what basis are you disagreeing here?

> RichardBuggs:
>
> If they had assumed that the human population had increased from a single couple to 7 billion individuals, I think the median TMR4A would be lower.

Its the exact opposite. If they had chosen a larger Ne, the estimated TMR4A would be higher, by a small amount. I'm not sure how you are forming your intuitions here. As I've explained, I've looked at the code carefully. What I first wrote about this still applies…

> Swamidass:
>
> To draw analogy, it's like we measured the weight of widgets, with the weak starting belief that the average weight of these widgets is 200 lb. After weighing several of them, and taking the prior into account, we compute the average weight is 420 lb. The fact we used a prior could be an argument that the real average is greater than 420 lb, but that is not a plausible argument that the true average is less than 420 lb. **The prior, in our case is biasing the results downwards, not upwards.**

Which once again gets to a key point…

> RichardBuggs:
>
> I still think that the footnote in the paper under Table 1 shows that even though ARGweaver can allow for changes in Ne, they did not use this ability in their analyses of the human dataset.

> RichardBuggs:
>
> My original point here was that all our methods (that I know of) that calculate Ne from genetic diversity will give a high value of Ne over the time period of a short, sharp bottleneck.

That is just as I've explained, but does not reduce confidence, because ArgWeaver ***is not attempting to estimate Ne***. It is merely measuring the trees (i.e. the D in the formula above), while taking recombination into account.

@RichardBuggs I'd quickly acknowledge if I'd made a mistake here or if you have a point. Honestly, however, I am not seeing your point. I think the 500 kya (with about 20% CI) is a pretty solid lower bound on a single couple origin. I hope you'll agree so we can move on to more interesting data.

> RichardBuggs:

> However, this does not mean that if there were such a bottleneck it would not have profound population genetic effects even if it were undetected by our methods. It would cause sharp increase in the number of coalescence. I think (though I am not completely sure) that **@DennisVenema** may be correct in his Part 2 blog in response to me that 25% of polymorphic genes will have coalescence events at a bottleneck of two.

That is accurate. Which is why I need to do the simulations to test this. I think this will push a plausible bottleneck back to about 800 kya, but I'm not sure.

> RichardBuggs:
>
> However, I think that these will be hard to detect, as the inaccuracy of our estimates of TMRCAs will mean that the coalescence events will appear to us with our estimates to be smeared out over a longer period of time and we will detect a small drop in Ne, rather than a bottleneck (BTW, this is one reason why PSMC struggles to detect bottlenecks).

> RichardBuggs:
>
> So I think what I am saying is that even if in the real history of a population there is a short sharp bottleneck that causes a burst of coalescence, we will struggle to pick that up, and thus will thus miss the bottlenecks and the effects we might expect it to have on rates of coalescence.

Yeah I agree with this.

On a theoretical note, I think there will be a relationship between the distribution of TMR4A, TMR3A, and TMR2A and the time range under which a bottleneck is detectable. The fewer lineages at a particular point in time (which reduce the farther back we go), the less of an increase in the coalescent rate.

You are right though that a sharp bottleneck will not be observed as sharply by PSMC, or really any coalescence based method, including ABC. I agree, it is hard to tell what is the effect of time (length of bottleneck) and population size. From a theoretical point of view, both have the exact same impact on coalescence rate, so it appears they are indistinguishable by looking at coalescence rate alone.

Closing out on TMR4A.

The reason why we measured TMR4A is because it provides an easy to understand lower bound, and is easier to robustly measure with fewer assumptions than coalescent rate (which is a second order or third order statistic). If there is a single couple bottleneck, we should no more than 4 lineages when it occurs.

One again, I do hope you can endorse that finding. In the end, it proves your critique of Venema is essentially correct.

Of course, we can imagine better ways of measuring TMR4A. When I get around to it, I might make some improvements myself. However, what's been put forward is a solid starting point that is not going to see wild revisions downwards without large changes to mutation rate.

RichardBuggs (Richard Buggs) 2018-02-03 18:11:37 UTC #477

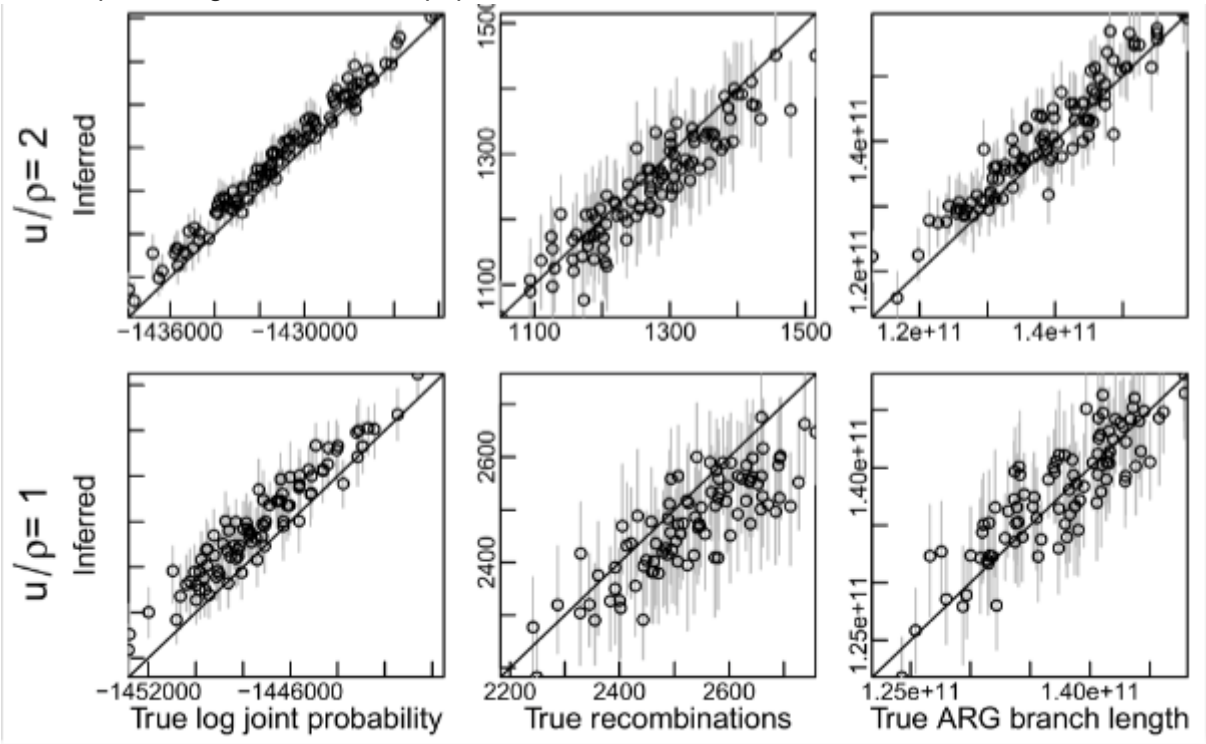
(2) Recombination rates and TMRCA estimated in Ramussen et al (2014)

Thank you **@Swamidass** for the information that the ratio of mutation rate to recombination rate (mu/rho) used in the ARGweaver analyses of human population data is around 1.13. My reading of the paper is that this means that (as

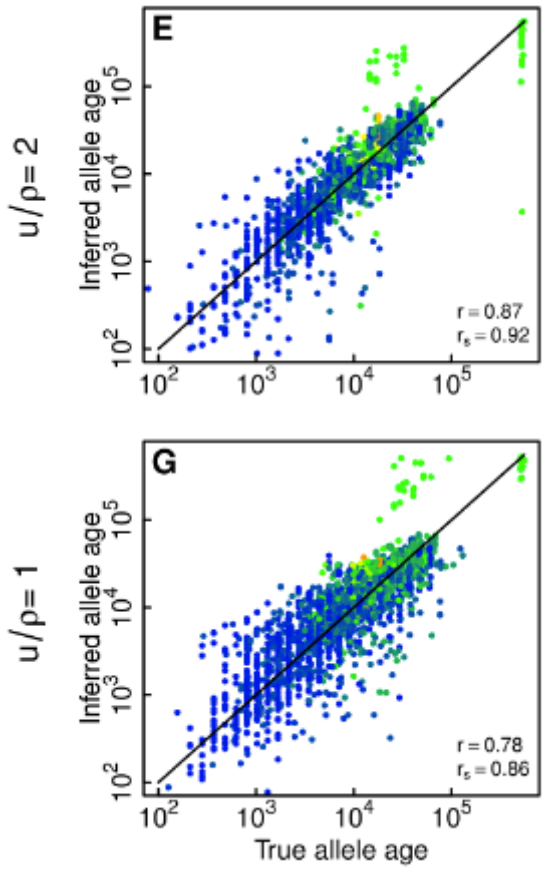
Joshua has also said) they will miss some recombination events. I agree with Joshua that:

> Swamidass:
>
> the recombinations that are detectable are those that will reduce the TMRCA substantially

However, I think that the lack of detection of other recombination events will have an effect of the TMRCA, causing it to be overestimated.
Here is part of Figure S4 from the paper:



Note that it is the lower set of charts that is for the value of mu/rho that is closest to 1.13. This shows (middle row) that the number of recombinations is systematically underestimated by ARGweaver with this low mu/rho value, and the error in estimating branch lengths is higher than would be the case if mu/rho were higher.
Here is part of Figure S7



This shows that the error in estimating allele age is greater at mu/rho = 1 than at mu/rho =2 . Whether or not there is a degree of systematic overestimation of allele age at mu/rho=1 is hard to tell from eyeballing the chart as we can't see the density of the clusters very well. There is a cluster of alleles with high derived allele frequency (coloured green) that have a true age of under 10^5 but are estimated to have an age of over 10^5 and this effect is greater at mu/rho = 1 than at mu/rho = 2.

It is also worth noting from Figure S8 that at mu/rho = 1 only about 60% of tree topologies are correct in ARGweaver. My guess is that incorrect trees are likely to be less parsimonious than correct trees, and so would elevate the TMRCA.

RichardBuggs (Richard Buggs) 2018-02-03 18:48:07 UTC #478

(3) "Exotic" effects

> Swamidass:
>
> Can you clarify what you are getting at here?

The main point I was making from the Lenski experiment is this:

> RichardBuggs:
>
> It is a very very different system to human populations, but in many ways it should be a simpler system, and therefore easier to model. It underlines the difficulty of going from models to real evolution.

I agree with your point that a "mutator" phenotype as extreme as those seen in some of the Lenski populations is unlikely/impossible a human population, and that you have done your best to account for the effects of balancing selection.

However, we do know that mutation rates can vary to some extent between human populations. As Kelley Harris wrote recently in Science

Reading the genome like a history book

One way to study a genome is to read it like an instruction manual. It contains genes that are easily decoded into the protein building blocks of cells, as well as much more cryptic regulatory codes that dictate when and where each protein should be...

"it is very clear that some mutagenic force became overactive in the European population during the past 20,000 years or so since Europeans and East Asians started differentiating into separate populations.
This contradicts the popular “molecular clock” model (13), which posits that mutation rates evolve very slowly over perhaps tens of millions of years. Rather, it suggests that DNA replication fidelity is a lot like other biological traits, sometimes evolving by leaps and bounds for reasons that usually elude us."

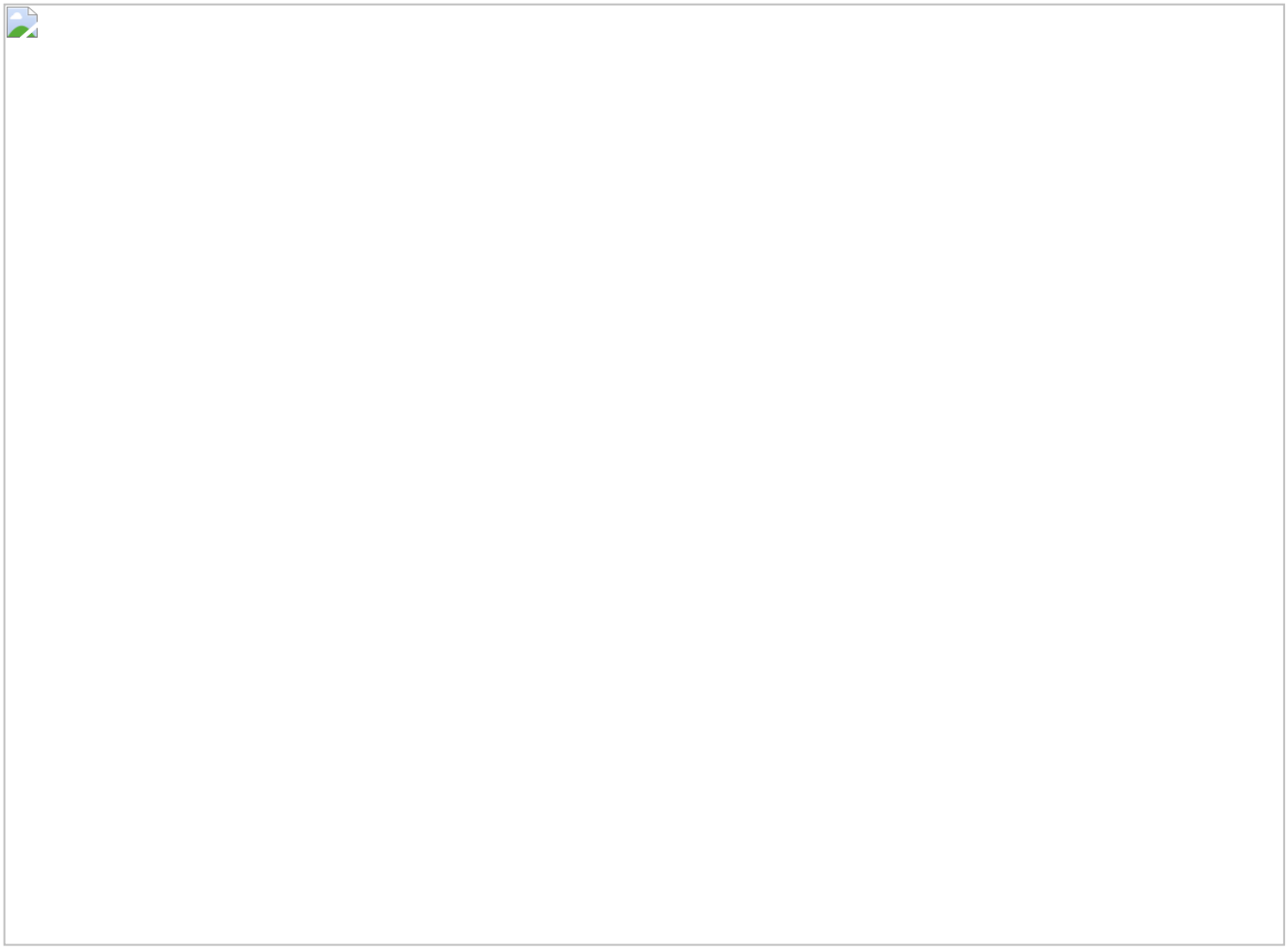
Swamidass (Dr. S Joshua Swamidass) 2018-02-03 19:08:52 UTC #479

> RichardBuggs:
>
> However, I think that the lack of detection of other recombination events will have an effect of the TMRCA, causing it to be overestimated.

> RichardBuggs:
>
> However, we do know that mutation rates can vary to some extent between human populations. As Kelley Harris wrote recently in Science

I agree these are all sources of error. That is nothing new. I’ve noted both these effects more than once over this conversation.

In regards to mutation rate, I has been measured by several independent methods covering a large range of time ranges to be about 0.5e-9 per year.



https://www.sciencedirect.com/science/article/pii/S0959437X16301010

This means…

> 1. If TMR4A was at 100 kya, we would expect the mutation rate to be 2.1e-8 per generation, or 4x more than observed.
> 2. If TMR4A was at 6 kya, we would expect the mutation rate to be 32e-8 per generation, or 64x more than observed.
> **https://discourse.peacefulscience.org/t/heliocentric-certainty-against-a-bottleneck-of-two/61/11?u=swamidass**

Notice that there is still a strong correlation between the estimated and true TMRCA. Also, most of the genome has a u/p > 2, so most of the time the correlation will be stronger than the u/p=1 plot indicates.

I agree that these are sources of error, but I do not think they take the uncertainty much beyond +/- 20%.

What do you think the error rate is? Would you say 20% too, or 30%? Or what exactly? It would be helpful if you would attempt to quantify your degree of uncertainty about these numbers. Perhaps we are not even disagreeing at this point. **To what extend do you think these factors increase the spread of our TMR4A estimate?**

GJDS (GJDS) 2018-02-03 23:13:04 UTC #480

> Lynn_Munter:

> To be clear, this is about our common ancestor, but not our sole common ancestor

agreed.

> Lynn_Munter:
>
> And the only living descendants of any post-chimpanzee-split hominins are us, modern humans.

can the modelling be calibrated in some manner so that one may obtain a method for assessing errors?

> Lynn_Munter:
>
> I'm still not sure I'm getting at what you're asking

I am interested in why accounting for genetic diversity by modelling some type of past and non-verifiable event(s) is treated with such certainty re past events by some proponents on this site.

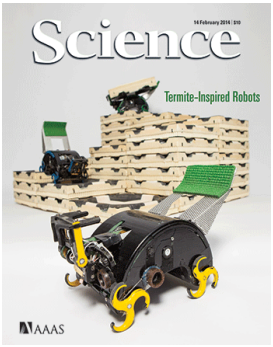
> Lynn_Munter:
>
> I'll agree with you that it's complicated!

amen to that brother, and I would add, uncertain as a way of providing a history of the human population over lengthy periods.

Swamidass (Dr. S Joshua Swamidass) 2018-02-03 23:17:35 UTC #481

> GJDS:
>
> can the modelling be calibrated in some manner so that one may obtain a method for assessing errors?

We can validate with known historical events…



A Genetic Atlas of Human Admixture History

Admixture, the result of previously distant populations meeting and breeding, leaves a genetic signal within the descendants' genomes. However, over time the signal decays and can be hard to trace. Hellenthal et al. (p. [747][1]) describe a method,...

GJDS (GJDS) 2018-02-04 00:36:15 UTC #482

Thanks for the reference **@Swamidass** . This adds to my impression of a very complicated simulation, and I note this goes back a few thousand years - I have paste two portions that may be helpful to this discussion.

A comparison with the historical record becomes progressively more difficult for older episodes. Even when events are well attested, their exact genetic impacts (if any) are rarely if ever known, motivating our approach. Nevertheless, we have identified nine groups of populations showing related events, incorporating almost all (19/20) with the strongest GLOBETROTTER admixture evidence (*9*). Results are presented as online maps (*26*). Some events appear to match well with particular historical occurrences, such as the so-called Bantu Expansion into Southern Africa (*9*). Events affecting a group of seven populations (Fig. 2D, purple box 4) correspond in time to the rapid expansion, initiated by Genghis Khan, of the Mongol empire (1206 to 1368 CE) (*31*), one of the most dramatic events in human history. These populations, including the Hazara (*32*, *33*), the Uygur (*34*), and the Mongola themselves, were sampled from within the range of the Mongol empire and show an admixture event dating within the Mongol Period, with one source closely genetically related to the Mongola that progressively decreases in proportion westward, to 8% in the Turkish (Fig. 2D).

Our results demonstrate that it is possible to elucidate the effect of ancient and modern migration events and to provide fine-scale details of the sources involved, the complexity of events, and the timing of mixing of groups by using genetic information alone. Where independent information exists from alternative historical or archaeological sources, our approach provides results consistent with known facts and determines the amount of genetic material exchanged. In other cases, novel mixture events we infer are plausible and often involve geographically nearby sources, supporting their validity. Admixture events within the past several thousand years affect most human populations, and this needs to be taken into account in inferences aiming to look at the more distant history of our species. Future improvements in whole-genome sequencing, greater sample sizes, and incorporation of ancient DNA, together with additional methodological extensions, are likely to allow better understanding of ancient events where little or no historical record exists, to identify many additional events, to infer sex biases, and to provide more precise event characterization than currently possible. We believe our approach will extend naturally to these settings, as well as to other species.

gbrooks9 (George Brooks) 2018-02-04 05:38:44 UTC #483

> RichardBuggs:
>
> My original point here was that all our methods (that I know of) that calculate Ne from genetic diversity will give a high value of Ne over the time period of a short, sharp bottleneck. However, this does not mean that if there were such a bottleneck it would not have profound population genetic effects even if it were undetected by our methods.

I have to wonder about this pair of sentences:

"… [it] does not mean that if there were such a bottleneck it would not have profound population genetic effects…" < [Meaning, it **could** have profound genetic effects]

"… even if it were undetected by our methods."

How profound could the effects be if we couldn't detect them?

What would be an example of such a profound effect?

Swamidass (Dr. S Joshua Swamidass) 2018-02-05 04:31:21 UTC #484

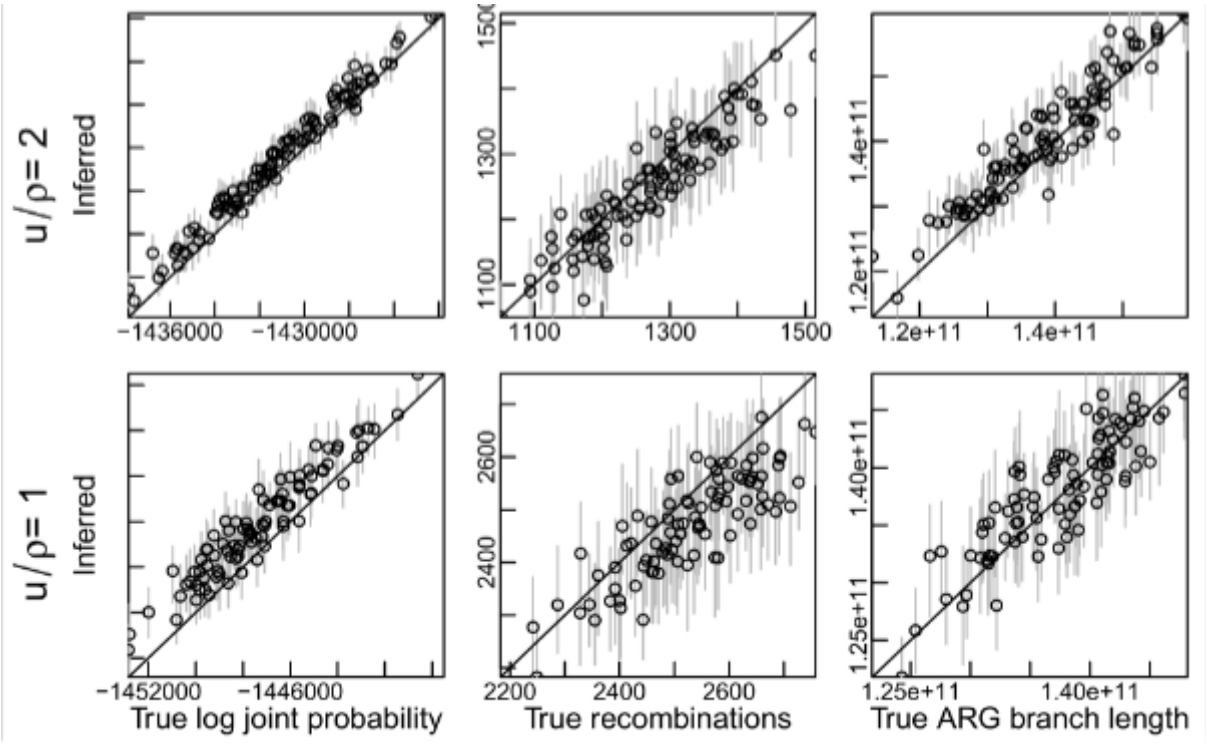
I thought this post required a more detailed follow up…

> RichardBuggs:
>
> (2) Recombination rates and TMRCA estimated in Ramussen et al (2014)

> RichardBuggs:
>
> However, I think that the lack of detection of other recombination events will have an effect of the TMRCA, causing it to be overestimated.

This is a great hypothesis but it is not borne out in the data marshaled. It confirms, instead, my point that the effect is only small on TMRCA. At the core of this is misunderstanding of the statistics at play.

Case in point is S4:

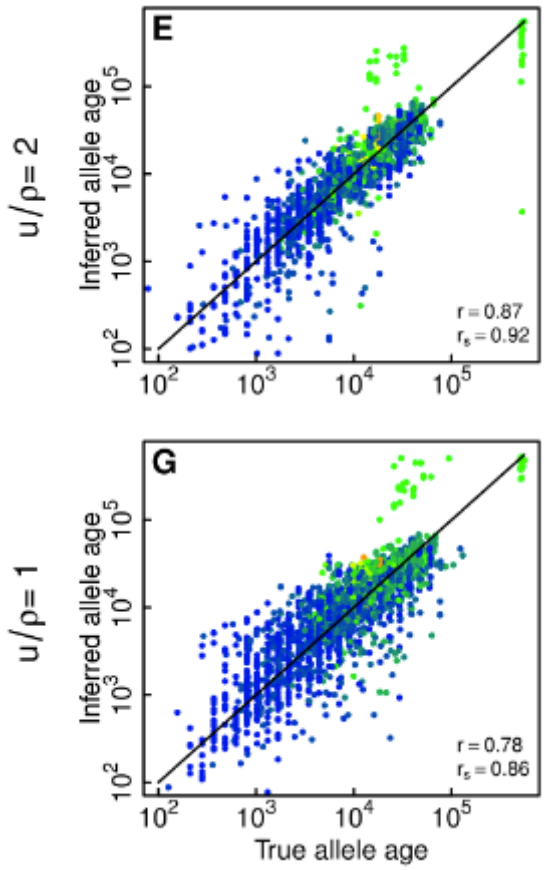


Look at the last column where it shows the true ARG branch length. We see that the variance of the estimate increases but **there is no systematic error that is shifting estimates upwards from the true value**. This is a critical point. Remember we are taking the median of the TMR4A, which only depends on where the distribution is centered, not its spread. That is why we chose median, not mean. **This graph is very strong evidence that the recombination inference errors are NOT increasing the TMR4A, just as I hypothesized.**

In fact, even when recombinations are underidentified (bottom row, middle column), ARG length is still measured about the same, but with higher variance (bottom row, right column). We chose an estimator that does not depend on variance, however, so this has zero impact on TMR4A.

We see the exact same pattern in S7. Even though you write…

> RichardBuggs:
>
> This shows that the error in estimating allele age is greater at mu/rho = 1 than at mu/rho =2 . Whether or not there is a degree of systematic overestimation of allele age at mu/rho=1 is hard to tell from eyeballing the chart as we can’t see the density of the clusters very well.



The correlation between the true and estimated TMRCA drops a little, from 0.87 to 0.78, but if there is systematic error, it is very low. We cannot tell precisely this graph, *but we can from the prior graph*. **The median of each distribution is going to be very close to each other.** Taken with the prior figure, this is evidence that the under inference of recombination is not a major source of error. In fact, these data points show that recombination inference mistakes do not change the average/median TMRCA estimates. Also, TMRCA has much higher variance than TMR4A, and TMR4A will be even less susceptible to these types of errors.

In the end, these figures validate pretty clearly my alternate hypothesis, which I formed based on knowledge of how this algorithm works.

> Swamidass:
>
> The clarify this last point, the recombinations that are detectable are those that will reduce the TMRCA substantially. Those that do not reduce the TMRCA are much more difficult to detect, so they are missed.

Remember, I am a computational biologists, and I build models for biological systems like this in my “day job,” so I am working from a substantial foundation of firsthand experience in how these algorithms work. This is not an appeal to authority (trust or distrust me as you like), but an explanation of why I had some confidence in this in the first place. What we see is what I guessed. There is increased variance in the estimate, but no clearly evidence that the TMRCA is increased more than it is decreased.

> RichardBuggs:
>
> It is also worth noting from Figure S8 that at mu/rho = 1 only about 60% of tree topologies are correct in ARGweaver. My guess is that incorrect trees are likely to be less parsimonious than correct trees, and so would elevate the TMRCA.

This hypothesis seems false. We can see from figure S4 and S7 that about 50% are less parsimonious than the correct tree (higher TMRCA) and about 50% are more parsimonious (lower TMRCA). Remember, we do not expect the trees to be precisely correct. There are just estimates, and we hope (with good reason) that the errors one way are largely cancelled by the errors the other way when we aggregate lots of estimates.

Finally, we are aggregating a lot of estimates together to compute the TMR4A across the whole genome. This is important, because by aggregating across 12.5 million trees, we reduce the error. While our estimate in a specific part of the genome might have high error, that error cancels out when we measure across the 12.5 million trees. This is a critical point.

The statistics here substantially increases our confidence in these numbers.

Just about any source of error we can identify will push some of the TMRCA estimates up and some of them down. However, because we are looking at the median of all these estimates, this increase in variance does not affect the accuracy much. A great example of this is mutation rates.

Yes, there is variation in mutation rate. We can measure it in different populations, and we can even detect some differences in the past. These variations, however, in humans are all relatively small. These variations, also, are not always to higher mutation rates, but also to lower mutation rates. So yes, it is likely that mutation rates were ***slightly*** higher in particular populations or points in the past (let's say within 2-fold per year), but it is also likely they were ***slightly*** lower at times too. For the most part, this just averages out over long periods when looking at the whole human population. That is not 100% true, but the law of averages is why variation in mutation rate is not going to dramatically increase our confidence interval on TMR4A by much.

Let's remember why we are here:

> Swamidass:
>
> We need to know the Time to Most Recent 4 Alleles (TMR4A). This is not a standard computed number in genetics.

> RichardBuggs:
>
> This is exactly my point. Thank you for stating it so concisely. To my mind, the way ahead would be to write a programme that computes the TMR4A for each haplotype block of the human genome, and work out a reasonable time frame using data from all blocks. **Until that has been done, I do not think we can say that the bottleneck hypothesis has been rigorously tested.**

> Swamidass:
>
> I took him up on the challenge and computed it across the whole genome.

I think it's fair to say at this point that I did rigorously test the bottleneck hypothesis. Right?

Perhaps there will be improved follow on analysis that will refine my estimates, and I encourage that. However, TMR4A is a feature of the data. It is the length (in units of time, computed by mutational length / mutation rate) of the most parsimonious trees of genome wide human variation. This is **not** an artifact of a population genetics modeling effort. Rather, it is a way of computing the time required to produce the amount of variation we see in human genetics.

Also, this analysis is very generous to to the bottleneck hypothesis. Though I'm not certain yet (and plan to do the studies to find out), bottlenecks going back as far as 800 kya might be inconsistent with the data we see. There are

some large unresolved questions about how a bottleneck effects coalescence rate signatures before the median TMR4A, and if they are detectable.

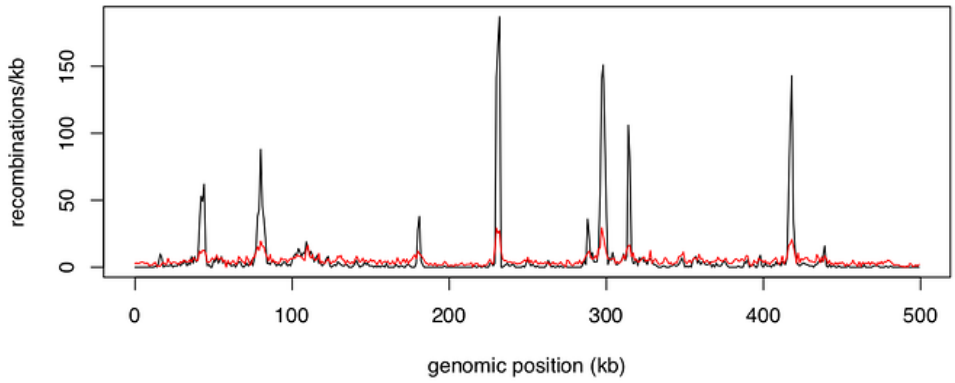
I hope there can be some agreements on these points, as a conclusion to this portion of the conversation would be valuable. It would be great to move on to more interesting data.

Swamidass (Dr. S Joshua Swamidass) 2018-02-05 05:38:19 UTC #485

> Swamidass:
>
> In the end, these figures validate pretty clearly my alternate hypothesis, which I formed based on knowledge of how this algorithm works.

I should also add that the referenced supplementary figures (S4 and S7) appear to be using only 20 sequences. Accuracy improves dramatically as more sequences are added. For the data we used, there were 108 sequences, so we expect better accuracy than the figures shown.

Also, S6 is an important figure, that shows the inferred vs true recombination rates for simulation using the known distribution of recombination rates across a stretch of the genome.



A few things to note about this.

1. For most of the genome, recombination rate is low (corresponding to high u/p), but only is jumps up at recombination hotspots (the places where u/p is low).

2. The model picks up some of the recombinations, but not all of them. Most of the recombination inference errors are there, in the recombination hotspots, which are confined to a very small proportion of the genome.

3. At recombination hotspots, the trees will span shorter amounts of the genome than the rest of the genome. Trees with low bp span are signature for high recombination rate.

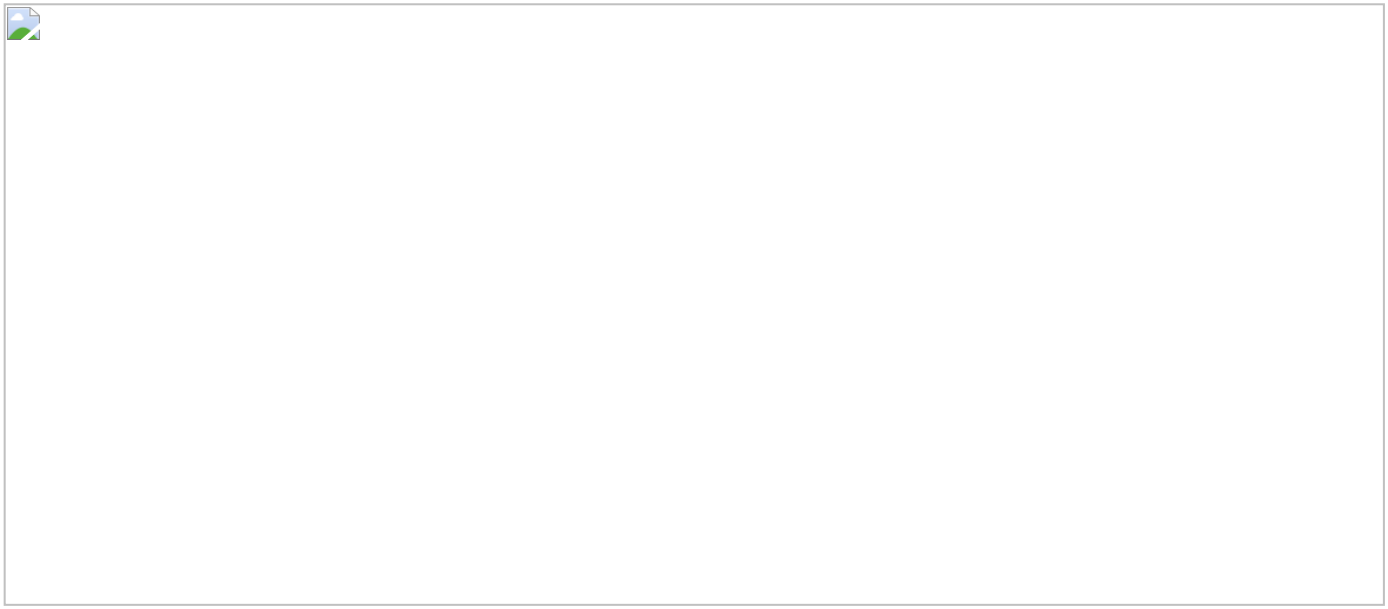
4. That means that most of the genome has a high u/p and is being estimated accurately, but there is only difficulty at recombination hotspots where u/p is low.

5. By weighting trees by the number of base pairs they cover, we can dramatically reduce any error that might be introduced by recombination inferences. That's because recombination hotspots are were the vast majority of the errors are, and these hotpots are just a few percent of the genome.

And that is exactly what I did. Rather than reducing the TMR4A estimate, downweighting the error prone recombination hotspots (by weighting by bp span of trees) ***increases*** the TMR4A estimate.

> Swamidass:
>
> > At the moment, all coalescents are weighted equally. This biases the averages to high recombination areas, which might be biased towards upward errors in TMRCA estimates. It would be wiser to average weighting by the length of the DNA segment to which the phylogeny applies.
>
> I finally got around to correcting this part of the code, and recomputing the TMR4A. Here is what we arrive at, a TMR4A of 495 kya, nearly 500 kya. This is a better estimate.

I'm going back over all this to point out I was already thinking about the effect of recombination and correcting for it in a plausible way. There are always sources of error in any measurement. This is no exception. The fact there is error however, does not mean the error is large. Clearly, we are only computing an estimate, but this is a good estimate of TMR4A.



Of note, correcting for recombination errors by downweighting recombination hotspots ***increases*** the TMR4A estimate. It does not decrease it. Thats because for trees spanning only short segments of the genome, they will be more influenced by the prior. That's because in short segments of the genome, there is not enough data/evidence to overwhelm the prior, so it takes over. On longer genome segments, the data is strong enough to disagree with the prior. As we have seen, the prior pull the TMR4A estimates downwards on real data. So in the end, reducing the effect of recombination hotspots just increases the TMR4A estimate. This is appropriate, because we want the TMR4A least dependent on the prior.

This may seem surprising, and in conflict with the the S4 and S7 data. It is not. In the S4 and S7 experiments, the prior matched the simulation, and did not pull the results up or down. In the real data, the prior pull the TMR4A estimates down, and pulls them down most in recombination hotspots because their bp spans are smallest. So this counterintuitive effect makes sense as an interaction with the prior and recombination hotspots. This error is important to understand, because **unlike most types of errors**:

1. it is biased in one direction (towards artificially lowering TMR4A)
2. its impact is large (about 70 kya, or about 15% relative effect)

Note, also, that I identified this source of error and corrected for it several weeks ago. Even in my first estimate, I disclosed it was going to be an issue.

> Swamidass:
>
> At the moment, all coalescents are weighted equally. **This biases the averages to high recombination areas, which might be biased towards upward errors in TMRCA estimates**. It would be wiser to average weighting by the length of the DNA segment to which the phylogeny applies.

Before I looked at the prior, however, I guessed wrong on the direction of the effect. I cannot identify any other sources of error likely to have this large an effect. Also, this adjustment was within my +/-20 confidence interval, which shows even my original estimate was not overstated.

Moreover, I have at this point corrected for it. A better correction might take this further, by just excluding the trees with small bp lengths, thereby excluding all regions where recombination rate is high. This refinement, will certainly increase the TMR4A estimate. I'm more inclined to improve this estimate with a different program first. That would likely have more value in the long run.

RichardBuggs (Richard Buggs) 2018-02-06 21:32:45 UTC #486

Hi Joshua,
Thank you for your patience with me regarding Ne and ARGweaver. I think I have misunderstood something, and I am just having more of a think about this. As I go back over your posts, I am struck by how many times you have made the same point to me, without me really taking it on board:

> Swamidass:
>
> That means the TMR4A (and all TMRCAs) are determined primarily using the formula: D = T * R, where D is mutational distance, T is time, and R is the mutation rate. That is the key determinants of the TMR4A.

> Swamidass:
>
> The key formula we are relying upon to compute times is D = R * T, or the number of differences equals the product of mutation rate with time.

> Swamidass:
>
> I've already explained that they are not estimating Ne, but have a weak prior on the trees computed using Ne. They do not estimate Ne in the past, nor do they assume specific value.

> Swamidass:
>
> It is just a simple formula that is relevant here: D = R * T. We can directly measure D and R (number of differences and mutation rate).

> Swamidass:

> The purpose of argweaver is not to estimate Ne, so they do not estimate it. They instead are estimating phylogenetic trees. The times on trees is determined not by population modeling but by the formula:
>
> D = R * T

Sorry I have not taken this on board sooner! Can I try to paraphrase this. What you seem to be saying is that they are simply taking a molecular clock approach to estimating TMRCA. Time is the number of differences divided by the mutation rate. They are building phylogenetic trees and dating them.

The reason why I have been so preoccupied with Ne is because I thought this was a coalescent analysis, where time to coalescence is proportional to effective population size. The bigger the population size, the longer it takes to get back to a MRCA, even in the absence of mutation. The reason why I was thinking that a bottleneck followed by exponential population growth to 7 billion individuals would reduce TMRCA in such an analysis is encapsulated in this figure from Barton et al's textbook "Evolution" published by CSHL (note especially part C)

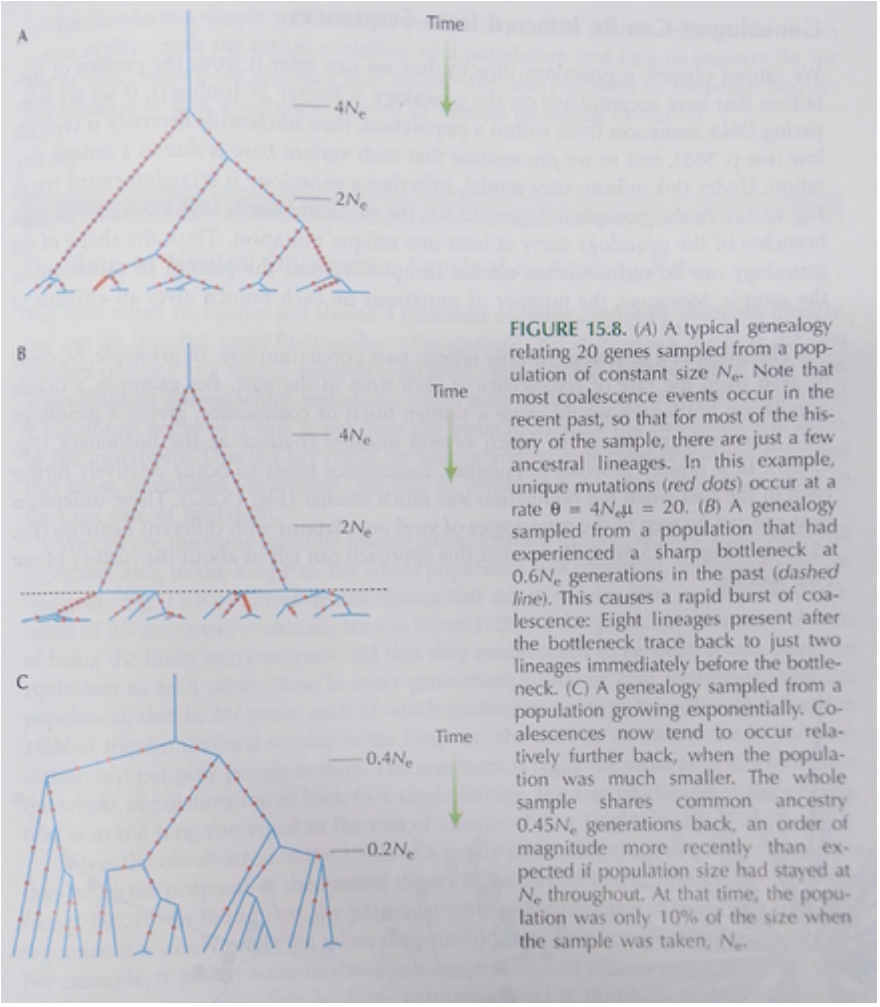


FIGURE 15.8. (*A*) A typical genealogy relating 20 genes sampled from a population of constant size N_e. Note that most coalescence events occur in the recent past, so that for most of the history of the sample, there are just a few ancestral lineages. In this example, unique mutations (*red dots*) occur at a rate $\theta = 4N_e\mu = 20$. (*B*) A genealogy sampled from a population that had experienced a sharp bottleneck at $0.6N_e$ generations in the past (*dashed line*). This causes a rapid burst of coalescence: Eight lineages present after the bottleneck trace back to just two lineages immediately before the bottleneck. (*C*) A genealogy sampled from a population growing exponentially. Coalescences now tend to occur relatively further back, when the population was much smaller. The whole sample shares common ancestry $0.45N_e$ generations back, an order of magnitude more recently than expected if population size had stayed at N_e throughout. At that time, the population was only 10% of the size when the sample was taken, N_e.

If ARGweaver is not doing coalescent analysis in this sense, then I can see that Ramussen et al are simply taking a molecular clock approach, as you seem to be saying.

I am not sure that you are saying that exactly though, as you also seem to be saying that the Ne value they choose is placing a prior on the TMRCA:

> Swamidass:
>
> The only way Ne affects things is by putting a weak prior on T

> Swamidass:
>
> If they had chosen a larger Ne, the estimated TMR4A would be higher, by a small amount.

This sounds to me like a coalescent analysis, not a simple phylogeny and molecular clock.
I'm sorry, but I seem to be misunderstanding something here.This is why you have had to repeat yourself so much, and I am sorry it is taking me so long the understand what is going on here.

---

gbrooks9 (George Brooks) 2018-02-06 22:18:43 UTC #487

> RichardBuggs:
>
> This sounds to me like a coalescent analysis, not a simple phylogeny and molecular clock.
>
> I'm sorry, but I seem to be misunderstanding something here.This is why you have had to repeat yourself so much, and I am sorry it is taking me so long the understand what is going on here.

@RichardBuggs

Are the results of this abstract consistent with your expectations? Or do you think they are making a fundamental error somewhere?

GENETICS journal
2016 Nov; 204(3): 1191–1206.
Published online 2016 Sep 15.

Inferring Past Effective Population Size from Distributions of Coalescent Times
by Lucie Gattepaille, Torsten Günther,and Mattias Jakobsson

Abstract
Inferring and understanding changes in effective population size over time is a major challenge for population genetics. Here we investigate some theoretical properties of random-mating populations with varying size over time.

In particular, we present an exact solution to compute the population size as a function of time, Ne(t), based on distributions of coalescent times of samples of any size. This result reduces the problem of population size inference to a problem of estimating coalescent time distributions.

To illustrate the analytic results, we design a heuristic method using a tree-inference algorithm and investigate simulated and empirical population-genetic data. We investigate the effects of a range of conditions associated with empirical data, for instance number of loci, sample size, mutation rate, and cryptic recombination.

We show that our approach performs well with genomic data (≥ 10,000 loci) and that increasing the sample size from 2 to 10 greatly improves the inference of Ne(t) whereas further increase in sample size results in modest improvements, even under a scenario of exponential growth. We also investigate the impact of recombination and characterize the potential biases in inference of Ne(t). The approach can handle large sample sizes and the computations are fast. We apply our method to human genomes from four populations and reconstruct population size profiles that are coherent with previous finds, including the Out-of-Africa bottleneck. Additionally, we uncover a potential difference in population size between African and non-African populations as early as 400 KYA.

In summary, we provide an analytic relationship between distributions of coalescent times and Ne(t), which can be incorporated into powerful approaches for inferring past population sizes from population-genomic data.

Inferring Past Effective Population Size from Distributions of Coalescent Times

Inferring and understanding changes in effective population size over time is a major challenge for population genetics. Here we investigate some theoretical properties of random-mating populations with varying size over time. In particular, we...

Swamidass (Dr. S Joshua Swamidass) 2018-02-07 05:19:50 UTC #488

@RichardBuggs thanks for your last post. I think you honed in on the point of confusion. Thanks for elucidating it.

> RichardBuggs:
>
> Thank you for your patience with me regarding Ne and ARGweaver. I think I have misunderstood something, and I am just having more of a think about this. As I go back over your posts, I am struck by how many times you have made the same point to me, without me really taking it on board:
>
> > That means the TMR4A (and all TMRCAs) are determined primarily using the formula: D = T * R, where D is mutational distance, T is time, and R is the mutation rate. That is the key determinants of the TMR4A.

You are right, that is the key point. I'm glad we are getting chance to explain it.

> RichardBuggs:
>
> What you seem to be saying is that they are simply taking a molecular clock approach to estimating TMRCA. Time is the number of differences divided by the mutation rate. They are building phylogenetic trees and dating them.

That is exactly right. That is what they are doing, with a few bells and whistles. Essentially, this is exactly what MrBayes does (**http://mrbayes.sourceforge.net/**), except that unlike MrBayes, ArgWeaver can handle recombination. Technically, it is constructing ARGs (ancestral recombination graphs), not phylogenetic trees. ARGs (of the sort argweaver computes) can be represented as sequential trees along the genome. That's convenient representation that is easier for most of us to wrap our heads around, but the actual entity it is constructing is that ARG.

> RichardBuggs:
>
> The reason why I have been so preoccupied with Ne is because I thought this was a coalescent analysis, where time to coalescence is proportional to effective population size.

Except, as you are coming to see, this is not a coalescence simulation at all.

To clarify for observers, there are three types of activities/programs relevant here.

1. ***Phylogenetic tree inference***. Starting DNA sequences -> find the best fitting phylogenetic tree (or ARGs when using recombination) -> assign mutations to legs of tree (or ARG) -> use #mutations to determine length of legs. (see for example MrBayes)

2. ***Coalescence simulation***. Starting from a known population history -> simulated phylogenetic trees (or ARGs when using recombination) -> simulated DNA sequences. (see for example ms, msms, and msprime)

3. ***Demographic history inference***. Many methods, but one common way is compute #1. Starting from DNA sequences -> Infer phylogenetic trees / args (task #1) -> compute the ***coalescent rate*** at time windows in the past -> Ne is the reciprocal of the coalescent rate. (see for example psmc and msmc).

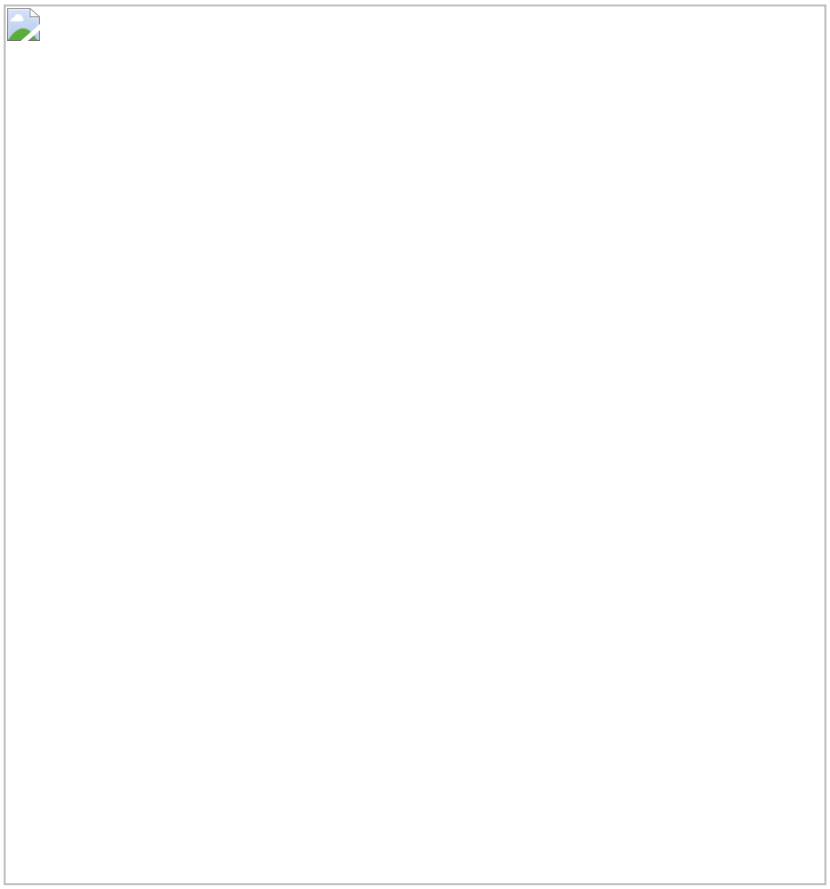
It seems that there was some confusion about what ArgWeaver was doing. Some people thought it was doing #2 or #3, but it is actually just doing #1. The confusion arose because it used a fixed Ne as parameter, which seemed only to make sense if it was doing #2, and might make its results suspect if it was doing #3. However, ArgWeaver was never designed to do #2 or #3. Instead, it is doing #1.

So what is the Ne for? One of the features of ArgWeaver is that it uses a prior, which is good statistical practice. They were using Ne to tune the shape of the prior, but ultimately this does not have a large effect on the trees. It's only important, in the end, when there is low amounts of data. As I've explained several times too, the prior they used pushed the TMR4A downwards from what the data showed too.

How This All Gets Confusing…

In defense of the confused, one of the confusing realities of population genetics is that the same quantities can be expressed in several different units. Often they are all used interchangeably without clear explanation, and its really up to the listener to sort out by context what is going on.

At the core of this is the units we choose to measure the lengths legs a phylogenetic tree. To help explain, let's go back to a figure from much earlier in the conversation:



http://www.genetics.org/content/172/2/1139.long2

.

In this figure, the dots are mutations assigned to legs in tree, the scale bar is in units of time (years in this case), and the leaves of the tree are observed DNA sequences obtained from actual humans. I've seen several units of tree length pop in this conversation and the literature…

1. Number of mutations (dots in figure, or D in my formula)

2. Years (scale bar in figure)
3. Generations (argweaver)
4. Coalescence units (number mutations / sequence length, or D in my formula)

A critical point it that the mutations are observed in the data, and the number along each leg is used to estimate the time. All these things are all just unit conversions, provided we clarify mutation rates, the length of the sequence, and (sometimes) generation time. So all these units are essentially interconvertible if we know the mutation rate. If we just express them as coalescence units or number of mutations, then they do not even require specifying a mutation rate and they are a fundamental property of the data itself.

Though, as we have discussed, we have reasonable estimates of mutation rates. For example, ArgWeaver uses a generation time of 25 years / generation, and a mutation rate of 1.25e-8 / bp / generation. This is equivalent to using a mutation rate of 0.5e-9 / bp / year.

Maximum Likelihood Estimation (MLE) of Lengths

One of the easiest ways to estimate a leg length is with a MLE estimate. Let's imagine we observer 10 mutations in a 10,000 bp block (or 1e4). For illustration, we can convert this to all the units we've mentioned, using the argweaver defaults.

1. 1e-3 coalescent units (or 10 mutations / 1e4 bp).
2. 2,000,000 years (1e-3 coalescent units / 0.5e-9 mutation rate per year)
3. 800,000 generations (1e-3 coalescent units / 1.25e-8 mutation rate per generation)

In actual trees, it is a little more complex, because some branch points have multiple legs. In these cases, we are going to average lengths computed across the data in each leg if we are building an *ultrametric* tree (distance from tip to each leaf is the same). In this application, the *ultrametric* constraint makes a lot of sense (because we all agree these alleles are related), and this gives a way to pool data together to get a higher confidence estimate that is not sensitive to population specific variation in mutation rates.

Nonetheless, these units are so trivially interchangeable, that they are not consistently used. While coalescence units is the most germaine to the data, it is also the most archain. So it is very common for programs to use different units to display results more understandably. Argweaver and msprime, for example, use "generations."

Maximum A Posteriori (MAP) Length

So MLE is great when we have lots of data, but it is very unstable when there is only small amounts of data.

1. For example, what if the number of bp we are looking at is really small, let's say exactly zero. In this case, what is the mutation rate? 0 mutations / 0 bp is undefined mathematically, and creates problems when taking recombination into account, some trees can end up having 0 bp spans in high recombination areas.

2. How about if the number of bp is just 100, and the observed mutations is zero. What is the mutation rate then? From the data we would say **zero**, but that's not true. We know it is low, but its not zero.

So how do we deal with these problems? **One way to solve this problem is to add a weak prior to the mutation rate computation.** There is a whole lot of math involved in doing this in a formal way (using a beta prior), but I'll show you a mathematically equivalent solution that uses something called pseudocounts.

With pseudocounts we preload the estimate with some fake data, pseudo data. If the mutation rate is 0.5e-9 / year and we think this leg should be about 10,000 years long, we can use this to make our fake data. In this case, we will say the fake data is a 100 bp stretch, where we observed 0.0005 mutations (100 * 10000 * 0.5e-9). This is fake data so we can make fractional observations like this. We choose 100 bp to make this easily overwhelmed by the actual data.

Now, we estimate the mutation rate by looking at the data + pseudo data, instead of the data alone. If, for example, we are looking at no data. We would end up with a length of 10,000 years instead of the nasty undefined 0/0 we get in the MLE. Likewise, if we look at a real tree over a 2,000 bp region where 3 mutations are observed.

1. We can make a MLE estimate of the length in coalescent units, at 0.0015 (or 3 / 2000), which is equivalent to 3 million years.
2. We can also make MAP estimate of its length (using our pseudo counts), at 0.001428 (or 3.0005 / 2100, which is equivalent to 2.8 million years)

There are a few observations to make about this example.

1. These numbers can be converted into other units as discussed above.

2. The MLE estimate and MAP estimate are pretty close. The more data there is, the closer they will be.

3. Even though our prior was 10,000 years, it's totally overwhelmed by the data in this case, to give an estimate of millions of years.

4. Only a few mutations is enough to increase the estimate of the length, which is why individual estimates have very high error (they will both be above and below the true value). We really need to see estimates from across the whole genome. NOnetheless, this example is not quite typical (just for illustration) and had 3 mutations in a tiny stretch of 2000 bp. That is a really high amount of mutations.

5. In the end, we want to choose a prior that will have little impact on the final results, but will help us in some of corner cases where things blow up in the MLE estimate. That is why were use a ***weak*** prior (low pseudocounts).

This is just an illustration, designed to be easy to understand without requiring statistical training. It is not precisely how argweaver works, for example, but is a very close theoretical analogy.

ArgWeaver Works Like MAP

ArgWeaver works very close to a MAP estimate. Our median TMR4A estimate is very much like a MAP estimate of TMR4A. What are the differences, however, with how ArgWeaver works from MAP…

1. ArgWeaver is not making a single MLE or MAP estimate (as described above). Instead, it is sampling ARGs based on fit to the data (likelihood) and the prior. This called Markov Chain Monte Carlo (MCMC) and is closely related to a MAP estimate when a prior is used in sampling (as it is here).

2. ArgWeaver prior is not implemented using pseudo counts, instead they are using an explicit prior distribution. Using a prior distribution (rather than psuedocounts) is the preferred way of doing this, as it is less *ad hoc*, more flexible, has clear theoretical justification, and clarifies upfront the starting point of the algorithm.

3. The ArgWeaver prior does not use a fixed time (we used 10,000 years above), but a range of times. This is how the Ne comes in. They use the distribution of times expected from a fixed population of 11,534. I have no idea why the chose such a specific number.

4. The ArgWeaver prior is on the time of coalescence, not the length of a leg in the tree. This is subtle distinction, but the TMR4A is actually the sum of several legs in the tree. The prior ArgWeaver uses says that we expect (not having looked at data) for that TMR4A time (which is a sum of leg lengths in the tree) to be at about 100 kya. As implemented, it's a weak prior, and is overwhelmed by the data. Ultimately, the tree lengths computed in the by ArgWeaver are not strongly influenced by the prior.

5. Though I have explained this as actions on trees, ArgWeaver is applying this to branch lengths on the ARGs (the ancestral recombination graph). This is important because ARGs end up using more information (larger lengths of sequences) to estimate the length than naively trying to estimate phylogenetic branch lengths independently

for each tree. The trees we have been using are an alternative representation of an ARG that is less efficient, but easier to use for many purposes (like estimating TMR4A).

In the end, to ease interpretation, ArgWeaver reports results in “generations” but its converting using the equations I’ve already given. So we can easily convert back and forth into any of these units. Most importantly, at its core, we are just using the fundamental formula:

```
D = R * T
```

Mutational distance is the product of mutational rate and time. That’s all that is here. That is what enables the conversions. The fact that argweaver makes the surprising decision to use Ne to parameterize its weak prior is just a non issue. As I have explained, the prior it uses for TMR4A is lower than TMR4A, so it’s just pulling the estimate down any ways. Getting rid of it will only increase the estimate (only a small amount). MAP estimates, also, are considered vastly superior to MLE estimates, so it just makes no sense to doubt this result for using a better statistical technique.

A Prior Is Not an Assumption

It should be clear now why it is just incorrect (despite that footnote in the paper) to call a prior an assumption. It is also incorrect to say that argweaver is “simulating” a large population. All it is doing is using a *weak* prior on the tree lengths, and that is a good thing for it to do that makes the results more stable.

As an aside, the language of prior and posterior is chosen intentionally. The terms are defined in relation to taking the data into account. In Bayesian analysis, the prior is updated by the data into the posterior. Then, the posterior becomes the new prior. We can then look at new data, to update it again. So priors, by definition, are not assumptions. They are starting beliefs that are updated and improved as we look at more data. It is just an error to call them assumptions.

Okay, I know that is a lot, but I figure that some people will find this useful. This is a good illustrative case of the fundamentals of Bayesian analysis. While the rigorous treatment requires a lot of math, this should give enough for most observers to follow what is going on here.

Chris_Falter (Chris Falter) 2018-02-07 06:25:02 UTC #489

My favorite post ever! Thanks a gazillion for taking the time to explain the analysis so clearly.

DennisVenema (Dennis Venema) 2018-02-07 06:52:42 UTC #490

Agreed. Thanks, **@Swamidass** !

RichardBuggs (Richard Buggs) 2018-02-07 22:03:35 UTC #491

Thank you Joshua **@swamidass** for such a clear explanation. I am very glad to have got to the bottom of where I was misunderstanding the ARGweaver paper. I will have to have a bit of a think now about what this means for the various critiques I was offering before.

---

gbrooks9 (George Brooks) 2018-02-07 23:28:10 UTC #492

> Chris_Falter:
>
> My favorite post ever! Thanks a gazillion for taking the time to explain the analysis so clearly.

Swami's posting … link below… is now for the history books:

Posting 481 in Thread 37039 !

> Swamidass:
>
> @RichardBuggs thanks for your last post. I think you honed in on the point of confusion. Thanks for elucidating it. You are right, that is the key point. I'm glad we are getting chance to explain it. That is exactly right. That is what they are doing, with a few bells and whistles. Essentially, this is exactly what MrBayes does (http://mrbayes.sourceforge.net/), except that unlike MrBayes, ArgWeaver can handle recombination. Technically, it is constructing ARGs (ancestral recombination graph…

Swamidass (Dr. S Joshua Swamidass) 2018-02-08 05:50:25 UTC #493

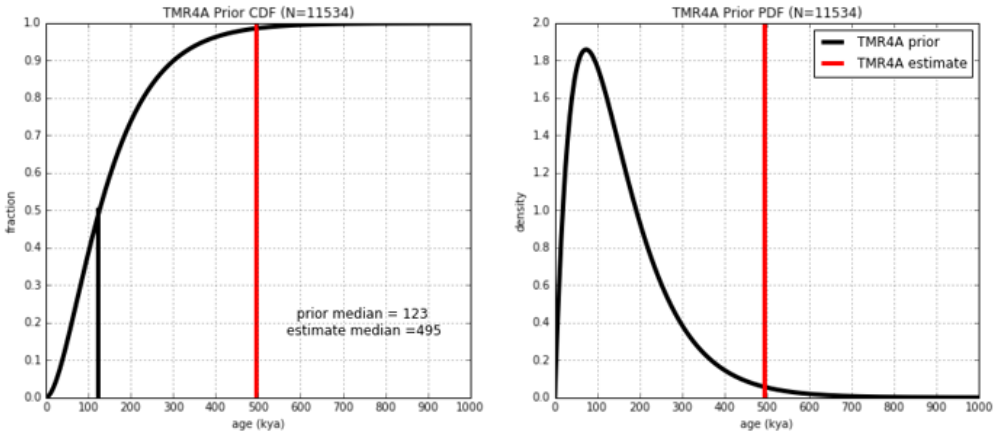
Hello all. When I make mistakes, I like to correct them as quick as possible, even if they do not have an impact on my overall point. I try to do so quickly, but please do keep in mind that this is not my real job. I do this on the side to serve everyone that cares about these questions. So, unfortunately, sometimes it takes me a bit longer then I'd prefer.

Fixing the Prior

For a while, I had been saying that the ArgWeaver prior was using a Ne = 10,000, leading to a prior TMR4A of 100 kya. That turns out not to be precisely correct. Instead…

> Swamidass:
>
> They use the distribution of times expected from a fixed population of 11,534.

This was pointed out to me in private a couple weeks ago, and since then I have been able to confirm it. So some of my earlier figures (and statements) were not precisely correct. The median of the prior of TMR4A is 123 kya, and the median estimate (the posterior) of TMR4A is 495 kya. You can see the figure below.



> Swamidass:
>
> In Bayesian analysis, the prior is updated by the data into the posterior. Then, the posterior becomes the new prior. We can then look at new data, to update it again. So priors, by definition, are not assumptions. They are starting beliefs that are updated and improved as we look at more data.

So the prior is 123 kya for TMR4A, but the data updates this posterior to 495 kya. Does this change affect any of my key points? Not that I can see. Still I did want to make the correction. I wish I had enough time for this to have retracted it sooner.

About Retractions in Science

One of the counterintuitive things about science is that we respect those who retract their errors quickly. Scientific work is difficult, and we know firsthand that even the best of us make mistakes. Though our instinct is to never admit mistakes, we really reward scientists that admit their mistakes.

As surprising as this may be, I'm not sure BioLogos as an organization is accustomed to this part of scientific culture. It is a very non-intuitive thing. Making a retraction ultimately increases our reputation. I do hope that, given what we are doing here, that some thought will be given to retracting statements that have gone beyond the evidence.

I think, for example, that there is a "Part 3" of **@DennisVenema** 's response to **@RichardBuggs** scheduled. It's curious that it has not yet been published. I'm hopeful that figuring out the right way to do this (and perhaps getting it approved) is why it has been delayed. That would be a very good thing, and a great outcome of this conversation. If that is what happens, eventually, it's important to remember that the best scientists make retractions, it is one of the ways we recognize honestly, and it's something worth respecting.

DennisVenema (Dennis Venema) 2018-02-08 06:07:36 UTC #494

> Swamidass:
>
> I think, for example, that there is a "Part 3" of **@DennisVenema** 's response to **@RichardBuggs** scheduled. It's curious that it has not yet been published. I'm hopeful that figuring out the right way to do this (and perhaps getting it approved) is why it has been delayed.

It's been delayed because I've been working with Charles Cole - the person that **@RichardBuggs** cited regarding PSMC modelling - to use PSMC models to directly test Richard's hypothesis as best we can. Charles has been busy, I've been busy, the modelling wasn't straightforward, and it'll be a bit yet before I've got it together. I'll probably invite **@Swamidass** and **@RichardBuggs** to look over the data before putting the post up so we can perhaps put our heads together on it. I'm hoping Cole will also join us here for that discussion. It should be interesting. Intuitively, one would think that PSMC modelling should see something if Ne went to 2 - but testing is better than intuition.

I also think we've reached a point in the conversation where the evidence is solidly showing to **@RichardBuggs** 's satisfaction that we can reasonably exclude a bottleneck to 2 in the last 350,000 years - am I correct there, Richard? If so, that pretty much means that we are in agreement. My certainty level in Adam and the Genome was only to 200,000 years ago, though I've said that I'm ok pushing that back to 300,000 plus or minus. This is of course excluding interbreeding with Neanderthals and Denisovans. **@Swamidass** , as I mentioned to you via PM, I'm really talking about ancestors to present-day sub-saharan Africans over this timeframe. Any species definition is going to break down, especially with hybridization going on. Once we include hybridization, we're back past 500,000 years as far as I can see.

Thanks again for your really nice exposition of the Argweaver paper. Kudos. I don't know that I'll actually do anything on LD - I think the argweaver paper more or less covers that territory better. I think the next part will be the PSMC results and we'll leave it at that.

Swamidass (Dr. S Joshua Swamidass) 2018-02-08 16:54:53 UTC #495

@DennisVenema I'll take this as your version of a retraction.

You made two claims, both of which you have backed off of in this post. That is good news, and should be received as such.

Claim 1: Homo sapiens never go to a single couple

> 1. Homo sapiens specifically do not dip down to a single couple in 300 kya to the confidence we have in **heliocentrism**.

But population size estimates are always of Homo sapiens + all of our other ancestors at the time. The finding that our ancestors do not go to a single couple tells us nothing about Homo sapiens specifically, because Homo sapiens are not our only ancestors past about 50 kya.

The Ecological Fallacy.: *Homo sapiens* go to zero, so why couldn't they go to two?

Now, as you explain here…

> DennisVenema:
>
> My certainty level in Adam and the Genome was only to 200,000 years ago, though I've said that I'm ok pushing that back to 300,000 plus or minus. This is of course excluding interbreeding with Neanderthals and Denisovans. **@Swamidass** , as I mentioned to you via PM, I'm really talking about ancestors to present-day sub-saharan Africans over this timeframe. Any species definition is going to break down, especially with hybridization going on.

Which seems like a long way of saying that you cannot demonstrate with heliocentric certainty that Homo sapiens never go to a single couple. After all, they go to zero, so they might very well start with a single couple by some definitions.

That is a pretty important concession, as claims of heliocentric certainty really seem to have provoked the whole debate in the first place. It looks like you have backed of that claim, because you cannot defend it.

Claim 2: Our ancestors never go to a single couple after 3 mya.

> 2. Our ancestors as a whole do not dip down to a single couple between 300 kya and 3 mya with very high confidence, but maybe not as high.

That is a bit of a soft pedal too, because at times you have made the claim they never go to a single couple since well before they diverged from chimpanzees. However, now…

> DennisVenema:
>
> It's been delayed because I've been working with Charles Cole - the person that **@RichardBuggs** cited regarding PSMC modelling - to use PSMC models to directly test Richard's hypothesis as best we can. Charles has been busy, I've been busy, the modelling wasn't straightforward, and it'll be a bit yet before I've got it together. I'll probably invite **@Swamidass** and **@RichardBuggs** to look over the data before putting the post up so we can perhaps put our heads together on it. I'm hoping Cole will also join us here for that discussion. It should be interesting. Intuitively, one would think that PSMC modelling should see something if Ne went to 2 - but testing is better than intuition.

That is really excellent that you are doing this. I shows a sensitivity to the question and a desire go engage the data. I think this is a really important effort, and I'll look forward to seeing the results. Of course, its on my to-do list too, so we'll

see who finishes it first.

However, that study is also an admission that you are going of instinct, not settled scientific work. Given that the TMRCA for humans is about 1.8 million, we just do not expect that anything based on coalescence inference like PSMC or MSMC will be able to detect a couple after 1.8 million, which is clearly before 3 million, and also well after Homo erectus arises: the first “human” as understood by **@agauger** . Maybe there will be a surprise here, but it seems that this claim too is ending up unsubstantiated.

The fact that new research is being commissioned is a good thing, but it also makes clear that we are at the frontiers of scientific inquiry, not established scientific findings. Clearly, a mistake was make when instincts about this frontier were presented as settled scientific findings.

Retractions are Good

So, of course, it is a good thing that the original claims are being walked back. It would better to acknowledge the mistake more clearly, because I think that **@RichardBuggs** deserves some credit here. Though it took some help from me to make the case, his instincts on the big points appears to have been borne out. Honestly, it is not what I expected. **@RichardBuggs** deserves some credit for helping us see this more clearly.

What about Tran-species Variation?

This might seem preemptive, in light of additional data (e.g. HLA haplotypes), to observers. However, there has been substantial behind the scenes conversation that shows that this is not nearly as strong evidence as I first thought. At this point, we may have to just take my word for it. Hopefully, we will get a chance to get into it. Of course, if my assessment (totally unjustified right now) ends up being wrong, its possible that Dennis might gain some ground on claim 2.

DennisVenema (Dennis Venema) 2018-02-08 17:10:50 UTC #496

> Swamidass:
>
> **@RichardBuggs** deserves some credit for helping us see this more clearly.

I would certainly agree with this. This whole conversation has been very helpful and has increased my understanding of this area, to be sure. Richard’s questions and contributions have been a significant part of that, so credit where credit is due.

I do think Richard is being a bit too skeptical, though. Perhaps he can clarify - he seems to be looking for any possible reason to doubt the evidence - even going back to his final replies to **@glipsnort** about the allele frequency spectrum. He also seems to be doing the same sort of thing with your discussion of the Argweaver paper - I just don’t see how the Lenski work relates to that at all. I’m all for critical thinking and skepticism, but there comes a point where it looks like a duck and quacks like a duck. I haven’t even yet seen **@RichardBuggs** say that he’s in agreement with no bottleneck to 2 in the last 300-350KYA - but I might have missed it. Are we in agreement, Richard?

The next thing to consider, in my mind, is how reasonable Richard’s proposed bottleneck is (biologically - not really thinking theology here, but that’s an issue too). A population drop from ~10,000 down to 2 in a single generation followed by exponential population growth - how exactly did this happen? I can’t think of a reasonable biological explanation for this. Our lineage was widely dispersed in Africa at the proposed time of this event - what happened to wipe all of them out but just two? Richard - thoughts?

Jonathan_Burke (Jon) 2018-02-08 17:22:22 UTC #497

> Swamidass:
>
> Which seems like a long way of saying that you cannot demonstrate with heliocentric certainty that Homo sapiens never go to a single couple. After all, they go to zero, so they might very well start with a single couple by some definitions.

Are there any published studies which say homo sapiens emerged from a single couple rather than emerging from a population? Thus far I have seen no evidence to contradict the statement that “Homo sapiens specifically do not dip down to a single couple in 300 kya to the confidence we have in heliocentrism”. All I’ve seen in response is “Well maybe it happened but it did so in a special way which left absolutely no evidence and is totally undetectable”. That’s just YEC reasoning, like the idea that God did a big “cleanup” after the flood to remove all the evidence of meteors and volcanoes and comets and other silly ideas.

Swamidass (Dr. S Joshua Swamidass) 2018-02-08 17:25:26 UTC #498

> Jonathan_Burke:
>
> Are there any published studies which say homo sapiens emerged from a single couple rather than emerging from a population? Thus far I have seen no evidence to contradict the statement that “Homo sapiens specifically do not dip down to a single couple in 300 kya to the confidence we have in heliocentrism”. All I’ve seen in response is “Well maybe it happened but it did so in a special way which left absolutely no evidence and is totally undetectable”. That’s just YEC reasoning, like the idea that God did a big “cleanup” after the flood to remove all the evidence of meteors and volcanoes and comets and other silly ideas.

@DennisVenema do you agree with **@Jonathan_Burke** on this assessment?

If we are so certain that it did not happen, why can no evidence be marshaled in support of the claim?

Jonathan_Burke (Jon) 2018-02-08 17:28:29 UTC #499

> Swamidass:
>
> If we are so certain that it did not happen, why can no evidence be marshaled in support of the claim?

Actually my statement was aimed at your claim, not his. You seem to be the one saying “Well maybe a recent homo sapiens bottleneck did happen but it did so in a special way which left absolutely no evidence and is totally undetectable”. In terms of evidence, all the genetic population studies (including your own), seem to demonstrate repeatedly that there’s no evidence for such a bottleneck even when testing specifically and robustly for such a bottleneck.

Additionally, you keep saying that since the homo sapiens population was zero at one point, it might very well have been a single couple at one point. I don’t understand the reasoning for this.

Christy (Christy Hemphill) 2018-02-08 17:41:16 UTC #500

> Jonathan_Burke:

> Additionally, you keep saying that since the homo sapiens population was zero at one point, it might very well have been a single couple at one point. I don't understand the reasoning for this.

I don't understand this either. If the boundary lines between species are fluid, it is populations that get designated a divergent species, not individuals. Using the language analogy, you could never identify the "first couple who spoke French." It would be a whole population that would be called French speakers that diverged at some point from the ancestral Latin form that became French over time. The only way I can imagine a population of two homo sapiens is if the rest of the homo sapiens (or whichever species we are talking about) got killed off somehow, not as two special individuals emerging from a population of non-homo sapiens.

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gbrooks9 (George Brooks) 2018-02-08 17:50:00 UTC #501

> DennisVenema:
>
> A population drop from ~10,000 down to 2 in a single generation followed by exponential population growth - how exactly did this happen? I can't think of a reasonable biological explanation for this. Our lineage was widely dispersed in Africa at the proposed time of this event - what happened to wipe all of them out but just two? Richard - thoughts?

@DennisVenema I believe the YEC position is that God could have arranged for Adam and Eve to have the diversity **as if** they were the only survivors of a 10,000 population. We could even **also** assume that God made the pair to genetically emulate the result of surviving a 10 million population, right?

But does this really change things much? Isn't there a point in the curve where it really doesn't matter how big the "hypothetical prior population" is? There is only room for a certain number of alleles… so maybe even 10,000 is well past that point in the curve?

Jonathan_Burke (Jon) 2018-02-08 17:50:14 UTC #502

> Christy:
>
> Using the language analogy, you could never identify the "first couple who spoke French." It would be a whole population that would be called French speakers that diverged at some point from the ancestral Latin form that became French over time.

That is exactly why I find this fixation on the idea that homo sapiens emerged as a single couple so odd. The language analogy is widely used to explain the non-intuitive idea that homo sapiens **did not** emerge as a single couple. The only reason I can see for insisting on a single couple origin of homo sapiens, is theological; specifically to give the YECs a foot in the door and to imply that they can legitimately oppose evolution.

---

gbrooks9 (George Brooks) 2018-02-08 17:52:25 UTC #503

> Jonathan_Burke:
>
> The language analogy is widely used to explain the non-intuitive idea that homo sapiens did not emerge as a single couple. The only reason I can see for insisting on a single couple origin of homo sapiens, is theological;

Yep… this is what it look like.

But I don't think 10,000 or 10,000,000,000 is going to change things much.

Jay313 (Jay Johnson) 2018-02-08 18:02:09 UTC #504

> DennisVenema:
>
> A population drop from ~10,000 down to 2 in a single generation followed by exponential population growth - how exactly did this happen? I can't think of a reasonable biological explanation for this. Our lineage was widely dispersed in Africa at the proposed time of this event - what happened to wipe all of them out but just two?

Exactly. There is the Toba super-eruption during the timeframe of the previously calculated bottlenecks associated with the Out of Africa event. In the case of a bottleneck to two, we are talking about an extinction-level event that would have to wipe out all other hominins except for one breeding couple. Is there anything comparable to Toba that would account for this? Even if one held to the *de novo* creation of Adam & Eve, we are still talking about all other hominin species suddenly going extinct, and then God presumably "starting over" with A&E. Is there any evidence of such a cataclysmic event?

Jonathan_Burke (Jon) 2018-02-08 18:06:15 UTC #505

> Jay313:
>
> Is there any evidence of such a cataclysmic event?

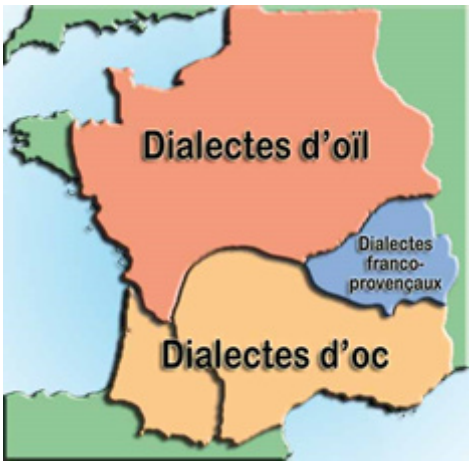
Of course there is, the Genesis flood!

AMWolfe (A.M. Wolfe) 2018-02-08 18:55:16 UTC #506

> Christy:
>
> I don't understand this either. If the boundary lines between species are fluid, it is populations that get designated a divergent species, not individuals. Using the language analogy, you could never identify the "first couple who spoke French." It would be a whole population that would be called French speakers that diverged at some point from the ancestral Latin form that became French over time. The only way I can imagine a population of two homo sapiens is if the rest of the homo sapiens (or whichever species we are talking about) got killed off somehow, not as two special individuals emerging from a population of non-homo sapiens.

It's interesting to think about this, though.

I mean, I agree. But suppose you had a particular shibboleth that was thought to be The Indicator for the French language — say, the use of "oui" versus the use of "òc", from which we get "**Languedoc**." This is the most widely known difference separating French from the Occitan language. (Anyone interested can see the subsection "History of the Modern Term" at the Languedoc Wikipedia link.)



So, from a certain popular perspective, could not the first person to say *oui*, back when it was still pronounced *oïl*, be thought of as the "first French speaker"?

Of course, it's not at all scientific, because [1] there are lots of differences between French and Occitan, [2] the language, and indeed even the specific use of *oïl*, really did evolve in a speech community, [3] the difference actually started as a difference in saying 'yes' between Latin *hoc* (this) and Latin *hoc illud* (this [is] it), which then evolved into *oïl*, and [4] the difference was only recognized in retrospect, by Dante in the 13th century, not precisely when it first happened.

But I wonder if a parallel here could be drawn, particularly if (as **@swamidass** has been urging) we allow for some fluidity between the biological definition of *H. sapiens* and the theological definition of Adamic human. Couldn't one imagine Adamic humanity as the origin of one particular indicator (or cluster of indicators) of what makes us "human"?

Of course, playing the devil's advocate against myself, I have to ask myself whether such philosophical gymnastics are actually useful or just trifling.

Swamidass (Dr. S Joshua Swamidass) 2018-02-08 21:12:07 UTC #507

@DennisVenema claimed in his book…

> DennisVenema:
>
> As our methodology becomes more sophisticated and more data are examined, we will likely further refine our estimates in the future. That said, **we can be confident** that **finding evidence** that we were created independently of other animals or **that we descend from only two people just isn't going to happen**. Some ideas in science are so well supported that it is highly unlikely new evidence will substantially modify them, and these are among them. The **sun is at the center of our solar system**, humans evolved, and we evolved as a population."

First, this statement was shown to be incorrect by genealogical science. That was want our dust up was last June. Good news too, the PSCF article showing this mistake **@DennisVenema** made is in press, and BioLogos even endorsed the science behind it as correct. It turns out that we do all descent from individual couples. **@DennisVenema** Did not clarify that in his book, and this is material to the conversation. This is an unintentional error **at best**, and intentionally misleading at worst.

Leaving that aside, let's look at how he clarified what he meant by this block of text. He first clarified that by "human" he means Homo sapien. So its claims here are meant to be understood as…

> 1. ***Homo sapiens*** specifically do not dip down to a single couple in 300 kya to the confidence we have in **heliocentrism**.

We came to understand this from asking him to clarify his statements in the book. He agreed that this is what he meant and we moved forward from it. Then it became clear that this is false. Let me give several reasons why.

Dennis No Longer Defends It

First off, it is notable that since January 1, **@DennisVenema** has no longer defended this claim. That is because, it seems, he has been convinced it is indefensible. Yes, others have leapt to his defense, but notice that he is not offering his agreement.

If he meant something different, of course, he should clarify his earlier statements. If he still has heliocentric certainty that original claim is correct, he can certainly offer evidence. Since Jan 1, however, he has not done this. Rather than trying to defend him, it's worth asking him to explain his process on this.

In the end, its not terribly clear to observers, but I think this is **@DennisVenema** 's way of retracting things. I give him credit for backing of his clearly false claim, but its not fair to everyone else if they do not recognize it for what it is. Of course, if I'm misreading this, I welcome **@DennisVenema** to make the case.

The Claim Relies on a Logical Error

However, it would not be wise to defend that claim. It relies on a clear logical error. Let us grant everyone for a moment that we have high certainty from genetics that…

> 1. ***Our ancestors*** do not dip down to a single couple in the last 300 kya.

I understand some may dispute this (not sure how), but lets just all concede this point for the purpose of understanding the logical flaw. This finding in population is NOT equivalent to…

> 2. **Humans** do not dip down to a single couple in the last 300 kya.

Moreover, it is NOT equivalent to…

> 3. ***Homo sapiens*** do not dip down to a single couple in the last 300 kya.

One logical level, #1 can only be offered as support for #2 if "our ancestors" = "human". If ***any*** of our ancestors during this time are not "human," than #2 does not follow from #1. Even if #2 is true, #1 is not evidence of #2. **Likewise**, #1 can only be offered as support for #3 if "*Homo sapiens*" = "our ancestors." If ***any*** of our ancestors during this time are not *Homo sapiens*, then #3 does not follow from #1. Even if #3 is true, #1 is not evidence of #3.

That is the logical error. We cannot substitute "our ancestors" for "human" or "Homo sapiens" as **@DennisVenema** does.

It's Self-Contradictory

If we knew **@DennisVenema** 's claim with heliocentric certainty, we would not be able to produce multiple counter examples that (1) contradict his statement, and (2) are 100% consistent with the data. Yet that is exactly the case we have. This partly because **@DennisVenema** himself agrees that:

1. Our ancestors != human alone. He agrees that our ancestors = humans + others. For this reason, we can imagine several scenarios where the number of “humans” dips down to zero. In fact, Dennis himself subscribes to one of these scenarios. If we think there are ZERO “humans” at 300 kya, it is self-contradictory to claim that “humans” never dip below a few thousand. The two claims are in contradiction with each other, so we know one must be false.

2. Our ancestors != Homo sapiens alone. He agrees that ancestors = Homo sapiens + others. The same logic applies. If we think there are ZERO *Homo sapiens* at 300 kya, it is self-contradictory to claim that *Homo sapiens* never dip below a few thousand. The two claims are in contradiction with each other, so we know one must be false.

We know exactly which one is false too. Its the claim that **@DennisVenema** makes, which is just not substantiated. We cannot use “our ancestors” and “human” and “Homo sapiens” interchangeably. That was the source of the error.

> Jonathan_Burke:
>
> Additionally, you keep saying that since the homo sapiens population was zero at one point, it might very well have been a single couple at one point. I don’t understand the reasoning for this.

The reasoning is that self-contradictory positions are false.

What “Really” Happened Is Beside the Point

> DennisVenema:
>
> The next thing to consider, in my mind, is how reasonable Richard’s proposed bottleneck is (biologically - not really thinking theology here, but that’s an issue too). A population drop from ~10,000 down to 2 in a single generation followed by exponential population growth - how exactly did this happen? I can’t think of a reasonable biological explanation for this. Our lineage was widely dispersed in Africa at the proposed time of this event - what happened to wipe all of them out but just two? Richard - thoughts?

First off, there are both theological and scientific reasons to wonder if we begin as a single couple. I’m not going to elaborate this, because it will be more fun to let it play out of time. Also, it’s probably worth a publication in its own right, and I do not want to scoop myself. For the curious wanting a hint, you can wonder about “grasshoppers.”

Second, this is all really beside the point. We are not arguing about what really happened, but whether **@DennisVenema** ’s representation of the scientific evidence is accurate. He had heliocentric certainty in a statement cannot be substantiated (whether or not it’s true). It’s a separate question entirely whether this is what really happened or not. **@DennisVenema** ’s conclusion might be ultimately right, but currently his argument for this conclusion has not been sustainable.

Where Confusion Lies

> Christy:
>
> I don’t understand this either. If the boundary lines between species are fluid, it is populations that get designated a divergent species, not individuals. Using the language analogy, you **could never identify** the “first couple who spoke French.”

Just because we could never identify who is the first could who spoke French does not mean that French (by some definition) does not begin with a single couple. As is well put…

> AMWolfe:
>
> So, from a certain popular perspective, could not the first person to say oui, back when it was still pronounced oïl, be thought of as the “first French speaker”?

So we can imagine a context were a specific definition of French could plausibly lead to a “first speaker” of French. Of course, we do not need to specifically ***identify*** this first speaker to posit that he or she exists. In fact, if such a person existed, we do not expect to identify him.

To flesh out the analogy, here are several possibilities regarding “humans” (none of which I will defend as normatively correct).

1. Perhaps “humans” are those with eternal souls, and are ***defined*** as such.
2. Perhaps “humans” are those given the divine appointment to represent God on earth, and are ***defined*** as such.
3. Perhaps “humans” are those with knowledge of God, and are ***defined*** as such.
4. Perhaps “humans” are the genealogical descendents of a specific single couple, and are ***defined*** as such.

In all these cases, it is possible that “humans” arise as a single couple. In the third case, it is ***guaranteed*** they arise as a single couple. A similar case can be made for the taxonomic category *Homo sapiens* on biological characteristics or (much easier) on behavior. In the end, it comes down to the fact that we just because thing are blurry from a distance does not mean there was never theological (or taxonomical) distinctions up close. It’s a grand leap to jump from one to the other.

Where We Are Now

Well, like I said about retractions…

> Swamidass:
>
> As surprising as this may be, I’m not sure BioLogos as an organization is accustomed to this part of scientific culture. It is a very non-intuitive thing. Making a retraction ultimately increases our reputation. I do hope that, given what we are doing here, that some thought will be given to retracting statements that have gone beyond the evidence.

However, it does seem that this claim of heliocentric certainty is not sustainable. Case in point, **@DennisVenema** is no longer making the claim. That is a good thing. Given that he has backed away from it, perhaps it’s a good moment for the rest of us to back away from it too.

Swamidass (Dr. S Joshua Swamidass) 2018-02-08 21:32:20 UTC #508

@RichardBuggs I think **@DennisVenema** makes a fair point.

> DennisVenema:
>
> I do think Richard is being a bit too skeptical, though. Perhaps he can clarify - he seems to be looking for any possible reason to doubt the evidence - even going back to his final replies to **@glipsnort** about the allele frequency spectrum. He also seems to be doing the same sort of thing with your discussion of the Argweaver paper - I just don’t see how the Lenski work relates to that at all. I’m all for critical thinking and skepticism, but there

> comes a point where it looks like a duck and quacks like a duck. I haven't even yet seen **@RichardBuggs** say that he's in agreement with no bottleneck to 2 in the last 300-350KYA - but I might have missed it. Are we in agreement, Richard?

As I understand it, you are rethinking much of this…

> RichardBuggs:
>
> Thank you Joshua **@swamidass** for such a clear explanation. I am very glad to have got to the bottom of where I was misunderstanding the ARGweaver paper. I will have to have a bit of a think now about what this means for the various critiques I was offering before.

As I understand it, you are trying to pressure test any claims being made. I can appreciate that, and am fine with that. At the same time, I think it is important to be honest with the Church about what the evidence appears to show, at least at this point in the conversation.

So I do hope that you can, after contemplation, agree that…

> Swamidass:
>
> I think it's fair to say at this point that I did rigorously test the bottleneck hypothesis. Right?
>
> Perhaps there will be improved follow on analysis that will refine my estimates, and I encourage that. However, TMR4A is a feature of the data. It is the length (in units of time, computed by mutational length / mutation rate) of the most parsimonious trees of genome wide human variation. This is not an artifact of a population genetics modeling effort. Rather, it is a way of computing the time required to produce the amount of variation we see in human genetics.
>
> Also, this analysis is very generous to to the bottleneck hypothesis. Though I'm not certain yet (and plan to do the studies to find out), bottlenecks going back as far as 800 kya might be inconsistent with the data we see. There are some large unresolved questions about how a bottleneck effects coalescence rate signatures before the median TMR4A, and if they are detectable.
>
> I hope there can be some agreements on these points, as a conclusion to this portion of the conversation would be valuable. It would be great to move on to more interesting data.

Jonathan_Burke (Jon) 2018-02-08 21:52:56 UTC #509

> Swamidass:
>
> Moreover, it is NOT equivalent to…
>
> Homo sapiens do not dip down to a single couple in the last 300 kya.

But this is precisely the question that I am interested in, regardless of Dennis never meaning it. I want to know about our homo sapiens ancestors. Otherwise this has absolutely no relevance to the issue of Adam and Eve at all.

All I have seen from your own scientific bottleneck testing is that there's no bottleneck going back even 500,000 years which could remotely be identified as evidence that either homo sapiens or our ancestors were bottlenecked down to a single pair.

> Swamidass:
>
> The reasoning is that self-contradictory positions are false.

I don't see how this establishes your claim.

> Swamidass:
>
> Just because we could never identify who is the first could who spoke French does not mean that French (by some definition) does not begin with a single couple.

But it's incredibly unlikely that it was only one person who started it; it was more likely to be a group of people. I just don't find other scientists saying what you're saying. I find them saying things like "**There was no first human**". And they say things like **this**.

> The first thing you see is obvious: our ancestors went through two different phases of population "bottlenecking" (constriction): one occurred about three million years ago, when a large population declined to around 10,000 individuals. The authors note that while this may reflect population size decline associated with the origin of hominins after our split with the lineage that produced modern chimps, they also say that this could be an artifact of ancient genetic polymorphisms maintained by natural selection.
>
> The second bottleneck is the one of interest, for it's the one associated with a reduced population size as humans left Africa. For the Chinese, Korean, and European genomes, effective population size fell from about 13,500 (at 150,000 years ago) to about 1200 between 20,000 and 40,000 years ago. Now this is the effective population size, almost certainly an underestimate of census size, but that only makes the problem worse: we never went through a bottleneck of anything near two individuals, as the Biblical Adam-and-Eve story suggests. This, of course, means that theologians have to scramble to save that story, turning it, as always, into a "metaphor". (In science, a falsified hypothesis gets tossed on the scrap heap; in religion, a falsified hypothesis becomes a metaphor.) And it also suggests that Jesus died for that metaphor.
>
> But enough of Biblical exegesis. While the bottleneck for non-European populations was probably associated with a group leaving Africa and subsequently colonizing the world, we also see a somewhat less severe bottleneck in the African samples: from about 16,100 people about 100,000-150,000 years ago to 5,700 about 50,000 years ago. It's not clear why the populations in Africa bottlenecked as well.

Jay313 (Jay Johnson) 2018-02-08 22:22:20 UTC #510

> Swamidass:
>
> **First, this statement was shown to be incorrect by genealogical science.** That was want our dust up was last June. Good news too, the PSCF article showing this mistake **@DennisVenema** made is in press, and BioLogos even endorsed the science behind it as correct. It turns out that we do all descent from individual couples. **@DennisVenema** **Did not clarify that in his book, and this is material to the conversation. This is an unintentional error at best, and intentionally misleading at worst.** (emphasis added)

Sorry, but this makes no sense. *Adam & the Genome* was published in Jan. 2017. You first published something on "genealogical science" on your blog in April 2017. How, exactly, did you expect Dennis to take into account a "discovery" that was still four months away from being published? And to imply that it might have been a case of "intentionally misleading" people is just irresponsible, unless you think that somehow Dennis had advance knowledge of

what you might publish about “genealogical science” back in 2016, but he intentionally choose to conceal his knowledge of the future from the rest of us.

Swamidass (Dr. S Joshua Swamidass) 2018-02-08 22:26:14 UTC #511

> Jay313:
>
> Sorry, but this makes no sense. Adam & the Genome was published in Jan. 2017. You first published something on “genealogical science” on your blog in April 2017. How, exactly, did you expect Dennis to take into account a “discovery” that was still four months away from being published?

Thanks for asking to clarifying this point.

> Jay313:
>
> you think that somehow Dennis had advance knowledge of what you might publish about “genealogical science” back in 2016, but he intentionally choose to conceal his knowledge of the future from the rest of us.

@DennisVenema ***did*** have advanced knowledge. He claims to have known about this for years (since graduate school), and the two of us had discussed this several times over 2016. In 2017, I was honestly surprised that he had not included in *Adam and the Genome*.

Regardless, let me be clear that **I do NOT think he was being *intentionally* misleading**. I think he did not understand that significance to the conversation. So it is better understood as an ***unintentional error*** to omit this. The error was in being imprecise in his language, and not realizing how some people would find this important. A lot of people made the same mistake. **@DennisVenema** is not unique here, and he certainly is not to blame any more than everyone else who did the same over the last couple decades.

Swamidass (Dr. S Joshua Swamidass) 2018-02-08 23:04:41 UTC #512

> Jonathan_Burke:
>
> I find them saying things like “There was no first human”. And they say things like this.

Yes, that is correct. Jerry Coyne makes illogical statements, and random youtubers misunderstand science. This is a widespread misunderstanding. Even many scientists are making these logical errors. No big surprise there.

That is the great thing about science though; its self correcting, and scientists themselves are not the ones having a problem with what I am saying. I’ve made the case, and its correct. In the end, appeals to what others are saying are an ineffective rebuttal when clear logical and scientific errors are identified.

> Jonathan_Burke:
>
> > Homo sapiens do not dip down to a single couple in the last 300 kya.
>
> But this is precisely the question that I am interested in, regardless of Dennis never meaning it. I want to know about our homo sapiens ancestors. Otherwise this has absolutely no relevance to the issue of Adam and Eve at all.

Well it's a good question. From a scientific point of view, we know that they go down to ZERO, so they certainly dip below 10,000. The exactly generation-by-generation counts at their origin are unknown, and likely unknowable, and likely dependent on the precise definition of *Homo sapien* we use.

Though, this may or may not have any relevance to Adam or Eve. There is no *a priori* reason to think Homo sapiens = the "adams" of Scripture.

Jonathan_Burke (Jon) 2018-02-08 23:11:35 UTC #513

> Swamidass:
>
> Yes, that is correct. Jerry Coyne makes illogical statements, and random youtubers misunderstand science. This is a widespread misunderstanding. Even many scientists are making these logical errors. No big surprise there.

So you are saying that the "real science" is that humans originated from a single couple, not as a population? I would love to see all the other scientists saying this, but I haven't found any yet.

> Swamidass:
>
> Though, this may or may not have any relevance to Adam or Eve. There is no a priori reason to think Homo sapiens = the "adams" of Scripture.

This doesn't seem like a sensible statement to me. It looks like an apologetic dodge.

Christy (Christy Hemphill) 2018-02-08 23:13:58 UTC #514

> Swamidass:
>
> For this reason, we can imagine several scenarios where the number of "humans" dips down to zero.

I cannot imagine this scenario. How is this possible? You are saying there were humans and then because of some event, were no longer any humans. But then humans reemerged at some point in time?

> Swamidass:
>
> If we think there are ZERO "humans" at 300 kya, it is self-contradictory to claim that "humans" never dip below a few thousand.

I don't understand. The word "dip" implies a population that falls to a lower number, not a population that simply doesn't exist yet. What kind of semantic game is this? I assume when anyone says that there are zero humans at 300 kya it is not because their population has "dipped" to zero, but because their population has not yet arisen. If the entire evolving population in which the boundaries between species are fluid and in which the designation "human" is philosophical, not genetic or biological, why does it matter exactly when a part of the population gets what label? If there was no two person bottleneck along the whole continuum, then there was no two person bottleneck.

I don't understand this contradiction you are pointing out. The question was whether or not there was a two-individual (whether they are designated ancestor, homo sapien, or human to me is irrelevant) bottleneck in the last 300,000 years. The answer was no, right?

> Swamidass:
>
> Just because we could never identify who is the first could who spoke French does not mean that French (by some definition) does not begin with a single couple. As is well put…

I disagree. French does not begin with a single couple. Any such designation would be totally arbitrary and not based on linguistic realities. It takes generations for given linguistic distinctives to solidify in a population. As transitions are happening speakers go back and forth. **@AMWolfe** 's "first people to say “oui” almost certainly also said “oïl” some or most of the time. Plus one linguistic distinction doesn’t make a new language out of two speakers. Those things are only useful in retrospect. No one in a given population would have recognized a single individual or pair of individuals in their population as speaking a different language. Similarly species don’t have solid boundaries. Anyone who labels a particular individual “the first homo sapien” is making an arbitrary choice that is not based in genetic or biological realities. “Human” is different because it is a different construct than “species” but if you want the first “humans” to not belong to a large population of other creatures who share their same biological species and live contemporaneously, we agree that did not happen within the last 300,000 years, correct? And pushing the designation of “human” back beyond 300,000 years ago to me sounds quite controversial and dubious.

“Human ancestors” has two meanings, depending whether you mean “ancestors of humans” or “ancestors who are human.” For the record, when I say “human ancestors” I mean “ancestors who are human” not “ancestors of humans.” Is it not true that our human ancestors (wherever in time you arbitrarily designate “human”) did not dip down to two?

Jonathan_Burke (Jon) 2018-02-08 23:15:33 UTC #515

> Christy:
>
> “Human ancestors” has two meanings, depending whether you mean “ancestors of humans” or “ancestors who are human.” For the record, when I say “human ancestors” I mean “ancestors who are human” not “ancestors of humans.” Is it not true that our human ancestors (wherever in time you arbitrarily designate “human”) did not dip down to two?

That is exactly how I have been reading this.

Swamidass (Dr. S Joshua Swamidass) 2018-02-08 23:23:53 UTC #516

> Jonathan_Burke:
>
> So you are saying that the “real science” is that humans originated from a single couple, not as a population? I would love to see all the other scientists saying this, but I haven’t found any yet.

You have to be much more precise in your language. That is not what I am saying.

The claim is not about the the origins of Homo sapiens, but whether they go below 10,000 in the last 300 kya. Everyone who thinks that Homo sapiens arise later than 300 kya will say that they dip below 10,000. That is just an obvious statement.

Whether they arise as a population or not depends on how we define them. Whether or not this has anything to do with Adam and Eve (which think not) depends on how we define the “adams” of scripture.

> Christy:

> I cannot imagine this scenario. How is this possible? You are saying there were humans and then because of some event, were no longer any humans. But then humans reemerged at some point in time?

No. That is not it.

For example, Dennis has argued that “humans” = Homo sapiens, and they arise about 200 kya ago. That means they do not exist at 250 kya. That means their population count at 250 kya is ZERO, which is less than 10,000. So the population count of humans is then less than 10,000.

This is just one scenario where they dip down to zero as we look back in time.

> Christy:
>
> I don’t understand. The word “dip” implies a population that falls to a lower number, not a population that simply doesn’t exist yet. What kind of semantic game is this?

Its about if we are using reverse or forward time. It’s common in population genetics to talk reverse time, which means we start in present with a high population and it “dips” as we go back in the past. Another direction insensitive way of making the same claim is that “humans never have less than 10,000 members”. That is just false.

It’s not a semantic game. It’s just taking a claim seriously and seeing if it is supported in the evidence or not. It’s worth asking, also, why **@DennisVenema** is no longer defending that claim. The reason, it seems, is that it is not defensible.

> Christy:
>
> If the entire evolving population in which the boundaries between species are fluid and in which the designation “human” is philosophical, not genetic or biological, why does it matter exactly when a part of the population gets what label?

It matters if there is a sharp theological or cultural transition at some point. Remember we are talking about Adam and Eve too, so at the core the theological question is whether or not Adam and Eve existed and if their is a sharp theological transition that comes about because of them. Ultimately, we are going to be dependent on our understanding of Scripture and theology to definitively answer these questions. Science does rule out some possibilities (it seems) but it certainly does not answer them.

> Christy:
>
> “Human ancestors” has two meanings, depending whether you mean “ancestors of humans” or “ancestors who are human.”

That is true! In context with Dennis, we clarified his meaning, but perhaps others take a different meaning.

> Christy:
>
> For the record, when I say “human ancestors” I mean “ancestors who are human” not “ancestors of humans.” Is it not true that our human ancestors (wherever in time you arbitrarily designate “human”) did not dip down to two?

> Jonathan_Burke:

> That is exactly how I have been reading this.

Using your definition, we just do not know from science. The question is underspecified because there are so many ways to understand “human”, and we both agree that our ancestors include at some point ancestors that are not “human.” At any generation, or the first generation, was there just a single couple of “human”? There is no way to know from science. It is certainly not settled, as there is raging debates about what “human” is in anthropology, and they are not considering things like “The Image of God” and “souls” and a historical Adam etc. From a purely biological point of view we cannot answer the question. Neither can we come to consensus when taking theology into account.

Christy (Christy Hemphill) 2018-02-08 23:31:41 UTC #517

> Swamidass:
>
> Everyone who thinks that Homo sapiens arise later than 300 kya will say that they dip below 10,000.

To “dip below 10,000” presumes a population of 10,000 exists, though right? At some arbitrary point in time a population that was once labeled, “pre-Homo Sapiens” gets labeled “Homo-sapiens.” The population is a continuum. Or do you conceptualize that individuals “emerge from their ancestor population” one at a time and form a new species population, so at some point in time there were fewer Homo sapiens than the total population of the species continuum?

Christy (Christy Hemphill) 2018-02-08 23:34:24 UTC #518

> Christy:
>
> Is it not true that our human ancestors (wherever in time you arbitrarily designate “human”) did not dip down to two?

Can you answer this yes or no, if we are going with the anthropological definition of human, not a theological one: that is, anatomically and behaviorally human.

AMWolfe (A.M. Wolfe) 2018-02-08 23:39:00 UTC #519

(also **@swamidass**)

I don’t really have more time to clarify my thoughts too much today (big move coming up) but just to agree:

My comment about “first speakers of French” only makes sense (if at all) with an *absurdly* reductionist definition of “French,” and after the fact, almost as a useful fiction, one might say.

In the linguistics version of this sort of shift, at least, the change is gradual in several respects. (In fact, I don’t know to what extent the metaphor even holds at this level of detail!)

I mean, yes, as **@Christy** said, speakers have variation from one communicative setting to the next. But also, initially, probably all Franco-Occitan speakers said both *hoc* and *hoc illud* in different contexts, and one community gradually conventionalized things so that when someone asked a question, they would tend to use *hoc illud* more than *hoc*. (This is sort of like, if you imagine a hypothetical English-speaking community where people started using the word “exactly” to mean “yes.” They would say “exactly” in many other situations, and only over time would people realize that “exactly” had come to mean “yes.”)

Then you have the gradual loss of the medial consonant *c* until it was *[h]o[c]il[lud]*, which probably happened over generations of reanalyzing, like when one of my kids started writing and wrote “gragon” for “dragon” because that initial “d” had come to sound like a “j” to her. This sort of reanalysis happens extremely gradually and probably went something like [k] > [g] > [ɣ] > ø over successive generations.

In genetics, I imagine there are similar complications when you try to isolate the particular innovative string of AGTC that you’re going to artificially designate to be The Thing That Makes Us Human. But I’m not a geneticist, so I’ll leave that question to others.

Jay313 (Jay Johnson) 2018-02-08 23:40:11 UTC #520

> Swamidass:
>
> I think he did not understand that significance to the conversation. So it is better understood as an unintentional error to omit this. The error was in being imprecise in his language, and not realizing how some people would find this important.

If you didn’t explicitly connect your conversation about pedigree collapse to Adam and Eve, I do not see how you can fault Dennis for not making the connection himself. I could go back and look up a conversation about pedigree collapse right here on the forums that many of us participated in, and none of us made that connection at the time. I might as well ask why you didn’t publish in 2016, if you had that conversation way back then.

> Swamidass:
>
> the two of us had discussed this several times over 2016. In 2017, I was honestly surprised that he had not included in Adam and the Genome.

The fact that you would be surprised that a conversation you had in 2016 was not reflected in a book published in Jan. 2017 just reflects your own ignorance of the book publishing process. I would bet that final proofs were due to the printer at least 8 weeks before the book actually went on sale, and the author would have turned in his “final” draft months before that.

But, I should let Dennis speak for himself, if he cares to revisit the subject at all. Personally, I’m done with it.

Swamidass (Dr. S Joshua Swamidass) 2018-02-08 23:42:46 UTC #521

> Christy:
>
> To “dip below 10,000” presumes a population of 10,000 exists, though right?

In reverse time, it is self evident that there is > 5 billion people alive now. So as we go back in time, we see the population “decrease” or “dip” over the last 10,000 years (its increasing in forward time). In that sense we will see a dip at origins. But we are also conflating our ancestral population with “human”.

> Christy:
>
> Or do you conceptualize that individuals “emerge from their ancestor population” one at a time and form a new species population, so at some point in time there were fewer Homo sapiens than the total population of the species continuum?

What I would insist upon is that there is a distinction between taxonomic categories and theological categories. In science, we only deal with taxonomic categories that are themselves very poorly defined (e.g. Homo sapiens). However, in theological origins, we are talking about the origin of a particular theological category. It is the dangerous type of concordism to equate a taxonomic kind with the theological kind.

So the real question is how do the theological category of “adams” arise. That is the story told in Genesis, and it is concordism (i.e. eisogesis) read *Homo sapiens* into “adams.” To understand how this theological kind arises, we have to think about different models. In many models already proposed by others (e.g. Kinder and Walton), “adams” arise as a single couple, even though Homo sapiens may or may not arise as a couple.

> Christy:
>
> Can you answer this yes or no, if we are going with the anthropological definition of human, not a theological one: that is, anatomically and behaviorally human.

So if they are anatomically ***and behaviorally*** human, we are talking ***behaviorally modern humans***? The answer is that we do not know. We do not have the resolution down to a single generation to know if all these cultural innovations (or the critical ones) arise from a single couple or not. We just do not know.

> AMWolfe:
>
> In genetics, I imagine there are similar complications when you try to isolate the particular innovative string of AGTC

Yes there are, but in a complex way. If we are going to identify *Homo sapien* by a genetic sequences (dubious) then it arises in a single person, but is not going to transmit to all his/her offspring reliably.

However, if we are going to identify “humans” behavior, that can reliably transmit.

> Jay313:
>
> But, I should let Dennis speak for himself, if he cares to revisit the subject at all. Personally, I’m done with it.

Agree. Let him speak for himself, or let’s just let sleeping dogs lie. I’ve just said it was an *unintentional* error that a lot of others have made too. He should not be scapegoated over that. A lot of other people made the same mistake.

Swamidass (Dr. S Joshua Swamidass) 2018-02-08 23:43:46 UTC #522

> AMWolfe:
>
> I don’t really have more time to clarify my thoughts too much today (big move coming up) but just to agree:
>
> My comment about “first speakers of French” only makes sense (if at all) with an absurdly reductionist definition of “French,” and after the fact, almost as a useful fiction, one might say.
>
> In the linguistics version of this sort of shift, at least, the change is gradual in several respects. (In fact, I don’t know to what extent the metaphor even holds at this level of detail!)

Just an analogy. We should just let it be, as the analogy will eventually break down. Probably already has.

Christy (Christy Hemphill) 2018-02-09 00:16:21 UTC #523

> Swamidass:
>
> What I would insist upon is that there is a distinction between taxonomic categories and theological categories. In science, we only deal with taxonomic categories that are themselves very poorly defined (e.g. Homo sapiens). However, in theological origins, we are talking about the origin of a particular theological category. It is the dangerous type of concordism to equate a taxonomic kind with the theological kind.

Where did I equate taxonomic kind with theological kind? In the part you quoted I only talked about homo sapiens and the number of individuals in the population continuum. That is all I am concerned about at the moment. Where you assert “humanity” in that 300,000 years doesn’t affect the question did the population of organisms that eventually transitioned to Homo sapiens ever have a bottleneck of two. The answer is no, correct?

GJDS (GJDS) 2018-02-09 01:05:21 UTC #524

> Christy:
>
> You are saying there were humans and then because of some event, were no longer any humans. But then humans reemerged at some point in time?

The puzzle as I see it is to identify the start of the human race. From what I have read here, the modelling cannot identify a time when “any” number can be given to a start of humans, and try as I may, a time when the model states, “here we are modelling human beings of an x number”.

I am also puzzled by an absence of any evidence of events that are thought to eliminate populations of any number of pre-humans in the model.

These are important concerns to those such as myself, who are not overly concerned with modelling techniques, and more interested in a narrative derived from such work, that identifies a start, and subsequent development, of human beings and communities.

Christy (Christy Hemphill) 2018-02-09 02:29:36 UTC #525

> GJDS:
>
> The puzzle as I see it is to identify the start of the human race. From what I have read here, the modelling cannot identify a time when “any” number can be given to a start of humans, and try as I may, a time when the model states, “here we are modelling human beings of an x number”.

Okay, that puzzle cannot be addressed by science.

But we can answer the question “In the population of organisms from which humans emerged at some point over the last 300,000 years, was there ever just a single pair?” The answer is no as I understand it. The fact that science can’t prove that there never was a possible two organism bottle-neck somewhere in some population of organisms that are a common ancestor with humans a million years ago is totally irrelevant to me personally.

Swamidass (Dr. S Joshua Swamidass) 2018-02-09 03:15:35 UTC #526

Hey @Christy with this…

> Christy:
>
> Where you assert “humanity” in that 300,000 years doesn’t affect the question did the population of organisms that eventually transitioned to Homo sapiens ever have a bottleneck of two. The answer is no, correct?

> Christy:
>
> But we can answer the question “In the population of organisms from which humans emerged at some point over the last 300,000 years, was there ever just a single pair?” The answer is no as I understand i

I think I can see what you mean, and think you are correct. However, your phrasing is not precise enough to be clear. There are some conceptions of it that may be possible. I do not think that, however, is what you mean. So the answer is “no”, it does not appear so.

First, a more clear way to phrase this that is precise…

> It seems that in the last 300 kya, our ***ancestors*** never had a generation with just a single couple.

Here ancestors would include all ancestors, without raising questions about who is human or not. We could also add…

> There seems to be ***strong genetic evidence*** that in the lsat 300 kya, our ***ancestors*** never had a generation with just a single couple.

However, we should always be aware, that this is an assessment made while barring ongoing miracles. That is a standard caveat in scientific findings, but seems worth pointing out here. If we allow for God’s action, and for unusual biology in Adam and Eve (e.g. if they were mosaics) it might be possible that at our origin (with one big miracle) there is a single couple, less than 300 kya ago. Of course, this last possibility is not “what the data looks like” but it is technically possible.

I’m not just being difficult or playing with words. Precision in stating the claims of science is important. Its part of honesty here. The evidence shows us some things. I does not show us others.

> Christy:
>
> …is totally irrelevant to me personally.

Even if these options are personally not relevant to us, they may be relevant to others. And we have the responsibility to honestly explain what it does and does not say. I think this cuts both ways.

1. I think @DennisVenema has the responsibility to acknowledge what the data does *not* say here. (as has been detailed in the last several posts).

2. I think also (once he has settled this for himself) that @RichardBuggs has a responsibility to acknowledge what data does seem to say (i.e. that a single couple bottleneck before 300 kya seems ruled out).

Both types of public acknowledgement are important. I press for ***BOTH*** of them to be honest about what the data does and does not seem show. It cuts both ways. Part of our service as scientists in the Church is to be honest about these

things, not selectively but in full. Honesty is just extremely important.

AMWolfe (A.M. Wolfe) 2018-02-09 03:22:11 UTC #527

> Swamidass:
>
> If we are going to identify Homo sapien by a genetic sequences (dubious) then it arises in a single person, but is not going to transmit to all his/her offspring reliably.
>
> However, if we are going to identify “humans” behavior, that can reliably transmit.

That’s a helpful correction, especially with the caveat you give prior to that…

> Swamidass:
>
> So if they are anatomically and behaviorally human, we are talking behaviorally modern humans? The answer is that we do not know. We do not have the resolution down to a single generation to know if all these cultural innovations (or the critical ones) arise from a single couple or not. We just do not know.

If it doesn’t work to say that Adam was the first “human” in terms of genetics or behavior, we can, of course, still say that God initiated a special kind of relationship with him as (or as being “in”) His “image,” and posit that this was passed down to others. That is, **it could be a relational definition rather than genetic or behavioral.** This is not something that science could ever really speak to, though, as it completely divorces the categories “Adamite” and “modern H. sapiens.” If I understand correctly, this is roughly what you’ve suggested elsewhere, or it’s compatible with it anyway.

I will add that the whole exploration of the linguistic metaphor above actually really helped me to get my mind around just how difficult it is to talk about some individual early human being singled out as “the first *H. sapiens*.” I started with the idea that surely there must have been some kind of first 100% *H. sapiens* (intuitively this has long been a hard notion for me to shake… there’s that intuition thing again), but it quickly became apparent how problematic that really is when you try to zoom in and look at the issue in high resolution, as it were. So I want to thank you and **@Christy** for helping me do that.

Swamidass (Dr. S Joshua Swamidass) 2018-02-09 03:44:39 UTC #528

> AMWolfe:
>
> If it doesn’t work to say that Adam was the first “human” in terms of genetics or behavior, we can, of course, still say that God initiated a special kind of relationship with him as (or as being “in”) His “image,” and posit that this was passed down to others. That is, it could be a relational definition rather than genetic or behavioral. This is not something that science could ever really speak to, though, as it completely divorces the categories “Adamite” and “modern H. sapiens.” If I understand correctly, this is roughly what you’ve suggested elsewhere, or it’s compatible with it anyway.

You are starting to get it =).

The relational definition is exactly the one that **@Jon_Garvey** has been developing on his blog.

However, it actually could make sense to see Adam and Eve as the first with a certain behavior. That does make sense. Or at least it can make sense. Its not at all different than proposals by John Walton about original sin. Defining them genetically, however, is more difficult.

Regarding the Image of God, it all depends exactly what you mean. Though Scripture barely speaks about the Image of God, it's a very loaded term. Some people have a difficult time with interbreeding between those with and without the "Image of God" because of a lot of meaning they import into the term. If we just mean "appointed to a role" (as many people believe), then this need not be a problem. If we mean "of different intrinsic capability" or "with a soul" then there might be some problems that arise.

I think it is clearer to explain that Adam and Eve (the first theological "humans") are defined by a particular relational status with God, and they eventually (by one of several possible means) transmit this relational status to all of us. I would associate this relational status more with the Fall than with the Image of God, but that is just me. I think, for example, **@Jon_Garvey** understands God's Image as "appointment to a purpose" so he is less concerned about saying that Adam's descendents are the only ones with this Image.

Ultimately, all these options should be on the table, as long as we affirm the unity of all mankind in the present day. So both my inclination and **@Jon_Garvey** 's are both in the zone of safety. Of course, that status can transfer to all of us many ways, and different theological models can take different paths. Most importantly, whether or not its important, genealogical descent is available as one method of transmission if that is what is needed within theology.

GJDS (GJDS) 2018-02-09 04:17:22 UTC #529

> Christy:
>
> Okay, that puzzle cannot be addressed by science.

So we are left with a question, which very simply may be phrased as, "Why do we seem to turn to science for answers that science cannot provide?"

Swamidass (Dr. S Joshua Swamidass) 2018-02-09 04:31:42 UTC #530

> GJDS:
>
> So we are left with a question, which very simply may be phrased as, "Why do we seem to turn to science for answers that science cannot provide?"

> The fundamental error here is summed up in an old joke scientists love to tell. Late at night, a police officer finds a drunk man crawling around on his hands and knees under a streetlight. The drunk man tells the officer he's looking for his wallet. When the officer asks if he's sure this is where he dropped the wallet, the man replies that he thinks he more likely dropped it across the street. Then why are you looking over here? the befuddled officer asks. Because the light's better here, explains the drunk man.

http://discovermagazine.com/2010/jul-aug/29-why-scientific-studies-often-wrong-streetlight-effect

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Christy (Christy Hemphill) 2018-02-09 04:38:29 UTC #531

> GJDS:
>
> So we are left with a question, which very simply may be phrased as, "Why do we seem to turn to science for answers that science cannot provide?"

I turned to science for the answer to the question, “Did humans emerge from a population that has not dipped down to two organisms within the last 300,000 years?” Science answered my question just fine.

GJDS (GJDS) 2018-02-09 04:57:05 UTC #532

But surely **@Christy** this simplistic approach poses more questions than answers. As a scientific question, we need to know what are these humans within the model, when did they “emerge” (whatever that means), and why are we confined to an elaborate analysis of genetic diversity in examining these matters. We have abundant data from archeology, history and perhaps geo-chemistry to seek answers to scientific questions - questions on human history, and “emergence” of the human race can only be answered adequately with science, by providing a coherent approach that uses all available data.

It is worth noting that modelling that looks at genetic diversity over the past few thousand years can be shown to be consistent with population modelling of humanity based on available recorded data. I will indulge in speculation (since this seems the fashion) by posing a thought that a history spanning 10-30,000 years would be sufficient to answer our questions of ancestry and the theological/spiritual behaviour of true humans.

In any event, I remain unconvinced that any modelling of bottlenecks would have relevance to the matters pertaining to Adam and Eve as discussed within Christianity.

Christy (Christy Hemphill) 2018-02-09 05:26:18 UTC #533

> GJDS:
>
> We have abundant data from archeology, history and perhaps geo-chemistry to seek answers to scientific questions - questions on human history, and “emergence” of the human race can only be answered adequately with science, by providing a coherent approach that uses all available data.

Come again? The whole point of half these discussions is that “theological human” is a different construct than the “modern human” construct proposed by anthropology. We do not have “abundant data” to answer the question “when did humans emerge” in theological terms. We have Genesis and a bunch of creative speculation.

> GJDS:
>
> In any event, I remain unconvinced that any modelling of bottlenecks would have relevance to the matters pertaining to Adam and Eve as discussed within Christianity.

Oh, I totally agree with that.

Swamidass (Dr. S Joshua Swamidass) 2018-02-09 05:45:24 UTC #534

> GJDS:
>
> But surely **@Christy** this simplistic approach poses more questions than answers.

Exactly. However…

> GJDS:

> “emergence” of the human race can only be answered adequately with science, by providing a coherent approach that uses all available data.

Don’t forget your question. It still applies…

> GJDS:
>
> So we are left with a question, which very simply may be phrased as, “Why do we seem to turn to science for answers that science cannot provide?”

So **@Christy** is right…

> Christy:
>
> Come again? The whole point of half these discussions is that “theological human” is a different construct than the “modern human” construct proposed by anthropology. We do not have “abundant data” to answer the question “when did humans emerge” in theological terms.

GJDS (GJDS) 2018-02-09 05:50:11 UTC #535

> Christy:
>
> The whole point of half these discussions is that “theological human” is a different construct than the “modern human” construct proposed by anthropology

I cannot make sense of this comment - I am aware of details of tribes and civilisations that span thousands of years, which all show various cultures and spiritual outlooks. All of these, as far as I know, are considered modern humans. Adam and Eve are a specific couple that is part of the Jewish /Christian tradition.

My impression has been that BioLogos has sought to turn Adam and Eve as either into a myth, or as unscientific by showing that it cannot fit into the modelling of genetic diversity, as the latter would need to show a primordial “bottleneck” of a single couple in the model.

I have questioned the premise underpinning the modelling effort and am unconvinced the model has provided any worthwhile insights regarding Adam and Eve.

GJDS (GJDS) 2018-02-09 05:51:31 UTC #536

I am questioning the distinction put by Christy - see my comment to her.

---

gbrooks9 (George Brooks) 2018-02-09 07:17:26 UTC #537

> Jay313:
>
> Exactly. There is the Toba super-eruption during the timeframe of the previously calculated bottlenecks associated with the Out of Africa event.

@Jay313

If we are going to entertain the idea of the creation of a special mating pair in the middle of another population, we might as well give them the maximum latitude for what the genetic diversity can be … locked up in the genes of the single mating pair. It's a wild card I'm willing to let them play … but only once.

@DennisVenema , no doubt it rubs you the wrong way … because you are trained not to look at things as God enabled… but I don't think it really changes things. Does it? If it does, now is the time to discuss it.

Lynn_Munter (Lynn Munter) 2018-02-09 09:52:06 UTC #538

Hi, @Swamidass . I'm going to go over some of these details from your post bringing back the whole issue of the heliocentric claim, since (as I did before) I still think you're being overly harsh on it.

> Swamidass:
>
> > DennisVenema:
> >
> > "As our methodology becomes more sophisticated and more data are examined, we will likely further refine our estimates in the future. That said, we can be confident that finding evidence that we were created independently of other animals or that we descend from only two people just isn't going to happen. Some ideas in science are so well supported that it is highly unlikely new evidence will substantially modify them, and these are among them. The sun is at the center of our solar system, humans evolved, and we evolved as a population."
>
> First, this statement was shown to be incorrect by genealogical science.

Sorry, I think this statement (with Dr. Venema's original correction) still stands, from everything I've seen. Your argument that

> Swamidass:
>
> we do all descent from individual couples

does not falsify it since your plural couples != "*only* two people."

What happened here is that you restated the claim in a way that turned out to be false, and @DennisVenema incautiously agreed to it. But his original claim, with his minor clarification, is not false, yet you persist in calling your erroneous restatement his claim.

> Swamidass:
>
> Its the claim that @DennisVenema makes, which is just not substantiated. We cannot use "our ancestors" and "human" and "Homo sapiens" interchangeably. That was the source of the error.

I think it doesn't take much to realize he meant the subset of "our ancestors" which are reasonably considered "human" or "homo Sapiens." When a word is clarified, it retains the original meaning but is limited in scope by the clarifying word. The context of his clarification was clearly that he did not mean the set of "our ancestors" stretching back to the other great apes.

But let's return to his original wording. There are actually two separate claims here to which he did not feel tarnished by comparison to heliocentric certainty (the claim does not even state we are 'as sure' of them):

> we can be confident that finding evidence that we were created independently of other animals or that we descend from only two people just isn't going to happen.

> humans evolved, and we evolved as a population.

Now the later clarification that by "people" or "humans" he means "homo sapien," not older human ancestors.

The first statement remains true. We do not descend from only two Homo sapiens. The suggestion of interbreeding cannot help you with this because if we descended from two Homo sapiens and some Neanderthals, that is not the same as descending from **only** two Homo sapiens.

Plus, it is not enough to demonstrate we cannot rule this option out: in order to falsify this claim, we must find actual positive evidence.

The second claim is what the actual humans=homo sapiens clarification applies to, and I think we can see that it works just fine with that substitution. "Homo sapiens evolved, and we evolved as a population." Clearly this does not take out the 'we' meaning once 'Homo sapiens' is substituted in. Crossover events with closely related species is still "we evolved as a population." If your only argument in refutation of this statement is that Homo sapiens could theoretically have had a population of only two at some point in time and we just wouldn't be able to see it because of all the other non-Homo sapiens that subsequently exchanged genetic material with us, that is still "we evolved as a population."

@DennisVenema may have gotten tired of defending this statement (or of grammatical hairsplitting), but as far as I can see nothing in this discussion has invalidated it.

It is unfortunate indeed that the conversation has gotten sidetracked by your (less well-worded) claim. If you wish to continue saying he should retract his agreement with it, you have a right to, certainly, as long as you stop conflating it with his.

Christy (Christy Hemphill) 2018-02-09 14:10:53 UTC #539

> GJDS:
>
> I cannot make sense of this comment

I don't know how to clarify. How do you envision science coming up with anything useful pertaining to questions about eternal souls, the image of God, the Fall, evidence of God relating to humanity, or any of the other theological elements used to designate "theological human". I can't envision how science would shed any light on these questions.

Lynn_Munter (Lynn Munter) 2018-02-09 15:17:56 UTC #540

> Lynn_Munter:
>
> The first statement remains true. We do not descend from only two Homo sapiens. The suggestion of interbreeding cannot help you with this because if we descended from two Homo sapiens and some Neanderthals, that is not the same as descending from only two Homo sapiens.

I kept thinking about this after I posted because I wanted to be sure I was being fair. There is a grammatical ambiguity in this sentence, and it might be where a lot of this confusion has come from. It's been long enough since my college linguistics classes that I'm not up to diagramming the sentence to show it, but I think it comes down to "(descend from **only**) (two people)" vs "(descend from) (only two **people**)." The difference is whether the statement allows for us to descend additionally from non-people.

Grammatical ambiguities like this are common in English (and, I imagine, other languages) and usually are resolved by looking at the context in which they were written. I think this ambiguity is entirely resolvable for two reasons. The first reason is that common sense tells us he is refuting the tradition of the sole progenitorship of Adam and Eve.

If we are still uncertain, however, we need only go to the end of the paragraph to see him restate the claim, *we evolved as a population*, this time making clear that it is the first sense (there were more than two) and not the second sense (there was a point when only two of our ancestors were human).

In case there is any doubt that what he is doing is restating the claim, we need only compare the first and second clauses, which are restated in order (parentheses mine):

1a: we were created independently of other animals
1b: we did not descend from only two people
2a: humans evolved (from other animals)
2b: we evolved as a population (more than two individuals)

P.S. I have now officially given up any hope I ever had of not being too nitpicky about this, but at the very least I seem to be in good company for it so I hope you will all forgive me!

Swamidass (Dr. S Joshua Swamidass) 2018-02-09 16:12:46 UTC #541

> Christy:
>
> I don't know how to clarify. How do you envision science coming up with anything useful pertaining to questions about eternal souls, the image of God, the Fall, evidence of God relating to humanity, or any of the other theological elements used to designate "theological human". I can't envision how science would shed any light on these questions.

I totally agree with you here.

Post Hoc Defense

@Lynn_Munter I'm not sure what your goals are here.

@DennisVenema is part of this conversation too, and he can certainly clarify his points and explain himself. He does not need a lawyerly defense from other people. In fact, it appears he has already retracted (in his way) the points you are defending. If I am wrong, he can explain himself. The fact that he is not should tell us something.

> Lynn_Munter:
>
> Sorry, I think this statement (with Dr. Venema's original correction) still stands, from everything I've seen. Your argument that

Except its not correct.

> Lynn_Munter:
>
> does not falsify it since your plural couples != “only two people.”

There is *no* model in which we do not all descend from multiple couples. Even in Ken Ham’s young earth creationist model, we all descend from many couples. This is scientifically a mistaken and incoherent defense. If you are take this definition, there is not a single model proposed that fits this criteria, not even the most YEC of YEC models.

> Lynn_Munter:
>
> I think it doesn’t take much to realize he meant the subset of “our ancestors” which are reasonably considered “human” or “homo Sapiens.”

> Lynn_Munter:
>
> Now the later clarification that by “people” or “humans” he means “homo sapien,” not older human ancestors.

Exactly. And there is ZERO evidence that they do not begin as a single couple. Zero evidence. So how do we come to heliocentric certainty about a claim substantiated by zero evidence?

> Lynn_Munter:
>
> The first statement remains true. We do not descend from only two Homo sapiens.

Except the statement is false. We do descend from only two Homo sapiens.

> Lynn_Munter:
>
> I kept thinking about this after I posted because I wanted to be sure I was being fair. There is a grammatical ambiguity in this sentence, and it might be where a lot of this confusion has come from.

Except there is no confusion; at least Dennis and I do not appear confused. As written, the statement that “We do not descend from only two Homo sapiens” is just false. There is more than one way to take it, and one way is not contradicted by the evidence. This is not nearly as ambiguous as you are making it. Unqualified, it’s just a false statement.

Of course, in context, it is possible other things were meant. However, clear explanations would have broken it down showing, (1) if you mean in this way, the answer is ‘no’, but (2) if you mean it this way, the answer is ‘yes’. Given that we are talking about a book designed to elucidate the key issues to the public this is a major error. It’s most clearly consequential in that McKnight concludes that a genealogical Adam is not consistent with science. Dennis’ own co-author is so confused by the this error he misunderstands a central fact about the science. That is Dennis’s co author, by the way, making his most controversial theological point based on a misunderstanding of the science.

It is rare to see a consequential error of this magnitude. It’s better to retract errors like this than give lawyerly defenses.

Now, once again, I think this was an unintentional error. Everyone has been making this error. It is, nonetheless, and unambiguous error that misrepresents what we know about the science. Going forward, no one has an excuse about this any more. These post hoc, word parsing only erode trust. The people that will be trust are the ones that fix this scientific error in their future work. Those that are trusted will own up to the oversight.

@Lynn_Munter you are welcome to disagree with me, but I'm 100% sure that @DennisVenema does not need your defense. I've been inviting him to correct it for over a month now, and he has demurred. Wisely, because I am not misrepresenting him.

Of course, a clearer retraction from him would serve you. However, that does not appear to be his style. This is how @DennisVenema makes retractions.

Christy (Christy Hemphill) 2018-02-09 16:32:11 UTC #542

> Swamidass:
>
> We do descend from only two Homo sapiens.

What?

How is the statement "we descend from a population that did not dip below 10,000" true and yet "we do not descend from (a population of) only two" false?

Jonathan_Burke (Jon) 2018-02-09 16:34:35 UTC #543

> Christy:
>
> What?

He's probably speaking of genealogical Adam.

Swamidass (Dr. S Joshua Swamidass) 2018-02-09 16:35:20 UTC #544

> Christy:
>
> What?
>
> How is the statement "we descend from a population of 10,000" true and yet "we do not descend from only two (i.e. significantly less than a population of 10,000" false?

We've gone over this several times. There is ambiguity in the grammar there. More precisely, we do all descend individually from two specific Homo sapiens. These two specific Homo sapiens are not unique, in that large number of others could be substituted in the place (from a scientific point of view). This is true of all models, including Ken Ham's model.

> Jonathan_Burke:
>
> He's probably speaking of genealogical Adam.

Yup.

Jonathan_Burke (Jon) 2018-02-09 16:37:18 UTC #545

> Swamidass:
>
> These post hoc, word parsing only erode trust.

This is ironic since it's your word parsing that has eroded my trust.

Christy (Christy Hemphill) 2018-02-09 16:41:57 UTC #546

> Jonathan_Burke:
>
> He's probably speaking of genealogical Adam.

Which is not the topic of conversation. The topic of conversation is population genetics. We all should not be expected to constantly mentally refer to genealogical Adam when making fairly straightforward statements about other topics.

Swamidass (Dr. S Joshua Swamidass) 2018-02-09 16:43:20 UTC #547

> Christy:
>
> Which is not the topic of conversation. The topic of conversation is population genetics. We all should not be expected to constantly mentally refer to genealogical Adam when making fairly straightforward statements about other topics.

Genealogical science is part of population genetics. Clarity in language is important, or a lot confusion persists. It's not my intention to keep going there, but we can't use language in a way that ignores that finding of population genetics.

However, you do have a point…

> Swamidass:
>
> Exactly. And there is ZERO evidence that they do not begin as a single couple. Zero evidence. So how do we come to heliocentric certainty about a claim substantiated by zero evidence?

In this case, I am not making reference to genealogical science. This is just correcting the ecological fallacy.

There is strong evidence that **our ancestors** do not dip to a single couple in the last 500 kya, but that does ***not*** mean ***Homo sapiens*** specifically do not go to zero, or even a single couple at their origin.

> Jonathan_Burke:
>
> This is ironic since it's your word parsing that has eroded my trust.

Its not word parsing to clarify what people mean by statements, and then see if the evidence holds to it. It is not word parsing to seek clear language that does not miscommunicate the details of the science. Much of this would not matter if the science was clearly understood by everyone. However, that is not the case. Most people are missing key things. Until that is resolved, its going to require reworking our language.

In the conversation with Dennis, we are working off his clarification of what he original wrote. Not the precise language he originally wrote. Still, we can't move the goal posts after those clarifications are made.

Lynn_Munter (Lynn Munter) 2018-02-09 16:56:50 UTC #548

> Swamidass:
>
> As written, the statement that "We do not descend from only two Homo sapiens" is just false. There is more than one way to take it, and one way is not contradicted by the evidence. This is not nearly as ambiguous as you are making it. It's just a false statement.

If that statement appeared out of nowhere, there would indeed be ambiguity and two ways to take it. However, it did not, and within its original context, it is very clear which way it was meant and it is not false at all.

I will give you that substituting in 'Homo sapiens' lends emphasis to your alternative meaning, because another way to tell how to parse a sentence is to look for the most specific words ('two' is more specific than 'people,' but 'Homo sapiens' is more specific than either) but that is no reason to change our established understanding of the sentence: We do not descend from only two people. (We evolved as a population.) I'm sorry but it's more than adequately clear.

> Swamidass:
>
> And there is ZERO evidence that they do not begin as a single couple

We don't care at all how some arbitrarily defined population of Homo sapiens *begins;* we care if we are *descended from* a single couple and *only* a single couple. That is the topic of discussion. Is there or is there not a single couple from whom alone we all descend?

I am not qualified to converse at as high a scientific level as Dennis Venema and Richard Buggs. It's great that you are qualified, and have provided a lot of very valuable contributions to the discussion. But if you're going to pursue this issue of grammar as you have been doing, I do consider myself qualified to disagree with your conclusions as I have been doing.

I have not seen anyone else take the meaning from the statement that you do. If McKnight did and disagrees with your genealogical Adam on the grounds of it, I will be extremely surprised: I think it more likely that there is some other miscommunication happening there. I don't know if you're referring to a public conversation or a private one?

Christy (Christy Hemphill) 2018-02-09 16:59:16 UTC #549

> Swamidass:
>
> but that does not mean Homo sapiens specifically do not go to zero, or even a single couple at their origin.

But this violates the concept of species, doesn't it? How is there ever "the first" mating pair of a species? Species transition over time as a population. Any divisions are arbitrary divisions on a development continuum that does not have precise boundaries down to individuals. Now it looks like you are conflating Homo sapiens with human.

AMWolfe (A.M. Wolfe) 2018-02-09 17:03:10 UTC #550

> Christy:

> But this violates the concept of species, doesn't it? How is there ever "the first" mating pair of a species? Species transition over time as a population. Any divisions are arbitrary divisions on a development continuum that does not have precise boundaries down to individuals. Now it looks like you are conflating Homo sapiens with human.

If there's one thing I thought I'd learned in this conversation (the most recent part of it — yesterday and today), it was that you may be able to meaningfully say that there was a first "human" couple if you define human relationally or theologically, but you can't say that there was a first "human" couple if you define human genetically (*H. sapiens*) or behaviorally ("behaviorally modern" humans).

If I've got this wrong, I hope Joshua will clarify.

Biological Definition of "Mankind"

Jonathan_Burke (Jon) 2018-02-09 17:03:12 UTC #551

> Christy:
>
> Which is not the topic of conversation. The topic of conversation is population genetics. We all should not be expected to constantly mentally refer to genealogical Adam when making fairly straightforward statements about other topics.

I agree. This is the kind of parsing to which I referred in my previous post. One minute a term means X, the next minute it means Y, then still later it's swapped out for Z. It feels horribly like a bait and switch is happening each time.

Lynn_Munter (Lynn Munter) 2018-02-09 17:03:54 UTC #552

> Christy:
>
> How is there ever "the first" mating pair of a species?

It is possible one could recognize a sharp species boundary at a point when the number of chromosomes changed, making interbreeding difficult although probably not impossible. That did happen once between the chimp split and us but I doubt it was at a human-defining moment we'd think much of. Other than that I couldn't say.

Christy (Christy Hemphill) 2018-02-09 17:04:51 UTC #553

So the number of chromosomes changed in only two individuals? How is that possible? And they happened to find each other and mate?

Lynn_Munter (Lynn Munter) 2018-02-09 17:10:47 UTC #554

It would change in one first (identical twins tangent … no, not going there) but then they'd have a kid? And either inbreeding, or the chromosome number isn't as much of a fertility issue early on as it becomes later.

Lynn_Munter (Lynn Munter) 2018-02-09 17:19:49 UTC #555

> Swamidass:
>
> In the conversation with Dennis, we are working off his clarification of what he original wrote. Not the precise language he originally wrote. Still, we can't move the goal posts after those clarifications are made.

His clarification was about three words. What you appear to be going off of is your further clarification/restatement which he agreed to, which is fine for some purposes, but not for saying he should put a retraction in the next edition of his book.

Jay313 (Jay Johnson) 2018-02-09 18:12:09 UTC #556

> Swamidass:
>
> So the real question is how do the theological category of "adams" arise. That is the story told in Genesis, and it is concordism (i.e. eisogesis) read Homo sapiens into "adams." To understand how this theological kind arises, we have to think about different models. In many models already proposed by others (e.g. Kinder and Walton), "adams" arise as a single couple, even though Homo sapiens may or may not arise as a couple.

I really wish you would stop saying "adams". The Hebrew in Gen. 1:26 is *adam*, which is a collective noun meaning "mankind". It is not a Hebrew plural, formed by adding -im, so what you're doing is, in effect, talking about "mankinds" every time you say "adams".

In any case, if you're trying to define a theological category of "adams" in contrast to the biological category of "mankind," I reject the distinction. We can have a theological definition of mankind and a biological definition of mankind, and they may be entirely different. But that is a far different thing than saying God created a "theological mankind" separately and at a later date than his creation of "biological mankind."

All of humanity developed through one evolutionary process of creation. That is parsimony.

Biological Definition of "Mankind"

T.j_Runyon (T J Runyon) 2018-02-09 18:42:05 UTC #557

I agree. Some of this word play is just becoming silly and I am quickly losing interest in this thread. I'm interested in if Homo sapiens, a species that is 350kya give or take ever dipped down to two. And the way I read Dennis' book was that the view that we are the descendants of two individuals that were created de novo is false and this as certain as heliocentrism. I couldnt care less if Erectus dipped down to two. And as someone who dedicates much of his time to Erectus, the view that Adam couldve been Erectus just doesn't match the data. I just want to know did our species ever dip down to two and is if even possible without that pair being descended from a larger pre Sapiens ancestral population?

DennisVenema (Dennis Venema) 2018-02-09 19:25:17 UTC #558

Lynn has the correct sense of things. I too am not really interested in grammatical hair-splitting! Nor do I see a need to revise the book. "Descending from just two people" is talking about populations and genetics, not genealogy. Yes I was aware of the genealogy issue - that is why "only" is in there. In other places, I'm careful to say we don't descend "uniquely" from just two people, etc.

DennisVenema (Dennis Venema) 2018-02-09 19:36:29 UTC #559

Oh, and chromosome number change by fusion isn't a speciation mechanism (in vertebrates, anyway). It happens in one individual, who then mates with others with the usual set. In the human lineage, this occurred before Neanderthals and Denisovans branch off.

48 --> 47 --> over time, more individuals with 47

47 mates with 47 —> some have 46

Over time, 48, 47 become less common, and our lineage fixes on 46.

Lynn_Munter (Lynn Munter) 2018-02-09 20:00:04 UTC #560

> DennisVenema:
>
> Oh, and chromosome number change by fusion isn't a speciation mechanism (in vertebrates, anyway).

Thanks for the clarification! Does it not cause fertility issues at all, or just not issues sufficient to prevent offspring?

GJDS (GJDS) 2018-02-09 20:00:11 UTC #561

Perhaps we misunderstand each other - I read your statement to mean there should be two classifications of humanity (eg non-theological and theological). The subsequent comments show some type of biological change and this excites others into speculation regarding Adam and Eve.

I think I will leave this conversationit at this point.

Christy (Christy Hemphill) 2018-02-09 20:23:25 UTC #562

> GJDS:
>
> I read your statement to mean there should be two classifications of humanity (eg non-theological and theological).

I don't personally think that, but yes, that is how some people talk about it. There is the species Homo sapiens (biological human) and then people speculate that within the species (or an earlier one) there arose a group or a couple that were the first "theological humans;" the first to have a relationship with God, or moral accountability, or an eternal soul, or the image of God, or whatever it is that one uses to define "human" theologically.

DennisVenema (Dennis Venema) 2018-02-09 20:44:18 UTC #563

The fertility issues are mild.

This sort of thing still happens - there's an example of a man in China with 44 chromosomes - his parents both have 45, and the fused pair they have they inherited from a common ancestor.

AMWolfe (A.M. Wolfe) 2018-02-09 20:44:29 UTC #564

> Christy:

> I don't personally think that, but yes, that is how some people talk about it. There is the species Homo sapiens (biological human) and then people speculate that within the species (or an earlier one) there arose a group or a couple that were the first "theological humans;"

For what it's worth, I think that a number of folks here (or perhaps just **@swamidass** and I) don't even necessarily feel this distinction is the best way forward for ourselves, but have been exploring it for the sake of those who cannot bear to accept evolution if it means jettisoning a singular historical Adam.

This sort of "**saving the phenomena**" approach seems to be tiring folks on this thread, though, and it's not properly speaking the topic of the thread…

Peter_Wolfe (Peter Wolfe) 2018-02-09 22:00:16 UTC #565

Yay! Have folks actually agreed on something? Isn't it the same thing we started with?! Can I go back under my rock now 🤓.

GJDS (GJDS) 2018-02-10 00:29:21 UTC #566

It seems to me there are as many versions as people to promote them.

I think we begin with one human species, and within these one couple that were created by God for a special relationship wit Him, that communed with God in a sacred place. We may draw an analogy from today - all of us are human, but some of us are Christians. With Adam and Eve, we draw on the Bible for understanding and read this into the entire doctrine of salvation in Christ.

Chris_Falter (Chris Falter) 2018-02-10 00:37:14 UTC #567

> Swamidass:
>
> However, we should always be aware, that this is an assessment made while barring ongoing miracles. That is a standard caveat in scientific findings, but seems worth pointing out here. If we allow for God's action, and for unusual biology in Adam and Eve (e.g. if they were mosaics) it might be possible that at our origin (with one big miracle) there is a single couple, less than 300 kya ago. Of course, this last possibility is not "what the data looks like" but it is technically possible.

We could also say that God is miraculously transforming the vision of astronauts so that a truly flat earth appears round. We could also say that the sun only appears to be the gravitational center of our neighborhood in space due to miraculous, divine interventions in our observations, but in fact the sun and planets revolve around the earth in conformance with Calvin's exegesis of many Bible passages.

You offered your observation as an olive branch to those who disagree with you, Joshua. Your motives are admirable. However, sometimes the doctor has to tell her desperate patient that he has stage 4 cancer, and sometimes the scientific community has to tell a religious community that some tenet of their traditional natural history does not comport with reality.

The genealogical Adam idea is a worthy idea, though. Worth further investigation, for sure.

Grace and peace,
Chris

GJDS (GJDS) 2018-02-10 02:10:25 UTC #568

> Chris_Falter:
>
> We could also say that God is miraculously transforming the vision of astronauts

To join in this humorous vane, we may also marvel at the mysterious “natural” force(s) that miraculously made all manner of “pre-humans”, and once it saw the required genetic diversity was achieve, it culled this helpless population (of an unknown but large number) into just the right bottleneck, (of an inferred but smaller number) at just the right time, to give us our indisputable modelling of the current human genome - but wait, this clearly is as certain as the round (as opposed to a flat) earth, and wait, there is more astronomy to leave us with complete certitude.

Just having some fun.

Grace and Peace,

GJDS

DennisVenema (Dennis Venema) 2018-02-10 02:27:41 UTC #569

> Chris_Falter:
>
> The genealogical Adam idea is a worthy idea, though. Worth further investigation, for sure.

@Swamidass has done a lot of nice work on this idea, and it’s a valuable contribution to the conversation. He is also motivated to bring unity to the church wherever possible, and for that he has my respect. It’s not for everyone, but it’s quite important for some of our brothers and sisters in Christ.

Swamidass (Dr. S Joshua Swamidass) 2018-02-10 02:32:42 UTC #570

This seems to be mixing issues. Partly my fault. So sorry about that.

> DennisVenema:
>
> Lynn has the correct sense of things. I too am not really interested in grammatical hair-splitting! Nor do I see a need to revise the book. “Descending from just two people” is talking about populations and genetics, not genealogy. Yes I was aware of the genealogy issue - that is why “only” is in there. In other places, I’m careful to say we don’t descend “uniquely” from just two people, etc

Adam and Genome’s final theological point is against a genealogical Adam. Its sounds like you will continue to leave no mention of the fact that genealogical universal ancestors are common and recent. That leaves key information out. I’m not sure that is upfront given what we all know now.

Also genealogical science is part of population genetics. Moreover the the theological section focuses on genealogical ancestry, not genetic ancestry. Intentionally excluding established and relevant science is not going to serve readers. It’s certainly not upfront.

> DennisVenema:

> @Swamidass has done a lot of nice work on this idea, and it's a valuable contribution to the conversation. He is also motivated to bring unity to the church wherever possible, and for that he has my respect.

Thanks for the kind words. I hope you at least make mention of it. Yes, Scott McKnight (and you) do not think its important or taught in Scripture. I respect that, and being convinced this way I see why its not important to you. However, its only plausible to take that position for theological reasons, not scientific.

> Lynn_Munter:
>
> If McKnight did and disagrees with your genealogical Adam on the grounds of it, I will be extremely surprised:

I was surprised when he disagreed with it on scientific grounds too. He is seems to think it is pseudoscience. No surprise, on the other hand, because there is no mention of it in Adam in the Genome. How could he know unless scientists are upfront with him?

However, it is a side issue to this thread. Sorry about raising it here.

Much more importantly, however, is how you plan to rework the sections involving the claims that @RichardBuggs have raised. Clarifying how you plan to revise those sections would be interesting. It seems worth revising both to fix some of the errors, and also for clarity. Any thoughts on that yet?

Swamidass (Dr. S Joshua Swamidass) 2018-02-10 02:34:08 UTC #571

> AMWolfe:
>
> For what it's worth, I think that a number of folks here (or perhaps just @swamidass and I) don't even necessarily feel this distinction is the best way forward for ourselves, but have been exploring it for the sake of those who cannot bear to accept evolution if it means jettisoning a singular historical Adam.

From many theological starting points, a genealogical Adam has a great deal of consilience. I'm an agnostic about the details, but see a lot of beauty here.

Though this is not the only model I would put forward. I'm working on more than one.

Lynn_Munter (Lynn Munter) 2018-02-10 04:41:27 UTC #572

> Swamidass:
>
> However, it is a side issue to this thread. Sorry about raising it here.

It was background I wasn't aware of, and improves my understanding of your position. I also want to emphasize that I have enormous appreciation for the work you've done on genetic modeling, on breaking down and explaining that modeling for everyone so that it was highly accessible, and on your commitment to bridge-building. Despite keeping on with my "lawyerly defense," I do have great respect for what you're doing here and with the genealogical Adam concept!

> DennisVenema:

> @Swamidass has done a lot of nice work on this idea, and it's a valuable contribution to the conversation. He is also motivated to bring unity to the church wherever possible, and for that he has my respect. It's not for everyone, but it's quite important for some of our brothers and sisters in Christ.

Hear, hear!

Swamidass (Dr. S Joshua Swamidass) 2018-02-10 17:42:38 UTC #573

Getting back on topic, and setting aside genealogical science…

We know that @DennisVenema 's first claim is unsubstantiated by evidence. Whether or it is true or not, we do not know from evidence whether Homo sapiens were ever just a single couple. To think that population genetics forecloses this possibility is to proffer the ecological fallacy. Yet this is how heliocentric certainty was built; going well beyond an accurate account of science.

That, still, is a scientific error.

About the second claim (our ancestors as a whole were never just a couple after 3mya), its seems that has been walked back too. We still have to look at trans-species variation, but we likely will not get to high certainty as far back as 3 mya, and no one is even discussing 10 mya as was done in the start of this conversation. Maybe its true, but its not substantiated be evidence.

So the second claim, therefore, appears to be an error too (unless tran-species variation comes to the rescue).

Whether or not @DennisVenema decides to clearly retract these confident statements as anything more than hypotheses is beside the point. It seems that ultimately @RichardBuggs 's instincts ended up correct here.

Christy (Christy Hemphill) 2018-02-10 18:56:01 UTC #574

> Swamidass:
>
> Whether or it is true or not, we do not know from evidence whether Homo sapiens were ever just a single couple.

Can you point to any other examples from biology where two specific organisms are identified as "starting" the species? I remain completely unconvinced that this is how the concept of "species" works, but I know I might be wrong.

Swamidass (Dr. S Joshua Swamidass) 2018-02-10 23:22:01 UTC #575

> Christy:
>
> Can you point to any other examples from biology where two specific organisms are identified as "starting" the species? I remain completely unconvinced that this is how the concept of "species" works, but I know I might be wrong.

Great question. Turns out that sexual species *usually* arise as populations, but not always. In biology, there are always exceptions to the rule. One well known exception to the rule is grasshoppers, which (it turns out) frequently speciate from single couples. Plants are another exception. It is very common for them to speciate from a single couple or even a single individual.

The usual pattern with mammals is speciation as a population, but it is possible to speciate from a single couple. Without getting into the details, this is an open question in the human lineage. It is certainly technically possible. Evidence one way or the other is most likely going to be equivocal, so I doubt we will ever know for sure.

Among mammals, consider the infamous Mouflon sheep of Corsica. **https://en.wikipedia.org/wiki/Mouflon**

Let's imagine it's true that they descend from an initial founding couple, and have been isolated for the last 8,000 years. At some point, if not *already*, they will no longer be able to produce fertile offspring with other Mouflon, and would be a distinct species.

Even if it ends up not being true in this specific case, there is no reason to think that this mechanism of speciation would not work. As long as there is enough separation for long enough period of time (by geography, genetic incompatibility, behavior, etc.) we expect new species to arise. So as long as an isolated population can arise from a single couple, this is one possible way for a species to arise.

Great question though. Always remember, there are rules in biology, but there are almost always exceptions to the rules.

Christy (Christy Hemphill) 2018-02-11 01:09:42 UTC #576

> Swamidass:
>
> Let's imagine it's true that they descend from an initial founding couple, and have been isolated for the last 8,000 years. At some point, if not already, they will no longer be able to produce fertile offspring with other Mouflon, and would be a distinct species.

But the original founding couple would have simultaneously been a member of the other species, right? And many of their offspring would have been able to reproduce with the "original" species had they not been geographically isolated correct? So it is only looking back in time that one could identify a "founding couple," and it doesn't have to do with uniqueness from the rest of their population, just circumstances of their environment. And in these cases where one mating pair becomes isolated from the rest of the species and "founds" a new species, can't all the members of the new species be traced back to the "founding pair" genetically? Isn't that exactly what these genetic studies being discussed are showing didn't happen with Homo sapiens?

Jonathan_Burke (Jon) 2018-02-11 01:10:18 UTC #577

> Swamidass:
>
> The usual pattern with mammals is speciation as a population, but it is possible to speciate from a single couple. Without getting into the details, this is an open question in the human lineage. It is certainly technically possible. Evidence one way or the other is most likely going to be equivocal, so I doubt we will ever know for sure.

If we look in the relevant literature, how many scientists are saying homo sapiens speciated as a single couple, and how many are saying homo sapiens speciated as a population?

Swamidass (Dr. S Joshua Swamidass) 2018-02-11 02:08:17 UTC #578

> Christy:

> But the original founding couple would have simultaneously been a member of the other species, right? And many of their offspring would have been able to reproduce with the “original” species had they not been geographically isolated correct?

In the case of the Mouflon sheep, that is correct. In the case of plants and grasshoppers, it often is a new species in literally a single generation. They would not be the original species, and are not reproductively compatible.

> Christy:
>
> So it is only looking back in time that one could identify a “founding couple,” and it doesn’t have to do with uniqueness from the rest of their population, just circumstances of their environment.

Depends, as I just explained.

Looking back in time, however, I’m not sure we can even distinguish these two cases from genetics. The data would end up looking essentially the same.

> Christy:
>
> And in these cases where one mating pair becomes isolated from the rest of the species and “founds” a new species, can’t all the members of the new species be traced back to the “founding pair” genetically?

Yes!

However, from genetics alone, we would not be able to easily distinguish (it seems) between the grasshopper and Mouflon sheep scenarios.

> Christy:
>
> Isn’t that exactly what these genetic studies being discussed are showing didn’t happen with Homo sapiens?

Only within a time range. However, we are also looking at the “human lineage” (see Dennis’s claim #2), which include all our ancestors even before they are Homo sapiens.

Right now, we are looking at evidence against a single couple origin within the last 500 kya. With further analysis (e.g. using PSMC), I suppose that might increase up to about 700 or 800 kya, but we do not know for sure yet.

However, before that point, say at about 750 kya or 2 mya, I’m not sure we can rule out a single couple bottleneck in our ancestors. Those are interesting dates too. 750 kya is when Homo sapiens, Neanderthals and Denisovans (for which we only have a knuckle) share a common ancestor. This group of species (or subspecies if they are the same species) appear to be the only hominids with hyoid bones, which might be a marker for modern linguistic capability. 2 mya is when Homo erectus arises and becomes cosmopolitan, and here is where we think clothing might arise, as does language/tools beyond other animals, and more.

At either transition, ignoring theology entirely, was their a tight bottleneck? The consensus is, right now, that there was a very tight bottleneck, at least 2 mya. Perhaps not consensus, but definitely a live option when I have talked to anthropologists is a bottleneck 750 kya. How tight would those bottlenecks be? I’m not sure we can know from extant evidence.

@Christy , these are great questions. Thanks for putting them forward. Hopefully this clarifies where it seems the science stands.

Christy (Christy Hemphill) 2018-02-11 02:27:09 UTC #579

> Swamidass:
>
> Only within a time range. Right now, we are looking at evidence against a single couple origin within the last 500 kya. With further analysis (e.g. using PSMC), I suppose that might increase up to about 700 or 800 kya, but we do not know for sure yet.
>
> However, before that point, say at about 750 kya or 2 mya, I'm not sure we can rule out a single couple bottleneck in our ancestors. Those are interesting dates too.

I'm confused. Back that far, Homo sapiens did not exist as a species, correct? Homo sapiens is 200,000 kya and forward. So if we have "ruled out" a single pair bottleneck in the time frame when Homo sapiens emerged as a species, how can it be possible that as you say, "we do not know from evidence whether Homo sapiens were ever just a single couple"?

Swamidass (Dr. S Joshua Swamidass) 2018-02-11 02:28:47 UTC #580

> Christy:
>
> I'm confused. Back that far, Homo sapiens did not exist as a species, correct? Homo sapiens is 200,000 kya and forward. So if we have "ruled out" a single pair bottleneck in the time frame when Homo sapiens emerged as a species, how can it be possible that as you say, "we do not know from evidence whether Homo sapiens were ever just a single couple"?

Typo there that I fixed.

> Swamidass:
>
> Only within a time range. However, we are also looking at the "human lineage" (see Dennis's claim #2), which include all our ancestors even before they are Homo sapiens.

Though, the genetics data only is about "our ancestors" not about Homo sapiens in particular.

It is possible that Homo sapiens arise as a single couple, but then there is subsequent interbreeding with other hominids.

Christy (Christy Hemphill) 2018-02-11 02:32:20 UTC #581

Well, it is a misunderstanding that affects multiple posts and deleting all of them would affect the flow of the conversation. So, we are talking about a single couple in the ancestry of Homo sapiens, not a single couple within the species.

Christy (Christy Hemphill) 2018-02-11 02:33:00 UTC #582

> Swamidass:
>
> It is possible that Homo sapiens arise as a single couple, but then there is subsequent interbreeding with other hominids.

When would this have hypothetically had to to happen?

Swamidass (Dr. S Joshua Swamidass) 2018-02-11 02:33:01 UTC #583

> Christy:
>
> Well, it is a misunderstanding that affects multiple posts and deleting all of them would affect the flow of the conversation. So, we are talking about a single couple in the ancestry of Homo sapiens, not a single couple within the species.

That is what I originally meant, however…

> Swamidass:
>
> It is possible that Homo sapiens arise as a single couple, but then there is subsequent interbreeding with other hominids.

Swamidass (Dr. S Joshua Swamidass) 2018-02-11 02:52:00 UTC #584

> Christy:
>
> > It is possible that Homo sapiens arise as a single couple, but then there is subsequent interbreeding with other hominids.
>
> When would this have hypothetically had to to happen?

Probably sometime between 350 kya and 100 kya, depending on exactly when we think Homo sapiens arise in the fossil record. Substantial interbreeding before 100 kya would probably be undetectable (though, perhaps that date has to move back a bit).

Christy (Christy Hemphill) 2018-02-11 03:01:16 UTC #585

If there is substantial interbreeding, how can you definitely identify a species boundary? Aren't species boundaries usually identified when interbreeding stops?

Swamidass (Dr. S Joshua Swamidass) 2018-02-11 03:09:49 UTC #586

> Christy:
>
> If there is substantial interbreeding, how can you definitely identify a species boundary? Aren't species boundaries usually identified when interbreeding stops?

Sometimes. Sometimes not.

For example, we know Neanderthals interbred substantially with Homo sapiens. However, some scientists would still classify them as a different species. Homo sapiens are defined by a cluster of anatomical and behavioral traits, a cluster that some are certain do not apply to Neanderthals.

T.j_Runyon (T J Runyon) 2018-02-11 09:06:11 UTC #587

I just want a simple question answered. Is a two person bottleneck possible without common ancestry? Could we be descended from two people that were created de novo and not descended from a previous previous population or part of a larger population, but the sole progenitors of Homo sapiens (not taking into account ad hoc miracles)?

Jonathan_Burke (Jon) 2018-02-11 09:11:39 UTC #588

> T.j_Runyon:
>
> I just want a simple question answered. Is a two person bottleneck possible without common ancestry? Could we be descended from two people that were created de novo and not descended from a previous previous population or part of a larger population, but the sole progenitors of Homo sapiens (not taking into account ad hoc miracles)?

I raised that question some weeks back.

Lynn_Munter (Lynn Munter) 2018-02-11 10:06:17 UTC #589

> T.j_Runyon:
>
> Is a two person bottleneck possible without common ancestry? Could we be descended from two people that were created de novo and not descended from a previous previous population or part of a larger population, but the sole progenitors of Homo sapiens (not taking into account ad hoc miracles)?

If we didn't descend from a population related to the chimpanzees and other apes, God sure went to a lot of pains to make it look as though we did. The similarities go far beyond anything that would be explained by 'similar function, similar genes' and include endogenous retroviruses, which are virus-like bits of DNA that go around inserting themselves randomly into our DNA so they get copied down into perpetuity. Some of these retroviruses we find in our DNA we can match with the same retroviruses inserted into the exact same places in chimpanzee DNA. Coincidence? No. Either we both descend from the same ancient creature in which the original insertion took place, or some One really wanted us to think we did.

But on the bright side, it is not stated in the Bible how many humans God first created, nor does it specify how he created them.

"So God created mankind in his own image; in his own image God created them; he created them male and female." Genesis 1:27

The later story of Adam is set in an environment where there are already other humans in the land (Gen 4:14–17).

I will let **@Swamidass** clarify the discussion at hand. I have lost track of which claims he is referring to.

T.j_Runyon (T J Runyon) 2018-02-11 14:31:51 UTC #590

Was it answered? The thread has gone way beyond the point I felt like Dennis was trying to make and has just turned into word games. I just want this one question answered and no one seems interested in it but instead wants to play word games.

Bill_II 2018-02-11 14:57:38 UTC #591

> T.j_Runyon:
>
> I just want this one question answered and no one seems interested in it but instead wants to play word games.

As I understand the current word game the science says there has been no two person bottleneck in the last 200,000 to 300,000 years to a fair degree of certainty. Now it is possible that there was a couple 10,000 years ago who could be related to everyone alive today but not genetically. Said couple obviously being just one of many from that time period. Think how many grandparents you have if you go back 400 generations.

RichardBuggs (Richard Buggs) 2018-02-11 15:36:54 UTC #592

> Swamidass:
>
> As I understand it, you are trying to pressure test any claims being made. I can appreciate that, and am fine with that. At the same time, I think it is important to be honest with the Church about what the evidence appears to show, at least at this point in the conversation.

Absolutely, I think you and I both agree with the need to be as rigorous as possible in our science here, and be open with the Church about what we do and don't know, and when we change our views in the light of the evidence.

I have been thinking over the ARGweaver paper since you clarified for me what the authors were doing. My initial mis-understanding of the paper made me think that different assumptions about population sizes could be a game-change for your calculations of TMR4A, but now I understand the paper better I don't think this is the case. Thank you for helping me on that one. This was the most major of my criticisms, and now that this is removed I feel more confident in your conclusions.

As you have said, this is just a first attempt at an estimate of TMR4A, and a more rigorous approach would be possible, but would be a lot of work. As we have also noted, the results could be affected by revisions in the estimation of recombination rates and mutation rates. It could also be that if the phylogenetic trees were built in a way which sought to maximise the number of mutations in the first four diverging lineages, different topologies might emerge (I'm not sure about this, but it would be interesting to examine the possibility). Unexpected factors that we have not accounted for as yet could also come into play, as happened in the Lenski experiment in a very different context. We can never be completely sure, as science is always progressing.

However, despite this, the big picture is that I am very much in agreement with you, and it is probably not profitable at this stage to continue to belabour criticisms of your analysis.

I think at this stage, it would be helpful to the Church if we could come up with a statement that we can all agree on, that summarises where we have come to in this discussion. This has been a long discussion that many will not have the time to wade through, and if you, **@DennisVenema** and perhaps **@glipsnort** and I, could come up with a statement that summarises the degree of consensus that we are reaching, then that might be helpful to the Church at large.

From my reading of our discussion, though there are things that we still differ over, here is a statement that I think we could all agree on:

As Christian biologists, we have over the last few months reviewed the population genetic literature, asking if it is possible that all modern humans could descend from a single couple within a theistic evolution (or evolutionary creation) framework. We have assumed that humans share common ancestry with apes, and that God has not intervened with physical miracles. Our task has been difficult because the hypothesis of a bottleneck of two in the human lineage has not been directly addressed in the scientific literature using genome-wide human diversity data. Nonetheless, from those published studies of human diversity that we have reviewed, and based on our understanding of current theory, we have drawn tentative conclusions. We conclude that current human genetic diversity data does not rule out a bottleneck of two individuals in the human lineage between approximately 400,000 and 7,000,000 years ago, but neither do they show that such a bottleneck has happened. Current analyses and models suggest that a two-person bottleneck has not occurred below a threshold of approximately 400,000 years before present. More research is needed in this area, and we are open to new analyses moving this threshold up or down.

If **@swamidass** **@DennisVenema** and perhaps **@glipsnort** agree that this is a consensus we have reached, I suggest that we publicly affirm this. I am very happy to discuss modifications to this statement that would enable all of us to affirm it.

Jonathan_Burke (Jon) 2018-02-11 16:09:56 UTC #593

Yeah, not to my knowledge. Leaving it ambiguous is to the advantage of YECs and IDers, so I expect this won't be clarified.

T.j_Runyon (T J Runyon) 2018-02-11 16:40:10 UTC #594

Thanks for that clearly written statement, Richard. What I've been looking for

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Lynn_Munter (Lynn Munter) 2018-02-11 16:53:23 UTC #595

> RichardBuggs:
>
> We conclude that current human genetic diversity data does not rule out a bottleneck of two individuals in the human lineage between approximately 400,000 and 7,000,000 years ago, but neither do they show that such a bottleneck has happened.

Would it be more accurate to say they show no support for such a bottleneck, instead of saying they don't show it's happened? It seems to leave quite a lot of wiggle room as is.

Jonathan_Burke (Jon) 2018-02-11 16:54:13 UTC #596

It's certainly a lot longer than 300,000 years ago.

Swamidass (Dr. S Joshua Swamidass) 2018-02-11 17:44:22 UTC #597

> RichardBuggs:
>
> If **@swamidass** **@DennisVenema** and perhaps **@glipsnort** agree that this is a consensus we have reached, I suggest that we publicly affirm this. I am very happy to discuss modifications to this statement that would enable all of us to affirm it.

@RichardBuggs I think this is an excellent idea. In terms of hashing out details, I suggest we do this on a private thread. I'll start one for us.

Also, we need to discuss trans-species variation. It should not take too long. Within a couple days (maybe today), I'll post my analysis of this for comment.

Thanks for your contributions here. Your questions and effort have encouraged real progress in our understanding. I appreciate a great deal the example you have set in (1) being sensitive to the questions of the church, (2) being correctable in an area you are an expert, and (3) being honest with the Church about difficult findings in science. I hope we all can follow that example.

Swamidass (Dr. S Joshua Swamidass) 2018-02-11 22:28:25 UTC #598

As guide for people just joining the conversation, The key scientific points are condensed here. The bolded links at the bottom were just added today, and might have been missed otherwise. In particular, take a look at how this estimate might be adjusted if the whole genome was included (**https://discourse.peacefulscience.org/t/heliocentric-certainty-against-a-bottleneck-of-two/61/14?u=swamidass**). If you find any errors, please let me know. Thanks.

Claims of Heliocentric Certainty. What are the scientific claims in question?

The Ecological Fallacy.: *Homo sapiens* go to zero, so why couldn't they go to two?

TMRCA or Time to Most Recent 4 Alleles? TMR4A (not TMRCA) puts the bounds on a couple bottleneck.

Estimate with Median or Max? The statistically sound approach is the median.

TMR4A from Genome-Wide TMRCA. An initial estimate of TMR4A.

The ArgWeaver Genome Wide Phylogenies 424 GB of data with genome-wide answers.

Genome-Wide TMR4A. A better estimate of TMR4A.

ArgWeaver Does Not Assume Large Population. The computed TMR4A is biased downwards, not upwards, by the prior.

The Correct Mutation Rate. ArgWeager is using an experimentally confirmed mutation rate.

Correctly Weighting Coalescents. An improve esitmate of TMRCA is about 500 kya.

ArgWeaver works like MAP and MrBayes. Really, no assumptions of population size are made, and this is just a measure of human variation, converted to units of time.

A Estimate Robust to Correction. The TMR4A estimate is exceedingly stable. AJ Roberts from *Reasons to Believe* would want a correction for the amount of genome that is not yet sequenced.

What about Recombination? The errors we see in ArgWeaver do not effect TMR4A estimates.

Christy (Christy Hemphill) 2018-02-12 01:07:36 UTC #599

> RichardBuggs:
>
> As Christian biologists, we have over the last few months reviewed the population genetic literature, asking if it is possible that all modern humans could descend from a single couple within a theistic evolution (or evolutionary creation) framework. We have assumed that humans share common ancestry with apes, and that God has not

> intervened with physical miracles. Our task has been difficult because the hypothesis of a bottleneck of two in the human lineage has not been directly addressed in the scientific literature using genome-wide human diversity data. Nonetheless, from those published studies of human diversity that we have reviewed, and based on our understanding of current theory, we have drawn tentative conclusions. We conclude that current human genetic diversity data does not rule out a bottleneck of two individuals in the human lineage between approximately 400,000 and 7,000,000 years ago, but neither do they show that such a bottleneck has happened. Current analyses and models suggest that a two-person bottleneck has not occurred below a threshold of approximately 400,000 years before present. More research is needed in this area, and we are open to new analyses moving this threshold up or down.

Is anyone taking bets about whether or not Evolution News and Views will promptly publish an article about this part of the thread? 🤨

T.j_Runyon (T J Runyon) 2018-02-12 07:54:30 UTC #600

This whole thread has been quite a learning experience. While it was frustrating at times because I'm at the beginning of my genetics education I still feel like I benefited from this. But areas I do feel more than competent to discuss are paleoanthropology and archaeology. These areas are where the vast majority of my studies have taken place and where I have had the most training. So im wondering if I take the time to write up something about the viability of a non sapiens Adam and Eve and start a new thread to discuss it will people here be interested in doing so? I don't want to waste my time getting all of my sources together and writing it up if no one is interested in having that discussion. Thanks!

Christy (Christy Hemphill) 2018-02-12 13:40:22 UTC #601

> T.j_Runyon:
>
> So im wondering if I take the time to write up something about the viability of a non sapiens Adam and Eve and start a new thread to discuss it will people here be interested in doing so? I don't want to waste my time getting all of my sources together and writing it up if no one is interested in having that discussion.

Do it. People will discuss it.

RichardBuggs (Richard Buggs) 2018-02-14 09:31:11 UTC #602

In the beginning, when we were first debating this at Skeptical Zone, I noted:

"a creationist (in the conventional sense of the word) would not be concerned about this entire topic as it assumes common ancestry and creationism can have genetic diversity front-loaded into Eve's ova anyway, thereby avoiding the whole issue of genetic diversity. I suspect many Christians, Jews and Muslims would be interested in the idea of a half million year old ancestral bottleneck of two."

See: **http://theskepticalzone.com/wp/adam-and-eve-still-a-possibility/comment-page-3/#comment-198358**

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gbrooks9 (George Brooks) 2018-02-14 19:40:15 UTC #603

> Swamidass:

> . . . there is ZERO evidence that they do not begin as a single couple.
> Zero evidence. So how do we come to heliocentric certainty about a claim substantiated by zero evidence?

@Swamidass

I think this is the sword upon which you must, of necessity, fall.

I think the sentence you have here is false… and demonstrably so.

The sentence that I **thought** you were defending would be more like this:

“There is ZERO evidence that God did not create a unique mating pair (Adam & Eve) to contribute to the larger human population, anywhere between 10,000 years to 6,000 years ago.”

In order to defend your original statement, you would have to specify something that forces the discussion into a non-YEC context (being silent on the issue does not make the sentence more valid):

**"There is ZERO evidence that [hominids] did not begin as a single couple, more **
than 300,000 years ago… Zero evidence. So how do we come to heliocentric certainty about a claim substantiated by zero evidence?"

If you attempt to replace “hominids” with “humans” (i.e., Homo sapiens), then the lack of any human fossils from 60,000yr to 300,000yr old strata is the evidence that it didn’t happen.

What are your thoughts on this brief analysis, **@Swamidass** ?

---

glipsnort (Steve Schaffner) 2018-02-15 16:31:09 UTC #604

> RichardBuggs:
>
> I have been doing a bit more reading about the theoretical background of some of the methods we have been discussing here. I am not a mathematician, so much of this is outside of my area of expertise. However, I have come across three papers that suggest that seem to suggest that site frequency spectra (as presented earlier in this discussion) have severe limitations as a source of evidence about past population sizes. The second of these papers specifically examines scenarios of a bottleneck followed by exponential population growth.

Okay, I’m about a month late and the thread has moved on, but I said I would comment about these papers, so here I am.

> RichardBuggs:
>
> Simon Myers, Charles Fefferman, Nick Patterson **Can one learn history from the allelic spectrum**?

This is an interesting paper from a theoretical perspective, but the practical implications are really only addressed in later papers. The authors conclude that the allele frequency cannot uniquely identify the actual demographic history, but as noted in the third cited paper, the example they give is not biologically plausible.

Note: I know this paper fairly well, since I shared an office with two of the authors (Simon and Nick) at different times, including while they were writing the paper. The third author is a math heavyweight they had to bring in to get past a sticky bit. Nick had some trouble getting the paper published, not because there was anything wrong with it, but because a reviewer sat on the paper on the paper for well over a year. I was at a mathematical genetics meeting in Durham (where I really did not belong), where Nick gave a talk. He ended by pointing out that this paper had been out for review forever, that the reviewer was probably in the audience, and could he please do his job? He got the reviews back a few weeks later.

> RichardBuggs:
>
> Terhorst, Jonathan, and Yun S. Song. Fundamental limits on the accuracy of demographic inference based on the sample frequency spectrum.

This paper does indeed consider a population bottleneck followed by exponential increase in size, and concludes that there are fundamental limits on how accurately such a demography can be reconstructed solely from the site frequency spectrum. It is important to note, however, that the difficulty they demonstrate is in reconstructing demographic events *prior* to the bottleneck, not the existence of the bottleneck itself. This is clear from their discussion section: “Intuitively, as the severity of the bottleneck increases, the population is increasingly likely to find its most recent common ancestor (MRCA) during that time; farther back in time than the MRCA, no information is conveyed concerning the demographic events experienced by the population.” Similarly: “Additionally, an interesting aspect of our work is that our minimax lower bounds do not depend on the number n of sampled individuals; increasing n is not enough to overcome the information barrier imposed by the presence of a bottleneck.”

> RichardBuggs:
>
> Baharian, Soheil, and Simon Gravel. “On the decidability of population size histories from finite allele frequency spectra.”

This is the most interesting of the papers. It shows that the results of the first paper apply approximately for much more realistic demographies, and that tight bottlenecks can be invisible when just looking at the frequency spectrum. Again, though, there’s an important point to note: the bottleneck they simulate is still, compared to what we’ve been talking about, quite old: 2.5 times the usual 2N generations. Certainly well over a million years ago for humans. I have no trouble believing that demographic signals from that era can be erased. What I have always found implausible is that a signal from less than 0.5 x 2N could be erased, since it leaves insufficient time to accumulate new mutations and get them to high frequency.

Swamidass (Dr. S Joshua Swamidass) 2018-02-15 16:55:53 UTC #605

@glipsnort , always great to see you.

Help me understand this…

> glipsnort:
>
> What I have always found implausible is that a signal from less than 0.5 x 2N could be erased, since it leaves insufficient time to accumulate new mutations and get them to high frequency.

As I understand it, 2N is about 2 million years ago (approx genome wide TMRCA, right?). Your SFS studies show no signal for a bottleneck at 0.5 million years ago, which is 0.25x 2N. Though, as I think about it, your studies used smaller population sizes we expect (e.g. constant 10,000 at all times), so perhaps your 2N is a lot lower than 2 million years?

So where is my math wrong here? If possible…

1. square this with your prior simulations on SFS.
2. give extrapolate to the real human data for where that cutoff might be.
3. tell us if you think there is anything here that conflicts with the TMR4A work.

Thanks.

---

gbrooks9 (George Brooks) 2018-02-15 17:38:49 UTC #606

@Swamidass ,

I asked you a question at the end of this posting (located above) … It's passingly important for me to understand some of the discussions you are maintaining. I hope you can get to it sometime in the near future! 😃

> gbrooks9:
>
> **@Swamidass** I think this is the sword upon which you must, of necessity, fall. I think the sentence you have here is false… and demonstrably so. The sentence that I thought you were defending would be more like this: "There is ZERO evidence that God did not create a unique mating pair (Adam & Eve) to contribute to the larger human population, anywhere between 10,000 years to 6,000 years ago." In order to defend your original statement, you would have to specify something that forces the…

---

cwhenderson (Curtis Henderson) 2018-02-15 19:39:28 UTC #607

> Christy:
>
> Is anyone taking bets about whether or not Evolution News and Views will promptly publish an article about this part of the thread? 🤨

Thanks, Christy, I got a pretty good laugh out of that one!

Swamidass (Dr. S Joshua Swamidass) 2018-02-15 22:10:09 UTC #608

> gbrooks9:
>
> > . . . there is ZERO evidence that they do not begin as a single couple.
> > Zero evidence. So how do we come to heliocentric certainty about a claim
> > substantiated by zero evidence?
>
> **@Swamidass**
>
> I think this is the sword upon which you must, of necessity, fall.
>
> I think the sentence you have here is false… and demonstrably so.

It is not. If "human" = Homo sapien as explained by Venema, there is no evidence that, as you almost say…

> "There is ZERO evidence that God did not create a unique mating pair (Adam & Eve) **(perhaps the first Homo sapiens)** to contribute to the larger ***hominid*** population, **when Homo sapiens arise**."

In this case, there is no evidence against it, and Homo sapiens ("human" according to Dennis) begin with a single couple.

@gbrooks9 , regarding the the 6kya - 10 kya timeline, that is not really what I have put forward. For a genealogical Adam (not necessarily the first Homo sapien), they could arise ***anytime*** before 6 kya, not just in that narrow range.

Jay313 (Jay Johnson) 2018-02-15 22:47:38 UTC #609

> Swamidass:
>
> "There is ZERO evidence that God did not create a unique mating pair (Adam & Eve) (perhaps the first Homo sapiens) to contribute to the larger homind population, anywhere between 10,000 years to 6,000 years ago."
>
> In this case, there is no evidence against it, and Homo sapiens ("human" according to Dennis) begin with a single couple.

This doesn't make any sense. But before I get to that, here are the definitions of hominid and hominin according to the Australian Museum:

Hominid – the group consisting of all modern and extinct Great Apes (that is, modern humans, chimpanzees, gorillas and orang-utans plus all their immediate ancestors).

Hominin – the group consisting of modern humans, extinct human species and all our immediate ancestors (including members of the genera Homo, Australopithecus, Paranthropus and Ardipithecus).

I don't think that God specially created Adam & Eve to contribute to a larger population that included chimps, gorillas, and orangutans. haha. Sorry. In any case, the only hominin that wasn't extinct 10,000 years ago was us, formally known as *Homo sapiens* and colloquially referred to as human beings. A unique mating pair named *Adam and Eve* would not be the first *H. sapiens* by any definition, nor would they be the first humans, unless you want to strip even that fig-leaf of dignity away from these "pre-Adamic people" (or whatever moniker they may go by in your scheme).

Swamidass (Dr. S Joshua Swamidass) 2018-02-15 22:54:47 UTC #610

> Jay313:
>
> This doesn't make any sense.

It is common for **@DennisVenema** to use "hominid" in the same way I just did. Feel free to take that up with him. Perhaps I could be more clear…

> Swamidass:
>
> "There is ZERO evidence that God did not create a unique mating pair (Adam & Eve) (perhaps the first Homo sapiens) to contribute to the larger a population (which were not Homo sapien at the time of A&E).
> years ago."

Also, the time line needed to be dropped. This would obviously be well before 10 kya.

DennisVenema (Dennis Venema) 2018-02-16 00:19:05 UTC #611

> Swamidass:
>
> It is common for @DennisVenema to use “hominid” in the same way I just did. Feel free to take that up with him. Perhaps I could be more clear…

I do use hominid, but to refer to the common ancestral population that includes the lineage leading to chimpanzees (or further back). As far as I know, in Adam and the Genome, I use hominin - species more closely related to us than chimps. So, hominid isn’t a usual term I use. If you go far enough back in my writing, you’ll come to a time where I wasn’t consistent with my usage, but that is quite a ways back.

DennisVenema (Dennis Venema) 2018-02-16 00:21:07 UTC #612

> Jay313:
>
> Homo sapiens (“human” according to Dennis)

Just keep in mind that “human” in my mind is shorthand for anatomically modern human. Also keep in mind that species designations are a fallible human attempt to draw lines on a continuum.

Lynn_Munter (Lynn Munter) 2018-02-16 02:58:21 UTC #613

> gbrooks9:
>
> If you attempt to replace “hominids” with “humans” (i.e., Homo sapiens), then the lack of any human fossils from 60,000yr to 300,000yr old strata is the evidence that it didn’t happen.

There are (more or less) anatomically modern human fossils in this age range in Africa (and now Israel, too).

Jay313 (Jay Johnson) 2018-02-16 11:32:20 UTC #614

> DennisVenema:
>
> “human” in my mind is shorthand for anatomically modern human.

I gathered that. The “quote” you referenced was Swamidass’ words, not mine.

DennisVenema (Dennis Venema) 2018-02-16 16:38:26 UTC #615

I don’t know why it quoted you - I knew that the word’s were Josh’s, not yours. Strange.

RichardBuggs (Richard Buggs) 2018-02-16 18:58:33 UTC #616

Hi Steve,
Thank you for coming back to this, and for these useful comments, and for the anecdote about the Myers et al paper.

Regarding Terhorst and Song (2015):

> glipsnort:
>
> It is important to note, however, that the difficulty they demonstrate is in reconstructing demographic events prior to the bottleneck, not the existence of the bottleneck itself. This is clear from their discussion section: “Intuitively, as the severity of the bottleneck increases, the population is increasingly likely to find its most recent common ancestor (MRCA) during that time; farther back in time than the MRCA, no information is conveyed concerning the demographic events experienced by the population.” Similarly: “Additionally, an interesting aspect of our work is that our minimax lower bounds do not depend on the number n of sampled individuals; increasing n is not enough to overcome the information barrier imposed by the presence of a bottleneck.”

I agree, but they also seem to be saying that it is not just a bottleneck that is hard to see through, but also any order-of-magnitude expansion of effective population size. See p7680: “This implies that for populations that have experienced roughly an order-of-magnitude increase in effective population size during their history, accurate estimation of demographic events that occurred before this expansion is difficult using SFS-based methods.” I would imagine that in the recent past the population of Africa has gone through a rapid increase of effective population size of at least an order of magnitude through both population growth and increased mixing among sub-populations. Wouldn’t it be hard to see back beyond this using SFS-based methods? I have to admit I have not mastered the maths in this paper, so I am just having to go on their discussion section.

Swamidass (Dr. S Joshua Swamidass) 2018-02-18 01:36:44 UTC #617

Okay, here are my current thoughts on trans-species variation. I invite a deep dive in the literature to see if anyone can find a key paper I overlooked. Please prove me wrong if you can…

Trans-species variation. The evidence against an ancient bottleneck in trans-species variation is not as strong as I had thought.

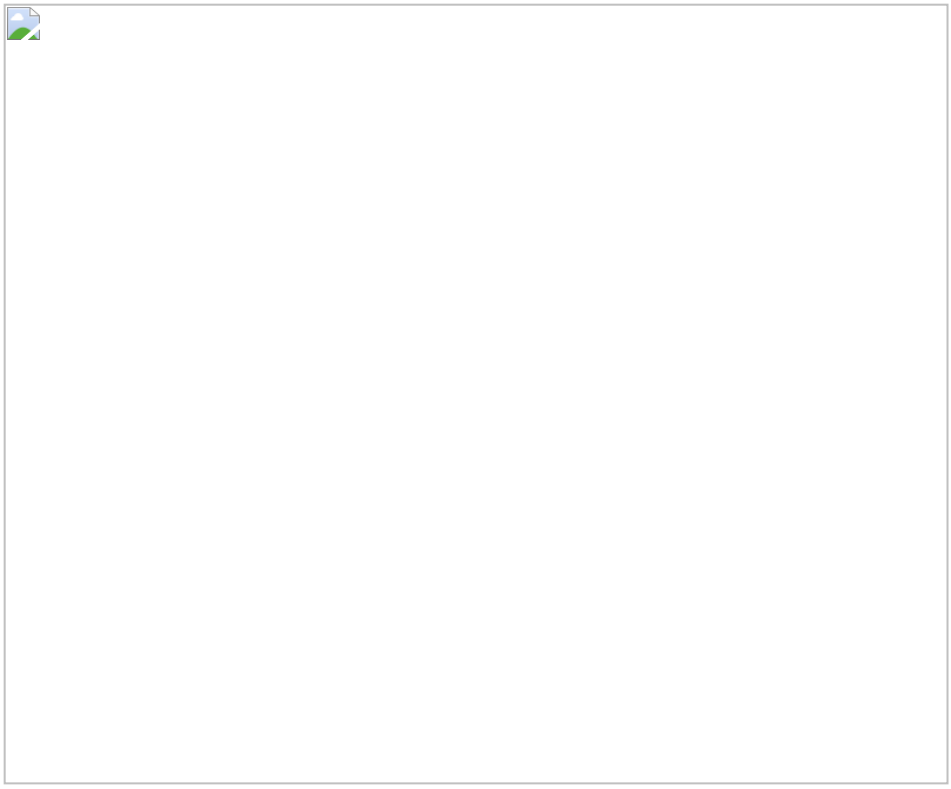
As we have seen, there is a limit how far back the evidence from **Human Variation** gives us confidence against a single couple bottleneck. Before about 500 kya, it is possible that such a bottleneck, if brief, would be undetected in by current population genetics models. The specific number may be adjusted upwards by further analysis, but it’s a good starting point for now.

However, this is not actually the strongest argument put forward against a single couple bottleneck since we diverged from chimpanzees. For that, we have to look more closely at **Trans-Species Variation**.

Trans-Species Variation

Human Variation and Trans-Species Variation are related but different. To measure human variation, we look at a large number of human sequences. To measure trans-species variation, we look at a large number of both human and non-human sequences, usually chimpanzee. From looking at this data, we might find evidence of alleles that appears ***both*** in chimpanzees (for example) and humans.

This figure illustrates what appears to be happening:



https://humgenomics.biomedcentral.com/articles/10.1186/s40246-015-0043-1

The key point is that along each of the colored lines, *several* lineages are being shared between different species at a single place in the genome. Normally, there would be just one lineage on these time scales, but balancing selection maintains *multiple* lineages of alleles. By counting the number of allele lineages shared between humans and others, we can put a hard-stop lower bound on a bottleneck going back before humans and chimps diverge. Whatever bottlenecks there are they have to be big enough to include all the trans-species lineages.

Molecular Clock Not Valid

One tempting argument, which is not quite right, is to just estimate the TMRCA (or TMR4A) of these alleles, the same as we did across the genome, and use this as an estimate of a bottleneck time. This however, is an error.

Something called “balancing selection” is critical for enabling variation to last long enough to be shared this long between humans and other species, and this usually happens in proteins important for our immune response. So we see trans-species in only a few regions of the genome.

However, balancing selection violates the conditions required to accurately date variation in DNA. We cannot use our formula D = R * T here, because, in this case, we do not have a valid way of estimating R over these time frames. While in neutral regions of the genome, the average mutation rate works in our favor, at times we expect balancing selection to be increasing the rate of change in unpredictable and untestable ways. This can happen very rapidly as balancing selection can even select for increased mutation rates within this region.

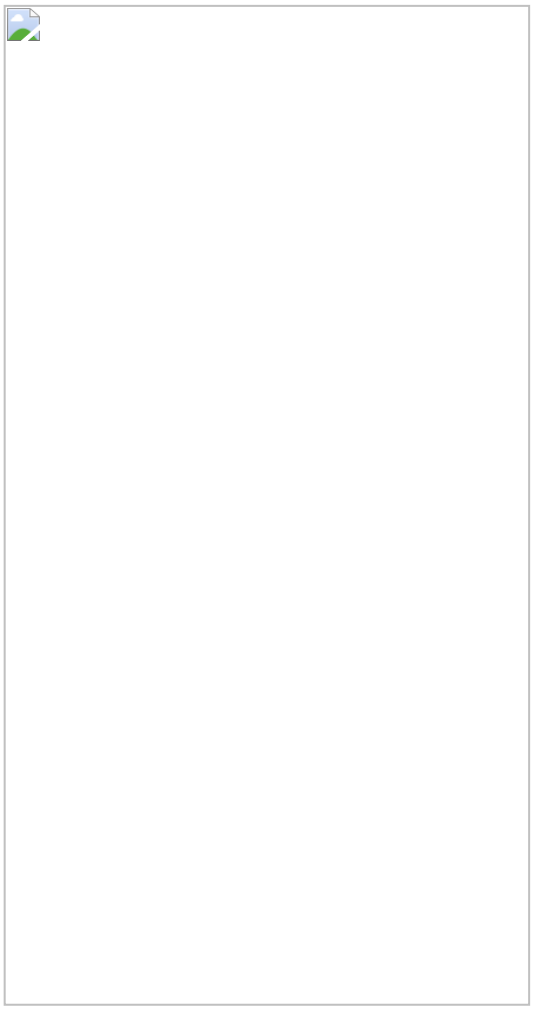
Ayala’s Argument Against a Bottleneck

The argument here is two part. First, from effective population size estimates, and second from trans-species variation. I’m not going to engage the argument about effective population size, because it appears to be incorrect. Very tight bottleneck can still have high effective population size, and it seems Ayala missed this point. But this just takes us back to the TMR4A work.

This is where **trans-species** variation becomes important. It gives an independent way of dating alleles. If an allele in humans is closer to non-human alleles, it appears that it existed before those two species diverged, and was

maintained by balancing selection to this day.

This study by Francisco Ayala was the first, to my knowledge, to make the case against a bottleneck by studying trans species variation HLA alleles. **https://www.sciencedirect.com/science/article/pii/S1055790396900135**



This figure from Ayala shows human alleles with other primate alleles joined by ***similarity***, not phylogenetic analysis that respects nested clades. I've highlighted the human alleles in this figure, and drawn red circles around 7 clusters of alleles which appear to be shared between human and other species. Remember, we can only put 4 alleles at each position in the genome of a couple, so this seems (at least on face value) to demonstrate there must have been at least 4 individuals in the tightest bottleneck of our ancestors.

Ayala's summary is:

> Figure 4 is a genealogy of the HLA alleles obtained by the UPGMA method, which assumes constant rates of evolution and thus aligns all 19 alleles at the zero- distance point that corresponds to the present. The ge- nealogy suggests that **8 allele lineages were already in existence 15 Myr ago**, at the time of the divergence of the orangutan from the lineage of African apes and hu- mans; and that **12 allele lineages were in existence 6 Myr ago, at the time of divergence of humans, chimps, and gorillas**.

The difference between his numbers and mine in how we determine lineages. There is some ambiguity in how we determine the cutoffs. Still, as long as we see more than 4 lineages with trans-species variation, its seems like evidence against a single couple bottleneck. From this, he argues,

> There is, however, no evidence supporting the claim that ex- treme bottlenecks of just a few individuals, such as postulated by some speciation models (Mayr, 1963; Car- son, 1968, 1986), have occurred in association with hominid speciation events, or with major morphological changes, at any time over that last several million years.

This is probably correct, in that there is no evidence *for* a bottleneck that I can see. But he means here to mean that a bottleneck has not happened: i.e. there is evidence *against* a bottleneck in the last several million years. That may be incorrect.

Some Technical Asterix

Generally speaking, this work has been understood in the field to definitely discount any notion of a single couple bottleneck. On face value, that is certainly what it looks like. However, there are some big caveats.

1. The molecular clock based dates computed in these studies, it does not appear to be well calibrated.
2. We do not really know the confidence on any of these clusters, because Ayala did not estimate them using modern bayesian methods.
3. He also used a similarity based method to build the trees, rather than a true phylogenetic reconstruction. This is important, because it can produce different clusters.
4. It does not appear convergent evolution was accounted for in this analysis. Convergent evolution, at this level, can create the appearance of shared history when there is none.
5. His population simulation used a bottleneck lasting 10 generations (e.g. 10 individuals for 10 generations), which is much longer than the bottlenecks we are considering (e.g. 2, to 10, to 500, to 2500, to 12500).

While these are interesting results, at some point, this analysis needs to be done with better methods to really determine how many lineages are persistent over the last 6 mya. Moreover, effort to correct for convergent evolution is important here too. On the simulation size, a brief bottleneck needs to be considered, rather than just those of 10 generations.

A Finding Not Replicated

Ayala focused his work on HLA-DBQ1 (one of the MHC genes), but similar work has shown trans-species variation at other locations in the genome. However, I could not uncover a single other study that shows more than 4 lineages with tran-species variation.

I cannot do a full review here, but we can see the balancing at other genes, with fewer lineages in the end. For example…

https://www.ncbi.nlm.nih.gov/pubmed/10866107

This figure is fairly typical of findings…

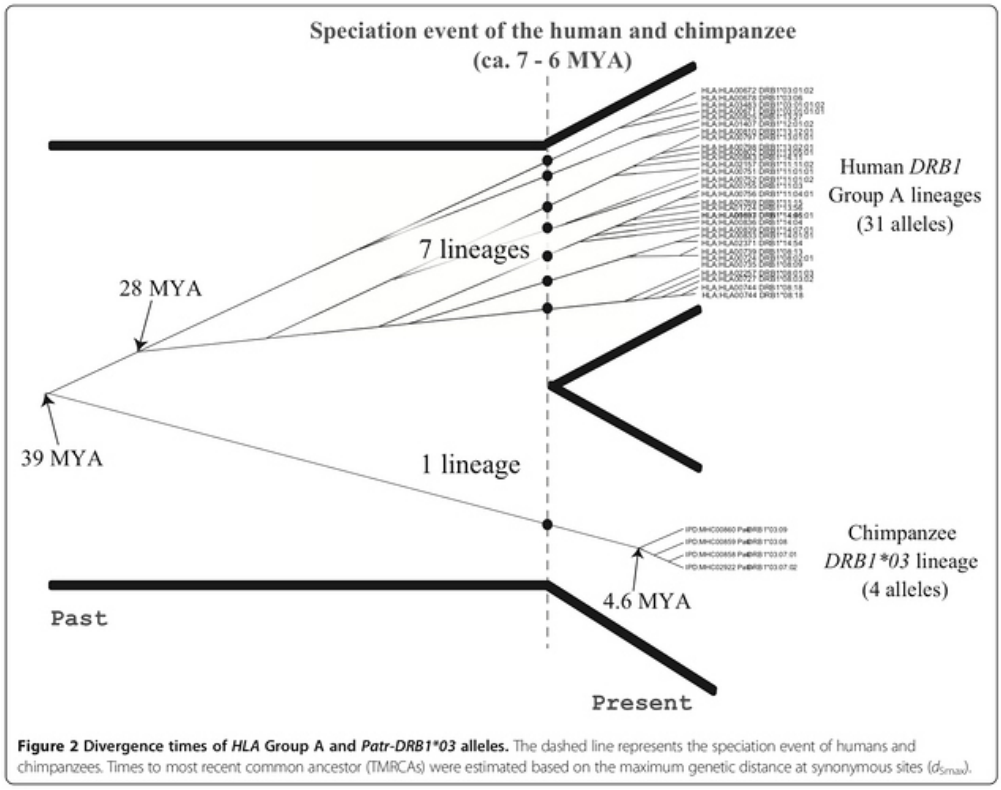
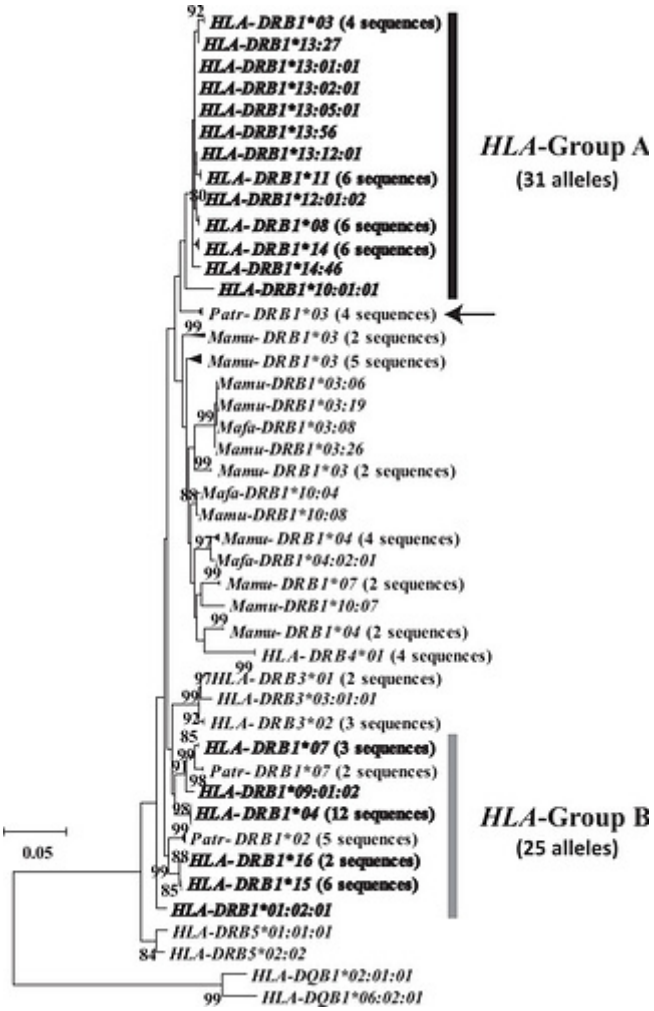


Figure 2 Divergence times of *HLA* Group A and *Patr-DRB1*03* alleles. The dashed line represents the speciation event of humans and chimpanzees. Times to most recent common ancestor (TMRCAs) were estimated based on the maximum genetic distance at synonymous sites (d_{Smax}).

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4072476/

This figure shows a molecular clock based estimate (which do not appear well-callibrated) of 7 lineages at 6 mya, however, less than four lineages (0 in this case) is shared with chimpanzee. **Reviewing several papers, I cannot find replication of Ayala's findings of more than 4 lineages being shared between humans and other species.**

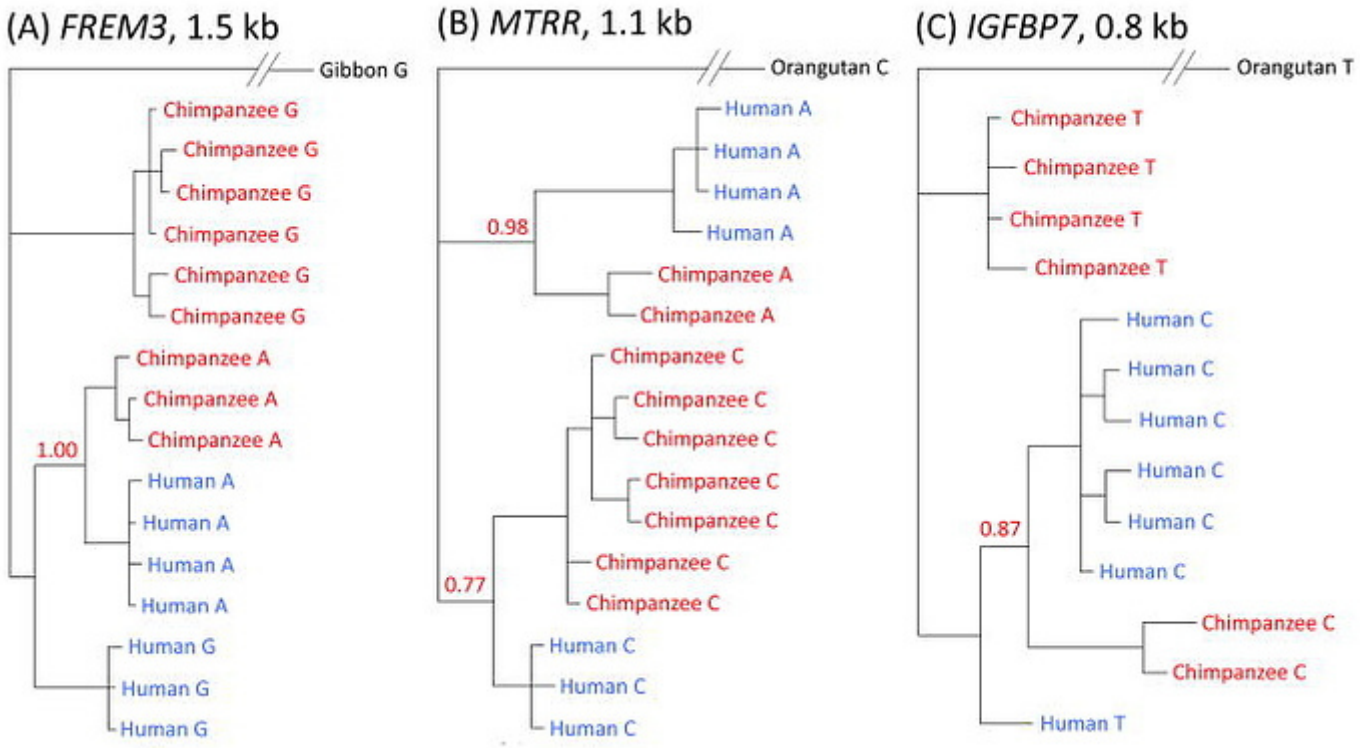
We can see this pattern in this figure too…



https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4072476

Here, the bold leaves are human sequences. Notice the difference between this figure and Ayala's. There is numbers on the edges (which indicate confidence) and we just do not see nearly as many lineages in common. The authors here conclude there is just ***one*** lineage in common.

Here is another typical results figure:



https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3612375/

Each tree is a different region of the genome. Notice, again, that there does not appear to be more than 4 clusters with both human + chimpanzee alleles.

While Ayala is an established scientist, his work was done in 1996, well before modern sequencing efforts, and modern bayesian analysis of phylogenetic trees. While no one has published on DBQ1 since he did, it is very surprising that no one else has replicated his result in the last 22 years on another locus. **Of course, if someone can find a study that does, please let me know!**,

The apparent failure to replicate this finding (with (1) much more data, and (2) improved methods), discounts substantially my trust in his findings. We just know much more about how analyze these sequences, and we have so many more of them. It is not surprising that our understanding might advance.

One Line of Evidence? One Paper?

At the moment, the Ayala paper appears to be the ***only*** study which shows more than 4 allele lineages with trans-species variation. His analysis, however, did not estimate confidence nor did it use phylogenetics to determine lineages. In 22 years, I cannot find a paper that replicates his finding. Certainly, trans-species variation has been observed, but not more than 4 lineages, as far as I can tell.

This is not enough evidence by which to make a confident claim against a single generation bottleneck.

The Way Forward

The right way forward, then, is to to study trans-species variation with the data we have now, but better methods than did Ayala. This takes some difficult work, however. I'm not 100% sure if we will give it a try here, but we might. This, also, is the most likely place a future study might uncover evidence against a single couple bottleneck.

Until that happens, however, I am not sure this is strong evidence against a brief bottleneck. I stand to be corrected, however, if someone can produce a study that shows this. If you find one, please send it to me.

Swamidass (Dr. S Joshua Swamidass) 2018-02-18 01:41:56 UTC #618

> Swamidass:
>
> Reviewing several papers, I cannot find replication of Ayala's findings of more than 4 lineages being shared between humans and other species.

Please, I want to know if I am wrong here. If you can find such a study, please let me know. Correct me if you can!

Swamidass (Dr. S Joshua Swamidass) 2018-02-18 23:11:06 UTC #619

I want to clarify a final point in public (as we hash out **@RichardBuggs** 's statement)…

Does Not Depend on Common Descent

Our conversation initially did presume common descent, however this result does not require this assumption. This result applies to everyone, not just those in the EC/TE camp.

The only way that common descent was used in this study was to determine the region specific mutation rate (which come out to an average of 0.7e-9 mutations / bp /year). The mutation rate, however, scaled down to 0.5e-9 mutations / bp / year, to be consistent with several independent studies that have directly measured genome wide mutation rates by many different methods. Read more about this here: **https://discourse.peacefulscience.org/t/heliocentric-certainty-against-a-bottleneck-of-two/61/11?u=swamidass**

We also know that the mutation rate estimated using common descent is well correlated across the genome with the experimentally measured one. Even if not, this will not shift the curve, but just increase the variance. A median TMR4A will not be affected by this error.

What We Can Expect From PSMC and MSMC Simulations

We can and should do simulated populations to see the sensitivity of PSMC and MSMC to detecting ancient bottlenecks. However, this will mean making some clearly incorrect assumptions about the population in the past. For example, we could use a population of 10,000 to simulate bottlenecks in the past, but the numbers we derive here will not apply to human data, because we know that at times there was more than a population of 10,000 in the past.

Still, my hope is those simulations would give some theoretical and empirical support for using TMR4A (or closely related measure) to determine sensitivity of PSMC and MSMC. With that aim, however, I do not anticipate large changes in the methodology. It is possible the 500 kya could move up to 800 kya or so, but not much more. Though as I have been looking at the data and working out the theory, that as not likely as remaining below 600 kya or so.

We never know until doing the analysis, but my instincts here have been largely correct.

Swamidass (Dr. S Joshua Swamidass) 2018-02-19 04:43:26 UTC #620

A few final thoughts on trans-species variation.

Convergent Evolution or Trans-Species Variation? A deeper look indicates convergent evolution, which violates the assumptions required for genetic clocks and undermines substantially the argument against a bottleneck using this line of evidence.

I wanted to further expand on this deficiency in Ayala's study.

> It does not appear convergent evolution was accounted for in this analysis. Convergent evolution, at this level, can create the appearance of shared history when there is none.

Convergent Evolution or Trans-Species Variation?

Convergent evolution, rather than shared history, is an alternate explanation of Trans-Specific variation. If we see several alleles in both humans and chimps clustered together, there are two possible explanations:

1. this could be because the allele lineaged existed in the common ancestor of the two species,
2. or it could be because of convergent evolution.

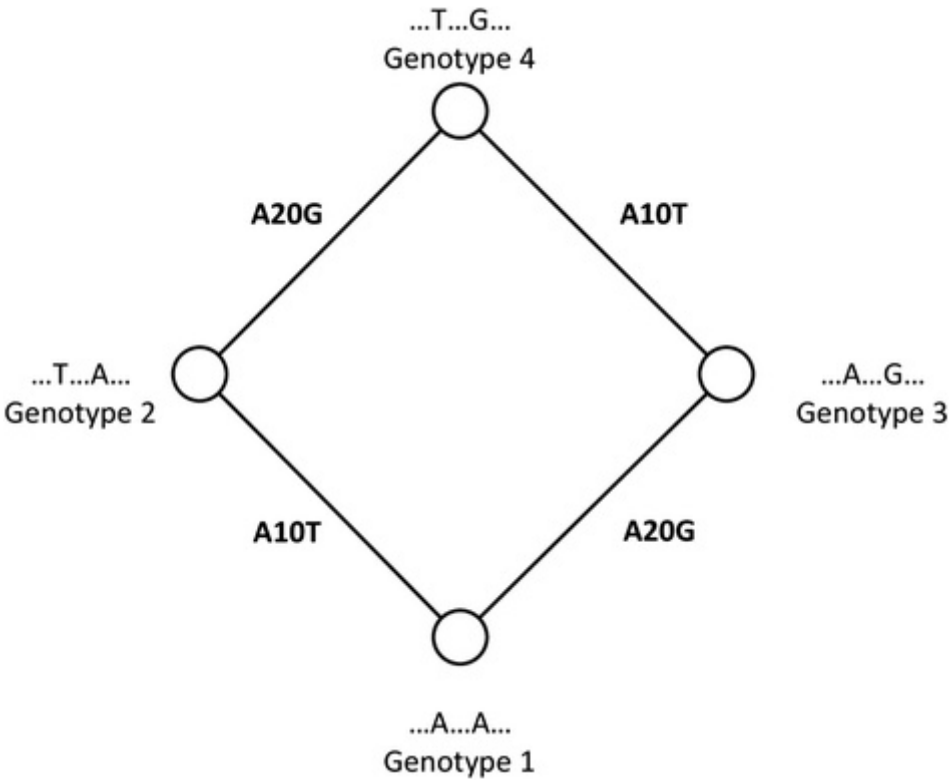
Ayala never considered or tested for this possibility. This is a critically important point, and why his use of similarity in phylogenetic analysis substantially undermines his point. In order to trust the tree, we need to know how many discordant mutations there are in the tree. However, he used similarity (not nested clades) to build the tree. He had no way to know if the data actually made sense as tree recapitulating common descent or not.

A basic feature of scientific thinking is to test hypotheses. Ayala's paper did not rule out the hypothesis of convergent evolution.

Testing for Convergent Evolution

The good news is that convergent evolution leaves a tell tale sign. We should see a large number of mutations that cannot fit into a tree like structure if convergent evolution is at play. It turns out that several groups have been studying convergent evolution on a genomewide scale, and HLA types regularly are outliers in these analyses.

For example, take a look at this study. **https://bmcevolbiol.biomedcentral.com/articles/10.1186/s12862-016-0722-0** It builds "allelic graphs", which I won't explain here in detail, except to say that when ever we see a cylcle, like this square, we know that it cannot fit into a tree structure:



https://bmcevolbiol.biomedcentral.com/articles/10.1186/s12862-016-0722-0

We expect a few of these in neutral evolution, but not many. If the data fit a tree, we would only see a single path from the top genotype to the bottom one. However, if we see both paths, we know that different alleles are taking different paths, which means that they do not actually share history here. It is a type of homoplasy, and it is a signature of convergent evolution. Notably, this signature is specific to convergent evolution, is not likely caused by Trans-Species variation.

If we see a large number of these squares in the genetic diversity of a particular part of the genome, that is evidence that the similarity we see between sequences is not actually a signature of common descent. Rather, in these cases, another hypothesis is favored: convergent evolution.

So what do the authors find?

Well, HLA genes have a massive excess of squares, a clear sign of pervasive convergent evolution. Ayala's gene HLA-DBQ1 is not mentioned in the text, but we find it in the supplementary data as one of the genes with clear evidence of convergent evolution.

Another gene, HLA-DRB1 is the most variable HLA gene. It is notable for having over 500 squares in the DNA of about merely 1,000 individuals, compared with an expected number of less than 10. That means if we had tried to put the DNA into a tree, we would see ***at least*** 500 mutations discordant with a phylogenetic tree. This is just a ***stunning*** result, because it means that HLA-DRB1 alleles are just not well described as a tree. The variation we see is evolving and re-evolving over and over again. Amazing.

It also validates my methodological concern about Ayala's work:

> He also used a similarity based method to build the trees, rather than a true phylogenetic reconstruction. This is important, because it can produce different clusters.

This is not exactly a new result, back in 2000, a test of Ayala's hypothesis was done on HLA-DBQ1. They also found strong evidence of convergent evolution. **https://www.semanticscholar.org/paper/Convergent-evolution-of-major-histocompatibility-c-Kriener-O'huigin/cf9f45169d245b7ab883a5a461f3a16fec62b751** However, the allele graph makes clear how much this affects the data. Perhaps more importantly, this *Nature* study from 1998 directly disputes Ayala's paper, arguing that this is rapid convergent evolution: **https://www.nature.com/articles/ng0398-237**.

It is just not an accurate view of the data to present HLA-DBQ1 in a tree based on a similarity matrix. We cannot even correctly determine ancestral history among human alleles themselves, let alone between species. The data seems to look more like convergent evolution than standard common descent, i.e. Trans-Species variation.

Remember, Ayala did not even consider convergent evolution. He did not test for it. This seems to a valid alternative hypothesis, which also seems to better explain the data.

Moreover it is not really accurate to present trans-species variation as a settled finding of genomic science. At best, it is one competing hypothesis among many. However, it might even be accurate to say that it is the disfavored hypothesis. There are many more papers disputing Ayala's findings than supporting it. No one should present this as as indisputable and settled evidence against a sharp bottleneck.

Perhaps the data will bear out Ayala's initial hypothesis, but a lot of work needs to be done to demonstrate this to be the case.

What About Common Descent?

Everyone believes these alleles share common descent (at least back to 4 alleles). However, this is good reminder that genetic data can pick up signatures that erase the nested clade signature we usually see in DNA. Homoplasy is a real

feature of the data, and expected even when there is common descent.

This is a great example of how there are rules in biology (e.g. DNA falls into nested clades), but there are exceptions (convergent evolution), that are very important to understanding this data.

Moreover, the next time someone points to mutations that do not fit the tree pattern in species, remember two things.

1. We expect a few discordant mutations, even in neutral evolution. That is not evidence against common descent.
2. Convergent evolution, also, can produce discordant mutations. Not usually ever as much as we see in HLA genes, but more than we expect from neutral evolution.
3. We observe homoplasy and convergent evolution in cancer (called recurrent mutations).
4. We observe homoplasy and convergent evolution in human variation (which everyone agrees shares common ancestry).

In case #2, we still expect to see a signature of common descent in most cases. However, it is such a pervasive pattern in HLA-DRB1 that it appears that the signature of common descent is erased, even though we all agree these alleles share common ancestry. And #3 and #4 are direct empirical evidence that convergent evolution is expected at a DNA level (#3) and thathomoplasy is observable in DNA everyone agrees shares common ancestry (#4).

Once again, the rule is that **most (but not all)** DNA fits into nested clades (a tree), but some does not. Neutral evolution produces nearly nested clade data, but positive selection (and balancing selection) can also lead to convergent evolution. Homoplasy (violations of nested trees) are ***expected*** in some genes, even more than we expect from neutral evolution.

The Median TMR4A Estimate Unaffected

It's important to understand how these findings interact with the TMR4A esitmates.

The convergent evolution creates homoplasy that will artificially increase TMRCA estimates upwards. Because a tree is a bad fit for the data, it will be impossible to find a parsimonious tree. This will inflate the TMRCA values substantially. This reinforces what I've said from the beginning. The molecular clock, in these regions, is not well calibrated.

Another indicator of this is that a much larger fraction of mutations in this region are non-synonymous (i.e. not neutral). This is an indicator that positive selection is driving most of the changes a far more rapid rate than neutral evolution. The end result of this is artificially inflated TMRCA estimates. Remember, that D = T * R only in regions where dynamics like this are not taking place.

This does not, however, create a problem for our estimate of a bottleneck limit. Remember that we used the ***median*** of TMR4A over the whole genome. So, this estimate is not really influenced much by a small portion of the genome in error. The estimate shifts only about 2 kya per 1% of the genome in error. That is the reason we used the median in the first place, it makes the estimate remarkably stable to errors like this.

Convergent evolution is really the exception to the rule in human variation. It is not accounted for by most phylogenomic methods, but that does not matter in our genome wide analysis. Our final estimate is not strongly influenced by this problem.

Swamidass (Dr. S Joshua Swamidass) 2018-02-19 05:02:41 UTC #621

> Swamidass:

> Moreover, the next time someone points to mutations that do not fit the tree pattern in species, remember two things.
>
> 1. We expect a few discordant mutations, even in neutral evolution. That is not evidence against common descent.
> 2. Convergent evolution, also, can produce discordant mutations. Not usually ever as much as we see in HLA genes, but more than we expect from neutral evolution.

Just to expand on this, some argue that homoplasy is evidence against common descent.

> Convergence is a common characteristic of life. This commonness makes little sense in light of evolutionary theory.
> *Convergence: Evidence for a Single Creator* by Fuz Rana of RTB
> **http://stag.reasons.org/explore/publications/facts-for-faith/read/facts-for-faith/2000/09/30/convergence-evidence-for-a-single-creator**

> The pervasive pattern of homoplasy, which is the term evolutionists use for similarities that cannot be explained by any conceivable pattern of common ancestry, undermines the logic of the argument. Common design explains all similarities, both homologies and homoplasies, but evolution cannot explain the pervasive homoplasies.3 The camera eye, evolutionists say, must have evolved independently six times! Labelling such things as due to 'convergent evolution' is pure circular reasoning and lacks any explanatory power.
> **https://creation.com/is-evolution-true**

Well, we see homoplasy in human variation, which ***everyone*** agree arise from common ancestors (at least down to 4 alleles). In fact, we see much more homoplasy in human HLA alleles than we do between species. That means we ***expect*** to see homoplasy in species level variation too.

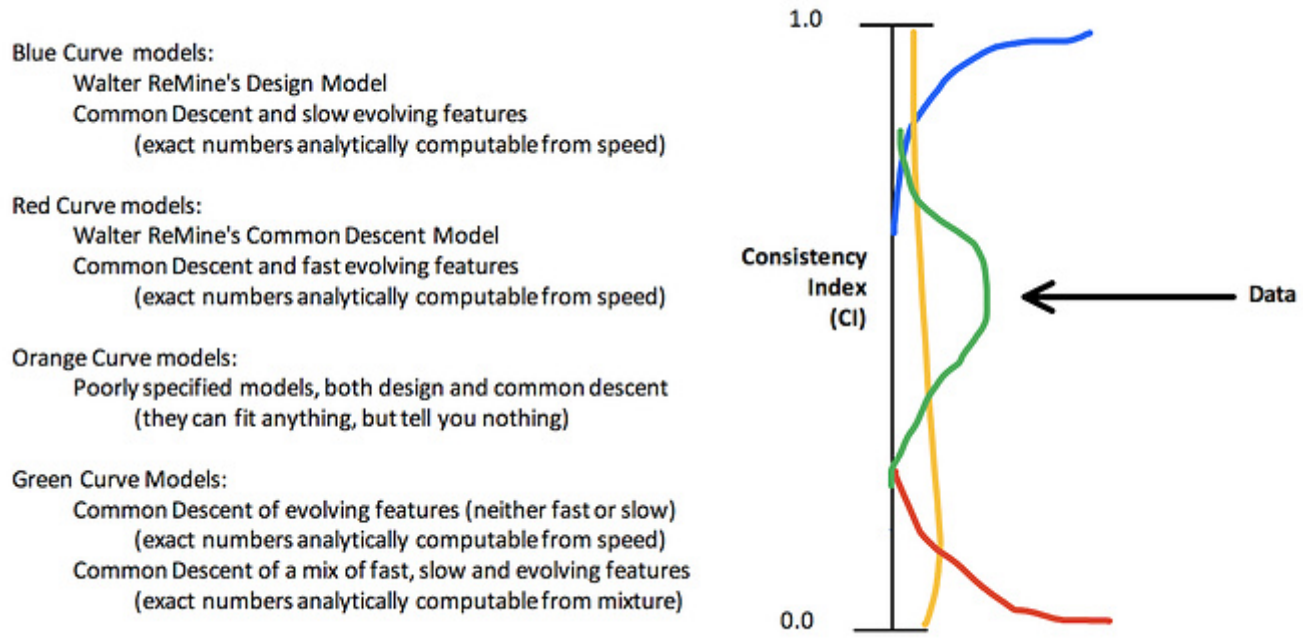
This is hardly evidence, then, against common descent. It is what we *expect* from non-neutral evolutionary processes.

For those who have been following this for a while, we also see homoplasy in cancer too (**https://biologos.org/blogs/guest/cancer-and-evolution**), but we refer to it by a different name. We call it in cancer biology "recurrent mutations," but we could just as easily call them homoplasies. The prediction from common descent is that DNA falls into nested clades, for the most part, but not exactly. We know there are processes that break this pattern.

Most DNA will fall into nested clades, but some will not. The structure of the biological world is nested clades, but not *perfect* nested clades. This not just a circular reasoning rescue for evolution, because we can see this arise in both cancer and human variation. So this is just an empirical and theoretical expectation of evoultion.

> Swamidass:
>
> In biology, there are always exceptions to the rule.

This, also is very closely related to some prior conversation with **@Cornelius_Hunter** about what common descent predicts vs design.



Signal and Noise

Notice that Remine argues that a common designer means natures should be in perfect nested clades (high CI). However, Fuz Rana argues that convergent evolution (which breaks the nested clade pattern) is evidence of a common designer (low CI). Instead, we find out that evolutionary theory (with common descent) can tell us why some features break the pattern, and others follow it.

The data fits neither Fuz or Remine's model of a creator. Instead we find that God designed us through a process of common descent. Or at least the evidence looks that way. This is not evidence against design, but it evidence that God's design principle was common descent.

Swamidass (Dr. S Joshua Swamidass) 2018-02-19 11:19:02 UTC #622

HLA Introns Appear Ancient (and Recent?)

> Swamidass:
>
> Please, I want to know if I am wrong here. If you can find such a study, please let me know. Correct me if you can!

So looking into this, I did find some additional evidence for very ancient lineages.

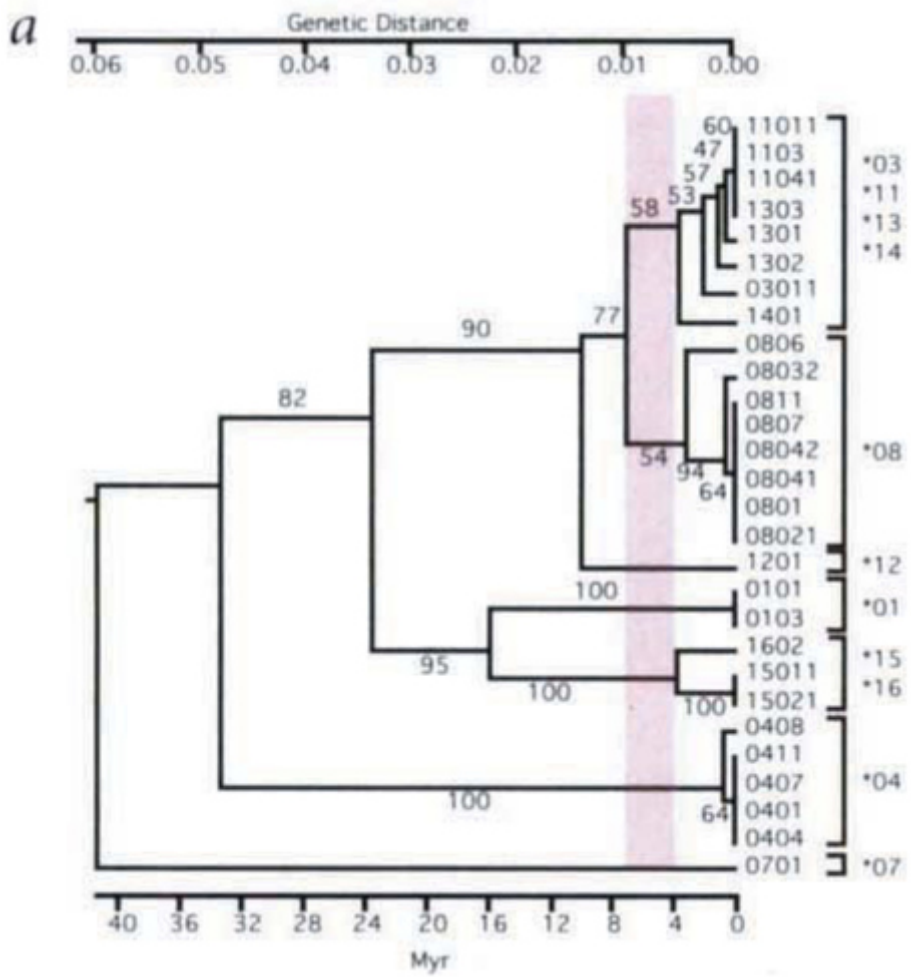
https://www.nature.com/articles/ng0398-237

This paper is interesting and has some valuable information. They show that the coding sequences of HLA-DRB1 likely arise recently, which is consistent with the convergent evolution work I previously explained. They did this by studying the introns, the non-coding regions adjacent to alleles.

They key observation they make is about the ***introns*** of HLA-DRB1 alleles lineages. The introns within a lineage are closely related, arising about 250 kya ago using a mutation rate of 1.4e-9 mutations / bp / year. This indicates that they are not ancient. This is the evidence that undermines significantly Ayala's argument.

However, the difference between introns in *different* lineages is much greater, suggesting they are much more ancient. This is an important finding, because introns are under much less selective pressure. For this reason, they will be more clock like. They estimate that there are about 7 lineages when humans and chimps diverge. This is much less lineages

one would compute by looking at the exons, but it is enough to put a minimum bottleneck at 4 individuals, if this corrects. Also the mutation rate here is high, about 3 times higher than the genome wide rate. So, in this sense, it is a conservative estimate.



The discussion in the paper is complex, and not really possible to summarize concisely. But for those studying this question, it is a must read.

One Line Of Evidence Against A Bottleneck?

This does count as one new line of evidence, that deserves some consideration. I'm still not sure how much confidence can place in this. Balancing selection can select for increased mutation rates in this region of the genome. There is also a lot of evidence that mutations often come in clusters, not as singletons. The introns will be more neutral than the exons, but I am not sure how much we can trust them as a clock in this case.

For me the most strange feature data is that, under the author's hypothesis, over 20 million years we almost never see recombination in this region in the introns . I am having a hard time believing that. It seems that a highly variable and high mutation rate in this region (and perhaps hitchhiking from mutational clusters) might be an alternate explanation for why the allelic lineages are this divergent. **One way to test the hypothesis of very ancient allelic lineages here is determine if the *introns* (not the exons) have trans-species variation with non-human primates.** That is a clear prediction of this model, which we really expect to see if these lineages are really this ancient.

However, this test of the model does not appear to have been done. It would be really interesting to see what the data might show. If we were to see trans-species variation of the introns, I might be enough to convince me. That, however, is a very difficult analysis to do correctly.

I'm particularly uncertain on how to square the high divergence between allelic lines with the absence of recombination reported here. If these are such ancient lines, we should see more recombination than the authors of these studies presume. This seems to be inconsistent with measured recombination in this regions, which appears to be very similar to the rest of the gnome (**https://academic.oup.com/hmg/article-abstract/4/3/423/588852?redirectedFrom=fulltext**). If these are such ancient alleles, why do we see no recombination? If they are missing recombination events too, then the allelic age will be overestimated. Though, there is some evidence that recombination here is selected against.

I'd be curious to hear comment from **@glipsnort** and **@RichardBuggs** on this. How do you weight this paper against everything else?

Swamidass (Dr. S Joshua Swamidass) 2018-02-19 20:10:07 UTC #623

Let me start by conceding that most colleagues will currently take the introns as *de facto* evidence against bottleneck. Maybe they are. However, there is this sticky problem of essentially no observable recombination in this model over literally tens of millions of year, even though we can directly observe recombination in this area.

> Swamidass:
>
> For me the most strange feature data is that, under the author's hypothesis, over 20 million years we almost never see recombination in this region in the introns . I am having a hard time believing that. It seems that a highly variable and high mutation rate in this region (and perhaps hitchhiking from mutational clusters) might be an alternate explanation for why the allelic lineages are this divergent.

With that, let me lay out the puzzling features of the data, and why this might be a better explanation.

The HLA Intron Puzzle

It all comes down to the age of the introns we observe in each lineage. However something is strange about the "clock" here.

1. If allele lineages introns have an **ancient** common ancestor (e.g. 20 mya), observed number of recombinations seems much **lower than observed recombination rate**.
2. If allele lineages introns have a **recent** common ancestor (e.g. less than 500 kya), observed number of mutations much ***higher*** **than the observed mutation rate**.
3. Whatever process we end up with, needs to explain why each alleles looks **young** by one measure (diversity within the allele) and **very old** by another (high divergence between allele lineages).

One thing that is particularly relevant here is that this paper is from 1998, so they are working from genomewide phylogenomic mutation rates, not directly observed and region specific mutation rates. We've now directly measured this in a regions specific way. So something is affecting these two clocks in opposite ways in a presumably neutral region of the genome. What could be going on to cause that? It seems that by concluding the allelic lineages coalesce anciently, the authors are just pushing the problem to recombination. This does not really solve the puzzle.

Developing Another Hypothesis

So, here is another option, that takes into account all that we know about genetics now, including information not available in 1998. I think that this pattern in the data might be in the interaction of several different processes. I am going to call this the **Bystander Mutation to Hitchhiker Model**.

First, remember what is going on in a directly adjacent area:

1. Very strong balancing, divergent, and positive **selection in an adjacent region** (the antigen binding exon).

2. Very high amounts of **gene conversion in the adjacent region** (the antigen binding exon).

Now to explain the extremely low amounts of recombination in the intron, I'll invoke a good explanation already put forward in the literature.

3. Strong **negative selection against exon shuffling recombination**, because the function of each exon is dependent on the varian of the exon t it is adjacent too, much more than usually is the case.

Then, to explain the very high amount of mutation in the intron, I'll recall some recently discovered information about mutation distributions.

4. **Mutations often come in clusters**, especially as a result DNA end-joining repair, which occurs in (for example) recombination and gene conversion. Other ways of putting this is that gene conversion events *cause* mutations. Or, mutations are often accompanied by adjacent mutations, ***much*** more than we expect by chance. We see a very clear signature of this in genetic variation data, confirmed by several studies, and also have clear molecular mechanisms for this process. **http://science.sciencemag.org/content/329/5987/82.full?rss=1**

5. There is much more convergent evolution happening in HLA exon than we had previously thought. So the rate of change in these exons is even higher than we thought.

[as an aside, this makes things like multiple mutations in a single exon or gene ***much*** more likely, thereby increasing the rate of evolution, and increasing the likelihood of crossing fitness barriers.] Now getting back to a key fundamental of genetic evolution is a "neutral process"

6. **Hitchhiking** is a process that can rapidly fix **neutral** mutations (like those in the introns) that are linked to selected mutations (like those in the exons). Because recombination is clearly suppressed somehow (likely negative selection) in this region, the hitchhiking effect will be stronger.

Now we are in a position to think about what the interaction between these affects will. Notably, this is a highly unusual cluster of evolutionary processes working together. It is not likely this is taking place in most the genome. It also seems to depend on co-dependency between exon variants, which may not be equally important to all HLA loci.

7. Finally, the process that produces introns that are very similar within allele lineages, but dissimilar between them, would be the **rare occurrence of a tolerated intron recombination**, followed by **very rapid evolution** of that new recombinant intron by **bystander mutation hitchhiking, that is also isolated from other lineages by negative selection of cross-allele recombination.** It is possible, once the functional space is filled by the exons associated with the new recombinant intron, the intron evolution rate would slow, and the **allelic introns *within* a lineage might be more neutrally evolving by drift and recombination-driven homogenization** (alongside continual convergent evolution in the exon).

This might be a place where the complex dynamics in the Lenski experiment (referenced by **@RichardBuggs**) might be relevant too. Yes this is a complex theory, but this is also complex data, that does not fit into the expectations of neutral evolutionary theory. Remember, we only trust our formula D = T * R if the region is evolving neutrally. That does not seem to be the case here.

From this proposal, we tentatively expect…

1. There to be much **lower recombination rate** in the introns than expected from a neutral process (because of negative selection) between allelic lineages, but *also* more **normal recombination rate** within allelic lineages. *So this will create very different dynamics between and within allelic lineages.*

2. There to be much **higher rate of change in the introns** than the population level mutation rate alone would tell you. The newly mutated exons that are being continually selected for are strongly *linked* to introns that have many bystander mutations caused by the same process that *caused* by the newly mutated exon's mutational process (e.g. gene conversion).

3. This process might produce phylogenies as observed, **with low intron diversity by drift and recombination *within* allelic lineages, but high intron divergence between each lineage.**

That means the introns are largely neutral with respect to function. Yes, there will be important sequences here, but most of the sequence is not under functional constraint. They are, however, ***not*** evolving neutrally, but strongly under the influence of the neighboring exons. Nor are they evolving at the same rate, but also in a highly variable rate.

Supported by Data?

I think that much more care needs to be carefully thinking through the implications of this proposal that I am giving here. This, after all, is not a scientific paper, but a forum post. However, it seems that this makes sense of the both the low recombination rate, and the discordance between the observed mutation rate in introns if the alleles is low. The two hypothesis, as I can tell, are:

1. The published hypothesis: **Ancient coalescences** of allele lineages, with the pattern caused by *extreme* negative selection on intron recombination over 20 million years, but neutral evolution of mutations in intron. THEREFORE, the molecular clock in introns is **valid**.

2. Bystander-Hitchhiker hypothesis: **much more recent coalescences** of allele lineages, with the pattern caused by *moderate to strong* negative selection on intron recombination, but *high rates of bystander mutations hitchhiking* along with the constant positive selection for new exon mutations. THEREFORE, the molecular clock in introns is **invalid at the most ancient scales**.

#2 was considered by the authors of the paper, but they did not know everything know now about mutation clusters and gene conversion. This changes the analysis substantially, by increasing the rate at which hitchhiking occurs by adding a strong correlation between selection and mutation in introns. Moreover, #2 seems to be more believable (at least to me) than extreme negative selection against recombination over 10s of millions of years.

Much more work could be done to work this out, and potentially validate this theory. First, we need to explicitly work on the math here. Second, we should look at other HLA genes, to see if there there is a discernible relationships predicted by that math. Third, we should look to see if the pattern in mutations matches that expected by gene conversion mutagenesis (they have some specific bias). Fourth, careful review of the evidence of direct measures (rather than phylogenetic inference) of mutation rate and recombination rates in this region are important. This is a truly massive effort to do correctly. I can tell you right now, that we are not going to do such a thing on a blog like this.

However, I #2 this seems like a hypothesis that makes more sense of the data we know right now from the literature. At the very least, it needs to be carefully considered and ruled out before we can have confidence in this as an argument against a bottleneck. As far as I can tell, I have not seen a paper that has done this. Though the literature in this area is vast. I might have missed it.

How Could We Date Them?

If this process is real, than the best date would be the age of the allelic lineages (250 kya), but not the dates of the coalescence of the distinct lineages (20 mya). However, I am not sure we could fully trust this either. A better theory or simulations might justify this somewhat. It would still be very difficult, because it requires having precise knowledge of the balance between several different mechanisms (e.g. negative selection on recombination, and bystander mutations), over long periods of time. And we also do not have a large number of loci to do error checking on. A priori, we also expect the selective pressures to be substantially changing over this period. I'm not sure it's possible to come to confident date estimate based on mutation or recombination clocks.

That leaves trans-species variation as the other way of dating them. This, it seems, also is something not yet done in the literature. It is also a very difficult analysis to do correctly, partly because we do not have access to much chimpanzee data in this region (as far as I can tell).

Hypothesis #1 here, however, requires there to be extremely high selection against intron recombination, so these chimp introns should very closely alignable with human introns. We should see a very strong signal for trans-species variation. And we should see more than 4 lineages too.

If, on the other hand, if we see a lot of recombination between the human and chimp alleles in the intron alignment, that is evidence against the very strong negative selection recombination rate the hypothesis requires model. This would give some strong support to Hypothesis #2.

Of course, we cannot know without looking at the data (and that is difficult in this case). I'll venture a guess that the observations of #2 are more likely.

Where Does that Leave Us?

I'm not sure this is strong evidence against a bottleneck in the end. There are some future studies we can imagine that could clarify the matter. However, based on current evidence, I do not think we can be sure the ages are well-calibrated in the HLA intron experiments.

So, it seems, **we are back to TMR4A**. Once again, the median estimate is validated as a wise early choice, as it automatically ignores outlier regions like this.

It is possible that better analysis of this data could change our minds. Wherever possible, I've tried to map out how future studies and evidence could help discriminate competing hypotheses. For those seeking to disprove a bottleneck, I think this is the most likely place that deeper analysis could change our view. For those really wanting to know what the data really tells us, this also is the place I think we might find the most important information.

However, at this point, we are not facing settled science at all, but the bleeding edge of inquiry into genomic science. I'm curious to see how this unfolds over the next decade. Until that is sorted out, I think our conclusion that a single couple bottleneck between 7 mya and ~500 kya is consistent with the data (not disproven by it), is still a reasonable interpretation.

RichardBuggs (Richard Buggs) 2018-02-19 21:45:34 UTC #624

Hi Joshua **@swamidass** thank you for these very interesting analyses of Ayala et al (1994) and Bergstrom et al (1998). As you know, I mentioned the Ayala paper **here** in my initial response to **@DennisVenema** 's part 1 response to me. At the time I said that I thought it was the strongest argument available against a bottleneck of two.

I was puzzled as to why Dennis did not refer me to it, and now I wonder if he perhaps anticipated some of the criticisms that you have made of it. He certainly seemed less confident than I did that it was crucial to his case.

You have made a far more convincing case against Ayala's paper than I could have done.

I think your point that Ayala's findings have not been replicated since the human genome project is an interesting one, and your attribution of this to methodological limitations in his tree building methods, and failure to consider the alternative hypothesis of convergence sounds convincing to me.

I would like to put out there another possibility in addition to these, and that is the possibility that before the human genome project, researchers on human MHC loci may sometimes have confused alleles and paralogs. I know from my own experience that before we have a full genome sequence for an organism, it can be very hard to analyse regions of the genome that contain families of highly similar genes: it is very easy to confuse paralogs with alleles. I don't know much about the DRB1 locus in humans and chimpanzees, but if there are paralogous copies of this gene, they might have been very challenging to identify before a highly accurate assembly of human MHC regions was complete. It is possible that this could be another reason why Ayala's findings have not been replicated since the human genome project. This is just a speculation, and is easily testable. I may well be wrong, but it is probably worth checking.

gbrooks9 (George Brooks) 2018-02-21 06:46:55 UTC #625

> Lynn_Munter:
>
> There are (more or less) anatomically modern human fossils in this age range in Africa (and now Israel, too).

@Lynn_Munter

If you read my posting carefully, it is a hypothetical that I am challenging **@Swamidass** with.

As best as I can tell, you are arguing on my side of the discussion in your posting above.

---

gbrooks9 (George Brooks) 2018-02-21 06:56:40 UTC #626

> Swamidass:
>
> . . . there is ZERO evidence that they do not begin as a single couple.
>
> Zero evidence. So how do we come to heliocentric certainty about a claim substantiated by zero evidence?

@Swamidass

Maybe you need to be more careful with the syntax?

Your statement that “there is ZERO evidence that humans do not begin as a single couple” is a statement embedded in the YEC context. And yet you try to avoid the YEC context by stripping your assertion of any chronological time frame!

All **@DennisVenema** has to do is demonstrate that the human population absolutely did not originate as a single couple at any time within the last 10,000 years, and he can be impressively certain that the YEC claims are false.

In contrast, **@Swamidass** , by your not being specific enough in your choice of words (for example, by intentionally excluding a time frame), you introduce confusion into what it is you think you are proving - - or at the very least, what it is you think you are proving to others.

Swamidass (Dr. S Joshua Swamidass) 2018-02-21 08:26:06 UTC #627

> gbrooks9:
>
> All **@DennisVenema** has to do is demonstrate that the human population absolutely did not originate as a single couple at any time within the last 10,000 years, and he can be impressively certain that the YEC claims are false.

You missed this.

> Swamidass:
>
> Also, the time line needed to be dropped. This would obviously be well before 10 kya.

Lynn_Munter (Lynn Munter) 2018-02-21 15:05:12 UTC #628

> gbrooks9:
>
> If you read my posting carefully, it is a hypothetical that I am challenging **@Swamidass** with.
>
> As best as I can tell, you are arguing on my side of the discussion in your posting above.

I read your posting about 3 times because I couldn't make sense of it. Having just read it again, I believe you were not reading Swamidass in the sense he meant to convey: that humans could have begun as a single couple (within a larger hominin population) or at least that there is zero evidence that they did not, within the conventionally accepted time range for the origin of humanity.

If it helps, you are hardly alone in this grammatical confusion!

---

gbrooks9 (George Brooks) 2018-02-21 17:12:14 UTC #629

> Swamidass:
>
> You missed this.
>
> "Also, the time line needed to be dropped. This would obviously be well before 10 kya."

@Swamidass

I didn't miss it. I was trying to decide what you meant by it!

What does "before 10 thousand years ago" mean ? Wouldn't you agree that "before 10,000 years ago" means 15,000 years ago, 20,000 years ago, and older and older? Your reference to "before 10 thousand years ago" seems perfectly design to cause problems for **@DennisVenema** , and yet ignoring the mortal damage he does to the YEC position - - which is really all that matters.

Did you actually mean After 10,000 years ago? - - as in 6000 or 5000 years ago?

This is what I mean by your use of syntax. It is difficult to imagine a sentence with more landmines in it than your adamant assertion that there is "ZERO evidence" etc etc etc…

And so now I'm going to discuss the confused posting of another one of your unintended victims: **@Lynn_Munter** .

Jay313 (Jay Johnson) 2018-02-21 17:40:46 UTC #630

> Swamidass:
>
> I think our conclusion that a single couple bottleneck between 7 mya and ~500 kya is consistent with the data (not disproven by it), is still a reasonable interpretation.

> gbrooks9:
>
> Maybe you need to be more careful with the syntax?
>
> Your statement that "there is ZERO evidence that humans do not begin as a single couple" is a statement embedded in the YEC context.

The entire phrasing strikes me as disingenuous. Claiming that a single-couple bottleneck is “consistent with the data” seems designed to confuse the issue. After 600+ posts, there is enough evidence to conclude that a single-couple bottleneck did not occur within the last 500,000 years, yet Swamidass’ conclusion is that there is ZERO evidence against a single couple. Huh?

What good is a conclusion when it says nothing? “A single couple bottleneck between 7 mya and ~500 kya is consistent with the data (not disproven by it).” The data provides ZERO evidence for a single couple in that time frame, yet the wording leaves the opposite impression. Somehow, a lack of data comes out as “consistent with the data.” A turn of phrase worthy of Doug Axe himself.

How about a straightforward answer: *The evidence shows that a single-couple bottleneck did not occur within the past 500,000 years. Prior to that date, our data and methods are incapable of answering the question.*

GJDS (GJDS) 2018-02-21 18:19:35 UTC #631

From what I understand of the modelling, it shows that it cannot provide a result that commences with a couple. This is a valid result from modelling - other results may or may not support a bottleneck - but it is valid to point out the model may not be able to deal with a bottleneck of two.

This should be viewed as the ,limitation of the modelling technique, and is not disingenuous.

Swamidass (Dr. S Joshua Swamidass) 2018-02-21 18:24:06 UTC #632

> Jay313:
>
> How about a straightforward answer: The evidence shows that a single-couple bottleneck did not occur within the past 500,000 years. Prior to that date, our data and methods are incapable of answering the question.

Sounds like exactly what i’ve said regarding our “ancestors as a whole”. However the same does not apply to homo sapiens specifically.

Bill_II 2018-02-21 18:34:03 UTC #633

> Swamidass:
>
> Sounds like exactly what i’ve said regarding our “ancestors as a whole”. However the same does not apply to homo sapiens specifically.

What exactly is the difference between “ancestors as a whole” and homo sapiens? I would assume homo sapiens would just be a subset of AAAW.

Lynn_Munter (Lynn Munter) 2018-02-21 18:52:50 UTC #634

> Bill_II:
>
> What exactly is the difference between “ancestors as a whole” and homo sapiens? I would assume homo sapiens would just be a subset of AAAW.

Well, because it's a subset, one can claim that 'homo sapiens' could have numbered two while 'our ancestors' were more numerous. The main difficulty lies in achieving some non-arbitrary definition of 'homo sapiens.'

As far as I can tell the main benefit of extending this argument was to make YECs feel less ganged-up on? But it's rather outlived its welcome in my un-humble opinion.

I'm still only halfway through catching up on **@Swamidass** ' last few posts, but I am immensely valuing the time he took to clearly set forth the status of the scientific evidence regarding interspecies variation and other matters! That is where the much more interesting stuff is.

Jay313 (Jay Johnson) 2018-02-21 19:04:15 UTC #635

> Swamidass:
>
> Sounds like exactly what i've said regarding our "ancestors as a whole". However the same does not apply to homo sapiens specifically.

There were no *H. sapiens* 500,000 years ago. Should we try again?

The evidence shows that *H. sapiens* has not experienced a population bottleneck to a single couple. Further, the evidence shows no single-couple bottleneck occurred among our ancestors as a whole in the last 500,000 years. Prior to that date, our data and methods are incapable of answering the question.

Jonathan_Burke (Jon) 2018-02-21 19:07:26 UTC #636

> Lynn_Munter:
>
> As far as I can tell the main benefit of extending this argument was to make YECs feel less ganged-up on? But it's rather outlived its welcome in my un-humble opinion.

Yes that's exactly right.

---

gbrooks9 (George Brooks) 2018-02-21 19:40:39 UTC #637

> Swamidass:
>
> Sounds like exactly what i've said regarding our "ancestors as a whole". However the same does not apply to homo sapiens specifically.

@Swamidass

What ?! I don't even think I can expect comprehensible answers from you in your current fugue state.

@DennisVenema , could you explain what **you** think **@Swamidass** is trying to say?

How can we have zero bottleneck within the past 500,000 years (which embraces 'ancestors as a whole'), but **not** if we look at just our Homo sapien ancestors within 500,000 years?

That sounds pretty nutty…

Bill_II 2018-02-21 19:49:25 UTC #638

> Lynn_Munter:
>
> Well, because it's a subset, one can claim that 'homo sapiens' could have numbered two while 'our ancestors' were more numerous.

But the no bottleneck result is applied to the entire set of AAAW so it should also apply to the subset.

Lynn_Munter (Lynn Munter) 2018-02-21 19:52:31 UTC #639

> Bill_II:
>
> But the no bottleneck result is applied to the entire set of AAAW so it should also apply to the subset.

Not necessarily. I can make a claim that none of my bags of M&Ms contain only two candies but it does not make it true that none of them contain only two green candies.

---

jpm (Phil) 2018-02-21 19:56:41 UTC #640

I think it is sort of like saying that all dogs may have arisen through a two wolf bottleneck in the distant past (I know they didn't but bear with me) but that all Chihuahuas never went through a a two Chihuahua bottleneck. I think.

---

gbrooks9 (George Brooks) 2018-02-21 21:36:51 UTC #641

@jpm

@Swamidass
I **wish** he was saying something like that. Let's look at his last sample:

> Swamidass:
>
> **@Jay313** writes:
> "How about a straightforward answer: The evidence shows that a single-couple bottleneck did not occur within the past 500,000 years.
>
> Prior to that date, our data and methods are incapable of answering the question."
>
> **@Swamidass** responds:
> Sounds like exactly what i've said regarding our "ancestors as a whole" [in reference to data being incapable of answering the question about a bottleneck]. However the same does not apply to homo sapiens specifically.

So, what does he mean "ancestors as a whole"? I can only interpret that to mean: all the hominids leading up to humans, Homo sapiens.

So, he concludes that data can answer the question regarding humans. So when I read it like this, I feel encouraged.

But then I remember that the problem is that Swamidass wants to be able to argue that science has **not** disproven a one-pair bottleneck back into the depths of time. So? Who cares about that?

YECs say that the bottleneck **has** to be within 6,000 years. So, let's give them more slack than they want… let's say it's all tolerable up to 10,000 years ago.

But this is where **@DennisVenema** is at his strongest. We know for a fact that it didn't happen within 10,000 years ago.

Swamidass (Dr. S Joshua Swamidass) 2018-02-22 06:36:18 UTC #642

> Bill_II:
>
> What exactly is the difference between "ancestors as a whole" and homo sapiens? I would assume homo sapiens would just be a subset of AAAW.

This is an example of the Ecological Fallacy, sometimes called the Fallacy of Division:

> A fallacy of division occurs when one reasons logically that something true for the whole must also be true of all or some of its parts.
> **https://en.wikipedia.org/wiki/Fallacy_of_division**

> Jay313:
>
> The evidence shows that H. sapiens has not experienced a population bottleneck to a single couple.

This is a *false* statement that relies on a logical fallacy. There is no value in advancing an illogical claim. There is no value in advancing a false claim. The evidence does not show homo sapiens never experienced a population bottleneck to a single couple.

> gbrooks9:
>
> How can we have zero bottleneck within the past 500,000 years (which embraces 'ancestors as a whole'),
>
> but not if we look at just our Homo sapien ancestors within 500,000 years?

Remember, our ancestors as a whole include both homo sapiens, but also others. So **@Lynn_Munter** explains it correctly…

> Lynn_Munter:
>
> Well, because it's a subset, one can claim that 'homo sapiens' could have numbered two while 'our ancestors' were more numerous.

However, this is not the primary benefit at all.

> Lynn_Munter:
>
> As far as I can tell the main benefit of extending this argument was to make YECs feel less ganged-up on? But it's rather outlived its welcome in my un-humble opinion.

I do not expect YECs will be happy with a single couple origin of Homo sapiens 200 kya. Rather, I think some may be intrigued by a recent genealogical Adam, which is an entirely different thing.

Rather, the primary reason to retract this claim is because it is absurd to confidently make illogical claims. There no value in advancing claims that depend on such clear fallacy. Moreover, difficulty in understanding why an illogical statement is logical is an opportunity to clarify our thinking on things. For example, it's clear that **@Lynn_Munter** understands what the evidence is telling us in relation to this question, and it also clear that others are confused. Purging that illogical claim, by understanding its fallacy, is an opportunity to clarify our thinking here.

Jay313 (Jay Johnson) 2018-02-22 14:13:49 UTC #643

> Swamidass:
>
> This is a false statement that relies on a logical fallacy. There is no value in advancing an illogical claim. There is no value in advancing a false claim. The evidence does not show homo sapiens never experienced a population bottleneck to a single couple.

I wish that just once you could state your claim without a double negative. In any case, I understand exactly where you're coming from. Positing that *H. sapiens* began with a single breeding pair may seem logical to you, but it looks like just another *ad hoc* hypothesis to me. Good to see you back on your high horse again, though!

Bill_II 2018-02-22 15:22:34 UTC #644

> Swamidass:
>
> This is an example of the Ecological Fallacy, sometimes called the Fallacy of Division:

I understand the problem of trying to say that a statistical measure of the whole set also applies to a subset. That makes sense. Using the Wikipedia example, the total or average ice cream consumption of the 2nd grade says nothing about how much ice cream a single student eats.

Let me illustrate what I hear from **@Swamidass** . If every 2nd grader eats a minimum of 1 pint of ice cream then any single student has eaten at least 1 pint of ice cream. Isn't this a correct logical argument? Am I just hearing you wrong?

Lynn_Munter (Lynn Munter) 2018-02-22 15:24:24 UTC #645

> Jay313:
>
> The evidence shows that H. sapiens has not experienced a population bottleneck to a single couple. Further, the evidence shows no single-couple bottleneck occurred among our ancestors as a whole in the last 500,000 years. Prior to that date, our data and methods are incapable of answering the question.

> Swamidass:
>
> This is a false statement that relies on a logical fallacy. … The evidence does not show homo sapiens never experienced a population bottleneck to a single couple.

“The evidence shows that we H. sapiens have not experienced a bottleneck of our ancestors to a single couple in the last 500,000 years. Prior to that date, our data and methods are insufficiently conclusive.”

There, I fixed it. Can we be good now?

Jay313 (Jay Johnson) 2018-02-22 16:08:46 UTC #646

> Lynn_Munter:
>
> Can we be good now?

Haha. Yes, you’re right. It’s become tiresome. I’m done with it.

Swamidass (Dr. S Joshua Swamidass) 2018-02-22 16:57:15 UTC #647

> Bill_II:
>
> If every 2nd grader eats a minimum of 1 pint of ice cream then any single student has eaten at least 1 pint of ice cream. Isn’t this a correct logical argument? Am I just hearing you wrong?

The problem is that you misunderstood the scientific claims. The genetics do not tell us that every 2nd grader eats a minimum number.

Rather, the total amount of ice cream eaten by the class is 5. However, if little billy tells you he got none, he might telling the truth.

Lynn_Munter (Lynn Munter) 2018-02-22 17:30:39 UTC #648

> Bill_II:
>
> Am I just hearing you wrong?

It all goes back to this grammatical ambiguity. If I say none of my bags contain only two green M&Ms, and then I produce a bag with five red M&Ms and two green M&Ms, was my statement true or false?

@Swamidass has been saying ‘false’ because there could have been a generation of our ancestors which had only two ‘H. sapiens’ and a bunch of other hominins. He has read the sentence one way, while many other people (including, I think, you, **@gbrooks9** , and **@Christy**) correctly inferred **@DennisVenema** ’s intended meaning from the original context. That is what we have to do with grammatical ambiguities like this. But once the statement is taken out of context and rephrased in a long discussion like this, it is very easy for mistakes to happen. I just want to make sure everyone sees clearly where everyone else is coming from here, because it takes a lot of careful reading to sort it all out at this point!

Christy (Christy Hemphill) 2018-02-22 17:51:07 UTC #649

> Lynn_Munter:

> If I say none of my bags contain only two green M&Ms, and then I produce a bag with five red M&Ms and two green M&Ms, was my statement true or false?

Grammatical ambiguity aside, I'm still hung up on the idea that species boundaries are subjective, so all the M&Ms in the bag are brown. Whether "only two" of them are subjectively identified as greenish brown instead of reddish brown is beside the point to me if we can count them and see there are clearly not "only two" M&Ms in the bag. It doesn't matter what color the M&Ms are. If there was no bottleneck of two individuals in the population, that is the relevant piece of information.

Lynn_Munter (Lynn Munter) 2018-02-22 18:00:49 UTC #650

> Christy:
>
> Whether "only two" of them are subjectively identified as greenish brown instead of reddish brown is beside the point to me if we can count them and see there are clearly not "only two" M&Ms in the bag.

Well said! Context is everything.

---

glipsnort (Steve Schaffner) 2018-02-22 23:03:37 UTC #652

> Swamidass:
>
> As I understand it, 2N is about 2 million years ago (approx genome wide TMRCA, right?). Your SFS studies show no signal for a bottleneck at 0.5 million years ago, which is 0.25x 2N. Though, as I think about it, your studies used smaller population sizes we expect (e.g. constant 10,000 at all times), so perhaps your 2N is a lot lower than 2 million years?
>
> So where is my math wrong here? If possible…
>
> square this with your prior simulations on SFS.
> give extrapolate to the real human data for where that cutoff might be.
> tell us if you think there is anything here that conflicts with the TMR4A work.

I would put long-term Ne at probably around 20,000, based on $\pi = 0.1\%$ and μ=1.25e-8. (Note: that's 20,000 diploid individuals, not 20,000 chromosomes). I used 10,000 and 20,000 generations in most of my simulations, corresponding to 2N/4 and 2N/2. 2N translates to about 1 million years (or somewhat more if the generation time is a little longer), and a TMRCA of 2 million years, since TMRCA is 4N for an ideal population.

Does that make sense?

Sorry for my very spotty attention to this thread, but life has been a little complicated lately.

---

gbrooks9 (George Brooks) 2018-02-23 00:55:59 UTC #653

> Swamidass:
>
> For example, it's clear that **@Lynn_Munter** understands what the evidence is telling us in relation to this question, and it also clear that others are confused. Purging that illogical claim, by understanding its fallacy, is an opportunity to clarify our thinking here.

@Swamidass

Make a flow chart or something… because your ability to use words “to make things clear” seems to have become attenuated by the bubbly enthusiasm you have developed regarding this topic.

If you intentionally strip out the time frame from your assertions, you are making an error.

If you carefully explain that the “Bottleneck of One Pair” is something that could have occurred 200,000 years ago… then I am fine with that.

But when you use confusing terminology “before 10 kya” (huh? which direction?!)… and the like, you are just asking for trouble - - especially when you combine it with a double negative and/or a subjunctive verb.

George (George #2, the **other** George)

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gbrooks9 (George Brooks) 2018-02-23 00:59:52 UTC #654

> Lynn_Munter:
>
> “The evidence shows that we H. sapiens have not experienced a bottleneck of our ancestors to a single couple in the last 500,000 years. Prior to that date, our data and methods are insufficiently conclusive.”
>
> There, I fixed it. Can we be good now?

@Lynn_Munter

Thank you for putting a time frame in that sentence… I believe you have single-handedly saved my sanity!

Lynn, I should let you know that I’m a single man again … 😉

RichardBuggs (Richard Buggs) 2018-02-24 22:11:38 UTC #655

Dear all,

I have now started to respond to **@DennisVenema** Part 2 blog reply to me. I have posted Part 1 of my response here:
http://www.richardbuggs.com/response_to_Dennis_Venema_Biologos_Part2_Adam_Eve_Coalescent.html
And placed it on the Biologos forum here:

> **Adam, Eve and Population Genetics: A Reply to Dr. Richard Buggs (Part 2)**
>
> Here is a copy of the text of my response at:
> **http://www.richardbuggs.com/response_to_Dennis_Venema_Biologos_Part2_Adam_Eve_Coalescent.html**
> In his blog “Adam, Eve and Population Genetics: A Reply to Dr. Richard Buggs (Part 2)”, Dr Dennis Venema raises the interesting issue of how much coalescence will occur at a bottleneck of two. This is a very relevant issue as rates of coalescence can be used to detect a long lasting bottleneck and it is possible that they might be able to detect a short, sh…

best wishes
Richard

Swamidass (Dr. S Joshua Swamidass) 2018-02-24 22:48:58 UTC #656

> RichardBuggs:
>
> I have now started to respond to **@DennisVenema** Part 2 blog reply to me. I have posted Part 1 of my response here:

Thanks **@RichardBuggs** , looking forward to reading it. Though, coalescence analysis is entirely encoded within ancestral recombination graphs. I'm not sure how relevant it is. The fact that TMR4A is at 500 kya is nearly at the point at which we have demonstrated that coalescence analysis cannot detect a single generation bottleneck of a single couple. I'm not sure his "part 2" requires a response.

Swamidass (Dr. S Joshua Swamidass) 2018-02-24 23:33:32 UTC #657

> RichardBuggs:
>
> **http://www.richardbuggs.com/response_to_Dennis_Venema_Biologos_Part2_Adam_Eve_Coalescent.html**

> RichardBuggs:
>
> I have now started to respond to **@DennisVenema** Part 2 blog reply to me. I have posted Part 1 of my response here:
>
> **http://www.richardbuggs.com/response_to_Dennis_Venema_Biologos_Part2_Adam_Eve_Coalescent.html**
>
> And placed it on the Biologos forum here:

Okay, got a chance to read it. I'm not sure your critique is correct. Can you help me understand? You point out two mistakes in this claim by **@DennisVenema** :

> his means that about 25% of the time, heterozygosity is lost, and that only one allele remains in the population for a given gene. If only one allele is present, then this is a coalescence point for that gene: going forward, we will have to wait for mutations to produce new alleles, and those new alleles will coalesce back to their single ancestral allele that survived the bottleneck. In the future, as new alleles are produced from the surviving allele through mutation, the new alleles will all coalesce within a few generations of the bottleneck. Their TMRCA values will thus be almost identical… Coalescent-based methods are thus an excellent way to detect bottlenecks—even really brief ones, if they are severe enough. Even a brief, severe bottleneck will still greatly increase the chances of alleles being lost, and the telltale signature of numerous genes that coalesce within a short time frame.

To clarify here, Ne (or effective population size) is just another unit conversion. It is the reciprocal of the coalescence rate as a function of time. Coalescence are the points in the tree where a merger happens, and they are normalized appropriately by the Kingman term. We just look at when they are, binning by time. This is the coalescence rate. One divided by that is Ne. That is why the TMRCA is relevant (of a subset of the alleles), as that is how the date is determined.

You say his wrong in this claim. I agree, but for a different reason than you. You write (dealing with each point differently)…

> I think that Dr Venema is wrong in making this claim. Let me explain why. I think that he is making at least two mistakes here.

> (1) In calculations that show that 75% of heterozygosity would be maintained after a bottleneck, the level of heterozygosity before the bottleneck is “known”. But coalescent models run backwards in time, and we can only “see” those lineages that survive the bottleneck. Thus we cannot directly know how many alleles were lost via sampling at the bottleneck. The loss of alleles via the sampling effect of the bottleneck will not show up as coalescence events in a coalescence model. These are two separate effects of a bottleneck.

First off there is a large conceptual difference between coalescence and heterozygosity. A very high amount of coalescence can take place, even as 75% heterozygosity is maintained. These are just different things.

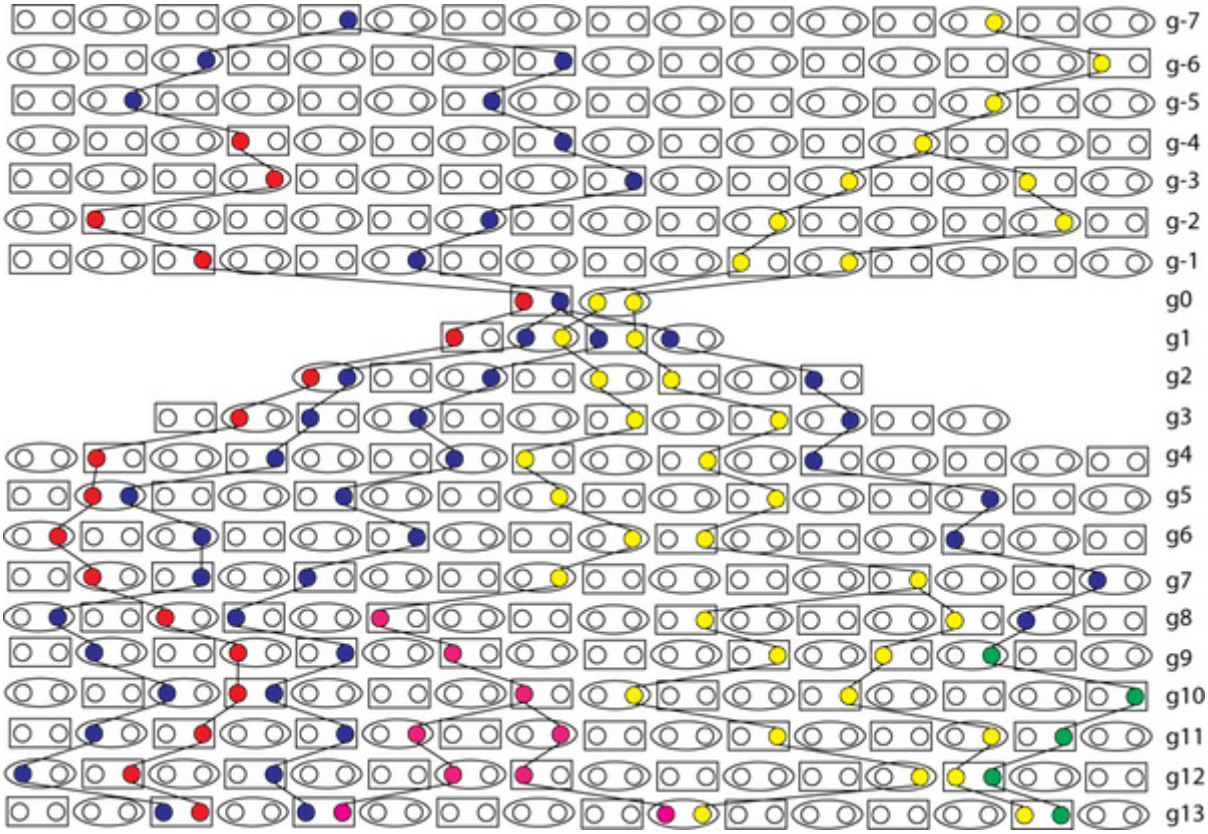
Moreover, the loss of alleles ***can*** show up as coalescence events. However, and this the critical point, our ability to detect them is very tightly dependent on the number of lineages entering (in backward time) the bottleneck. If there is only one surviving lineage, there will be zero coalescents, our ability to detect is zero. If there are 50 lineages, there will be a *very* high amount of coalescence (at least 46 lineages will coalesce), and we will almost certainly detect it. If there is 4 lineages, it seems that we would not detect it. To close the loop, the fact that there might by 75% heterozygosity after a bottleneck tells us nothing about how many lineages are coalescing at this point in time. These are different things, and are entirely separable.

Moreover, and this is a critical point. Coalescence analysis ***CAN*** detect bottlenecks, but only if there is sufficient surviving lineages to cause a spike in coalescence at the bottleneck. So **@DennisVenema** appears to be in error, in that he did not understand the or explain the lineage number dependence on coalescences when he wrote this. However, he is correct in his claim that coalescence can detect bottlenecks, ***if we limit ourselves to very recent timepoints.*** However, in the distant past, not so much.

> (2) Dennis is assuming that if only one allele is present in a population, then that allele has coalesced. This is a misunderstanding of coalescent theory. In coalescent theory, two gene lineages only coalesce when they reach a single copy in a single genome within a population. This means that if only one allele is present at a particular locus in a bottleneck of two, we know for sure that this allele has NOT coalesced, as it is present in four genomes (two in each person). It must therefore coalesce before the bottleneck. If the ancestral population is large, that coalescence will be a long time before the bottleneck.

I do not think this is his assumption. Coalescence does NOT make any statements about the number of alleles at a given time in history. Rather it make a statement about the number of lineages **that survive to this day by direct descent.** That is all that is modeled in coalescence theory. It does not presume that all alleles collapse to a single allele at coalescence, just that two alleles (potentially of many) collapse to one.

So once again, a lot of coalescence can take place, even when there is heterozygosity. Let’s look at your figures to make that clear.

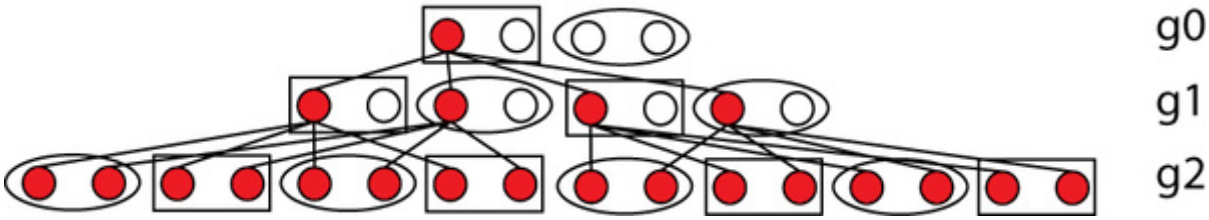


So, here, we see that the conditions put forward are not met. There is more than one lineage going through the bottleneck. The heterozygosity is high.

What about coalescence? Well, in that figure, there are THREE coalescence events between g0 and g1, all in the blue lineages. I cannot tell for sure (it gives me a headache to look to closely) but that seems to be the maximum number of coalescence in any generation. If we had more lineages going in there, we would have seen more coalescence. In fact we are guaranteed that there at least L - 4 coalescents through a single couple bottleneck if there are L lineages going into it (reverse time).

In this case, there was SIX lineages entering, and THREE coalesced. Notice how this nothing to do with heterozygosity. It is, rather, about reduction in number of alleles. It is, also, tightly influenced by the NUMBER of surviving alleles that are still in the population right after (time forward) the bottleneck.

It seems, however, **@RichardBuggs** you are confusing the several coalescence that appear with “THE coalescent,” which you identify in this figure:



There is not one coalescent at g0, but FOUR coalescents. This is a critical point. Really all merge points in a tree are coalescents, not just the top one.

> We can calculate the chances, because normally we would expect there to be a 0.5 chance of a parent passing a particular gene copy to their children. So the chances of what we see in generation g1 above are: 0.5 x 0.5 x 0.5 x 0.5 = 0.54 = 0.0625. The chances of what we see in generation g2, given what we see in generation g1, are 0.516 = 0.0000153. The overall probability of this is 0.520= 0.000000954.

> As we have four starting lineages at the bottleneck, we need to multiply by four, to find the overall chance of having coalescence to one lineage at the bottleneck. This gives us 0.00000381. So all in all, we expect coalescence to a single lineage 0.000381% of the time. Not 25% of the time.

This turns out not to be quite correct. Coalescence analysis does not deal with this. Privately, I had shared some similar computations, but also came to understand it was in error (notice it is not in public). However, this computations miss exactly what coalescence theory is doing, I missed this too the first time around, It is quite subtle.

Some subtle math errors notwithstanding, what is being computed here might be a reasonable estimate of the allele distribution we would expect after a bottleneck if we were to measure it. However, most of that diversity is going to die out (or be missed) before we get to our specific samples. So it is not really valid. What coalescence tries to do is, instead, reconstruct the history of all ***direct*** ancestral sequences of the data in our current day sample. There may be other alleles with the exact same DNA sequences alongside this direct ancestors, but coalescence only models the ***direct*** ancestors.

Keep in mind, the number of allelic lineages at different points in time, does not tell us the number of alleles in the population at that point in time. For example, lets say we are 3 mya, where the vast majority of the genome has coalesced to a single allele that survives till today. The population at that time, however, is not all homozygous for that allele. That allele, also, might even be low frequency. Rather, we are just saying none of those other alleles survive for 3 million years to present day.

For that reason, demonstrating heterozygosity is not lost does not really make the case here. Moreover, remember, no more than 4 alleles can pass through the bottleneck. Heterozygosity, however, does not tell us how many alleles there are.

> If my calculations are correct (and I stand ready to be corrected if they are not) then Dennis is quite wrong to think that 25% of genes would coalesce to one lineage at a bottleneck of two. Less than 1% would.

Neither your calculations nor **@DennisVenema** are correct. It turns out that the amount of coalescence is entirely ***dependent*** on the number of extant lineages that enter (backwards time) the bottleneck. The more lineages the more coalescence, the fewer lineages the fewer coalescence. Also his application of the Kingman coalescent to compute 25% is just incorrect. It is wrong.

One final point about a major conceptual error. Read this statement by **@DennisVenema** :

> Coalescent-based methods are thus an excellent way to detect bottlenecks—even really brief ones, if they are severe enough. Even a brief, severe bottleneck will still greatly increase the chances of alleles being lost, and the telltale signature of numerous genes that coalesce within a short time frame.

This is false. For all the reasons we discussed, but for one additional reason. “Severity” of a bottleneck includes two things: (1) the size of the bottleneck population AND (2) the number of generations in the bottleneck. Severe bottlenecks are a LARGE number of generations, with a SMALL population size. However, a SINGLE generation of a very SMALL population size (e.g. a single couple) is not necessarily a severe bottleneck. That is, remember, because severity is defined along two dimensions. In one dimension it is severe, but in another it is extremely mild.

Of note, I’ve had a chance to interact with some secular population geneticists about this. There is actually quite a bit in the literature that makes this point. It is common for papers here to note the limitations of this approach, that it cannot pick up brief bottlenecks.

That is, in fact, what makes this question so scientifically interesting. Essentially, we are asking if a bottleneck is extremely severe by one dimension, but extremely mild by another, is detectable? No one has tested that before

(though I just did!, data not shown), and we are finding out that the answer is “no we cannot detect it much before 500 kya.” It’s no surprise, because this falls out nicely from the math, justifying the use of TMR4A here.

In summary, **@RichardBuggs** I agree that **@DennisVenema** was in error, however, I’m not sure your argument is correct either. Can you clarify if I missed something here? I hope I did not misrepresent you. My critique here is based on my best understanding of what you wrote. However, please correct me if I missed something,

---

DennisVenema (Dennis Venema) 2018-02-25 01:33:13 UTC #658

I think you’re on the right track here, **@Swamidass** , yes - and I agree I was thinking about the size dimension of the bottleneck without properly appreciating the length aspect. (Though, I still have not seen a reasonable case for *why* such a bottleneck might have occurred - ~10,000 down to 2 and then back up to ~10,000 with exponential growth - that would be unlike anything we’ve ever noted in nature as far as I am aware).

I also think that the TMR4A is a better way of looking at this overall - it more directly addresses what we’re really interested in.

I’ll be sharing that PSMC modelling with you and **@RichardBuggs** shortly. Things got busy… it’ll be good to chew over those data together.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 02:55:14 UTC #659

> DennisVenema:
>
> (Though, I still have not seen a reasonable case for why such a bottleneck might have occurred - ~10,000 down to 2 and then back up to ~10,000 with exponential growth - that would be unlike anything we’ve ever noted in nature as far as I am aware).

A tight bottleneck followed by rapid expansion is a well known and observed manner of speciation. It is observed from single couples (and even single individuals) in some animals and many plants. There was a long standing debate about whether this is important in human speciation too, until the trans-species variation argument seemed to incorrectly end it.

The bottleneck can be caused, for example, by genetic interference or by near extinction events. Or by founder events too. Speciation can be a slow gradual process. It can also be rapid, even occurring in a single generation.

DennisVenema (Dennis Venema) 2018-02-25 03:11:32 UTC #660

> Swamidass:
>
> A tight bottleneck followed by rapid expansion is a well known and observed manner of speciation. It is observed from single couples (and even single individuals) in some animals and many plants. There was a long standing debate about whether this is important in human speciation too, until the trans-species variation argument seemed to incorrectly end it.
>
> The bottleneck can be caused, for example, by genetic interference or by near extinction events. Or by founder events too. Speciation can be a slow gradual process. It can also be rapid, even occurring in a single generation.

Sorry, I see that wasn't clear. I'm wondering about such an event *specifically for hominins* - which, we know from other lines of evidence, have been widely dispersed on the planet for the last 1.8 million years at a minimum.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 03:23:13 UTC #661

> DennisVenema:
>
> Sorry, I see that wasn't clear. I'm wondering about such an event specifically for hominins - which, we know from other lines of evidence, have been widely dispersed on the planet for the last 1.8 million years at a minimum.

From a geographic distribution point of view, it there were at least two, if not three times, that a species (or subspecies) in our lineage arose from a single location, spreading very quickly across the globe to become a cosmopolitan species. It is possible a bottleneck preceded, and perhaps was even casually interrelated, with these events.

There has been several theories put forward in the literature about this specific question. Like I said, this was a long standing debate. There are several speciation mechanisms that requires this, and the question is whether or not these mechanisms of speciation were important ever in our lineage. Some of these mechanisms, it turns out, can be testable. But that is way beyond our scope here. At this point, we can just settle into the fact that this is unknown.

Ultimately, I think it is beyond science to determine if it was precisely a single couple at these bottlenecks (if they exist). However, a single couple may not be implausible in some scenarios. Drift in these contexts is one the most potent and powerful forces of genetic change. The sharper the bottleneck, the more potent a force it might have been.

DennisVenema (Dennis Venema) 2018-02-25 06:08:08 UTC #662

> Swamidass:
>
> From a geographic distribution point of view, it there were at least two, if not three times, that a species (or subspecies) in our lineage arose from a single location, spreading very quickly across the globe to become a cosmopolitan species. It is possible a bottleneck preceded, and perhaps was even casually interrelated, with these events.

I hear what you're saying, but *10,000 down to 2 in a single generation* is what **@RichardBuggs** is proposing. I know of no case of a large mammal (or even any mammal) where anything analogous to this is thought to have happened. Do either of you know of a case? The literature is large, and I may well be missing something.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 06:34:51 UTC #663

> DennisVenema:
>
> I hear what you're saying, but 10,000 down to 2 in a single generation is what **@RichardBuggs** is proposing. I know of no case of a large mammal (or even any mammal) where anything analogous to this is thought to have happened. Do either of you know of a case? The literature is large, and I may well be missing something.

Perhaps Mouflon sheep.

If not, just because we haven't observed it doesn't mean it didn't happen. For example, just because we haven't observed abiogenesis, doesn't mean it didn't happen. It does not appear, to the point, that there is evidence against an ancient bottleneck.

Regarding how “likely” this is, it seems to depend tightly on what one thinks about Scripture. Because we have no evidence on way or the other, people are just going to reiterate their priors. Where is science is silent, theology has legitimate autonomy.

Jonathan_Burke (Jon) 2018-02-25 08:58:01 UTC #664

> Swamidass:
>
> Where is science is silent, theology has legitimate autonomy.

That sounds awfully like a God of the gaps. I don’t think it’s wise to tell people they can be confident basing their faith on things which “might” have happened, which science “hasn’t ruled out yet”.

---

glipsnort (Steve Schaffner) 2018-02-25 12:32:49 UTC #665

> Swamidass:
>
> From a geographic distribution point of view, it there were at least two, if not three times, that a species (or subspecies) in our lineage arose from a single location, spreading very quickly across the globe to become a cosmopolitan species.

What two or three times do you mean?

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 16:28:20 UTC #666

I think the example most relevant to this case is the spread of *Homo erectus* about 2 million years ago.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 20:35:16 UTC #667

> Swamidass:
>
> I think the example most relevant to this case is the spread of Homo erectus about 2 million years ago.

I see why this model of a very ancient Adam seems valuable to **@agauger** . We can avoid perceived “problems” of Adam interbreeding with others, and also give an account of “human”-like behavior in non-Homo sapiens.

However, I think **@Jon_Garvey** ’s theological critique from Christology and God’s nature is important.

http://potiphar.jongarvey.co.uk/2018/02/23/the-lord-is-not-slow/

If Adam fell 2 million years ago, that means God waiting 2 million years to redeem us by Jesus. Why would God wait so long? How was His plan of redemption set into motion 2 million years ago? This, to me, are large puzzle that need to be addressed by any ancient Adam model, including the RTB model (with Adam 100 kya) and Figurative Adam models linked to the origin of *Homo sapiens* too (such as **@DennisVenema** ’s model).

I’ve been looking for a good account of this, but have yet to find one already put forward. I’m stuck on this too, and cannot see quite how to answer this in an any ancient Adam scenario.

These Christological concerns are what pushes me towards a recent genealogical Adam. We could see the rise of civilization as both the Fall into Knowledge of Good and Evil, and God initiating His plan to redeem us through the Incarnation, Death, and Resurrection of Jesus. The testimony of Scripture, for example, seems predicated, at minimum, on written language. This instinct is rooted in my admittedly fallible understanding of God's nature, but there are legitimate theological questions I'd like to see engaged by ancient Adam advocates (e.g. **@DennisVenema** and **@agauger** and **@RichardBuggs**). In these models…

Why did God not send Jesus soon after the fall?

Why did God not just execute Adam and Eve and start over with a new couple? Or species (in **@DennisVenema** 's case)?

Why do we not see much evidence of the fall in the distant past, even if we see evidence of human-like behavior? In what way does the Fall radically reshape the world?

In a recent genealogical Adam model, the answers are more accessible. God does send Jesus soon after the fall. The reason God does not execute Adam and start over is because there are people outside the garden too, and allowing Adam to leave sows the seeds for redemption of people outside the garden. Moreover, the Fall does entirely reshape the world as human civilization rises. So we do see a radical transformation of the world, but this is associated more with the fall of Adam than the rise of the human mind.

Of course, maybe there is a way to make sense of this in an ancient Adam scenario. I'd be curious to hear how those who care about that scenario thinking about it. Until then, I see more coherence in **@Jon_Garvey** 's approach.

> Jonathan_Burke:
>
> That sounds awfully like a God of the gaps. I don't think it's wise to tell people they can be confident basing their faith on things which "might" have happened, which science "hasn't ruled out yet".

You should know by now that I encourage people to place the confidence in the thing that science ***HAS*** definitely ruled out: the Resurrection of the Son of God. Those who die do not rise again, yet this is the solid rock on which my faith finds confidence.

http://peacefulscience.org/swamidass-confident-fatih.pdf

As for Adam, there is a big difference between saying science does not know the details, and inferring God's action because there is a gap in our knowledge. Scripture does not teach of the mechanism of God's creative work, but some do feel it tells us of Adam. Any one who takes such a position is not resting their faith in science, but looking beyond it.

Of course, those how do not find the Scriptural account trustworth will think differently. Also, there are reasons why some might read that account differently, even if they do find the account trustworthy. This, however, has nothing to do with "God of the Gaps."

DennisVenema (Dennis Venema) 2018-02-25 21:04:42 UTC #668

> Swamidass:
>
> I see why this model of a very ancient Adam seems valuable to **@agauger** . We can avoid perceived "problems" of Adam interbreeding with others, and also give an account of "human"-like behavior in non-Homo sapiens.

There's not a lot of "human-like behaviour" in Homo at 2 million years ago. A significant issue for ancient Adam models is the conspicuous *lack* of behaviours we consider indicative of humanity at that time. No art, only simple stone tools, no

evidence of intentional burial or religious observance. The picture at 2 million years ago looks nothing like what is described in Genesis.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 21:07:18 UTC #669

> DennisVenema:
>
> There's not a lot of "human-like behaviour" in Homo at 2 million years ago. A significant issue for ancient Adam models is the conspicuous lack of behaviours we consider indicative of humanity at that time. No art, only simple stone tools, no evidence of intentional burial or religious observance.

This a matter of great debate within anthropology. You are certainly entitled to your private opinion. Let's just not equivocate your opinion with the scientific consensus. There is no consensus here. In fact, even the Natural Museum of History seems to be closer to **@agauger** 's position than yours.

> DennisVenema:
>
> The picture at 2 million years ago looks nothing like what is described in Genesis.

I agree. The same goes for your scenario. It is nothing like what is described in Genesis. Moreover, it raises the same questions as the ancient Adam view, along with several more of its own.

DennisVenema (Dennis Venema) 2018-02-25 21:09:07 UTC #670

> Swamidass:
>
> Perhaps Mouflon sheep.

Hmm. For those that don't know about it, that's a case where humans cause a bottleneck for one population of sheep by transporting them to a remote island. They certainly don't enjoy exponential growth afterwards either. Mouflon sheep in Europe continue on during this time. So, not many parallels to the proposed situation unless we're floating the idea that the postulated hominin bottleneck was intentionally caused by an intelligent agent.

DennisVenema (Dennis Venema) 2018-02-25 21:10:00 UTC #671

> Swamidass:
>
> The same goes for your scenario.

What are you saying is "my scenario"?

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 21:13:23 UTC #672

> DennisVenema:
>
> What are you saying is "my scenario"?

As I understand it, you hold that “humans” are Homo sapiens, and Adam is not a historical figure. Rather, God’s Image and our Fallen nature are instilled gradually over time as our species arises about 200 kya. “Adam” in Genesis is not a historical individual in our past, but perhaps an allegorical reference to the rise of *Homo sapiens*.

You acknowledge that Neanderthals do interbreed with “humans,” but we neither refer to them as “human” or “non-human” or “sub-human.” They are something else that has not been specified. Somehow, they are not the same thing as *Homo sapiens*, but they breed with *Homo sapiens*, and their origins need not be specified. (Epicycle?)

Of course, please do refine and clarify your view.

DennisVenema (Dennis Venema) 2018-02-25 21:14:16 UTC #673

> Swamidass:
>
> This a matter of great debate within anthropology. You are certainly entitled to your private opinion. Let’s just not equivocate your opinion with the scientific consensus. There is no consensus here.

I’m not aware of anyone proposing intentional burial, art, or religious activity at 2 million years ago. I’m open to being corrected on that, of course, if you know of any examples.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 21:26:09 UTC #674

> DennisVenema:
>
> I’m not aware of anyone proposing intentional burial, art, or religious activity at 2 million years ago. I’m open to being corrected on that, of course, if you know of any examples.

You are really not aware of this? That is surprising.

Most recently there has been a raging debate surrounding H nadelii. Some were arguing that they are a version of Homo erectus, burying their dead. It now seems these bones were dated around 250 kya, but for a while people were thinking much much earlier. That date, also, is certainly up for dispute and could be revised again.

https://www.nbcnews.com/science/science-news/early-human-homo-naledi-may-have-made-tools-buried-dead-n756916

Even if affirm the more recent dating, if we see this behavior in multiple species/subspecies at this time (which we do), we expect it actually arose much earlier, closer to the common ancestor of all of them (unless its convergent). So it is not unreasonable to suggest it arises even earlier that we have observed, well before humans arise.

Yes, you could disagree with this interpretation (and I personally have no stake here). However, that does not remove the raging debate on these points. There is precious little data to go off of, and many of the most populated areas are now covered by rising seas. We just do not know when intentional burial arises, and most think it arises long before Homo sapiens.

Likewise, large scale pigment mining also arises before Homo sapiens: **https://miningafricaonline.co.za/index.php/mining-features/mining-in-africa/2556-the-origins-of-pigment-mining**. It is almost expected that small scale pigment utilization is taking place long before that.

> Archaeological evidence suggests that the mining of minerals for use as pigments may have begun more than one million years ago

Of course, pigments are used often for art, and we do not expect art from 1 mya to last to this day, except perhaps in the most fortunate of extremely rare and lucky cases.

There is a repetitive quality to this part of the conversation. It seems there is a pattern of arguing that “because we do not detect it, it’s not plausible to wonder if it exists”.

I’d encourage a more scientific approach, where we propose several hypotheses, understand what evidence would be uncovered under each hypothesis (which may be nothing), and then consider what the data might tell us. In cases like Homo erectus 2 mya, there is not really much data. Most hypothesis are plausible, and that is why there is so much debate within anthropology. That ambiguity a fact of scientific inquiry, and pushing too quickly past it leads to errors.

DennisVenema (Dennis Venema) 2018-02-25 21:46:10 UTC #675

> Swamidass:
>
> You are really not aware of this? That is surprising.

I’m well aware of the evidence about H. naledii. I think they intentionally buried their dead. But they are nowhere near 2 million years ago, which is the time point we are discussing.

I’m also well aware of the evidence for pigment use in *Homo*. I have not seen a peer-reviewed article that places this evidence further back than 250-300 KYA. I’m of course open to new evidence as it arises. But again, there is none (that I know of) anywhere close to 2 million years ago.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 21:56:41 UTC #676

> DennisVenema:
>
> I’m well aware of the evidence about H. naledii. I think they intentionally buried their dead. But they are nowhere near 2 million years ago, which is the time point we are discussing.

That is under debate: **https://www.theguardian.com/science/2017/may/09/new-haul-of-homo-naledi-bones-sheds-surprising-light-on-human-evolution**

> DennisVenema:
>
> I’m also well aware of the evidence for pigment use in Homo. I have not seen a peer-reviewed article that places this evidence further back than 250-300 KYA. I’m of course open to new evidence as it arises. But again, there is none (that I know of) anywhere close to 2 million years ago.

That is openly contended by many anthropologists. **https://miningafricaonline.co.za/index.php/mining-features/mining-in-africa/2556-the-origins-of-pigment-mining**

> Early Homo species arose within the southern savannas of Africa and **left evidence of the collection of red ochre and specular haematite** (specularite). Some authors have suggested that these early Homo species therefore had enhanced aesthetic and symbolic capabilities. However, **the date and location of the emergence of ‘symbolic behaviour’ is still debated and may never be unequivocally resolved**.

I know it is tempting to speed past the controversies, but science does not end up resolving all the details. We are limited by what we can see, and that is a mere fraction of what has happened.

Things also have changed since you were in graduate school. Back then, your view was quite common, until the weight of evidence started to challenge it. Now, most anthropologists tell a different story. There has been a steady progress of finding evidence of symbolic thought earlier than Homo sapiens. That is part of the reason why **@agauger** is in closer agreement with the Natural History Museum than you.

Ultimately, we cannot really be sure. That makes it more interesting. Do not prematurely foreclose the conversation. It could be fun!

DennisVenema (Dennis Venema) 2018-02-25 22:02:30 UTC #677

> Swamidass:
>
> As I understand it, you hold that “humans” are Homo sapiens, and Adam is not a historical figure. Rather, God’s Image and our Fallen nature are instilled gradually over time as our species arises about 200 kya. “Adam” in Genesis is not a historical individual in our past, but perhaps an allegorical reference to the rise of Homo sapiens.
>
> You acknowledge that Neanderthals do interbreed with “humans,” but we neither refer to them as “human” or “non-human” or “sub-human.” They are something else that has not been specified. Somehow, they are not the same thing as Homo sapiens, but they breed with Homo sapiens, and their origins need not be specified. (Epicycle?)
>
> Of course, please do refine and clarify your view.

I’m not really understanding why you think this view - and I will clarify it a bit for you below - is somehow as at odds with the setting of Genesis as seeing Adam as *Homo erectus* at 2 million years ago. Not following you here.

My own personal view (and note, this is my own view, not any sort of an official BioLogos position, of course - and despite the title on these comments, I am no longer the Fellow of Biology for BioLogos) is my own sort of mash-up of Pete Enns’ Adam is Israel and Walton’s cosmic temple view. I think Genesis is operating on both levels here - telling the narrative of Israel’s God creating the world and echoing the exile at the same time. I’m ambivalent on whether historical individuals named Adam and Eve are part of that. My suspicion is not, but people I respect (Walton, N.T. Wright) are holding out for at least some form of that, so I’m happy to let the theologians discuss it and see where it goes.

All of this sits quite well with the Genesis narratives set in the neolithic, around 6,000 years ago. I don’t think Genesis has in mind at all any time frame before this.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 22:06:51 UTC #678

> DennisVenema:
>
> My own personal view (and note, this is my own view, not any sort of an official BioLogos position, of course - and despite the title on these comments, I am no longer the Fellow of Biology for BioLogos) is my own sort of mash-up of Pete Enns’ Adam is Israel and Walton’s cosmic temple view. I think Genesis is operating on both levels here - telling the narrative of Israel’s God creating the world and echoing the exile at the same time. I’m ambivalent on whether historical individuals named Adam and Eve are part of that. My suspicion is not, but people I respect (Walton, N.T. Wright) are holding out for at least some form of that, so I’m happy to let the theologians discuss it and see where it goes.

> All of this sits quite well with the Genesis narratives set in the neolithic, around 6,000 years ago. I don't think Genesis has in mind at all any time frame before this.

Sounds quite a bit like a recent genealogical Adam.

> DennisVenema:
>
> I'm not really understanding why you think this view - and I will clarify it a bit for you below - is somehow as at odds with the setting of Genesis as seeing Adam as Homo erectus at 2 million years ago. Not following you here.

Probably because of your strong stance against identifying Adam with anything other than the origin of "humans," by which you mean Homo sapiens. Yet, here, you identify Adam with Israel, who is certainly not the ancestor of all Homo sapiens.

Like I said, your position is very close to the recent genealogical Adam view. Surprising.

DennisVenema (Dennis Venema) 2018-02-25 22:07:23 UTC #679

> Swamidass:
>
> That is openly contended by many anthropologists. **https://miningafricaonline.co.za/index.php/mining-features/mining-in-africa/2556-the-origins-of-pigment-mining**
>
> Early Homo species arose within the southern savannas of Africa and left evidence of the collection of red ochre and specular haematite (specularite). Some authors have suggested that these early Homo species therefore had enhanced aesthetic and symbolic capabilities. However, the date and location of the emergence of 'symbolic behaviour' is still debated and may never be unequivocally resolved.
>
> I know it is tempting to speed past the controversies, but science does not end up resolving all the details. We are limited by what we can see, and that is a mere fraction of what has happened.

Again, everything I've seen in the literature is ~300KYA or later. I don't think the debate stretches back to 2MYA, but like I said, I may have missed a paper somewhere.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 22:12:59 UTC #680

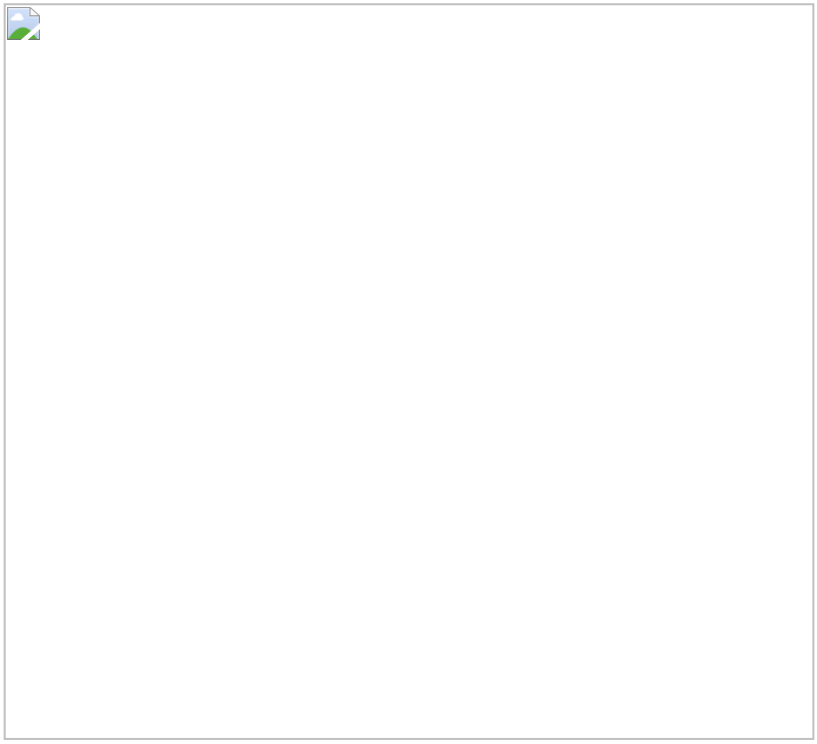
> DennisVenema:
>
> Again, everything I've seen in the literature is ~300KYA or later. I don't think the debate stretches back to 2MYA, but like I said, I may have missed a paper somewhere.

You've missed a whole body of literature, not just a single paper. See this one on art from 1.8 million years ago.

http://www.mdpi.com/2076-0752/3/1/135/pdf

I'm not presenting this as definitive evidence of art, but of definitive evidence of open debate. Many anthropologists hold that Homo erectus was fully human, with symbolic thought, art, and more.

> **Current archaeological evidence supports** the claim that **symbolic behavior, including palaeoart, first emerged in human evolution around 1 million years ago**. The purpose of this article is to review archaeological studies that might support the hypothesis that **the earliest palaeoart actually is evident around 2 million years ago.** This review identifies nine Oldowan artifacts that have been proposed as possible non-utilitarian and possibly symbolic behavior. Among seven stone tools, the three strongest candidates are the Olduvai Gorge, the FLK North grooved and pecked cobble, ~1.80 million years ago, and MNK Main subspheroid with hexagon shape framing an apparent natural dot-and-undulating-line motif, ~1.5–1.6 million years ago, both initially reported and described by Mary Leakey; and the curated Koobi Fora FxJj1 “broken core” with inner rhomboid shape, ~1.87 million years ago. All six stone tools from Olduvai Gorge need scientific re-examination to determine their chaîne opératoire and assess non-utilitarian features. If even one of the Olduvai Gorge artifacts were validated as symbolic behavior this would indicate the emergence of palaeoart one million years earlier than current proposals. It would also suggest that Homo habilis/rudolfensis or a very early Homo erectus had substantially more advanced cognitive, design and symbolic competencies than inferred in current theories. It would constitute a challenge to develop more advanced cognitive semiotic and art-theoretic analytical tools for illuminating the role of such palaeoart in hominin cultural evolution.



Like I said:

> Swamidass:
>
> Things also have changed since you were in graduate school.

> DennisVenema:
>
> and note, this is my own view, not any sort of an official BioLogos position, of course - and despite the title on these comments, I am no longer the Fellow of Biology for BioLogos

True, but you are also a speaker in the Voices Program, and have a long running blog on the site, and are the face of the scientific account of BioLogos. BioLogos does includes people of a wide range of views on Adam. True. However, it

only forefronts a small number of people, including you. That means something too.

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glipsnort (Steve Schaffner) 2018-02-25 22:45:09 UTC #681

What single location did *erectus* spread from?

DennisVenema (Dennis Venema) 2018-02-25 22:47:46 UTC #682

> Swamidass:
>
> You've missed a whole body of literature, not just a single paper. See this one on art from 1.8 million years ago.
>
> **http://www.mdpi.com/2076-0752/3/1/135/pdf**
>
> I'm not presenting this as definitive evidence of art, but of definitive evidence of open debate. Many anthropologists hold that Homo erectus was fully human, with symbolic thought, art, and more.

Thanks for the paper, I'll read up on it. It's not my area, so it's not something I keep close tabs on.

At first blush, it is as I suspected - the early evidence is pretty controversial. When the average Christian hears "art" or even "paleoart" they're not thinking about natural objects that may have been collected for aesthetic purposes, or a few lines on a bone that might have been intentionally made as opposed to the results of butchering with stone tools, or very crude natural figures that might be intentional or might just appear to us to be pareidolic. What we see is a gradient of behaviour. Just like species, there is no clear line of when "art" begins.

This is what we expect from a gradual progression, not "fully human" entities at 2MYA.

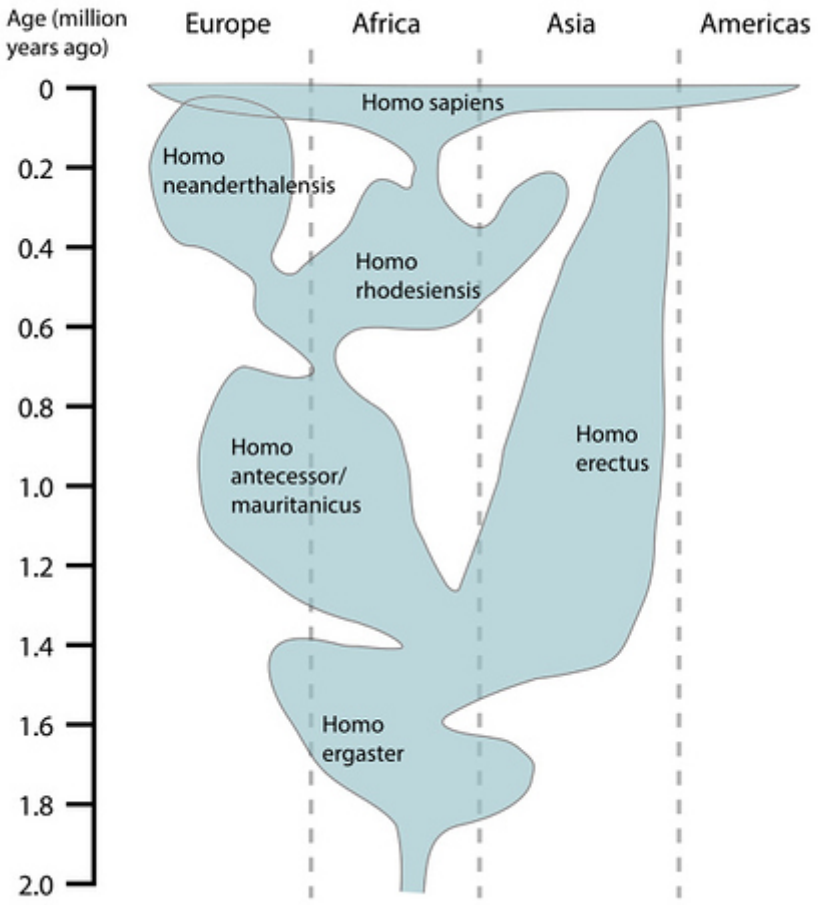
Genesis has art, agriculture, metallurgy, pastoralism, music, and so on within Adam's lifetime. It fits well with 6KYA.

Thanks again for the paper. It's a fascinating read thus far.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 22:47:53 UTC #683

> glipsnort:
>
> What single location did erectus spread from?

Africa, at the bottom of the figure ("eregaster" here).



https://en.wikipedia.org/wiki/Human_evolution

> DennisVenema:
>
> At first blush, it is as I suspected - the early evidence is pretty controversial.

Yes, but completely within mainstream speculation. Moreover, current views with much less controversy place first art about 1 mya, not just 300 kya. Either way, **@agauger** is just going with one view which is solidly within mainstream science when says "humans" arise 2 mya.

> DennisVenema:
>
> This is what we expect from a gradual progression, not "fully human" entities at 2MYA.

Yes, it is also what we expect in **@agauger** 's model.

> DennisVenema:
>
> Just like species, there is no clear line of when "art" begins.

Which is why we have to tolerate diversity and differences of opinion here. It is not really something science answers.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 22:53:30 UTC #684

> DennisVenema:
>
> Genesis has art, agriculture, metallurgy, pastoralism, music, and so on within Adam's lifetime. It fits well with 6KYA.

It is very interesting seeing you coming over to a recent genealogical Adam view of origins. If you start asking the questions you've been directing my way over the last year, you might move even farther.

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glipsnort (Steve Schaffner) 2018-02-25 22:55:46 UTC #685

> Swamidass:
>
> Africa, at the bottom of the figure ("eregaster" here).

In this context, an entire continent is not something I would consider a single location. (Actually, I can't think of any context in which I would consider Africa to be a single location. Interstellar travel, maybe?)

DennisVenema (Dennis Venema) 2018-02-25 22:56:01 UTC #686

> Swamidass:
>
> Which is why we have to tolerate diversity and differences of opinion here. It is not really something science answers.

I agree - there needs to be allowances for differences on disputable matters. FWIW, I'm happy fellowshipping alongside Christians of widely disparate views - YEC, OEC, ID, EC, and everything in between. I do draw the line (as nicely as I can) when folks start saying that one has to reject evolution to be a Christian (or similar), though.

DennisVenema (Dennis Venema) 2018-02-25 22:57:59 UTC #687

> Swamidass:
>
> It is very interesting seeing you coming over to a recent genealogical Adam view of origins. If you start asking the questions you've been directing my way over the last year, you might move even farther.

Not sure what you mean here - I've always thought that Genesis has 6KYA in mind, as far as I can recall. I want to take Genesis on its own terms. It doesn't have modern science in view, in my opinion.

Swamidass (Dr. S Joshua Swamidass) 2018-02-25 23:22:33 UTC #689

> glipsnort:
>
> In this context, an entire continent is not something I would consider a single location. (Actually, I can't think of any context in which I would consider Africa to be a single location. Interstellar travel, maybe?)

How about "somewhere in Africa".

Evidence is spotty. It does not seem they instantly appear everywhere. As I understand, the evidence of their tools is distinguishable from early creatures, but exactly how and where they arise will always be blurry.

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agauger (Ann Gauger) 2018-02-26 00:16:57 UTC #690

> DennisVenema:
>
> At first blush, it is as I suspected - the early evidence is pretty controversial. When the average Christian hears “art” or even “paleoart” they’re not thinking about natural objects that may have been collected for aesthetic purposes, or a few lines on a bone that might have been intentionally made as opposed to the results of butchering with stone tools, or very crude natural figures that might be intentional or might just appear to us to be pareidolic. What we see is a gradient of behaviour. Just like species, there is no clear line of when “art” begins.

Hi Dennis,

I just want to share my favorite evidence for the existence of art in Homo erectus/ergaster. This piece was found in South Africa at Kathu Pan, and dates to 750 KYR. It was made using many more flakes than required, and has a clear aesthetic quality

http://www.aggsbach.de/2011/09/short-history-of-the-acheulian-in-south-africa-the-chronology/

As far as anatomical similarity between Homo sapiens and Homo ergaster/habilis, see here

http://www.efossils.org/page/specimens/Homo%20ergaster

Thank you, **@Swamidass** , for the links to the evidence for neural development and art.

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agauger (Ann Gauger) 2018-02-26 01:53:34 UTC #691

> Swamidass:
>
> These Christological concerns are what pushes me towards a recent genealogical Adam. We could see the rise of civilization as both the Fall into Knowledge of Good and Evil, and God initiating His plan to redeem us through the Incarnation, Death, and Resurrection of Jesus. The testimony of Scripture, for example, seems predicated, at minimum, on written language. This instinct is rooted in my admittedly fallible understanding of God’s nature, but there are legitimate theological questions I’d like to see engaged by ancient Adam advocates (e.g. **@DennisVenema** and **@agauger** and **@RichardBuggs**). In these models…
>
> Why did God not send Jesus soon after the fall?
>
> Why did God not just execute Adam and Eve and start over with a new couple? Or species (in **@DennisVenema** ’s case)?
>
> Why do we not see much evidence of the fall in the distant past, even if we see evidence of human-like behavior? In what way does the Fall radically reshape the world?

@Swamidass , Hi Josh.

I have a great deal of respect for Jon Garvey, and you, Josh, but I am going to disagree with his and your claim that “God wouldn’t have done it that way.”

Jon left off a critical part of the context of his verse: 2 Peter 3:8.

8 But do not let this one fact escape your notice, beloved, that with the Lord one day is as a thousand years, and a thousand years as one day. 9The Lord is not slow about His promise, as some count slowness, but is patient toward you, not wishing for any to perish but for all to come to repentance.

And Habukkuk 2:1-3

> 1I will stand on my guard post
> And station myself on the rampart;
> And I will keep watch to see what He will speak to me,
> And how I may reply when I am reproved.
>
> 2Then the LORD answered me and said,
> “Record the vision
> And inscribe it on tablets,
> That the one who reads it may run.
>
> 3For the vision is yet for the appointed time;
> It hastens toward the goal, and it will not fail.
> Though it tarries, wait for it;
> For it will certainly come, it will not delay.

6000 years is a long time to us in terms of our life spans, but only 300-400 generations. 60,000 years is 10 times and 600,000 years 100 times that-- 30,000-40,000 generations. I hold to an old age for the universe. If God can take 14 billion years to form the universe we see, including the 4 billion year old earth, and then took more than 3 billion years to create life as we see it now, it’s clear he’s not in a hurry.

As to the awfulness of leaving so many generations in sin, there is this: there are many icons that depict Christ descending to the dead to redeem Adam and Eve. It’s probably based on these verses: 1 Peter 3:19 and following.

19 After being made alive,[d] he went and made proclamation to the imprisoned spirits— 20 to those who were disobedient long ago when God waited patiently in the days of Noah while the ark was being built.

Maybe there was the offer of redemption for those who had no opportunity before Christ. (This verse is interpreted in various ways. I have given the Catholic version here.)

Let the buyer beware. I am not a theologian. I have no axe to grind about Genesis interpretation (YEC or OEC) except for the historicity of Adam and Eve. I agree with Josh that the Gospel is central. Others have made the arguments about whether Adam was figurative, representative or a single actual person. I came to the idea of an old Adam because of the science, because I couldn’t reconcile multiple hominins running around with only some bearing God’s image. *H. erectus* is *so much* more similar to us than chimpanzees ever were. The chief argument against a *H erectus* Adam for me is that technology did not advance much, at least as far as we can tell. But then at that distance in time, the only things to preserved will be the kinds of things we see.

I also agree that some are exhibiting prejudice against “brow ridges”, and a tendency to underestimate the abilities of *H erectus* or Neanderthals.

As for the apparent presence a neolithic culture at the time of early Genesis (though written language?), I attribute that to whoever recorded the stories remembered from long long ago. The essence of the family history was preserved, but because they had no detailed description of things, anachronistic details were added.

Now I could well be wrong. It wouldn’t be the first time. But you asked.

Swamidass (Dr. S Joshua Swamidass) 2018-02-26 02:09:08 UTC #692

Thanks for the response.

> agauger:
>
> I have a great deal of respect for Jon Garvey, and you, Josh, but I am going to disagree with his and your claim that “God wouldn’t have done it that way.”

For the record, I do not know how God did it. I’m just curious how you are thinking about these things. I think there will be interesting things in the conversation. The goal, to be clear, is not to convince you to change. Any of us could be wrong about these distant details of the past, and it would not make any difference in the end.

> agauger:
>
> I have no axe to grind about Genesis interpretation (YEC or OEC) except for the historicity of Adam and Eve.

I think there are many that draw the line here too. Though I would say you also seem to think sole genetic progenitorship is important too. Why do you think genetic sole proprietorship is so important?

> agauger:
>
> I came to the idea of an old Adam because of the science, because I couldn’t reconcile multiple hominins running around with only some bearing God’s image.

Someday we’ll have to talk about a recent genealogical Adam model that does not have that problem. In the Genesis narrative, Adam is tied to the Fall, not God’s Image. Perhaps all our ancestors equally bear God’s Image at any given point in time, but Adam is more important for the Fall.

> agauger:
>
> As to the awfulness of leaving so many generations in sin, there is this: there are many icons that depict Christ descending to the dead to redeem Adam and Eve.

> agauger:
>
> disobedient long ago when God waited patiently in the days of Noah while the ark was being built.
>
> Maybe there was the offer of redemption for those who had no opportunity before Christ. (This verse is interpreted in various ways. I have given the Catholic version here.)

I’ve heard this view before. It is very catholic. =).

> agauger:
>
> I agree with Josh that the Gospel is central.

Amen.

DennisVenema (Dennis Venema) 2018-02-26 02:41:38 UTC #693

Thanks for your comments, Ann.

It's a beautiful axe, to be sure. I too "see a mind there" - but I also see minds of varying degrees in nature. My dog has more going on than the zebrafish in my lab. Among fish, cichlids like angelfish seem to have more going on than the zebrafish. Bowerbirds make things we think of as aesthetic. So do octopuses. Crows plan ahead and make / use tools. So, I guess I'm more comfortable with seeing a gradient of "mind".

I too agree that the gospel is central. I just don't see a historical Adam as part of that. When Paul summarizes the gospel, he does not reference Adam (and of all the New Testament authors I would expect to use Adam as part of the gospel, Paul would be the one). For example, here's 1 Cor 15 (the very chapter where Paul gets into Adam theology in the letter) in the NIV:

> Now, brothers and sisters, I want to remind you of the gospel I preached to you, which you received and on which you have taken your stand. 2 By this gospel you are saved, if you hold firmly to the word I preached to you. Otherwise, you have believed in vain.
>
> 3 For what I received I passed on to you as of first importance[a]: that Christ died for our sins according to the Scriptures, 4 that he was buried, that he was raised on the third day according to the Scriptures, 5 and that he appeared to Cephas,[b] and then to the Twelve. 6 After that, he appeared to more than five hundred of the brothers and sisters at the same time, most of whom are still living, though some have fallen asleep. 7 Then he appeared to James, then to all the apostles, 8 and last of all he appeared to me also, as to one abnormally born.

Similarly, in Romans 1 (also NIV):

> Paul, a servant of Christ Jesus, called to be an apostle and set apart for the gospel of God— 2 the gospel he promised beforehand through his prophets in the Holy Scriptures 3 regarding his Son, who as to his earthly life[a] was a descendant of David, 4 and who through the Spirit of holiness was appointed the Son of God in power[b] by his resurrection from the dead: Jesus Christ our Lord. 5 Through him we received grace and apostleship to call all the Gentiles to the obedience that comes from[c] faith for his name's sake. 6 And you also are among those Gentiles who are called to belong to Jesus Christ.

I see Jesus's lineage from David, his death, burial, resurrection, and exaltation as Lord as the key elements. I just don't see Adam on the radar here.

Now, I too am not a theologian, so, as you aptly said, "buyer beware". But I don't think a historical Adam is part of the gospel according to Paul.

Swamidass (Dr. S Joshua Swamidass) 2018-02-26 03:36:27 UTC #694

> DennisVenema:
>
> I too agree that the gospel is central. I just don't see a historical Adam as part of that.

To be clear, neither **@agauger** or myself are saying Adam is part of the Gospel. Several times I have made this point, often in your defense. This is a conversation between those of us together in the Church, and this community is defined by Jesus, not Adam.

> DennisVenema:

> It's a beautiful axe, to be sure. I too "see a mind there" - but I also see minds of varying degrees in nature. My dog has more going on than the zebrafish in my lab. Among fish, cichlids like angelfish seem to have more going on than the zebrafish. Bowerbirds make things we think of as aesthetic. So do octopuses. Crows plan ahead and make / use tools. So, I guess I'm more comfortable with seeing a gradient of "mind".

That is a valid interpretation too.

Right now, I think there is a lot up for grabs in our understanding of human origins. So much so that everything from **@agauger** position to yours is consistent with the evidence, at least somewhat represented within mainstream science.

Also, if the goal is merely to affirm a sole genetic progenitorship, we could possibly imagine that taking place about 700 kya with the common ancestors of Homo sapiens, Denisovans, and Neanderthals.

Chris_Falter (Chris Falter) 2018-02-26 05:16:53 UTC #695

> Swamidass:
>
> encourage people to place the confidence in the thing that science HAS definitely ruled out: the Resurrection of the Son of God.

Hi Joshua - I agree with you on the object of our confidence. However, I disagree with you that science rules out miracles. I would contend quite adamantly that a one-time miracle is not subject to scientific research, which requires repeatability.

Best,
Chris

Swamidass (Dr. S Joshua Swamidass) 2018-02-26 05:19:59 UTC #696

> Chris_Falter:
>
> I would contend quite adamantly that a one-time miracle is not subject to scientific research, which requires repeatability.

One time events are the subject of scientific study. That is how we study the Big Bang.

I would agree however, that science has not precisely ruled out the Resurrection. It does not consider God's action, so it is more accurately silent on the Resurrection. The claim is that God Himself rose Jesus from the dead, breaking the natural order of things. That is a hypothesis outside the realm of science.

The point, however, in context is that we believe things beyond science. The fact that science is silent does not mean nothing of interests exists in its blindness.

DennisVenema (Dennis Venema) 2018-02-26 06:47:07 UTC #697

> Swamidass:
>
> To be clear, neither **@agauger** or myself are saying Adam is part of the Gospel. Several times I have made this point, often in your defense. This is a conversation between those of us together in the Church, and this community

> is defined by Jesus, not Adam.

Exactly. Jesus is the gospel. There are some non-negotiables in the faith, and other matters which are open for discussion.

Thinking about fish, minds, and aesthetic artifacts reminded me of this video from the BBC on pufferfish. Imagine if we found a carving like this in the hominin record?

Why do puffer fish build sandcastles?

Puffer fish build delicate and intricate structures on the ocean floor, but what could they possibly be used for?

Jon_Garvey (Jon Garvey) 2018-02-26 11:26:43 UTC #698

@Chris_Falter
Hi Chris

I would agree with you that science properly only "does" repeatability, *except* that it may *document* unique phenomena on the possibility of future repeatability of some kind. But the recording itself is really history rather than science.

But on "ruling out miracles", a few years ago I set up (here) a scenario of an essentially miraculous overnight transformation in a lab petrie dish. Can't remember the details, but it was designed to ask "How would scientists deal with an apparent miracle?"

Almost universally I got the reply that the true scientist would *always* be looking for the natural cause, and suspend judgement on a miracle, even if no plausible natural possibility existed. Strictly speaking this is not to *exclude* a miracle - but if ones agnosticism is so absolute and unconditional, then effectively miracle *is* excluded.

Th question is what one actually means by "science does not rule out miracles". Since "science" always means "scientists," wouldn't it be true to say that a scientist practising methodological naturalism *consistently* cannot *accept* a miracle, including the resurrection? He/she either has to suspend the methodology in that case (in which case it becomes a methodology with ad hoc exceptions), or believe "as a human" whilst remaining agnostic "as a scientist".

The trouble is that the resurrection is not simply a factual proposition to be accepted or not, but a demand for total commitment - in other words, the scientist part of one has no warrant to cut itself off from that commitment to the risen Christ.

So on what basis can methodological naturalism continue for the person who has suspended it in the case of the resurrection? Is there any longer any rational basis to use naturalism as a reason to doubt, at least, an historical Adam if the methodology is no longer used to doubt the resurrection of the second Adam?

My own solution: free science from the dead hand of "naturalism" altogether and deal only with your excellent concept of "repeatability," which is entirely metaphysics-free. One can also allow the recording and investigation of isolated events, like the Big Bang (which can hardly be naturalistic as it preceded the laws of nature), and that also is metaphysics-neutral.

False metaphysics only gets a look in when (1) regularity is assumed to be an alternative to divine action, excluding the latter in favour of some demigod called “Nature” or (2) when metaphysically loaded (and spurious) concepts like “chance is a cause” are allowed in as explanations of non-regular phenomena.

Jon_Garvey (Jon Garvey) 2018-02-26 11:43:28 UTC #699

@DennisVenema
The “Adam was a puffer fish” hypothesis?? Good for the theory of universal redemption, I guess. Especially if diatoms get in on the act:

More seriously (slightly), unless one found human eggs at the centre of the artifact, it would in the hominin lineage be evidence of culture and symbolic thought, because it would be in direct continuity with *our* use of symmetry, and not that of teleosts or diatoms.

But that is only a problem if one has already taken the common conceptual leap of equating the defining nature of Adam in Scripture - ie the first physical being to come into covenant relationship with Yahweh - with some measurable cultural attainment in a particular area like symbolic thought.

But why on earth should those two be any more equivalent than expecting born-again Christians to be measurably more culturally advanced than unbelievers?

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glipsnort (Steve Schaffner) 2018-02-26 20:22:46 UTC #700

> Swamidass:
>
> How about “somewhere in Africa”.

It could have been one location, it could have been a broad range, or it could have been patchwork evolution across multiple locations with limited gene flow between them. We have lots of evidence for multiple range expansions by hominins, but they really don’t provide evidence for rapid expansions from a small founding population. My impression is that such a rapid expansion is unlikely, given what we know about the reproductive capacity of hunter-gatherers.

Jay313 (Jay Johnson) 2018-02-26 21:12:03 UTC #701

> glipsnort:
>
> It could have been one location, it could have been a broad range, or it could have been patchwork evolution across multiple locations with limited gene flow between them.

By 1.8 million years ago, just 100,000 years after *H. erectus* appeared, three different species of hominin and *A. sediba* were co-existing in East Africa, as well as the smaller-bodied *H. erectus* in Dmanisi, Georgia. Considering the mosaic of features present at the time, anthropologist Susan Anton termed this early phase of our evolution “a period of morphological experimentation." In which species did the literal Adam appear?

RichardBuggs (Richard Buggs) 2018-02-26 21:54:43 UTC #702

Hi **@Swamidass** , thank you for such a quick response. It looks as if you had a busy Sunday!

> Swamidass:
>
> I’m not sure his “part 2” requires a response.

I felt an obligation to give a response in that: (1) it is a loose thread that needs to be tied up, and (2) it is a public blog that mentions my name in the title and (3) because I said I would and (4) because it is interesting. I also feel obligated to continue to reply and deal with the four papers that **@DennisVenema** references in the blog, even though you have already dealt quite effectively in their conceptual content within this discussion forum. If Dennis were to formally retract the blog, I would not need to do this, but otherwise I need to do this for the sake of completeness.

I think that you and I are essentially in agreement, and where we appear to differ it is mainly because we have different interpretations of what **@DennisVenema** was saying in his blog, or you are making additional comments that complement mine, or you have misunderstood what I was seeking to say.

> Swamidass:
>
> To close the loop, the fact that there might by 75% heterozygosity after a bottleneck tells us nothing about how many lineages are coalescing at this point in time. These are different things, and are entirely separable.

I think you are saying the same thing as I was my statement:
“The loss of alleles via the sampling effect of the bottleneck will not show up as coalescence events in a coalescence model. These are two separate effects of a bottleneck.”

> Swamidass:
>
> If there are 50 lineages, there will be a very high amount of coalescence (at least 46 lineages will coalesce), and we will almost certainly detect it.

When you say this, do you mean (1) any lineage, or do you mean (2) a lineage that has a mutation that makes it a different sequence (allele) to other lineages?

> Swamidass:
>
> So once again, a lot of coalescence can take place, even when there is heterozygosity. Let’s look at your figures to make that clear.

I agree, and I agree that my figure shows that. That was not unintentional! 🙂

> Swamidass:

> So, here, we see that the conditions put forward are not met. There is more than one lineage going through the bottleneck. The heterozygosity is high.

I am not sure what conditions you mean. Yes, I deliberately showed three lineages going through the bottleneck, two in a heterozygote and one in a homozygote. I tried to illustrate as many processes as I could in the figure.

> Swamidass:
>
> What about coalescence? Well, in that figure, there are THREE coalescence events between g0 and g1, all in the blue lineages.

I agree: three identical alleles in three different individuals coalesce into a single identical copy in a one parent.

> Swamidass:
>
> It is, rather, about reduction in number of alleles.

I think we are misunderstanding one another here. There is no reduction in number of alleles from g1 to g0. There is a reduction in the number of copies of alleles (= a reduction in the number of lineages) but not a reduction in the number of alleles. By an allele here I mean a DNA sequence that is different in nucleotide sequence to the other alleles - as I explained in the text describing my figure, I show different alleles in different colours. There are three alleles in generation g1 (one red, one blue and one yellow, with copy number 1, 3 and 2 respectively) and three alleles in the g0 generation (one red, one blue and one yellow, with copy number 1, 1, and 2 respectively)

> Swamidass:
>
> There is not one coalescent at g0, but FOUR coalescents. This is a critical point. Really all merge points in a tree are coalescents, not just the top one.

I agree. In the text that accompanied this second figure I wrote:
“How would coalescence to one lineage occur after a bottleneck? Figure 2 shows a scenario in the minimum possible number of generations.” The figure does not claim to show a single coalescence - it claims to show the most rapid possible coalescence back to a single lineage that passed through a bottleneck of two. (The significance of this is that it was the nearest thing I could think of that would to some extent correspond with what Dennis seemed to be writing about in his blog. A problem here is that Dennis’ blog was so off the mark that it is hard to reinterpret it in terms of actual coalescent scenarios.)

> Swamidass:
>
> This turns out not to be quite correct. Coalescence analysis does not deal with this. Privately, I had shared some similar computations, but also came to understand it was in error (notice it is not in public). However, this computations miss exactly what coalescence theory is doing, I missed this too the first time around, It is quite subtle.

I think you are misunderstanding what I am seeking to do here.

> Swamidass:

> what is being computed here might be a reasonable estimate of the allele distribution we would expect after a bottleneck if we were to measure it

I agree that this could be developed into that, but my aim here was simply to show how unlikely it is that three lineages would be lost after a bottleneck of two, leaving just one of the four allele copies that was present in the parental pair.

> Swamidass:
>
> What coalescence tries to do is, instead, reconstruct the history of all direct ancestral sequences of the data in our current day sample. There may be other alleles with the exact same DNA sequences alongside this direct ancestors, but coalescence only models the direct ancestors.

I agree that coalescence analysis is normally done with a sample, not the whole population. This is why I wrote: "Similarly, if we only sample a subset of the lineages, the probability of all of our sample coalescing at the bottleneck is slightly higher than the probability of all lineages coalescing, but again, this will not make a huge difference. For example, if we sampled four individuals in generation g2 the probability of all sampled lineages coalescing in the bottleneck would be 0.000977. "

> Swamidass:
>
> Keep in mind, the number of allelic lineages at different points in time, does not tell us the number of alleles in the population at that point in time. For example, lets say we are 3 mya, where the vast majority of the genome has coalesced to a single allele that survives till today. The population at that time, however, is not all homozygous for that allele. That allele, also, might even be low frequency. Rather, we are just saying none of those other alleles survive for 3 million years to present day.

I agree. Coalescence and fixation are completely different things.

> Swamidass:
>
> For that reason, demonstrating heterozygosity is not lost does not really make the case here.

That was not my case. There seems to have been a degree of misunderstanding in your reading of my blog.

> Swamidass:
>
> It turns out that the amount of coalescence is entirely dependent on the number of extant lineages that enter (backwards time) the bottleneck.

I don’t dispute that, but the number of extant lineages in a coalescent analysis is simply our sample size. Every sample we take is a lineage. It doesn’t matter if they differ in their nucleotide sequence (i.e. are different alleles) or not.

> Swamidass:
>
> “Severity” of a bottleneck includes two things: (1) the size of the bottleneck population AND (2) the number of generations in the bottleneck. Severe bottlenecks are a LARGE number of generations, with a SMALL population size. However, a SINGLE generation of a very SMALL population size (e.g. a single couple) is not necessarily a

> severe bottleneck. That is, remember, because severity is defined along two dimensions. In one dimension it is severe, but in another it is extremely mild.

I agree. This is a point I have been trying to make all along in this debate.

> Swamidass:
>
> In summary, **@RichardBuggs** I agree that **@DennisVenema** was in error, however, I'm not sure your argument is correct either. Can you clarify if I missed something here? I hope I did not misrepresent you. My critique here is based on my best understanding of what you wrote. However, please correct me if I missed something,

In summary, Joshua, I am glad we agree on the big picture, but I think you have misinterpreted some of what I was trying to say, especially (a) the distinction between lineages and alleles, and (b) what I was seeking to show in figure 2 and the calculations accompanying it.

Swamidass (Dr. S Joshua Swamidass) 2018-02-27 01:01:36 UTC #703

> RichardBuggs:
>
> I felt an obligation to give a response in that: (1) it is a loose thread that needs to be tied up, and (2) it is a public blog that mentions my name in the title and (3) because I said I would and (4) because it is interesting. I also feel obligated to continue to reply and deal with the four papers that **@DennisVenema** references in the blog, even though you have already dealt quite effectively in their conceptual content within this discussion forum. If Dennis were to formally retract the blog, I would not need to do this, but otherwise I need to do this for the sake of completeness.

Okay, I'll mainly let **@DennisVenema** respond then.

> RichardBuggs:
>
> > If there are 50 lineages, there will be a very high amount of coalescence (at least 46 lineages will coalesce), and we will almost certainly detect it.
>
> When you say this, do you mean (1) any lineage, or do you mean (2) a lineage that has a mutation that makes it a different sequence (allele) to other lineages?

I mean #1. In coalescence, we only care about direct descent of the samples. At particular times, we entirely expect different "lineages" to have exactly the same sequence, such as right after they split.

> RichardBuggs:
>
> I think we are misunderstanding one another here. There is no reduction in number of alleles from g1 to g0. There is a reduction in the number of copies of alleles (= a reduction in the number of lineages) but not a reduction in the number of alleles.

But that is all that matters. In coalescence based estimates of Ne, we are just estimating where in time these coalescents fall. They can all be identical sequence, but they are still different lineages.

> RichardBuggs:
>
> (The significance of this is that it was the nearest thing I could think of that would to some extent correspond with what Dennis seemed to be writing about in his blog. A problem here is that Dennis' blog was so off the mark that it is hard to reinterpret it in terms of actual coalescent scenarios.)

I'll let Dennis defend himself. As in understand it, has already retracted several things from that post here on this thread. I suppose it's up to you how you would take it from here.

> RichardBuggs:
>
> > "Severity" of a bottleneck includes two things: (1) the size of the bottleneck population AND (2) the number of generations in the bottleneck. Severe bottlenecks are a LARGE number of generations, with a SMALL population size. However, a SINGLE generation of a very SMALL population size (e.g. a single couple) is not necessarily a severe bottleneck. That is, remember, because severity is defined along two dimensions. In one dimension it is severe, but in another it is extremely mild.
>
> I agree. This is a point I have been trying to make all along in this debate.

It seems now that **@DennisVenema** agrees now too. That it seems was the conceptual error that's been fixed.

> RichardBuggs:
>
> In summary, Joshua, I am glad we agree on the big picture, but I think you have misinterpreted some of what I was trying to say, especially (a) the distinction between lineages and alleles, and (b) what I was seeking to show in figure 2 and the calculations accompanying it.

Okay, I'll let you work it out with **@DennisVenema** then.

DennisVenema (Dennis Venema) 2018-02-27 01:05:06 UTC #704

> Swamidass:
>
> It seems now that **@DennisVenema** agrees now too. That it seems was the conceptual error that's been fixed.

Yes, I agree with this. I pointed that out ^ up there ^ somewhere.

RichardBuggs (Richard Buggs) 2018-02-27 09:17:23 UTC #705

Hi Dennis,
That's great. Would you also agree that the points made in the four papers you refer to in your "Part 2" blog have also been dealt with adequately on this thread, or would you like me to respond to them also?
best wishes
Richard

DennisVenema (Dennis Venema) 2018-02-27 15:17:18 UTC #706

I think so - I haven't read the entire thread, but I think we've covered what needs to be covered. Like I said to Josh before, I think that the ArgWeaver paper covers the same territory (and does it more thoroughly) than those papers. If we're agreed that a single - couple bottleneck is not supported in the last 400+ KYA then I don't really have a dog in the fight any longer, since that goes beyond even what the (now infamous) "heliocentric" statement in *Adam and the Genome* was defending. It simply becomes a question of "how far back can we exclude this?" now, which of course is very interesting in its own right.

I will be away for the next few days, but I'm hoping to get the PSMC modelling results from Charles Cole up on a private thread for you, myself and **@Swamidass** to look over later today (dv).

Hope you're doing well. I'll send a PM once the PSMC data is up.

RichardBuggs (Richard Buggs) 2018-02-27 20:47:55 UTC #707

Hi Dennis,

Thanks for your reply. I am glad to hear that you consider that the four papers you refer to in your "Part 2" blog have also been dealt with adequately on this thread. That potentially frees up a few of my evenings, for which I am very grateful!

> DennisVenema:
>
> If we're agreed that a single - couple bottleneck is not supported in the last 400+ KYA then I don't really have a dog in the fight any longer,

Just to be clear, are you saying that you now no longer hold this view, described on page 55 of Adam and the Genome:

"Put most simply, DNA evidence indicates that humans descend from a large population because we, as a species, are so genetically diverse in the present day that a large ancestral population is needed to transmit that diversity to us. To date, every genetic analysis estimating ancestral population sizes has agreed that we descend from a population of thousands, not a single ancestral couple. Even though many of these methods are independent of one another, all methods employed to date agree that **the human lineage has not dipped below several thousand individuals for the last 3 million years or more— long before our lineage was even remotely close to what we would call "human."** Thus the hypothesis that humans descend solely from one ancestral couple has not yet found any experimental support, and it is therefore not one that geneticists view as viable."

If that is no longer a "dog" you have in the "fight" then we have come to a good degree of agreement

> DennisVenema:
>
> I will be away for the next few days, but I'm hoping to get the PSMC modelling results from Charles Cole up on a private thread for you, myself and **@Swamidass** to look over later today (dv).

I am really glad that Charles Cole has done some more work on this. I will look forward to hearing more.

best wishes
Richard

RichardBuggs (Richard Buggs) 2018-02-27 20:49:32 UTC #708

Thanks Joshua. It seems we are entirely in agreement. 🙂

DennisVenema (Dennis Venema) 2018-02-27 21:53:20 UTC #709

> "To date, every genetic analysis estimating ancestral population sizes has agreed that we descend from a population of thousands, not a single ancestral couple. Even though many of these methods are independent of one another, all methods employed to date agree that the human lineage has not dipped below several thousand individuals for the last 3 million years or more— long before our lineage was even remotely close to what we would call "human."

This remains accurate, even with our ongoing conversation. All methods employed thus far do indicate that we descend from thousands. What we've been discussing is whether or not these methods have the power to detect the sort of bottleneck that you are proposing. That idea - 10,000 down to 2 in a single generation, followed by exponential growth - was not on my radar at all when I wrote that. Nor had I seen anyone else suggest anything similar. If I were to write the book today, I would discuss this idea and talk about what we have learned together (especially the ArgWeaver data). But it wasn't on my radar in 2016.

> Thus the hypothesis that humans descend solely from one ancestral couple has not yet found any experimental support, and it is therefore not one that geneticists view as viable."

This also remains the case. At best, we can say that your specific idea cannot be conclusively ruled out further back than 400 KYA. We do not have any evidence that *supports* the hypothesis - we only have a limit to our current methodology that does not allow us to rule it out in the deep past.

I hope to have the Cole data ready for later today, but it might be tomorrow.

T.j_Runyon (T J Runyon) 2018-02-28 04:19:34 UTC #710

Erectus did have some modern behavior. But also lacked some. What pretty much rules out an ancient Adam for me is its very unlikely Erectus could even speak. Like us at least. Definitely more complex than say chimps. But what we know about their anatomy I just don't see much speaking ability.

T.j_Runyon (T J Runyon) 2018-02-28 04:48:09 UTC #711

Regarding Naledi being a "primitive" Erectus, I'm assuming you are referring to Tim White's interpretation? The Erectus possibility has been shot down, most notably by John Hawks. Who as you know has a very close and intimate relationship with Naledi. Also for future reference Id be careful when you reference popular news sites. Reporting on human evolution is notoriously terrible.

T.j_Runyon (T J Runyon) 2018-02-28 06:56:14 UTC #712

I dont think anyone would argue Erectus lacked all Modern behavior. This is the impression I have got from my studies, classes, lectures, meetings, etc. anyway. But I also think you won't find anyone advocating Erectus had full behavioral modernity. Which seemed to arise around 50kya. Though I admit this is also controversial as is the whole behavioral modernity framework. See Shea for informstion on this:
http://www.jstor.org/stable/10.1086/658067#references_tab_contents
So I defintely think Erectus had some modern behavior. To put it in cladistic terms Id say Erectus is on the stem when it comes to modern behavior. Some not all. So if you are comfortable with Adam being not fully modern then cool. More power to you. But there is a lot more to being modern than art, aesthetics and symbolic thought. It's an interesting idea

that needs to be explored. Though the probable lack of any real meaningful speech in Erectus is troubling for me. As are some biblical issues. But it should defintely be explored.

AMWolfe (A.M. Wolfe) 2018-02-28 07:04:18 UTC #713

> T.j_Runyon:
>
> **http://www.jstor.org/stable/10.1086/658067#references_tab_contents**

Fascinating abstract. Is this opinion fairly mainstream, or has there been pushback since 2011?

Paging both **@aleo** and **@Jay313** , whose interest I think may be piqued by this.

T.j_Runyon (T J Runyon) 2018-02-28 07:08:21 UTC #714

Heres a good discussion of it : **http://blogs.plos.org/neuroanthropology/2011/02/22/john-shea-human-evolution-and-behavioral-variability-not-behavioral-modernity/**

Notice John Hawk's comment at the bottom. He views it as incoherent

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Swamidass (Dr. S Joshua Swamidass) 2018-02-28 07:31:56 UTC #715

Thanks for the thoughtful comments.

I think, for **@agauger** , the key thing is genetic sole progenitorship, without interbreeding with other kinds. I'm not sure if the specific time of 2 mya is really the hill she is dying on here. If that is the case, she has available to her a stronger option…

She could take a model were Adam and Eve are about 700 kya, with the common ancestors of Neandertal, Homo sapiens, Denisovans, and others (possibly even H. nadeli too, if we take the recent dates). Right now there is quite a bit of anthropologists that seriously doubt the Neandertal-Homo sapiens distinction. And a secular anthropologist here at WUSTL scoffed with great vigor at any notion of Denisovans even being a distinct type (all we have is a mere knuckle, now reduced to dust). To take a view that this is "human" is solidly within the accepted range of views. Moreover, there are several anatomical features unique to Neanderthal and Sapiens. As I understand it the hyoid bone is specific to the two of them, and some have suggested it gave greater ability to vocalize.

Regarding "modernity" there is very little understanding of how much, if any, of the 50 kya "transition" was genetic vs. cultural. Given how long it would have taken for genetic mutations to fix during this time, there is good reason to think that culture is driving a large part of that transition. Frankly, there is not real way to disentangle intrinsic biological capability from cultural development endowed behavior. Our instinct is to tightly link them, but this instinct is likely flawed.

Regardless, if I'm understanding the specific concerns motivating **@agauger** 's model, this 700 kya Adam is much more defensible. It avoids the murky questions about H. erectus. It is actually closer to the mainstream consensus than **@DennisVenema** 's equivocation of H sapiens with "human" (which many anthropologists would say is wrong).

T.j_Runyon (T J Runyon) 2018-02-28 07:37:07 UTC #716

Oh I agree if any non Sapiens could really vocalize it would be the Neanderthals. Their anatomy is right for it. But any other hominin, i strongly doubt

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T.j_Runyon (T J Runyon) 2018-02-28 07:43:21 UTC #717

Also, and take this with a grain of salt since my career is in its infancy, all anthropologists I've been been around would Define human as anyone belonging to the genus Homo. Homo Sapiens are broken down into Early Homo Sapiens, like the Jebel Irhoud specimens and anatomically modern humans. So Anne is arguing for an archaic Homo Sapiens (those that are morphologically and behaviorally between Erectus and Sapiens) Adam?

Swamidass (Dr. S Joshua Swamidass) 2018-02-28 08:20:05 UTC #718

> T.j_Runyon:
>
> Also, and take this with a grain of salt since my career is in its infancy, all anthropologists I've been been around would Define human as anyone belonging to the genus Homo.

That's the anthropologist I am around too. The've, once again, audibly scoff at the notion of "human" == Homo sapiens, as a totally backwards view, unless of course they are one of the few holdouts (or a BioLogos writer 😉). It is almost comical how large a swing this is from just a couple decades ago. In a lot of ways, it's quite fascinating. There has been a convergence between YEC's and secular anthropologists on how they understand "human" in the fossil record, though of course they totally disagree on the timeline. Both would usually say genus Homo is "human." However, to call that a consensus is not quite correct either, because there is just a roiling debate about this in science. Even if we say "human" is Homo, we stil have to determine which bones are Homo or not. Which bones are sapiens or not. Etc.

> T.j_Runyon:
>
> So Anne is arguing for an archaic Homo Sapiens (those that are morphologically and behaviorally between Erectus and Sapiens) Adam?

@agauger is not really arguing for very much.

> agauger:
>
> I came to the idea of an old Adam because of the science, because I couldn't reconcile multiple hominins running around with only some bearing God's image. H. erectus is so much more similar to us than chimpanzees ever were. The chief argument against a H erectus Adam for me is that technology did not advance much, at least as far as we can tell. But then at that distance in time, the only things to preserved will be the kinds of things we see.

The way I read her (and please correct me Ann if I am wrong) is that sole genetic progeintorship is important.

The issue of God's Image is, I would argue, a separable question. Because textually in Genesis 1 and 2, we can see that God's Image is not actually part of the Adam narrative. We can propose a model where God first creates mankind in the image of God, and then later creates a man, Adam, and places him in a Garden. He is not the only one with God's Image, so the problem she is concerned about is not there. Of course, perhaps we do not like this model, but its not wrong for the reason she puts forward here.

Regardless, given this high commitment to sole genetic progeintorship, she is willing to push Adam back ***as far as*** 2 mya, with the origin of the *Homo genus*. However, I do not sense that she is insisting it ***must be*** 2 mya. If there is a more plausible place to put Adam, consistent with the archaeological and genetic data, she would amenable. However, maybe she does feel H erectus is distinctly "human."

That flexibility could be a strength, because she can chose the most defensible position as it arises, which I think might actually be at 700 kya, not 2 mya. So I am an the one suggesting something after H erectus and before H sapiens, not her. It just seems like a stronger option, that is still consistent with her motivations. Though, she is certainly entitled to her own view of what is most defensible. Most likely, most of this is being held very provisionally right now, as we work out the some more of the studies here.

DennisVenema (Dennis Venema) 2018-02-28 08:53:29 UTC #719

> T.j_Runyon:
>
> To put it in cladistic terms Id say Erectus is on the stem when it comes to modern behavior.

This is how I see the data at present as well.

Edit: if anyone wants a primer on stem/crown groups, I discuss it at some length in the *Evolution Basics* series, **starting with this post**.

T.j_Runyon (T J Runyon) 2018-02-28 09:31:30 UTC #720

I think an archaic H. sapiens Adam is much more defensible. A H. heidelbergensis Adam perhaps? If you prefer the interpretation of H. heidelbergensis being the common ancestor of us and neanderthals anyway. That's something I could get behind. But I think i would need more than we can't rule out a bottleneck between 400kya and 7mya before I really could consider it. Where the bottleneck actually took place is really really important. Is it closer to the 7mya mark? Or the 400K mark? And this leads me to ask is it even possible in theory to detect a bottleneck that far back? If so, what needs to be done to determine if such a bottleneck existed in that timeframe?

Jonathan_Burke (Jon) 2018-02-28 09:42:58 UTC #721

> Swamidass:
>
> That flexibility could be a strength, because she can chose the most defensible position as it arises, which I think might actually be at 700 kya, not 2 mya

This shows she's doing apologetics, not science. And that's what this has been about all along.

T.j_Runyon (T J Runyon) 2018-02-28 09:43:15 UTC #722

And another thing, when I read Dennis' book and the part that dealt with the topic of this thread, I read it as though he was as certain that H. sapiens never started off as two people but were descedents of a larger population as he is heliocentrism. Not that a two person bottleneck never took place in the entire hominin evolutionary history. And it seems that is the conclusion that this thread reached. I owe a lot to Dennis. He had a huge part in bringing me back to Christianity. Helped show me I could be an intellectually fulfilled Christian evolutionary biologist. I owe him a lot. I just feel he has been read a little uncharitably here.

Jonathan_Burke (Jon) 2018-02-28 09:58:37 UTC #723

> T.j_Runyon:

> And another thing, when I read Dennis' book and the part that dealt with the topic of this thread, I read it as though he was as certain that H. sapiens never started off as two people but were descedents of a larger population as he is heliocentrism. Not that a two person bottleneck never took place in the entire hominin evolutionary history. And it seems that is the conclusion that this thread reached.

That's how I see it. This discussion has been full of apologetics along the line of "Since there are lots of stories of floods around the world, there was clearly a worldwide flood like Genesis says". Then you ask them when it happened, and they can't answer, but claim it hasn't been ruled out by science.

T.j_Runyon (T J Runyon) 2018-02-28 11:21:30 UTC #724

This tells me we need more than a few beautiful handaxes to draw any real conclusions

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T.j_Runyon (T J Runyon) 2018-02-28 12:17:27 UTC #725

can you explain to this new Christian what the recent genealogical Adam view is?

Jay313 (Jay Johnson) 2018-02-28 14:02:47 UTC #726

> T.j_Runyon:
>
> can you explain to this new Christian what the recent genealogical Adam view is?

I wish you hadn't asked that question …

> AMWolfe:
>
> Fascinating abstract. Is this opinion fairly mainstream, or has there been pushback since 2011?

It's all part of an ongoing discussion that mainly centers on two things: Was behavioral/cognitive modernity a "leap forward" (saltational), or was it the end of a long process? The other question involves what lies behind it all. The early answer from Tattersall and the archaeologists pointed either to language or Theory of Mind. The biologists and geneticists pushed back and sought an answer in biology. There was a lot of early enthusiasm for FOXP2, for example, until it was realized that there is no "language gene," just as there is no "cancer gene."

The consensus (there's that bad word) leans toward the co-evolution of the brain and language, although there are still partisans on both sides. An example on the language side would be Charles Taylor's **The Language Animal: The Full Shape of the Human Linguistic Capacity**. An example on the biological side would be Coolidge & Wynn's **The Rise of Homo Sapiens: The Evolution of Modern Thinking**. Coolidge & Wynn do not reject cognitive modernity; they just seek to explain it by some other (non-Eurocentric?) standard besides symbolic behavior. As they put it, "the modern mind is not … simply an archaic mind augmented by symbolism and language." In that, they're certainly correct. But in the end, their theory of "Enhanced Working Memory" falls back upon some presently unknown mutation that allowed fully symbolic language, a change they believe occurred between 100,000 and 40,000 years ago, when cognitive modernity fully flowered.

Painting with a broad brush, of course, but that's the general lay of the land. You can find a short example of how Coolidge & Wynn's theory plays out in this 20-min talk at TedxVictoria by anthropologist Genevieve von Petzinger, **The Roots of Religion**

T.j_Runyon (T J Runyon) 2018-02-28 14:06:32 UTC #727

I apologize haha

Jay313 (Jay Johnson) 2018-02-28 14:18:01 UTC #728

> T.j_Runyon:
>
> Oh I agree if any non Sapiens could really vocalize it would be the Neanderthals. Their anatomy is right for it. But any other hominin, i strongly doubt

Right. Neanderthals are (so far) the only other hominin with a hyoid bone, which helps suspend the larynx in the neck. That bone is necessary to vocalize the full range of speech, mainly vowel sounds. Other than that, *H. erectus/heidelbergensis* around 500 Kya seems like a good candidate for the first speaker of "words," although they probably wouldn't be sounds that we would recognize as such.

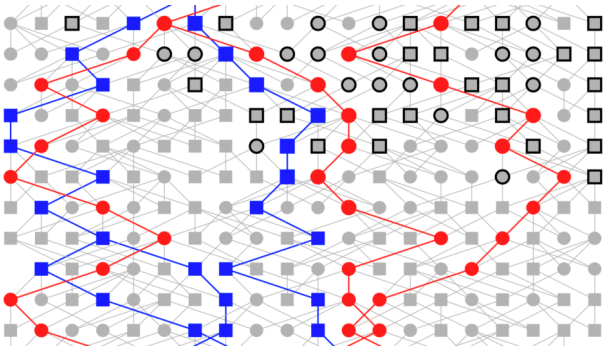
DennisVenema (Dennis Venema) 2018-02-28 14:54:33 UTC #729

> T.j_Runyon:
>
> I owe a lot to Dennis. He had a huge part in bringing me back to Christianity. Helped show me I could be an intellectually fulfilled Christian evolutionary biologist. I owe him a lot.

Your story is easily one of the most encouraging ones I know of for me. Evolution is such a cool area of science, and it's such a shame that so many Christians have such difficulties with it. I look forward to the day when there are just as many Christians in evolutionary biology (proportionately) as any other field. In my mind, you're part of the beginning of that trend…

Swamidass (Dr. S Joshua Swamidass) 2018-02-28 15:01:05 UTC #730

> T.j_Runyon:
>
> can you explain to this new Christian what the recent genealogical Adam view is?



A Genealogical Rapprochement on Adam? - Peaceful Science

A genealogical Adam will not solve the puzzle of Adam and Eve for everyone, but it will for many. Is a rapprochement possible?

Swamidass (Dr. S Joshua Swamidass) 2018-02-28 15:05:35 UTC #731

> T.j_Runyon:
>
> And this leads me to ask is it even possible in theory to detect a bottleneck that far back? If so, what needs to be done to determine if such a bottleneck existed in that timeframe?

It may not be possible to know from data with out some serious luck.

Swamidass (Dr. S Joshua Swamidass) 2018-02-28 15:12:14 UTC #732

> Jonathan_Burke:
>
> This shows she's doing apologetics, not science. And that's what this has been about all along.

A beautiful example of an apologetic statement for your position!

Sounds more like **@agauger** is trying to find a position consistent with her deeply held belief and what the evidence shows.

Swamidass (Dr. S Joshua Swamidass) 2018-02-28 16:25:49 UTC #733

> agauger:
>
> 000 years is a long time to us in terms of our life spans, but only 300-400 generations. 60,000 years is 10 times and 600,000 years 100 times that-- 30,000-40,000 generations. I hold to an old age for the universe. If God can take 14 billion years to form the universe we see, including the 4 billion year old earth, and then took more than 3 billion years to create life as we see it now, **it's clear he's not in a hurry.**

Very good point.

Swamidass (Dr. S Joshua Swamidass) 2018-02-28 18:06:34 UTC #734

> T.j_Runyon:
>
> He had a huge part in bringing me back to Christianity. Helped show me I could be an intellectually fulfilled Christian evolutionary biologist. I owe him a lot. I just feel he has been read a little uncharitably here.

@DennisVenema has been and is an important part of the conversation. I've also very much benefitted from his work and hope to see more from him.

However, we have not been misreading him, but going off how he has clarified what he meant. A key point is that he thought the bottleneck hypothesis was tested, and that psmc could detect these sorts of things very anciently. On both counts he was wrong, and he recently explain it wasn't even on his mind as an option. He would rewrite that portion of the book now based on how weve all clarified things together here (hopefully citing those that have brought this to his attention).

That is all good and respectable. We expect to make errors when doing scientific work. We respect scientists that retract there errors and oversights, as **@DennisVenema** has here.

DennisVenema (Dennis Venema) 2018-02-28 18:56:29 UTC #735

> Swamidass:
>
> A key point is that he thought the bottleneck hypothesis was tested, and that psmc could detect these sorts of things very anciently. On both counts he was wrong

On the second count I was wrong, yes, though it's not a major point for AatG. The point of AatG is that when anatomically modern humans arise, we do so as a population, and that all the methods we've used to date agree on a population of thousands, not a pair (regardless of what time we use). The first point still stands, though. There are papers in the literature that claim to exclude a bottleneck weaker than the one **@RichardBuggs** is proposing, and I've referenced them way up there ^^ somewhere early on in this conversation.

DennisVenema (Dennis Venema) 2018-02-28 19:14:42 UTC #736

> T.j_Runyon:
>
> Also, and take this with a grain of salt since my career is in its infancy, all anthropologists I've been been around would Define human as anyone belonging to the genus Homo. Homo Sapiens are broken down into Early Homo Sapiens, like the Jebel Irhoud specimens and anatomically modern humans. So Anne is arguing for an archaic Homo Sapiens (those that are morphologically and behaviorally between Erectus and Sapiens) Adam?

Remember that *Adam and the Genome* is a popular book for a lay audience. Most lay people think "human" means us. As I've mentioned before, I used it in AatG as shorthand for "anatomically modern human."

If you want an example of a paleoanthropologist using the same way of speaking, Tim White would be one (when speaking to popular audiences). For example, **in this lecture** he uses "human" the same way as I do in the book.

But of course, another key point in the book is that species designations are attempts to draw lines of demarcation on a continuous gradient. So whatever term one uses, it will have blur around the edges.

Edit: here's some of the transcript of the lecture that makes the point:

> Tim White:
>
> Let's go down the stack of rocks. We have to move a little bit to the north to do that. We move a little bit further down in time. Now we're at a half a million years. We have a specimen known as the Bodo man, a half a million years old; that's the next one in the line over there. We rotate this man into view, and now it's not a human anymore. We're looking at something that nobody would mistake for an anatomically modern human. What is it? Is it an ape? No. Is it a human? No. What is it? Well, we can put labels on these things, but biologically, it is an intermediate fossil in the record of human evolution. This man studied the record of the archaeology; his name was Desmond Clark, and he founded the project many years ago. And he found thousands of these hand axes at a million years, down a little bit further in the record. And then finally, one of the graduate students from Berkeley, doing a survey found this cranium eroding from the surface. We took it out, we cleaned it up, and this is this cranium. This one is about two-thirds as large as the one, that's the next one in line there. This is Homo erectus. It's well known; it was discovered, the species was discovered in Java many, many years ago.

A.Suarez's Treatment on a Pope's Formulation for Original Sin's Transmission!

A.Suarez's Treatment on a Pope's Formulation for Original Sin's Transmission!

Jonathan_Burke (Jon) 2018-02-28 19:32:53 UTC #737

> Swamidass:
>
> A beautiful example of an apologetic statement for your position!

It's nothing to do with my position.

> Swamidass:
>
> Sounds more like @agauger is trying to find a position consistent with her deeply held belief and what the evidence shows.

That's apologetics. In contrast, science is determining what the evidence shows, and then arriving at beliefs.

Swamidass (Dr. S Joshua Swamidass) 2018-02-28 19:33:25 UTC #738

> DennisVenema:
>
> The first point still stands, though. There are papers in the literature that claim to exclude a bottleneck weaker than the one @RichardBuggs is proposing, and I've referenced them way up there ^^ somewhere early on in this conversation.

I supposed you are entitled to your opinion, but I disagree. The bottleneck hypothesis of which Buggs was asking about was ***not*** tested in the literature. And the only ones in the literature I have seen are stronger along the timing dimension, not weaker. Moreover, observing if a bottleneck is detected is a distinct activity from testing a hypothesis.

---

aleo (Albert Leo) 2018-02-28 20:07:09 UTC #739

> Jay313:
>
> It's all part of an ongoing discussion that mainly centers on two things: Was behavioral/cognitive modernity a "leap forward" (saltational), or was it the end of a long process? The other question involves what lies behind it all. The early answer from Tattersall and the archaeologists pointed either to language or Theory of Mind. The biologists and geneticists pushed back and sought an answer in biology. There was a lot of early enthusiasm for FOXP2, for example, until it was realized that there is no "language gene," just as there is no "cancer gene."

I'm sure you understand my position, Jay, (since I've repeated it often on these posts) but for any new readers I want to be clear that I reject any "biological saltation" that would claim to explain the Great Leap Forward or the sudden appearance of Theory of Mind. If real, the GLF must have be a fortuitous but rare confluence of 'ordinary' biology (a larynx capable of sounds needed for language) and perhaps an epigenetic change in brain 'wiring' that promoted EWM (enhanced working memory) and expression of sophisticated thoughts through language.

In respect to the recent efforts (see @AMWolfe ; @T.j_Runyon) to render the term **'behavioral modernity' as unscientific** in reference to humankind's origins, I would suggest that depends on how one plans to use it. Paleo-anthropologists may prefer some statistical method of treating *'behavior variance*' as more reproducible and therefore

more comparable between research teams. However in explaining how Christian Faith can be seen as compatible with evolutionary science, it is quite acceptable to use layman's terms to emphasize humankind's uniqueness as the theological foundation for the Biblical term "In God's Image'.
Al Leo

Jon_Garvey (Jon Garvey) 2018-02-28 21:07:09 UTC #740

"The fallacious belief that we can quantify the unquantifiable… is responsible for scientism." (William Briggs)

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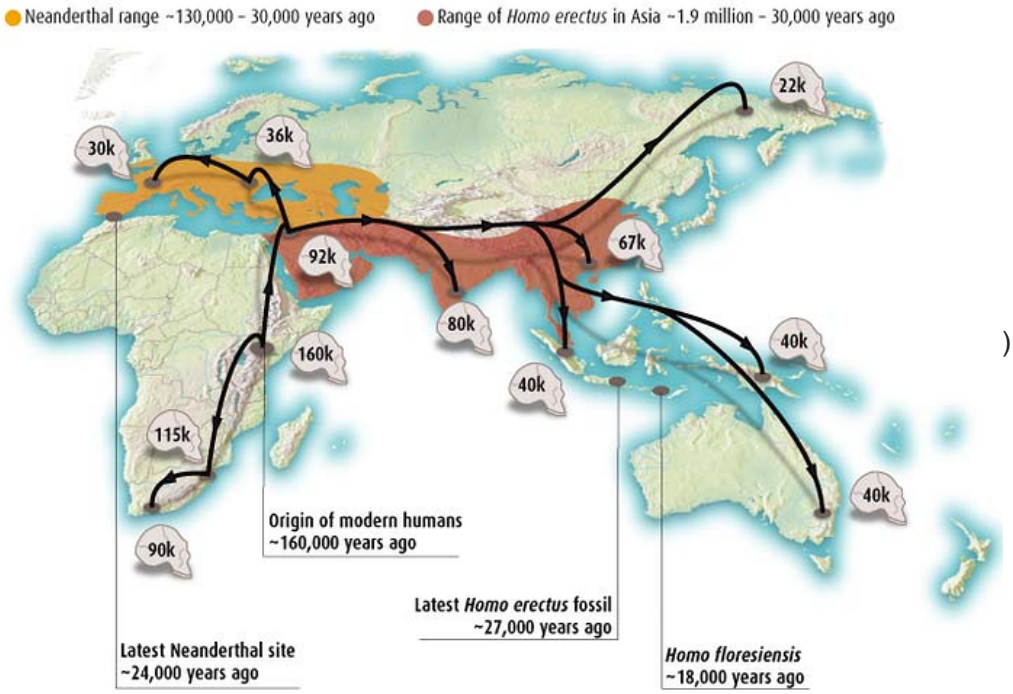
agauger (Ann Gauger) 2018-02-28 23:01:21 UTC #741

> Swamidass:
>
> Regardless, given this high commitment to sole genetic progeintorship, she is willing to push Adam back as far as 2 mya, with the origin of the Homo genus. However, **I do not sense that she is insisting it must be 2 mya. If there is a more plausible place to put Adam, consistent with the archaeological and genetic data, she would amenable.** However, maybe she does feel H erectus is distinctly "human."
>
> That flexibility could be a strength, because she can chose the most defensible position as it arises, which I think might actually be at 700 kya, not 2 mya. So I am an the one suggesting something after H erectus and before H sapiens, not her. It just seems like a stronger option, that is still consistent with her motivations. Though, she is certainly entitled to her own view of what is most defensible. Most likely, most of this is being held very provisionally right now, as we work out the some more of the studies here.

@Swamidass , you are correct that I am trying to understand how the genetics, population genetics, and paleoanthropology evidence fit together best if we start from the assumption of a first pair. This is, after all, a position that hasn't been tested, but needs to be. There are a lot of people invested in it.

In order to insure that later lineages (Neanderthals, Denisovans and H Sapiens: N, D, and H) that show signs of having interbred, and knowing that N and D are believed to share common ancestry with H erectus _and that_H erectus migrated into Asia very rapidly and very early on (about 1.8 mya? I don't know current estimates



), I chose to view H. erectus as the original pair. @Swamidass is right, though, my goal is to find the best explanation for *all* the data. The date 700 kya fits much of it, but I don't think it does for the (easily forgotten) Denisovans.

I really don't like the idea of interbreeding between N and H or D and H if they are far distant on the tree, and do not share the same nature (I mean that in a theological sense). I do not want any people now to have more or less share of the genetics of the first pair, where ever that first pair was in time. Sole progenitorship? You can call it that. The main concern is to be sure that we all come from the same stock.

2 mya, 1 mya, 7mya, 400 kya, 200 kya or smaller–if it fits the data best, any of those dates are OK. To be explained: time of origin: ancestry and ability to interbreed, morphology, cultural and technological artifacts, dispersal, population size and local origin, population genetics, and genetics, with the assumption of a first pair.

The last two categories of data are most important because they provide a historical record in a way that the others cannot. As anyone can see, the data are in tension with one another. It depends on which factors one emphasizes as to where one comes down on the time line as most likely. Or one can throw up one's hands and discard a first pair, or find a solution that does not involve sole progenitorship, or some other solution I haven't thought of.

BTW, my thanks to Buggs, Venema, Swamidass and Schaffner for a fine discussion. I have kept silent most of the time, but have observed. It has been worthwhile.

Chris_Falter (Chris Falter) 2018-02-28 23:11:46 UTC #742

Hi Jon - As always, I enjoy your posts. I do want to push back on your view just a bit. I think it's legitimate science to define the boundary of what the scientific method can ascertain. To say that the data we possess can neither refute nor confirm a certain kind of population bottleneck is good science, in my completely unauthoritative opinion. 🙂

Best,
Chris Falter

DennisVenema (Dennis Venema) 2018-02-28 23:12:42 UTC #743

> agauger:

> 400 mya

I assume that should be 400kya, unless Adam is back in the Devonian? 🙂

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agauger (Ann Gauger) 2018-02-28 23:31:21 UTC #744

@DennisVenema

Oops.

T.j_Runyon (T J Runyon) 2018-02-28 23:35:01 UTC #745

The real Adam

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agauger (Ann Gauger) 2018-02-28 23:40:56 UTC #746

😄

Now the required verbiage, and 😄 again.

Jonathan_Burke (Jon) 2018-03-01 03:09:36 UTC #747

> Chris_Falter:
>
> I think it's legitimate science to define the boundary of what the scientific method can ascertain. To say that the data we possess can neither refute nor confirm a certain kind of population bottleneck is good science, in my completely unauthoritative opinion.

I agree. I have not raised any objection to this. What I raise objection to, is pretending that motivations such as this do not exist.

> "…you are correct that I am trying to understand how the genetics, population genetics, and paleoanthropology evidence fit together best **if we start from the assumption of a first pair**. This is, after all, a position that hasn't

> been tested, but needs to be. **There are a lot of people invested in it**."

> "**I really don't like the idea of** interbreeding between N and H or D and H if they are far distant on the tree, and do not share the same nature (I mean that in a **theological** sense). **I do not want** any people now to have more or less share of the genetics of **the first pair**, where ever that first pair was in time. Sole progenitorship? You can call it that. **The main concern is to be sure that we all come from the same stock**."

> "To be explained: time of origin: ancestry and ability to interbreed, morphology, cultural and technological artifacts, dispersal, population size and local origin, population genetics, and genetics, **with the assumption of a first pair**."

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agauger (Ann Gauger) 2018-03-01 06:45:56 UTC #748

I was asked why I chose an old age for the first pair. The main reason was that 2 mya was the time that might most conform to the criteria I laid out. I chose those criteria as I did, "time of origin: ancestry and ability to interbreed, morphology, cultural and technological artifacts, dispersal, population size and local origin, population genetics, and genetics," because those are the data we potentially have available, or can test by modeling.

I stated my reasons for wanting sole progenitorship because it is the reason I prefer some models over others, and because Josh asked directly. His model does not support sole progenitorship, and has its own assumptions. I am sure others on this list have preferences also, such as not wanting a first pair to be true.

Third, when you make a model to test something, you have to start with some assumptions. I was on record, along with my coauthors, as wanting to test the possibility of a first pair. Nobody had tested the possibility of a first pair yet, until Richard Buggs' persistent questioning got Schaffner and Swamidass to make their own models. With the results we have seen.

No one is pretending that motivations do not exist. Dennis had his motivations for writing his book. Josh had motivations for making his model. Richard had is motivations for raising the issue, which he also stated clearly: there are a lot of people invested in this question, and the answer needs to be tested before categorical claims are made. You, I surmise, also have motivations.

---

gbrooks9 (George Brooks) 2018-03-01 21:13:10 UTC #749

> agauger:
>
> **@Swamidass** , you are correct that I am trying to understand how the genetics, population genetics, and paleoanthropology evidence fit together best if we start from the assumption of a first pair. This is, after all, a position that hasn't been tested, but needs to be. There are a lot of people invested in it.

@agauger

So, if a "first pair" actually works brilliantly… if you place the pair at 400 kya … would you then begin work to convince Young Earth Creationists that their Adam & Eve don't fit in the first 6000 years or even the first 10,000 years … and that they would have to reconcile their view of Genesis to a 400 kya time frame?

George

Swamidass (Dr. S Joshua Swamidass) 2018-03-01 21:18:51 UTC #750

Of all the most odd ad hominems:

> Jonathan_Burke:
>
> I agree. I have not raised any objection to this. What I raise objection to, is pretending that motivations such as this do not exist.

Of course people have motivations for doing research. That is a good thing. I entirely agree, also, that there has been no deception from **@agauger** , at least as far as I can tell. Or from **@RichardBuggs** .

> agauger:
>
> I stated my reasons for wanting sole progenitorship because it is the reason I prefer some models over others, and because Josh asked directly. His model does not support sole progenitorship, and has its own assumptions. I am sure **others on this list have preferences also, such as not wanting a first pair to be true.**

> agauger:
>
> No one is pretending that motivations do not exist. **Dennis had his motivations for writing his book.** Josh had motivations for making his model. Richard had is motivations for raising the issue, which he also stated clearly: there are a lot of people invested in this question, and the answer needs to be tested before categorical claims are made. You, I surmise, also have motivations.

The much more important question to ask is if people are ***honest*** enough to acknowledge where the evidence deviates from what they might prefer. One way to recognize honest is to see that they are willing adjust their beliefs based on evidence, just as **@agauger** has done:

> agauger:
>
> I was asked why I chose an old age for the first pair. The main reason was that 2 mya was the time that might most conform to the criteria I laid out. I chose those criteria as I did, “time of origin: ancestry and ability to interbreed, morphology, cultural and technological artifacts, dispersal, population size and local origin, population genetics, and genetics,” because those are the data we potentially have available, or can test by modeling.

That engagement with scientific data is exactly what we should admire. Instead of saying “*every detail I’ve imagined in Genesis is equally important, so I am going to stick my fingers in my ears and ignore the data*”, **@agauger** is engaged in a creative and productive exchange to form a new position in the origins debate. That is ***exactly*** the right thing to do, whether or not she ends up correct in the end.

I want to add also another recent action by **@agauger** that increases my trust in her work:

> agauger:
>
> The date 700 kya fits much of it, but I don’t think it does for the (easily forgotten) Denisovans.

She is not wanting an easy win based on only part of the evidence. Instead she really is trying to figure out what makes sense in light of the whole. It is harder to do this, but it does increase my ability to trust her when she can identify spoilers, and is working to make sense of them.

In particular, for her project, she really does need to include Neanderthal and Denisovan genetic data too. From what I know, they will all likely share a common ancestor about 700 kya, but no one has actually tested that with data. It certainly is not part of the argweaver paper or equivalent. Yet, for her to make that claim, she'd have to deal with it. She is already raising this weak point before we are.

This also distinguishes her effort here from the dishonestly inherent to one-sided polemics.

> gbrooks9:
>
> So, if a "first pair" actually works brilliantly… if you place the pair at 400 kya … would you then begin work to convince Young Earth Creationists that their Adam & Eve don't fit in the first 6000 years or even the first 10,000 years … and that they would have to reconcile their view of Genesis to a 400 kya time frame?

You are missing the point **@gbrooks9** . She is not a YEC. She is an OEC, and she will probably be on your side in moving YECs into a different timeline.

> agauger:
>
> I stated my reasons for wanting sole progenitorship

I'd just clarify you want sole ***genetic*** progenitorship. Sole ***genealogical*** progenitorship is still possible recently with a genealogical Adam model.

In the end **HONESTY** is in short supply, and fundamentally more important than the illusion of inquiry free of motivations. So cut **@agauger** some slack.

RichardBuggs (Richard Buggs) 2018-03-01 21:19:34 UTC #751

Hi Dennis,

> DennisVenema:
>
> This remains accurate, even with our ongoing conversation. All methods employed thus far do indicate that we descend from thousands.

But as we have shown at length in this discussion, they do not. They reconstruct ancestral effective population sizes (not census population sizes) by methods that would not detect a short census bottleneck of two even if one had occurred. These methods therefore do not "indicate that we descend from thousands".

> DennisVenema:
>
> That idea - 10,000 down to 2 in a single generation, followed by exponential growth - was not on my radar at all when I wrote that. Nor had I seen anyone else suggest anything similar. If I were to write the book today, I would discuss this idea and talk about what we have learned together (especially the ArgWeaver data). But it wasn't on my radar in 2016.

I don't think I have ever named 10,000 as the size of a pre-bottleneck population in this discussion – I have just been suggesting that it would be large enough for individuals within it to carry substantial polymorphism within them.

I am left wondering why you wrote a book on Adam and Eve at all, if the idea of the human race coming from a bottleneck of two polymorphic ancestors who had several children was not on your radar.

If you don't mind me asking, what was on your radar? What hypotheses did you consider that would allow a sole pair of human ancestors?

I note that you wrote on page 46 of *Adam and the Genome* "it is technically possible that a species could be founded by single ancestral breeding pair".

I am glad that you would write the book differently today, and that this discussion has not therefore been in vain. However, I am still very mindful of the fact that very few of the readers of *Adam and the Genome* will stumble across this discussion, and the few that do are unlikely to make it through the first 700 posts. I think that we all need to do all that we can to communicate to your readers that a single couple bottleneck in the lineage leading to modern humans is a possibility that is consistent with extant genetic diversity.

Swamidass (Dr. S Joshua Swamidass) 2018-03-01 21:28:38 UTC #752

> RichardBuggs:
>
> > This remains accurate, even with our ongoing conversation. All methods employed thus far do indicate that we descend from thousands.
>
> But as we have shown at length in this discussion, they do not…
>
> > That idea - 10,000 down to 2 in a single generation, followed by exponential growth…
>
> I don't think I have ever named 10,000 as the size of a pre-bottleneck population in this discussion – I have just been suggesting that it would be large enough for individuals within it to carry substantial polymorphism within them.

I agree with **@RichardBuggs** assessment here.

That is not actually the model that has been put forward. The substance of several AatG claims are no longer supported, or are now supported by analysis made after your book was published by other people. **You were claiming to be presenting settled science, and the evidence that supported it, NOT a hypothesis that would eventually be supported by work on ArgWeaver.** That claim turns out to be totally false. The data you were presenting as evidence was not sufficient to make your case. If had not helped you, you would still be struggling to make the case.

> agauger:
>
> Third, when you make a model to test something, you have to start with some assumptions. I was on record, along with my coauthors, as wanting to test the possibility of a first pair. Nobody had tested the possibility of a first pair yet, until Richard Buggs' persistent questioning got Schaffner and Swamidass to make their own models. With the results we have seen.

Also **@agauger** to be fair, both **@glipsnort** and myself have been responsive to this and engaging it long before Richard Buggs entered the conversation. Back in Sept 2016…

1. **Agreeing with a YEC critic**, I wrote a fairly detailed acknowledgement of the failure to directly test for a recent single couple in the literature.
2. In response, **@glipsnort ran his first SFS simulation for an outsider.**
3. Not public but true, I've been engaging with scientists across the origins debate to help them start asking and answering questions here. I've always acknowledged that the ancient Adam model has not been tested, and have encouraged effort here.

So we have been testing this, at least since Sept 2016, long before **@RichardBuggs** entered the conversation. The real problem is that this is just hobby for us (we have other jobs), and there was very little visibility on those contributions.

The real contribution of **@RichardBuggs** has been to press more tightly in on the LD and population reconstruction data, bring some new information to the table (the website on the PSMC bottleneck detection), and also to draw visibility to this question. This is nearly the most read thread on the forums now, it took quite a bit of effort to bring **@DennisVenema** to the table (and he is only here now thanks to **@RichardBuggs**). I'm very grateful to his contribution, but **@glipsnort** and I have been thinking about this problem for a while. I have encouraged inquiry into it, and have put a lot of personal time into answering it as soon a new path forward to tractably test it became available. It is not merely that **@RichardBuggs** raised the question, or it would have been missed.

I want to emphasize also that **@glipsnort** is part of BioLogos, even though I am not. Moreover, several Biologos scientists have been following this, very supportive of **@RichardBuggs** and my correction to the scientific account. So it is important that full credit is given where it is due. There are alot of people who have been unsympathetic to the questions of the Church, but there are several (including with in BioLogos) that have been sympathetic.

> RichardBuggs:
>
> I am left wondering **why you wrote a book on Adam and Eve at all**, if the idea of the human race coming from a bottleneck of two polymorphic ancestors who had several children was not on your radar.
>
> If you don't mind me asking, what was on your radar? What hypotheses did you consider that would allow a sole pair of human ancestors?

Very good questions. Not sure there is a good answer possible.

Remember, he put forward the strawman of the homozygous clone Adam and Eve?

It does not seem he was terribly engaged on the science here. As has been clear for a while (**henrycenter.tiu.edu/2017/06/a-genealogical-adam-and-eve-in-evolution/**), **@DennisVenema** presented a selective account that fit with his personal theological views.

> RichardBuggs:
>
> I am glad that you would write the book differently today, and that this discussion has not therefore been in vain. However, I am still very mindful of the fact that very few of the readers of Adam and the Genome will stumble across this discussion, and the few that do are unlikely to make it through the first 700 posts. I think that we all need to do all that we can to communicate to your readers that a single couple bottleneck in the lineage leading to modern humans is a possibility that is consistent with extant genetic diversity.

I agree. Which is why your public statement is a good idea **@RichardBuggs** . I hope Dennis is up for signing it.

Jay313 (Jay Johnson) 2018-03-01 22:04:53 UTC #753

> RichardBuggs:
>
> I am left wondering why you wrote a book on Adam and Eve at all, if the idea of the human race coming from a bottleneck of two polymorphic ancestors who had several children was not on your radar.
>
> If you don't mind me asking, what was on your radar? What hypotheses did you consider that would allow a sole pair of human ancestors?

> Swamidass:
>
> Very good questions. Not sure there is a good answer possible.
>
> Remember, he put forward the strawman of the homozygous clone Adam and Eve?
>
> It does not seem he was terribly engaged on the science here. As has been clear for a while (**henrycenter.tiu.edu/2017/06/a-genealogical-adam-and-eve-in-evolution/**), **@DennisVenema** presented a selective account that fit with his personal theological views.

> T.j_Runyon:
>
> I owe a lot to Dennis. He had a huge part in bringing me back to Christianity. Helped show me I could be an intellectually fulfilled Christian evolutionary biologist. I owe him a lot. **I just feel he has been read a little uncharitably here.**

Just a little? Ya think?

---

agauger (Ann Gauger) 2018-03-01 22:09:47 UTC #754

@gbrooks9
Fair question. But in that case I don't think my arguments would change many minds. As others on the list have pointed out, an old Adam does not agree with their reading of Genesis, and that won't change. That is a key issue for them.

---

agauger (Ann Gauger) 2018-03-01 22:36:54 UTC #755

> Swamidass:
>
> That engagement with scientific data is exactly what we should admire. Instead of saying "every detail I've imagined in Genesis is equally important, so I am going to stick my fingers in my ears and ignore the data", **@agauger** is engaged in a creative and productive exchange to form a new position in the origins debate. That is exactly the right thing to do, whether or not she ends up correct in the end.

@Swamidass
Thanks, Josh. I appreciate the generous words. I'll tell you what I would most like: positive evidence of a first pair, not just the finding that we can not rule them out past a certain age.

> Swamidass:
>
> Also **@agauger** to be fair, both **@glipsnort** and myself have been responsive to this and engaging it long before Richard Buggs entered the conversation. Back in Sept 2016…

> Agreeing with a YEC critic, I wrote a fairly detailed acknowledgement of the failure to directly test for a recent single couple in the literature.
> In response, **@glipsnort** ran his first SFS simulation for an outsider.
>
> Not public but true, I've been engaging with scientists across the origins debate to help them start asking and answering questions here. I've always acknowledged that the ancient Adam model has not been tested, and have encouraged effort here.
>
> So we have been testing this, at least since Sept 2016, long before **@RichardBuggs** entered the conversation.

And thank you for the correction of the record. I was not aware of your earlier efforts with **@glipsnort** on the question of a first pair.

---

agauger (Ann Gauger) 2018-03-01 22:48:59 UTC #756

> Swamidass:
>
> I agree. Which is why your public statement is a good idea **@RichardBuggs** .

> RichardBuggs:
>
> I think that we all need to do all that we can to communicate to your readers that a single couple bottleneck in the lineage leading to modern humans is a possibility that is consistent with extant genetic diversity.

@Swamidass **@RichardBuggs**

Will you two sign it without **@DennisVenema** ? I agree with Richard that a public statement would be great, especially if Dennis signs it as a clarification for his book. But if he doesn't want to, will you proceed without him?

---

glipsnort (Steve Schaffner) 2018-03-01 23:32:53 UTC #757

> Swamidass:
>
> I want to emphasize also that **@glipsnort** is part of BioLogos, even though I am not.

Hmm. While I have written one blog post for BioLogos, I have no formal affiliation with them. Hanging around here a lot doesn't count.

T.j_Runyon (T J Runyon) 2018-03-02 00:03:29 UTC #758

> **Homo erectus made world's oldest doodle 500,000 years ago**
>
> Shell markings are the oldest abstract signs ever discovered.

This may interest you as well

Chris_Falter (Chris Falter) 2018-03-02 01:49:13 UTC #759

> glipsnort:
>
> Hanging around here a lot doesn't count.

Counts with me, Steve!

Swamidass (Dr. S Joshua Swamidass) 2018-03-02 03:55:03 UTC #760

> RichardBuggs:
>
> I am left wondering why you wrote a book on Adam and Eve at all, if the idea of the human race coming from a bottleneck of two polymorphic ancestors who had several children was not on your radar.
>
> If you don't mind me asking, what was on your radar? What hypotheses did you consider that would allow a sole pair of human ancestors?

> Swamidass:
>
> Very good questions. Not sure there is a good answer possible.
>
> Remember, he put forward the strawman of the homozygous clone Adam and Eve?
>
> It does not seem he was terribly engaged on the science here. As has been clear for a while (**henrycenter.tiu.edu/2017/06/a-genealogical-adam-and-eve-in-evolution/**), **@DennisVenema** presented a selective account that fit with his personal theological views.

I should add to that response, by pointing to something I wrote quite a while back about this. Perhaps there is a good reason to why he should have written that book.

> Even in their support, I hope those who agree with Adam and the Genome will do so with humility. Science is a human effort. It is merely our best account of the world, without considering God's action. Many informed and intelligent people will still reject evolution. If they do so in obedience to their honest understanding of Scripture, they choose the better thing. There is real danger in unwittingly pressing science if it encourages disobedience to God.

> Even in their opposition, I hope those who disagree with Adam and the Genome will work hard to understand. I hope they will emphasize the voices in evolutionary creation with whom they most agree, like the many that affirm traditional Genesis interpretations. Even if it is false, evolution is the origin story of our modern world. **We need those with whom we disagree to articulate their positions, just as Venema and McKnight have done here.** Even if we disagree, they give truthful account of how most scientists understand our evolutionary origins. **http://peacefulscience.org/reviewing-adam-and-the-genome/**

I think those words still stand. The way how **@DennisVenema** explained the science was truthfully how most scientists understand our origins, even if it did have major errors. And we all benefit when people put together orderly accounts as Dennis did, so that we can then see what evidence and theology others are resting their positions.

I suspect that **@DennisVenema** did not understand how important it could be to his audience either (1) a recent genealogical Adam or (2) an ancient single-couple genetic origin. I suspect it was not malice, but inattention. As much as he has become the focal point, a large number of people have thought the same thing, and have been equally inattentive.

It seems he made several errors in how he justified his claims. Much of the strong evidence he had evaporated, and he seems to still communicate about it in a way that overstates the evidence (almost like he does not want to admit he made a mistake?). However, without help, he could not support his claims. Even if he was right on all claims (which he is not), he did not put forward the right reasons for why his claims were correct.

Perhaps, that is the value of the book, it has helped clarify how weak these confident claims really were. Many people make these claims all the time, but now we are clarifying what the evidence is really showing us.

> agauger:
>
> Will you two sign it without **@DennisVenema** ? I agree with Richard that a public statement would be great, especially if Dennis signs it as a clarification for his book. But if he doesn't want to, will you proceed without him?

It depends. I put forward some revisions to the language. **@RichardBuggs** has not responded. I suspect people are now waiting on him. It seems the ball is in his court at the moment.

I also want to acknowledge and thank the moderators, **@Christy** , **@BradKramer** , **@jpm** , and **@Casper_Hesp** . They actually are officially with BioLogos and have allowed a fairly unsettling conversation to progress on the forums. If it is not clear, they have been very fair, and not interfered in what happened here. They deserve credit for this, as this takes a great deal of work and they could have easily shut down this conversation when it has become uncomfortable.They deserve some credit too.

Moreover, even if **@glipsnort** apparently is not with BioLogos. Both of us affirm evolutionary science, and I do not believe he affirms a historical Adam. While I affirm a historical Adam, I'm not advocating any specific view of Adam. We are involved just to serve the Church with an honest account of the science, regardless of our personal positions.

Chris_Falter (Chris Falter) 2018-03-02 04:19:11 UTC #761

> Swamidass:
>
> that is the value of the book, it has helped clarify how weak these confident claims really were.

Really, Joshua, do you think that is the only value of Dennis' efforts in the book? I get that he made a mistake that needed to be corrected. Is that all that comes out of his writing, in your opinion?

Swamidass (Dr. S Joshua Swamidass) 2018-03-02 04:25:36 UTC #762

> Chris_Falter:
>
> Really, Joshua, do you think that is the only value of Dennis' efforts in the book? I get that he made a mistake that needed to be corrected. Is that all that comes out of his writing, in your opinion?

Of course that is not the only value.

As I wrote…

> Swamidass:
>
> Even if it is false, evolution is the origin story of our modern world. **We need those with whom we disagree to articulate their positions, just as Venema and McKnight have done here. Even if we disagree, they give truthful account of how most scientists understand our evolutionary origins.**

I also really appreciated hearing his back story, as that explains much of what motivates him. I think Adam and the Genome remains an accurate account of how many people see our origins. I also liked a great deal one of McKnights points:

> McKnight studies how Paul's Adam interacts with Jesus. He observes Paul could be reasoning from Jesus to Adam (p. 181). **Paul's Adam, rather than a starting point from which to define Jesus, is instead an explanatory contrast by which to expound a Jesus clearly seen by other means** (Heb. 1:1-3); a Jesus who stands alone, without need of Adam. McKnight's reframing is consistent with the rest of Scripture, which calls Jesus the "cornerstone" (Eph. 2:20),
> **http://henrycenter.tiu.edu/2017/06/a-genealogical-adam-and-eve-in-evolution/**

That was a strong point with which I agree, and had not thought of it that way before.

Nonetheless…

> *Adam and the Genome* is best understood as **a partial explanation of the relevant evolutionary science**. It also explains why some Christians do not affirm a historical Adam, but a better account would explain this without assuming science.
> **http://henrycenter.tiu.edu/2017/06/a-genealogical-adam-and-eve-in-evolution/**

That has value, of course, because we need people to tell us how they see origins. That is what Dennis did.

Swamidass (Dr. S Joshua Swamidass) 2018-03-02 04:54:12 UTC #763

@agauger and **@T.j_Runyon** curious your thoughts on this:

Tools and voyages suggest that Homo erectus invented language – Daniel Everett I...

Early hominins who sailed across oceans left indirect evidence that they might have been the first to use language

Did you know that there is ancient evidence of seafaring, at least 700 kya? I discovered it during my work on the genealogical Adam. Very interesting and surprising.

> **Seafaring in the Pleistocene | Cambridge Archaeological Journal | Cambridge Core**
>
> Seafaring in the Pleistocene - Volume 13 Issue 1 - Robert G. Bednarik

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agauger (Ann Gauger) 2018-03-02 05:19:53 UTC #764

> Swamidass:
>
> The way how **@DennisVenema** explained the science was truthfully how most scientists understand our origins

@Swamidass
This is the main point I would like to make. With regard to Adam and the Genome, Dennis was pretty much reflecting what I have seen in the literature: many papers, using different methods, that end up with an Ne of 10,000, plus or minus for our population 6 million or so years ago. He did not think of testing for a bottleneck of two directly, but then at least as far as I know, no one else did either. Until recently.

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agauger (Ann Gauger) 2018-03-02 05:58:57 UTC #765

@Swamidass
I had encountered this before also. When I first saw it I discounted it because of the sensationalism. This about sailing to Crete:

> "I was flabbergasted," said Boston University archaeologist and stone-tool expert Curtis Runnels. "The idea of finding tools from this very early time period on Crete was about as believable as finding an iPod in King Tut's tomb."

130 kya is the date I have seen, which could have been Neanderthal, but I assume it had to do with the style of the hand axe.

But more evidence is accumulating of seafaring at earlier dates, as you say. The oldest I have seen:

> While no remains of a boat used by H. erectus have been found (the oldest known vessels, Stone Age dugouts, are only a few thousand years old), potential evidence of the species' habitation on isolated islands suggests that it may have been able to travel many miles across the open sea.
>
> In 2008, Russian researchers found very primitive stone tools on Socotra, a completely isolated island more than 150 miles off the Horn of Africa and 240 miles off the coast of Yemen. … The researchers estimate their discoveries to be anywhere from 500,000 to 1 million years old, which is firmly within the time frame of H. erectus.
>
> (Jørn Madsen, "Who was Homo erectus," Science Illustrated (July/ August 2012), p. 23.)

Even the skeptics are on board.
http://www.aske-skeptics.org.uk/sailing_to_flores_and_crete.html

And about the Everett piece: he is something of a disputed figure. Some think him brave and insightful, others think him wild and a publicity hound. He challenged Chompsky's theory about universal language, on fairly flimsy grounds, in my opinion. So he is bound to favor a gradual development of language, and boat building in the early Pleistocene would support that.

Jonathan_Burke (Jon) 2018-03-02 06:18:04 UTC #766

> Swamidass:
>
> Of all the most odd ad hominems:

Please stop mis-using that term. An ad hominem is the use of a personal attack on someone's character, as the basis of an argument that their claim is wrong. I have done nothing of the sort.

> Swamidass:
>
> Of course people have motivations for doing research. That is a good thing.

Every time I make a statement you spin it subtly to deflect from what I am saying. I did not simply say "people have motivations for doing research". I objected to the fact that in this case a specific theological motivation (anti-evolutionism), is being treated as if it doesn't exist. Statements and research are being treated as if they are objective scientific exercises, instead of apologetic exercises aimed at trying to support a narrative which opposes evolution.

> Swamidass:
>
> The much more important question to ask is if people are honest enough to acknowledge where the evidence deviates from what they might prefer. One way to recognize honest is to see that they are willing adjust their beliefs based on evidence, just as **@agauger** has done:

The fact that she refuses to accept evolution, keeps on arguing against evolution, and makes arguments which are palpably in contradiction to the evidence ("**Is There Enough Time For Humans to have Evolved from Apes? Dr. Ann Gauger Answers**", "**Is Evolution True? Laying Out the Logic**", "**Is Evolution True? Laying Out the Logic, Part 2**"), indicates that her willingness to adjust her beliefs on evidence is not as robust as you are trying to depict it.

> Swamidass:
>
> That engagement with scientific data is exactly what we should admire.

Again, this is a highly selective description of her "engagement with scientific data". The way she engages scientific data is not a method we should admire.

> Swamidass:
>
> I want to add also another recent action by **@agauger** that increases my trust in her work:

If her work is so trustworthy, should we accept her anti-evolution views?

> Swamidass:

> In the end HONESTY is in short supply, and fundamentally more important than the illusion of inquiry free of motivations. So cut **@agauger** some slack.

I don't believe she's intellectually honest. I find that you spend a lot of time these days calling out scientists for (perceived), lack of honesty if they **accept** evolution, and praising them for honesty if they **reject** evolution. You set the bar for honesty and evidence very high for anyone who accepts evolution, but very low for anyone who rejects it. This is a curious pattern which does not appear to have a scientific motivation, but I guess it plays well to your intended audience.

> Swamidass:
>
> Remember, he put forward the strawman of the homozygous clone Adam and Eve?

As I pointed out, it was not a strawman. It was an argument which several creationist organizations have made; I even quoted them.

> Swamidass:
>
> As has been clear for a while (**henrycenter.tiu.edu/2017/06/a-genealogical-adam-and-eve-in-evolution/**), **@DennisVenema** presented a selective account that fit with his personal theological views.

The irony in this statement is palpable.

> agauger:
>
> No one is pretending that motivations do not exist.

I call it as I see it. This post of yours looks like just another effort to do exactly that; you talk about everything except the point I raised, your theological motivation for wanting sole genetic progenitorship.

> agauger:
>
> Richard had is motivations for raising the issue, which he also stated clearly: there are a lot of people invested in this question, and the answer needs to be tested before categorical claims

Yes, he was more transparent in his motivation.

> agauger:
>
> You, I surmise, also have motivations.

Yes. I want to know what the scientific data actually says, regardless of whether or not it conflicts with what I believe at present. I will change my beliefs according to the facts.

I used to believe in a global flood. I did my best to explain away the contrary evidence. I was doing apologetics. When I stopped doing apologetics and started seriously looking at the contrary evidence (both from the Bible and from the physical record in the earth), I found I could not sustain my belief in a global flood. I changed my mind. When I do apologetics, I don't pretend I'm doing science.

Swamidass (Dr. S Joshua Swamidass) 2018-03-02 06:25:22 UTC #767

> Jonathan_Burke:
>
> > Of all the most odd ad hominems:
>
> Please stop mis-using that term. An ad hominem is the use of a personal attack on someone's character, as the basis of an argument that their claim is wrong. I have done nothing of the sort.

You ***were*** making a classic ad hominem. You might want to look at the definition. From wiki:

> Ad hominem (Latin for "to the man" or "to the person"[1]), short for argumentum ad hominem, is a fallacious argumentative strategy whereby an argument is rebutted by attacking the character, ***MOTIVE***, or other attribute of the person making the argument, or persons associated with the argument, **rather than attacking the substance of the argument itself.** **https://en.wikipedia.org/wiki/Ad_hominem**

Dismissing an argument because of the motives of a person is an ad hominem. Denying it is ad hominem does not make it so.

> Jonathan_Burke:
>
> The fact that she refuses to accept evolution, keeps on arguing against evolution, and makes arguments which are palpably in contradiction to the evidence ("Is There Enough Time For Humans to have Evolved from Apes? Dr. Ann Gauger Answers", "Is Evolution True? Laying Out the Logic", "Is Evolution True? Laying Out the Logic, Part 2"), indicates that her willingness to adjust her beliefs on evidence is not as robust as you are trying to depict it.

Of course I disagree with Ann on evolution. I think she is wrong, and I have also debated with her extensively about common descent. However, I was surprised when she acknowledged when there was evidence for common descent uncovered in that conversation. Regardless, she can be wrong on evolution, and right on this. Can she not? And even if she is wrong, can she not be honest too? She could just be honestly wrong.

For that matter, I do not think **@DennisVenema** has been dishonest either. He was just wrong.

> Jonathan_Burke:
>
> Again, this is a highly selective description of her "engagement with scientific data". The way she engages scientific data is not a method we should admire.

Yes it is selective, to the specific data we are discussing here. We are not discussing common descent, but population genetics and Adam and eve.

> Jonathan_Burke:
>
> I don't believe she's intellectually honest. I find that you spend a lot of time these days calling out scientists for (perceived), lack of honesty if they accept evolution, and praising them for honesty if they reject evolution. You set the bar for honesty and evidence very high for anyone who accepts evolution, but very low for anyone who rejects it. This is a curious pattern which does not appear to have a scientific motivation, but I guess it plays well to your intended audience.

You have not being paying attention then.

T.j_Runyon (T J Runyon) 2018-03-02 08:13:28 UTC #768

So Everett has always kind of frustrated me. He attributes a lot of views to people that they just don't hold. This article is pretty frustrating as well. I think most people would grant Erectus had some type of language. Complex speech? No. I think **@agauger** is spot on about Everett. And me personally I find the evidence for seafaring pretty convincing. But it was defintely not a regular thing so I'm not going to call them seafarers. This is an area I haven't spent too much time on so who knows what I really think.

T.j_Runyon (T J Runyon) 2018-03-02 08:20:34 UTC #769

I mean you can kind of see what people think of Everett here

Chris_Falter (Chris Falter) 2018-03-02 13:10:14 UTC #770

At a level suitable for a broad audience, Dennis also spilled a good bit of ink describing the evidence for common ancestry, the various members of the hominid tree, and the reasons why many scientists are dissatisfied with the ID movement.

Since you are also interested in communicating to a broad audience, Joshua, I thought you might have something to say about Dennis' sections on these other topics. Do you?

AMWolfe (A.M. Wolfe) 2018-03-02 13:27:31 UTC #771

> aleo:
>
> recent efforts (see **@AMWolfe** ; **@T.j_Runyon**) to render the term ‘behavioral modernity’ as unscientific in reference to humankind’s origins

No such effort on my part! I merely chimed in that **@T.j_Runyon** ’s comments were interesting, and that they might be of interest to you and **@Jay313** , the two Forum regulars who (it seems to me) most often interact over the subject of a Great Leap Forward. My intent was to help you by calling this post to your attention during a season with lots of posts on the Forum. Didn’t mean to imply anything about your position or mischaracterize it. 🙂

Have a good day —
AMW

Swamidass (Dr. S Joshua Swamidass) 2018-03-02 13:51:38 UTC #772

> Chris_Falter:
>
> At a level suitable for a broad audience, Dennis also spilled a good bit of ink describing the evidence for common ancestry, the various members of the hominid tree, and the reasons why many scientists are dissatisfied with the ID movement.

Very good point!

I certainly am not in the ID camp, and I also affirm common descent. **@DennisVenema** work explaining this both on the blog and in his book has been very important.

AMWolfe (A.M. Wolfe) 2018-03-02 14:10:22 UTC #773

> Chris_Falter:
>
> > glipsnort:
> >
> > Hanging around here a lot doesn’t count.
>
> Counts with me, Steve!

…but **@swamidass** has written *four* blog posts for BioLogos, and spent lots more time hanging out with all of us… so I’d say Joshua is more part of BioLogos than Steve, by those measures! 🙂

(Sorry, don’t mean to be insensitive to political realities. Just expressing my naive wish that we could “all just get along” 🙂 … I very much appreciate all the voices in this conversation and the time generously given to this important conversation!)

Jay313 (Jay Johnson) 2018-03-02 14:17:56 UTC #774

> T.j_Runyon:
>
> This may interest you as well

Yes, interesting article. There's a really good paper that came out of an interdisciplinary symposium on cultural evolution that ties together all of these things pretty well. **The Nature of Culture: an eight-grade model for the evolution and expansion of cultural capacities in hominins and other animals** Here is the key section:

Due to the virtual nature of notional modules
it is often difficult to detect undoubted evidence
of notional cultural capacity within the archaeological
record. Pigments and cut marks on different
raw materials are often claimed to implicate
symbolic content (d'Errico & Henshilwood,
2011; d'Errico et al., 2012; Mania & Mania,
1988), a fact which can hardly be proven without
other unambiguous hints from the archaeological
context (cf. Garofoli & Haidle, 2014).
Recently, ca. 500 ka old shells from Trinil on Java,
Indonesia have been reported as showing engravings
in a geometrical pattern (Joordens et al.,
2014). However, it is not clear that the engravings
are deliberate, let alone evidence of Homo
erectus having attempted to signify something.
Eagle claws from 130 ka old layers at Krapina
suggest at least a Neandertal affection for special
objects (Radovčić et al., 2015); if possible ornaments
as such are a proof of symbolism is debated
(Garofoli, 2014). It is only around 40 ka ago that
undisputable elements of figurative art occur in
the archaeological record, which are accepted
by most archaeologists as carriers of notional
information (but see Malafouris, 2007 for an
alternative conception of cave paintings). From
that time, ivory sculptures depicting animals and
females have been discovered from several cave
sites of the Swabian Jura in Southern Germany
(Conard, 2003, 2009; Higham et al., 2012).
As early evidence of notional concepts artistic
representations of probably supernatural beings
are counted like the ca 40 ka lion-man from
the Hohlestein-Stadel cave in South Germany
(cf. Kind et al., 2014; Wynn et al., 2009), the
'adorant' from the Geißenklösterle cave nearby
(Hahn, 1994), and the small figurine interpreted
as a lion-man from Hohle Fels cave (Conard,
2003). A stone figurine from Stratzing in Austria
(Neugebauer-Maresch, 1989), paintings on rock
fragments from Fumane Cave in Northern Italy
(Broglio et al., 2005), and the paintings from
Grotte Chauvet in France (Clottes, 2001) are of

roughly comparable age. The oldest cave paintings, so far, have been dated in Northern Spain back to more than 40.8 ka (Pike et al., 2012). Outside Europe, the oldest evidence for figurative depictions was found in the Maros caves on Sulawesi, Indonesia dating back to more than 35 ka (Aubert et al., 2014) and in 27.5 ka old layers at Apollo 11 Cave in Namibia (Vogelsang, 1998).

Edit: I should also clarify that *H. erectus* did not speak “language” but proto-language, which began with one-word utterances. This doesn’t require full symbolicity, as the symbols are processed one-at-a-time.

AMWolfe (A.M. Wolfe) 2018-03-02 14:42:31 UTC #775

> agauger:
>
> And about the Everett piece: he is something of a disputed figure. Some think him brave and insightful, others think him wild and a publicity hound. He challenged Chompsky’s theory about universal language, on fairly flimsy grounds, in my opinion. So he is bound to favor a gradual development of language, and boat building in the early Pleistocene would support that.

This is probably too far afield, but just to say: Challenging Chomsky’s theory on universal grammar is tricky, because the theory is virtually unfalsifiable. Everett took one of Chomsky’s more memorable but narrow claims and attempted to falsify it. The argument may appear flimsy because it’s narrow, but in Everett’s defense, this was probably one of the only ways to pin down Chomskian theory and falsify (some portion of) it.

That said, Everett is certainly a controversial figure, not least for his highly public deconversion as a former member of a well-known evangelical mission that counts at least three regular BioLogos Forum contributors in its ranks. 🙂

Swamidass (Dr. S Joshua Swamidass) 2018-03-02 15:07:30 UTC #776

> AMWolfe:
>
> …but **@swamidass** has written four blog posts for BioLogos, and spent lots more time hanging out with all of us… so I’d say Joshua is more part of BioLogos than Steve, by those measures! 🙂
>
> (Sorry, don’t mean to be insensitive to political realities. Just expressing my naive wish that we could “all just get along” 🙂 … I very much appreciate all the voices in this conversation and the time generously given to this important conversation!)

Do not despair.

I am no longer associated with BioLogos or consider it my “tent”, however, I still have good relationships with people here. We can get along, and we are not enemies. There are no hard feelings on my end, and neither do I think there are on theirs. We have a great deal of common ground, despite our very real disagreements.

That being said, as is entirely evident on this thread, the moderators have been very accommodating and tolerant of me.

BioLogos places a vital role in the conversation, which I support. We are just cross-purposes with each other in this season. Who knows what the future holds.

gbrooks9 (George Brooks) 2018-03-02 15:21:46 UTC #777

> Swamidass:
>
> This also distinguishes her effort here from the dishonestly inherent to one-sided polemics.
>
> **gbrooks9 wrote:**
> **So, if a "first pair" actually works brilliantly… if you place the pair at 400 kya … would you then begin work to convince Young Earth Creationists that their Adam & Eve don't fit in the first 6000 years or even the first 10,000 years … and that they would have to reconcile their view of Genesis to a 400 kya time frame?**
>
> **swamidass responds:**
> You are missing the point **@gbrooks9** . She is not a YEC. She is an OEC, and she will probably be on your side in moving YECs into a different timeline.

@Swamidass ,

Didn't you read any of this thread? Or this post in particular?:

> **New book explaining why EC is wrong**
>
> Thank you for the heads-up, **@Bill_II** ! Here are the Editors, including our recent visitor, Ann Gauger. Bill, in your opinion, which criciticm of the book draws the most blood… or comes closest to breaking the skin? **[image]**

The thread deals with this book:
"Theistic Evolution: A Scientific, Philosophical, and Theological Critique Edited by J.P. Moreland"

Despite her extensive involvement with this book, as far as I have been able to determine, Dr. Gauger, (**@agauger**) , at no time, attempted to rectify the Young Earth position by explaining that humanity is much, much, much older than 6,000 or even 10,000 years.

So, what exactly convinces you that Dr. Gauger is **not** a YEC?

The concerns I raise are essentially the very same concerns raised by **@Jonathan_Burke** :

> Jonathan_Burke:
>
> **jonathan_burke writes:**
> The fact that she refuses to accept evolution, keeps on arguing against evolution, and makes arguments which are palpably in contradiction to the evidence ("Is There Enough Time For Humans to have Evolved from Apes? Dr. Ann Gauger Answers", "Is Evolution True? Laying Out the Logic", "Is Evolution True? Laying Out the Logic, Part 2"), indicates that her willingness to adjust her beliefs on evidence is not as robust as you are trying to depict it.
>
> **Swamidass writes:**
> "That engagement with scientific data is exactly what we should admire."
>
> **jonathan_burke counters:**
> Again, this is a highly selective description of her "engagement with scientific data". The way she engages scientific data is not a method we should admire.

gbrooks9 (George Brooks) 2018-03-02 15:30:17 UTC #778

> agauger:
>
> **@gbrooks9**
>
> Fair question. But in that case I don't think my arguments would change many minds. As others on the list have pointed out, an old Adam does not agree with their reading of Genesis, and that won't change. That is a key issue for them.

@agauger

But what you write in the book "Theistic Evolution" is far and away the opposite of what your scientific position, as described here and there on these BioLogos boards, would indicate.

You are either keeping "a secret" from the Young Earth Creationists … or keeping "a secret" from the BioLogos audience. How can one person write your answer to me above, and also write what we see in the book "Theistic Evolution"?

You can see that it is not just me who is wondering what is going on here… **@Jonathan_Burke** has written far more about your views than I have even contemplated.

Can you resolve this mystery for us?

---

agauger (Ann Gauger) 2018-03-02 18:59:59 UTC #779

@gbrooks9 , **@Jonathan_Burke** ,

I'd like to make several points.

1. *Science and Human Origins*, published in 2012, was when I was first beginning to grapple with this problem. It lays out why I think/ thought an unguided process could not account for human evolution. It did not mention an age for Adam. I had not begun to think about it. It does touch on the problem of special creation but says the evidence is not in yet.

2. There are four things that are separable.
   Did God use special creation to produce Adam or not?
   Did God use guided evolution and we can detect it?
   Did God use guided evolution and we can't detect it
   It all happened by natural causes, with God having set everything in motion.
   I am either 1 or 2. Still considering. Most of my writing does challenge evolution, but that depends on how you define evolution. What I challenge is 3 and 4.

3. I began thinking about the evidence available about dates for a bottleneck/ first pair after that. I have a power point from a talk I gave in 2014 that demonstrates that. At that point I was convinced of an old date and a first pair but did not have firm evidence. So I didn't argue the point publicly.

4. I began to pursue a model to test the Ne of 10,000 and dates in 2014.
   By 2016 we had a model to publish, which we did. The possibility of either a young age or an old one is discussed in those papers.

5. The manuscript for my chapters in the TE book were submitted in 2016. The article on the population genetics models restates what our more scientific paper said: there are two options for a first pair (or bottleneck), as stated

above. I said nothing on the age of the earth because it was irrelevant, AND it should be clear from other writings that I accept an old earth. If it's not clear to you, then let me say it here: I ACCEPT AN OLD EARTH. I gave no firm dates for Adam because at that time we still didn't have a model working to test the possibility. NOTE: the articles in the TE book were submitted long before any of this discussion had happened.

6. It is only recently that we have a real argument for a possible bottleneck older than 400 kya. I have been waiting for a public statement. But with Swamidass having addressed the HLA problem, we have several lines of argument/evidence, so it is a good time for me to say something about this publicly. The only caveat is our model has not been run to test the dates yet. That is in progress. It will be interesting to see what it shows, because it uses different assumptions.

Nothing hidden. No secrets. No deception. Just an unwillingness to state a date without evidence.
I can't spend more time on this. You will either have to accept my word, or let your prejudices color your reading of what I am saying in ways I cannot predict.

Chris_Falter (Chris Falter) 2018-03-02 19:55:10 UTC #780

Thanks for summarizing your research so clearly, Dr. Gauger. Could you kindly provide links to the papers you reference?

---

gbrooks9 (George Brooks) 2018-03-02 20:17:52 UTC #781

> agauger:
>
> I said nothing on the age of the earth because it was irrelevant, AND it should be clear from other writings that I accept an old earth. If it's not clear to you, then let me say it here: I ACCEPT AN OLD EARTH. I gave no firm dates for Adam because at that time we still didn't have a model working to test the possibility. NOTE: the articles in the TE book were submitted long before any of this discussion had happened.

@agauger

I thank you for your clarifying details. Timelines are certainly important in the development of your views.

But I do struggle with just one point: You say you accept Old Earth. I must assume that your acceptance of an Old Earth is part of what came **after** you submitted your chapters in the TE book. Otherwise, I would have expected that your chapters would reflect Old Earth views, and that your submissions would not have been included in the TE book.

Since you have an "insiders'" view… can you list a few names of any other experts in the I.D. field (other than you or Dr. Behe):

Who are *Definitively* and *Simultaneously*:
1) Old Earthers, where humanity, not just the Earth, was created well before 10,000 years ago;
and
2) that God formed present-day Humanity by influencing the step-by-step genetic progression of a population (or populations) of pre-humans - - who would thus be the legitimate biological ancestors of modern humans.

Let's start things on an easy gradient, Dr. Gauger. Can you confirm that your views currently satisfy both of the points above? If not, which point seems to be the problem?

I worded the two-way criteria above to accomplish a few things at once:
A) To accommodate some of **@Swamidass** 's scenarios, without doing specific harm to evolutionary scenarios.

B) To defeat dodgy equivocations by some who say they are Old Earthers but still insist that humanity came from a single pair 6000 years ago, with evolution not even being a consideration.
C) To satisfy many BioLogos supporters who see no controversy in the idea that God guided evolution.

---

agauger (Ann Gauger) 2018-03-02 21:59:13 UTC #782

@Chris_Falter

http://bio-complexity.org/ojs/index.php/main/issue/view/30 This lists both papers, with links.
Ola Hössjer, Ann Gauger, and Colin Reeves are the authors.

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agauger (Ann Gauger) 2018-03-02 22:47:50 UTC #783

> gbrooks9:
>
> But I do struggle with just one point: You say you accept Old Earth. I must assume that your acceptance of an Old Earth is part of what came after you submitted your chapters in the TE book. Otherwise, I would have expected that your chapters would reflect Old Earth views, and that your submissions would not have been included in the TE book.

> gbrooks9:
>
> Old Earthers, where humanity, not just the Earth, was created well before 10,000 years ago;

@gbrooks
I think you have several things run together which need to be separate. *It is possible to hold that the earth is old, and not have a position on the age of humanity.* There is a great deal of evidence that the earth is old, which I accept, and disputed evidence about when humans first appeared and whether common descent is true. Those last two are what I am working on.

My chapters do not discuss old earth views. Neither do they propose a young earth. Casey Luskin's discussion of fossils clearly does. And not discussing something does not indicate disagreement with it.

Concerning the opinions of other ID supporters, I can't answer because I don't know. I haven't taken a poll. Some may be on the fence, some may be on either side of the fence. And I said, you need to separate your categories.

I am glad that many Biologos supporters believe that God guided evolution. I guess the question that might distinguish my position from theirs is whether we can detect that guidance.

> gbrooks9:
>
> 1. Old Earthers, where humanity, not just the Earth, was created well before 10,000 years ago; and
> 2. that God formed present-day Humanity by influencing the step-by-step genetic progression of a population (or populations) of pre-humans - - who would thus be the legitimate biological ancestors of modern humans.

1. I don't know when humanity was created. I am still waiting on the results of our model. I favor an older origin but don't consider it settled yet.
2. I can't affirm 2. I don't affirm common descent, at least where humans are concerned. I am open to evidence.

> gbrooks9:
>
> I must assume that your acceptance of an Old Earth is part of what came after you submitted your chapters in the TE book.

No. I was old earth from the beginning. I don't know why you think otherwise.

---

agauger (Ann Gauger) 2018-03-02 23:12:00 UTC #784

@AMWolfe

Thanks for your response. Admittedly I am basing my evaluation on a book by Tom Wolfe 🙂
and I am not a linguist. However, I discount Everett's story for this reason:
He challenged Chomsky on one particular grammatical feature that Chomsky said was universal, by saying that the tribe he worked with did not have this feature in their language. Fair enough, but tribe members who moved to locations where they had to learn other languages picked up that grammatical feature without trouble. So it's not that they lacked the structure in their brain, just that it wasn't being used until necessary.

Everett does have his supporters. The article concerning *Homo erectus* and boat building had a favorable quote from Kenneth Laland I believe. He is a member of the group that wants to see an extended synthesis for evolution.

---

agauger (Ann Gauger) 2018-03-03 08:59:30 UTC #785

@gbrooks9

One more thing. After your questions about why I didn't declare myself on the age of the earth in the TE book, I remembered something. The editors decided well before I joined the team to not bring up the age of the earth. This was discussed in Wayne Grudem's intro.

> A. What This Book Is Not About
> This book is not about the age of the earth. We are aware that many sincere Christians hold a "young earth" position (the earth is perhaps 10,000 years old), and many others hold an "old earth" position (the earth is 4.5 billion years old). This book does not take a position on that issue, nor do we discuss it at any point in the book.

So nobody discussed this subject, and that reveals nothing about anybody's position. Certain chapters discussed material that required the use of dates–those chapters used old earth dates.

I understand that you see the YEC position as inimical, and you would like for someone somehow to persuade them of the truth. At least that's how I read what you have written. You think I have not declared my position to avoid offending them. No, I will declare what I see as happening, but not declare what I see as not firmly settled as if it were settled. And BTW, my taking up an old Adam position will not change anybody's mind.

Another thing, it's one thing to propose an idea, and another thing to hang one's hat on it. I have stated my reasons for why I think an old Adam would fit the data best, but that choice depends on which data are emphasized and which are left out. Other choices can be made.

A good deal of science is living in tension with conflicting data, and trying to find a way to explain both sides. I find the science/faith dispute about origins is similar. I know a little, and what I do know I hold very gently, because I can be wrong. There is a great deal more that I do not know, and even more that I don't know I don't know 🙂

BradKramer (Brad Kramer) 2018-03-03 23:33:02 UTC #786

A post was split to a new topic: **Question for Ann Gauger**

A.Suarez's Treatment on a Pope's Formulation for Original Sin's Transmission!

---

glipsnort (Steve Schaffner) 2018-03-03 22:45:39 UTC #787

> Swamidass:
>
> Moreover, even if **@glipsnort** apparently is not with BioLogos. Both of us affirm evolutionary science, and I do not believe he affirms a historical Adam.

That is correct: I do not affirm a historical Adam. That's not really based on scientific considerations – the way I view the Bible operating as scripture doesn't give me any reason to think Adam would have been a historical figure.

---

gbrooks9 (George Brooks) 2018-03-04 02:30:21 UTC #788

> glipsnort:
>
> That is correct: I do not affirm a historical Adam. That's not really based on scientific considerations – the way I view the Bible operating as scripture doesn't give me any reason to think Adam would have been a historical figure.

@glipsnort ,

You don't find some of the scenarios being explored by **@Swamidass** appealing?

The one I like is that God uses special creation to create the Adam and Eve pair, and they shape the course of the entire human race by having their descendants blend into the ancient human lineage(s) that have evolved on Earth . . . not realizing they were prepared for the arrival of Adam and Eve.

---

glipsnort (Steve Schaffner) 2018-03-04 03:21:19 UTC #789

> gbrooks9:
>
> You don't find some of the scenarios being explored by **@Swamidass** appealing?

No. I might find it appealing if I thought the authors of Genesis were intending to talk about a historical figure, and if I thought they had access to information about such a figure. But since I don't believe either of those things, estimating the time of genealogical Adam is of no more interest to me than, say, estimating the date of the first human with blonde hair, or the first human who was lactose tolerant.

Swamidass (Dr. S Joshua Swamidass) 2018-03-04 03:30:14 UTC #790

> glipsnort:
>
> No. I might find it appealing if I thought the authors of Genesis were intending to talk about a historical figure, and if I thought they had access to information about such a figure.

Makes a lot of sense to me why **@glipsnort** does not care.

Our views on a genealogical Adam will be tightly defined by how we read Scripture. I'm fine with that.

Jonathan_Burke (Jon) 2018-03-04 03:32:31 UTC #791

> Swamidass:
>
> You were making a classic ad hominem. You might want to look at the definition. From wiki:

Yes look at the definition.

> Ad hominem (Latin for "to the man" or "to the person"[1]), short for argumentum ad hominem, is a fallacious argumentative strategy whereby **AN ARGUMENT IS REBUTTED** by attacking the character, motive, or other attribute of the person making the argument, or persons associated with the argument, **RATHER THAN ATTACKING THE SUBSTANCE OF THE ARGUMENT ITSELF**. **https://en.wikipedia.org/wiki/Ad_hominem**

I did not make any attacks on Ann's character, motive, or other attribute, and in particular (and most relevant), I did not use any such comments to try and rebut her argument. I did not say "Ann is motivated by her desire for a historical Adam, so her bottleneck argument is wrong", or anything like that. My comments were made specifically about your representation of Ann, not about Ann's argument.

> Swamidass:
>
> Dismissing an argument because of the motives of a person is an ad hominem. Denying it is ad hominem does not make it so.

But I did not dismiss her argument based on her motives. I did not dismiss her argument at all. As I have said, I was addressing your representation of Ann, not Ann's argument.

> Swamidass:
>
> Regardless, she can be wrong on evolution, and right on this. Can she not? And even if she is wrong, can she not be honest too? She could just be honestly wrong.

Yes all of this can be true. But my confidence in the integrity of her approach to scientific data is not improved when she makes comments like this.

1. "there is not enough evolutionary time for all these coordinated changes to have happened by the mutation/selection process"
2. "Thus the evidences for common ancestry put forward by various scientists are not as solid as they might seem"
3. "The more we learn about our human genome, the more it seems to be brilliantly and uniquely designed."
4. "I would say that unless somebody figures out how to go back in time, we will never be able to establish for certain that we arose from an evolutionary process"
5. "I actually believe that we will someday falsify Darwinism, which will be great because then the question arises, "If it didn't happen by a gradual process, how did it happen?""
6. "It used to be said that only two to three percent of our genome coded for protein, and the rest was junk, speaking loosely. Well, the ENCODE project is revealing that this is a complete falsehood"

7. (interview with Ann Gauger) "Regarding a couple of Swawidass's points, Sarah Chaffee asks at one point, "Are those serious arguments?" "**No, they're not**." "Scary arguments?" **You can hear Dr. Gauger suppress a laugh**. "No."

If she is "honestly wrong" in her statements about well known and settled science, then she is unreliable at best, and should be identified as such. If I were to make these statements, especially here on Biologos, I would be called out for scientific ignorance. Given her professional position, and given the influence she has, holding her to at least the same standard of accuracy, is entirely reasonable. Given your aim is to "serve the Church with an honest account of the science, regardless of our personal positions", surely it is reasonable to expect her to do the same.

> Swamidass:
>
> You have not being paying attention then.

You wouldn't accept that kind of dismissive comment if it were aimed at the concerns of someone who is ID or YEC. The fact is I am not the only person who has expressed concern with your approach. Look at this comment.

> Chris_Falter:
>
> Really, Joshua, do you think that is the only value of Dennis' efforts in the book? I get that he made a mistake that needed to be corrected. Is that all that comes out of his writing, in your opinion?

It's clear that you're coming across as rather one sided (to put it mildly), to more than one person. For example, you called out Dennis, saying he "presented a selective account that fit with his personal theological views". But you haven't done the same with Ann.

Christy (Christy Hemphill) 2018-03-04 04:23:01 UTC #792

@Jonathan_Burke
@Swamidass

Please do not have any further public discussion about what is or is not ad hominem. If you really must further adjudicate this particular instance, do it via PM. Thank you. 🙂

---

gbrooks9 (George Brooks) 2018-03-04 04:23:33 UTC #793

> glipsnort:
>
> No. I might find it appealing if I thought the authors of Genesis were intending to talk about a historical figure, and if I thought they had access to information about such a figure. But since I don't believe either of those things, estimating the time of genealogical Adam is of no more interest to me than, say, estimating the date of the first human with blonde hair, or the first human who was lactose tolerant.

But here's the rub, **@glipsnort** , because you don't care, and you reject the whole idea of an historical Adam being **inserted** into the Evolutionary scenario (as per **@Swamidass** constructions)… you are not likely to populate the "bridge" between some YEC and some BioLogos scenarios.

I had been wondering if Prof **@agauger** might serve as a bridge… but she tells me that she pretty much rejects the idea of primates as a common ancestor for the base population of humans.

So she's out of the equation too.

Swamidass (Dr. S Joshua Swamidass) 2018-03-04 04:27:42 UTC #794

> gbrooks9:
>
> I had been wondering if Prof @agauger might serve as a bridge… but she tells me that she pretty much rejects the idea of primates as a common ancestor for the base population of humans.

She said she is not sure about common descent yet.

> gbrooks9:
>
> But here's the rub, @glipsnort , because you don't care, and you reject the whole idea of an historical Adam being inserted into the Evolutionary scenario (as per @Swamidass constructions)… you are not likely to populate the "bridge" between some YEC and some BioLogos scenarios.

Not so. @glipsnort is important because he has been consistently honest about the data, and not overstated it.

---

gbrooks9 (George Brooks) 2018-03-04 04:37:36 UTC #795

> Swamidass:
>
> Not so. @glipsnort is important because he has been consistently honest about the data, and not overstated it.

Hey, @Swamidass , **we are all important.**

My comments were specifically addressing the service of "bridging"… not "anchoring".
I don't think @glipsnort will be bothered by this …

Swamidass (Dr. S Joshua Swamidass) 2018-03-06 21:52:34 UTC #796

Don't miss this piece by @agauger .

https://evolutionnews.org/2018/03/is-there-a-first-human-couple-in-our-past-new-evidence-and-arguments/

Overall, I think she did a good job.

> Then two new scientists entered the debate with Venema and Buggs. Remarkably, neither is an ID advocate, both affirm evolutionary theory, and both came to similar conclusions by different routes. A population geneticist named Dr. Steve Schaffner of the Broad Institute in Cambridge, Massachusetts, ran a simulation to determine whether a bottleneck of two individuals was possible. He found that, at dates older than 500,000 years ago, a bottleneck could not be ruled out. His analysis of allele frequencies could not distinguish between allele frequencies obtained after a bottleneck of two and those from current genetic data. Dr. Joshua Swamidass, assistant professor in the Department of Pathology and Immunology at Washington University in St. Louis, estimated the time to the most recent four alleles in the genome. An allele is a version of a gene. We all carry two copies of each gene (setting sex chromosomes aside), so a bottleneck of two individuals would have a maximum of four alleles per gene. His analysis likewise showed that the most recent time at which a bottleneck of two individuals, or four alleles, could

> have occurred was about 500,000 years ago. Both researchers used experimentally validated mutation rates in their models, and the precise details are worth looking at closely.

RichardBuggs (Richard Buggs) 2018-03-06 21:54:45 UTC #797

Hi Steve **@glipsnort** please could I just doublecheck some details with you? The simulations you ran earlier in this discussion were for:

1. A constant effective population size of 16,384 and a mutation rate (1.6e-8/bp/generation)
2. A constant effective population size of 16,384 then a bottleneck of two **100,000** years ago, with population doubling each generation for 14 generations (350 years) until it reaches a population size of 16,384 after which the population has constant size (mutation rate 1.6e-8/bp/generation)
3. A constant effective population size of 16,384 then a bottleneck of two **250,000** years ago, with population doubling each generation for 14 generations (350 years) until it reaches a population size of 16,384 after which the population has constant size. (mutation rate 1.6e-8/bp/generation)
4. A constant effective population size of 16,384 then a bottleneck of two **500,000** years ago, with population doubling each generation for 14 generations (350 years) until it reaches a population size of 16,384 after which the population has constant size. (mutation rate 1.6e-8/bp/generation)
5. A constant effective population size of 16,384 then a bottleneck of two **1,000,000** years ago, with population doubling each generation for 14 generations (350 years) until it reaches a population size of 16,384 after which the population has constant size. (mutation rate 1.6e-8/bp/generation)
6. A constant effective population size of 16,384 then a bottleneck of two 250,000 years ago, with population doubling each generation for 14 generations (350 years) until it reaches a population size of 16,384 after which the population has constant size. (**mutation rate 2.0 x 10^-8**)
7. A **rapidly expanding effective population size prior to the bottleneck rising to 1.4 million** then a bottleneck of two 250,000 years ago, with population doubling each generation for 14 generations (350 years) until it reaches a population size of 16,384 after which the population has constant size (mutation rate 1.6e-8/bp/generation)
   I think that is what you did, but just wanted to double check with you.
   many thanks
   Richard

Christy (Christy Hemphill) 2018-03-07 02:19:18 UTC #798

Except when you throw in sentences like:

> The 500 thousand year date also does not rule out other dates based on other approaches and different assumptions.

I guarantee a certain percentage of the readership hears "If you don't have atheist evolutionist assumptions about millions and billions of years, it's totally plausible that Adam and Eve could have existed 6,000 years ago. Maybe not totally Ann Gauger's fault, but still unfortunate.

Also, how many of the readers understand that the "we" in this sentence is not homo sapiens?

> It cannot be ruled out between about 500,000 years ago and 7 million years ago, when **we** supposedly split from chimps.

Jonathan_Burke (Jon) 2018-03-07 03:10:52 UTC #799

> Christy:
>
> I guarantee a certain percentage of the readership hears "If you don't have atheist evolutionist assumptions about millions and billions of years, it's totally plausible that Adam and Eve could have existed 6,000 years ago. Maybe not totally Ann Gauger's fault, but still unfortunate.

Exactly. That has been the entire aim all along.

> Christy:
>
> Also, how many of the readers understand that the "we" in this sentence is not homo sapiens?

Yep. And note "supposedly split from chimps", intended to communicate clear denial of common descent.

Christy (Christy Hemphill) 2018-03-07 03:25:17 UTC #800

Also:

"The claim that our population was never smaller than thousands is wrong."

So, "our population" is hominins who lived more than 500,000 years ago? I wonder how many people would agree that counts as "our population"? Plus, is it wrong, or just unprovable? It is true to say there is no evidence that our population was smaller than thousands, correct? Even using that very generous and not intuitive definition of "our population"?

---

gbrooks9 (George Brooks) 2018-03-07 04:38:43 UTC #801

> Swamidass:
>
> Quoted from **@Agauger** 's Article on "First-Human-Couple…"
> Dr. Joshua Swamidass … estimated the time to the most recent four alleles in the [current human] genome. . . . His analysis likewise showed that the most recent time at which a bottleneck of two individuals, or four alleles, could have occurred was about 500,000 years ago.

@Christy and **@Jonathan_Burke**

As the narrative is formulated above, as conveyed to us by **@Swamidass** , it seems pretty emphatic that the studies being discussed permit no Single-Pair Bottleneck at any time **within half a million years of the present**!

This statement seems rather immune to any obfuscating influences caused by pre-human hybridization or any related consideration. No matter what you throw at this paragraph, regardless of the theoretical possibilities, the very best case is no Single-Pair Bottleneck, regardless of any possible extra-sapiens inter-breeding, can be detected any time sooner than 500kya.

This can be stated emphatically, because we are not projecting forward from some kind of sober estimate of what these proto- or quasi-humans genomes might have been like. No. We are taking the modern human genome as it is right now … and casting backwards - - looking for soonest time a Single-Pair bottleneck of all Humanity could have existed - - that would have left some unmistakable signs on our genome.

Don't I have that right? Isn't this a pretty strong conclusion for unhinging the Young Earth Creationists from their fetish for literal interpretations of Genesis.

@Swamidass , thoughts?

Swamidass (Dr. S Joshua Swamidass) 2018-03-07 05:20:15 UTC #802

> gbrooks9:
>
> As the narrative is formulated above, as conveyed to us by @Swamidass , it seems pretty emphatic that the studies being discussed permit no Single-Pair Bottleneck at any time within half a million years of the present!

> gbrooks9:
>
> This statement seems rather immune to any obfuscating influences caused by pre-human hybridization or any related consideration.

I think that @agauger has made some ambiguous statements, but has also made some clear statements. I would take @gbrooks9 's view, that the clear statements are not negated by the ambiguous ones. She is certainly not hiding her position.

> gbrooks9:
>
> Don't I have that right? Isn't this a pretty strong conclusion for unhinging the Young Earth Creationists from their fetish for literal interpretations of Genesis.

Yes on @agauger , but there is no problem with a literal interpretation of Genesis per se. A lot of Christians read the Bible literally and do not believe it teaches a young earth.

Swamidass (Dr. S Joshua Swamidass) 2018-03-11 22:11:56 UTC #803

Brief update for the curious, that I hope @RichardBuggs and @DennisVenema will fill in more completely.

1. Another line of evidence appears to be Neanderthal and Denisovan DNA, which are different enough that they do not look like Homo sapien DNA. But if Adam is ancestor of them, we need to have enough time for his lineage to produce the diversity we see in them too.
2. It appears that probably pushes the plausible CA date back from 500 kya to 700 kya. This is hardly something new, as we have made reference to this a few times. At this point, the error bars are going to range from about 800 kya to 500 kya, and would meaning identifying "human" with more than just Homo sapiens.
3. I posit that an Adam at about 700 kya introduces no more theological questions, and probably less scientific problems, than one at 400 kya. I'm not sure the theological difference between 400 kya vs 700 kya vs 2mya are important; they are broadly very similar.
4. I think the conclusion (which I hope @RichardBuggs and @DennisVenema will develop) is that it is seems like scientifically solid ground to wonder about an Adam at 700 kya.
5. To those intent on disapproving a bottleneck, we do not expect this to be overturned without a total revolution of our understanding of HLA sequences and trans-species variation (not likely happening soon).
6. To those intent on proving a bottleneck, it appears that this just places a bottleneck outside our view, beyond the horizon of genetic data. I'm not sure how demonstrating a bottleneck back that far could be possible. Though, you are welcome to try. Even if it were possible, that is still a long way off from unsettling common descent, or

from demonstrating that the bottleneck was the Adam and Eve of Scripture. Those claims are likely well beyond science.

7. So, reaching the limits of the scientific account, it might be good to encourage diversity in our views on Adam.

This still needs to be fleshed out. For those of you who can, we will be covering this all in detail at the ASA conference. I'm doing a workshop on the "**Reworking the Science of Adam and Eve"**, and I hope you can join us. **http://network.asa3.org/mpage/ASA2018 Friday, July 27th, 2018, 2pm to 5pm at the ASA Conference in Gordon College, Boston.**

At this time, I'd be curious to hear comment from **@Paul_Nelson** , whom I know is following this conversation closely.

---

gbrooks9 (George Brooks) 2018-03-11 23:03:28 UTC #804

> Swamidass:
>
> Another line of evidence appears to be Neanderthal and Denisovan DNA, which are different enough that they do not look like Homo sapien DNA. But if Adam is ancestor of them, we need to have enough time for his lineage to produce the diversity we see in them too.

@Swamidass ,

This is one of those areas I do not think you will prosper in. Let someone else carry the water for the Neanderthal and Denisovan. They are clearly on the "non-Adam" side, right?

So let the Neanderthal and Denisovan compete with the attention of the newly evolved and arrived Sapiens … and by the time of Adam's special creation in 4000 BCE, all the genetic oddities have been played out.

I feel you need to keep your time frame for Adam at 4000 BCE. You will win no friends moving off of that period… and it allows plenty of time to become a Universal Ancestral pair by the time Jesus arrives.

As you can see, from this perspective, Neanderthal and Denisovan as issues will have been completely finished up by 4000 BCE.

---

gbrooks9 (George Brooks) 2018-03-11 23:04:30 UTC #805

> Swamidass:
>
> I posit that an Adam at about 700 kya introduces no more theological questions, and probably less scientific problems, than one at 400 kya. I'm not sure the theological difference between 400 kya vs 700 kya vs 2mya are important; they are broadly very similar.

@Swamidass

Okay … who is it that you think is clamoring for the Special Creation of Adam at either 700,000 or 400,000 years ago? It's not the YECs, right? So who?

Swamidass (Dr. S Joshua Swamidass) 2018-03-11 23:49:39 UTC #806

> gbrooks9:

> Okay … who is it that you think is clamoring for the Special Creation of Adam at either 700,000 or 400,000 years ago? It's not the YECs, right? So who?

I think is **@agauger** and **@RichardBuggs** and any other Christian more uncomfortable with people outside the garden then losing the Genesis timeline. Obvious, right?

Personally, I like the diversity but am more drawn to a recent genealogical Adam.

---

gbrooks9 (George Brooks) 2018-03-12 00:04:24 UTC #807

> Swamidass:
>
> Personally, I like the diversity but am more drawn to a recent genealogical Adam.

@Swamidass ,

I think anyone who opposes Common Descent **and** wants you to defend a 400,000 year old Adam is just trying to "sink" the entire work. There's nothing about a 400,000 year old Special Creation of Adam that makes a lick of sense. It just makes things more difficult all the way around.

If you are going to have a special creation, you might as well have it at 4000 BCE.

Why would a scientist argue that it is more scientific for Special Creation to have happened 400,000 or more years ago? That wouldn't fit anything. It wouldn't fit the physical evidence **nor** the Biblical assertions. it's pretty much guaranteed to discredit both your science and your biblical interpretation.

Shake that dust off of you, doctor … if someone wants that scenario badly enough, let them make sense of it on their own.

Swamidass (Dr. S Joshua Swamidass) 2018-03-12 03:24:02 UTC #808

> gbrooks9:
>
> Shake that dust off of you, doctor … if someone wants that scenario badly enough, let them make sense of it on their own.

I'm just trying to serve the Church with an accurate account of the science. There is value in this scientifically and theologically. It serves the common good.

If helping them make sense of it is received as a work of peace, this serves the common good too.

Though I do agree with you…

> gbrooks9:
>
> If you are going to have a special creation, you might as well have it at 4000 BCE.

There appear to be problems introduced by a sole-genetic origin from a de novo Adam that a genealogical Adam avoids. **@agauger** , however, is undecided on common descent. So maybe de novo creation is not critical for her.

T.j_Runyon (T J Runyon) 2018-03-12 05:48:28 UTC #809

I've been trying to find something to do this summer. Maybe that's what I'll do!

RichardBuggs (Richard Buggs) 2018-03-13 18:27:26 UTC #810

Hi all,

> DennisVenema:
>
> I've been working with Charles Cole - the person that **@RichardBuggs** cited regarding PSMC modelling - to use PSMC models to directly test Richard's hypothesis as best we can. Charles has been busy, I've been busy, the modelling wasn't straightforward, and it'll be a bit yet before I've got it together. I'll probably invite **@Swamidass** and **@RichardBuggs** to look over the data before putting the post up so we can perhaps put our heads together on it. I'm hoping Cole will also join us here for that discussion. It should be interesting. Intuitively, one would think that PSMC modelling should see something if Ne went to 2 - but testing is better than intuition.

Just for completeness I would like to note that Dennis has shared Charles Cole's new analyses with me, **@Swamidass** and **@glipsnort** in a private forum back in February. These analyses do not demonstrate that PSMC could detect a bottleneck of two followed by rapid population growth. Rather, they add evidence that this method could not detect such a bottleneck. I am not sure if Dennis is still intending to share these analyses here on the public forum or not.

My understanding is that **@DennisVenema** now agrees that PSMC estimates of past effective population sizes could not detect a bottleneck of two followed by rapid population growth.

---

gbrooks9 (George Brooks) 2018-03-14 19:07:36 UTC #811

> RichardBuggs:
>
> My understanding is that **@DennisVenema** now agrees that PSMC estimates of past effective population sizes could not detect a bottleneck of two followed by rapid population growth.

@RichardBuggs

Meaning, it did not have the capacity ? Or that it does, and it found no evidence for such?

RichardBuggs (Richard Buggs) 2018-03-15 22:08:14 UTC #812

Of possible interest:

> **Advances in human behaviour came surprisingly early in Stone Age**
>
> Excavations in Kenya suggest improvements in stone tools and other human changes are linked to variations in climate.

"Evidence collected at sites in the basin suggests that early humans underwent a series of profound changes at some point before roughly 320,000 years ago. They abandoned simple hand axes in favour of smaller and more advanced blades made from obsidian and other materials obtained from distant sources. That shift suggests the early people living there had developed a trade network — evidence of growing sophistication in behaviour. The researchers also

found gouges on black and red rocks and minerals, which indicate that early Olorgesailie residents used those materials to create pigments and possibly communicate ideas…The team cannot say exactly how long before 320,000 years these changes happened because an extended period of erosion at the site wiped out the archaeological record there between 499,000 and 320,000 years ago.”

RichardBuggs (Richard Buggs) 2018-03-15 22:11:33 UTC #813

It does not have the capacity. Thanks for asking for clarification. This is my understanding of **@DennisVenema** ’s view. I am sure he will provide an update on his own views soon, as I may be an imperfect messenger.

T_aquaticus 2018-03-15 22:17:02 UTC #814

Sorry, couldn’t help it.

---

gbrooks9 (George Brooks) 2018-03-17 00:51:27 UTC #815

@RichardBuggs

Thanks for the link to that article!

> RichardBuggs:

> Of possible interest:
> **https://www.nature.com/articles/d41586-018-03244-y**

Great final two paragraphs…

Some information could come from several projects that drilled into ancient lake beds in Kenya and Ethiopia to collect a detailed record of environmental and ecological changes in the region6. Potts and his team drilled two of those cores in the southern Olorgaseilie Basin, and Potts says the cores cover the entire period that is missing from the archaeological record. Comparisons with cores drilled elsewhere in East Africa should help scientists to differentiate between events happening locally and broader regional climatic trends.

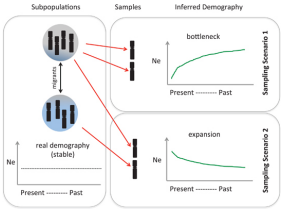
“The drill cores I hope will be a game changer, because of the precision of the environmental record and hopefully the precision of the dating,” Potts says. Then it’s a matter of working to understand how animals and people might have responded to the changing environment, Potts says. “Only then can we say anything about how climate is really affecting human evolution.”

Swamidass (Dr. S Joshua Swamidass) 2018-03-17 20:26:23 UTC #816

d[quote=“RichardBuggs, post:813, topic:37039, full:true”]
It does not have the capacity. Thanks for asking for clarification. This is my understanding of **@DennisVenema** ’s view. I am sure he will provide an update on his own views soon, as I may be an imperfect messenger.
[/quote]

That is my understanding of the evidence, and also my understanding of how **@DennisVenema** sees it.

This post is important to go over:



Opening Pandora’s box: PSMC and population structure

Essentially, all models are wrong, but some are useful. — George Box Publication of the Li and Durbin’s 2011 paper titled “Inference of human population history from individual whole-genome sequenc…

> However, PSMC has several considerable limitations that should be kept in mind.
>
> 1. **It doesn’t recover sudden changes in Ne**
> 2. Nor does it recover recent changes, e.g. younger than 10,000 years BP in humans (Li and Durbin 2011).
> 3. Simulation suggest that **it also performs worse in case of very ancient changes in Ne** (Mazet et al. 2015).
> 4. Using incorrect mutation rate or generation time can cause bias in the interpretation.
> 5. The change in Ne in a PSMC plot can be actually caused by population structure.

Another must read paper is here, Mazet et al 2016

On the importance of being structured: instantaneous coalescence rates and human evolution--lessons for ancestral population size inference?

O Mazet, W Rodríguez, S Grusea, S Boitard and L Chikhi, *Heredity*, Apr 2016

> Most species are structured and influenced by processes that either increased or reduced gene flow between populations. However, most population genetic inference methods assume panmixia and reconstruct a history characterized by population size changes. This is potentially problematic as population structure can generate spurious signals of population size change through time. Moreover, when the model assumed for demographic inference is misspecified, genomic data will likely increase the precision of misleading if not meaningless parameters. For instance, if data were generated under an n-island model (characterized by the number of islands and migrants exchanged) inference based on a model of population size change would produce precise estimates of a bottleneck that would be meaningless. In addition, archaeological or climatic events around the bottleneck's timing might provide a reasonable but potentially misleading scenario. In a context of model uncertainty (panmixia versus structure) genomic data may thus not necessarily lead to improved statistical inference. We consider two haploid genomes and develop a theory that explains why any demographic model with structure will necessarily be interpreted as a series of changes in population size by inference methods ignoring structure. We formalize a parameter, the inverse instantaneous coalescence rate, and show that it is equivalent to a population size only in panmictic models, and is mostly misleading for structured models. We argue that this issue affects all population genetics methods ignoring population structure which may thus infer population size changes that never took place. We apply our approach to human genomic data.

Jon_Garvey (Jon Garvey) 2018-03-18 08:35:14 UTC #817

Very relevant, Joshua. The problem with models of the distant past is partly, as these articles relate, the possible problems we know that we know - like possible changes in mutation rate.

But models in the real world are potentially - and often actually - falsified by actual failed outcomes: the medical intervention one models doesn't *actually* alter the death rate, so you go back, invstigate, and find factors you didn't include in the model.

One very tragic and graphic example - we're told that the accelerated building technique for the bridge at Florida International University hadn't been used before. But you can bet it was extensively modelled, and found good. But something was missed in the model - as in many other engineering examples. Only reality cruelly uncovers the flaws in the modelling.

In the end, for the past population of humanity we wouldn't *need* a population genetics model if we had sufficient information about the deep past to validate it. And it's vanishingly unlikely that the fossil record contains enough information for us ever to be able to correct any unknown problems with the models from actual data.

"All models are wrong, but some are useful." That's very true, but we must always remember what it means: models show us what kind of data to look for in the real world: their *usefulness* is entirely about their match to reality. Internal consistency is satisfying to the modeler, but not "useful".

Chris_Falter (Chris Falter) 2018-03-19 16:26:08 UTC #818

Hi Jon,

Hope things are going well on your side of the pond.

When scientists build a model well, they use statistical terminology to define how much uncertainty needs to be acknowledged. Joshua **@Swamidass** has done a good job of this IMO, and stated IIRC that the TMR4A is 500kya ± 100k.

Do you have any reason to dispute the boundaries of the cone of uncertainty that **@Swamidass** has placed around his model? If so, how would you quantify the uncertainty so we appreciate it better?

Thanks,
Chris

Jon_Garvey (Jon Garvey) 2018-03-19 17:08:03 UTC #819

Chris, it's snowy here, but we should be able to burst out to the outside world tomorrow.

My point was, essentially, about things we don't know that we don't know. That can be checked on a bridge by building a bridge, or on model for widget marketing by marketing widgets.

But factors operating half a million years ago, on an unknown number of individuals in an unknown geographic distribution and even an unknown number of species or subspecies, and with the mechanisms of speciation not fully understood are potentially legion.

If you have a way of quantifying what one doesn't know that one doesn't know, you're a better clairvoyant than I am!

---

gbrooks9 (George Brooks) 2018-03-19 18:18:58 UTC #820

> Jon_Garvey:
>
> "All models are wrong, but some are useful." That's very true, but we must always remember what it means: models show us what kind of data to look for in the real world: their usefulness is entirely about their match to reality. Internal consistency is satisfying to the modeler, but not "useful".

@Jon_Garvey

Fortunately for **@DennisVenema** , his methodology is more secure in the first 25,000 years than at any other time.

Chris_Falter (Chris Falter) 2018-03-19 23:59:18 UTC #821

Hi Jon, Now I understand why England athletes excelled at the winter games!

> Jon_Garvey:
>
> If you have a way of quantifying what one doesn't know that one doesn't know, you're a better clairvoyant than I am!

Based on my reading of the scientists' discussion, I think they have been able to quantify the impact of the unknowns you cite.

As for the unknown unknowns, I leave the last word to my invisible Martian friend, ÷=/_<>××:

> *//=x>[÷÷_</=÷x66==÷<>>*

Very compelling, ÷=//_<>××! Thanks for sharing your perspective!

Jon_Garvey (Jon Garvey) 2018-03-20 08:09:45 UTC #822

Ah - “Statistical Analyses are the assurance of things hoped for, the conviction of things not seen.” (Heb 11:1, American Scientistic Version)

> “The epidemiologist fallacy is also richer than the ecological: it occurs whenever an epidemiologist says, “X causes Y” but where he never measures X *and* where he uses classical statistics to claim proof of a cause - based on, say, wee *p*-values or large Bayes factors; [citation]. Over-certainty is guaranteed.” (William Briggs)

X, in this case, is the original ancestral population that gives rise to the population we have now, which we are trying to ascertain and which we *cannot* measure, even if we want to. If we really *can*, through models alone, allow for all the factors that we don’t know we don’t know, then science is back to the Greek model, where reason replaces empirical examination of the world.

Unknown Martians are an unlikely factor here, in my humble view. But unknown biological mechanisms, and unknown historical contingencies, are not only likely but turn up every year - what do we know now from actual data about the radiation of humanity that we did not know this time last year? Wasn’t “Out of Africa” not long ago an uncomplicated and more or less uncontested understanding of where we came from?

One possible confounding factor for this particular discussion, as regards the final truth of the matter, is the ultimate point at issue (correctly excluded by Richard for the scientific discussion) - a *known* God who, according to many following the traditional understanding of the Scriptures, created the first humans as a single couple *de novo*.

I have no dog in the fight - I don’t believe an Adam >200K years ago is consistent with Genesis. But I do know that once one has done the excellent modelling that Joshua, in particular, has worked on, then what one has achieved is a fuller exploration of the model(s) currently in use, and a bigger range of possibilities than was previously thought - but by no means a certainty about the deep past on which to stake your life.

Or even a reliable quantification of what surprises the world may have for you.

Jonathan_Burke (Jon) 2018-03-20 09:50:59 UTC #823

> Jon_Garvey:
>
> If we really can, through models alone, allow for all the factors that we don’t know we don’t know, then science is back to the Greek model, where reason replaces empirical examination of the world.

Let me guess, you also dispute anthropogenic climate change.

Jon_Garvey (Jon Garvey) 2018-03-20 10:35:39 UTC #824

> Jonathan_Burke:
>
> Let me guess, you also dispute anthropogenic climate change.

Guess wrong. The forecasts of climate change can be tested by direct data… not that I’ve checked the records on how they’re doing currently.

Jonathan_Burke (Jon) 2018-03-20 10:49:17 UTC #825

What happened to all the things that we don’t know that we don’t know?

Jon_Garvey (Jon Garvey) 2018-03-20 11:15:42 UTC #826

Jon

I think you missed the point. When real-world data defy the predictions, the model is proven wrong. If the data is unavailable, as it is for the deep past, the agreement of as many independent models as you like does not “prove” a single one of them. They may only suggest probabilities - but the real world’s certainties have a habit of overturning assessments of probability.

I don’t know what your own working experience is in science, but I spent my entire career in clinical medicine. Every intervention was based on models built, to speak crudely, from applying current theory to available data to determine beneficial outcomes. That applied to therapeutics, surgical procedures, epidemiology, or anything else.

Over four decades, I saw possibly a majority of those models falsified, invariably when someone got round to looking more closely at the real-world outcomes. Sometimes that just meant factoring in new variables to tweak the model, but often it meant an entire reversal of previous “evidence-based” practice. That’s no criticism of my profession - except when it was so certain of the models that nobody bothered to test them against reality, of which I could name many examples. In every case you can go and look up the research on which those faulty models were built, and why they were wrong - in retrospect.

Ask any old doctor, and they will agree that, new drugs etc aside, it’s only because people’s bodies are so resilient that we got away with much of what we did in the 1970s.

Ten years after retirement, when I speak to my colleagues it’s clear that, if I returned to work, much of the advice or treatment I gave would have become outmoded: but only by the replacement of the models were were using back then by new ones based on data from the real world forcing a change of theory and, hence, a different model.

Your experience of science may be more ideal - in my world it is messy and provisional.

Jonathan_Burke (Jon) 2018-03-20 11:29:26 UTC #827

> Jon_Garvey:
>
> If the data is unavailable, as it is for the deep past…

In this case, what data is unavailable?

Jonathan_Burke (Jon) 2018-03-20 14:21:11 UTC #828

> Jon_Garvey:
>
> Guess wrong. The forecasts of climate change can be tested by direct data… not that I’ve checked the records on how they’re doing currently.

So you would reject the claims of people like Roy Spencer who say the current warming is a natural cycle?

Christy (Christy Hemphill) 2018-03-20 14:24:07 UTC #829

@Jon Garvey’s personal views on climate change aren’t relevant to the discussion. If you two would like to delve into this topic, do it via PM.

Jonathan_Burke (Jon) 2018-03-20 14:54:36 UTC #830

Given the fact that they form part of his argument against the genetic evidence for human evolution ("Models are unreliable; we can't be certain of this genetic information because it's based on an unverifiable model, just like we can't be certain of the arguments for AGW because it's based on an unverifiable model"), as Jon has written publicly elsewhere, I think they are relevant. But ok.

Chris_Falter (Chris Falter) 2018-03-20 15:37:25 UTC #831

Hi Jon,

> Jon_Garvey:
>
> "The epidemiologist fallacy is also richer than the ecological: it occurs whenever an epidemiologist says, "X causes Y" but where he never measures X and where he uses classical statistics to claim proof of a cause - based on, say, wee p-values or large Bayes factors; [citation]. Over-certainty is guaranteed." (William Briggs)

I'm not sure why you think the epidemiologist fallacy applies here: There is no inference of causation from correlation. The model we are discussing simply estimates minimum population size at some point in the past based on current DNA data + knowledge about rates of change in DNA. (**@RichardBuggs** **@Swamidass** **@glipsnort** please correct me as needed.)

Consider this analogy, Jon: If a comet passes near the earth with a certain velocity, astronomers might pull out their slide rules and determine that the comet was in the Van Oort cloud 200,000 years ago. (Or maybe, just maybe, they would use computers.) They would say, "we have data about the current state of the comet and about the rate of change; these allow us to build a model that projects backwards in time."

I would be astonished, simply astonished, if some theologian would enter a discussion about comet trajectories and chastise the astronomers for their overconfidence about the location of the comet 200,000 years ago. And if the theologian would justify his skepticism on the basis of the fact that astronomers are learning more and more about astronomy every year, the astonishment would increase. And if theologian were to further argue that there is a confounding factor of a known God who, according to many following the traditional understanding of the Scriptures, created the earth less than 10,000 years ago, so maybe the comet didn't even exist 200,000 years ago, what would I think?

I would think about the argument between Galileo and Cardinal Bellarmine. It was Bellarmine, after all, who so adamantly argued that Galileo could say what he wanted about celestial mechanics *as long as Galileo declared that the scientific findings were hypothetical*.

The analogy between celestial mechanics and population genetics is sufficiently clear, I think, so I will not belabor the point further.

Have a great day on the eastern side of the pond, Jon!

Chris

Jonathan_Burke (Jon) 2018-03-20 15:57:33 UTC #832

> Chris_Falter:

> I would be astonished, simply astonished, if some theologian would enter a discussion about comet trajectories and chastise the astronomers for their overconfidence about the location of the comet 200,000 years ago. And if the theologian would justify his skepticism on the basis of the fact that astronomers are learning more and more about astronomy every year, the astonishment would increase. And if theologian were to further argue that there is a confounding factor of a known God who, according to many following the traditional understanding of the Scriptures, created the earth less than 10,000 years ago, so maybe the comet didn't even exist 200,000 years ago, what would I think?

What I would think is that I'm hearing people who believe Ken Ham's "You weren't there" argument has some kind of value. Every time I hear "But we can't know about that stuff in the deep past", that's what it sounds like.

Chris_Falter (Chris Falter) 2018-03-20 16:10:11 UTC #833

Hi Jon,

While I was writing a reply to a previous message, you made a very interesting post based on your experience as a medical practitioner. This helps me understand your general skepticism about models. However, I do think that your experience in medicine does not apply to hard sciences like physics and population genetics for 3 reasons:

1. The medical field is far, far behind the scientific fields with respect to experimental methods and evidence-based decision making. It has come a long way, to be sure, but it still has a long way to go.

2. Causality is very hard to identify in medicine given the ethical and financial constraints on experimental methods, along with the inherent complexity of human body systems. Of course complexity also exists in population genetics, but the fog is much thinner.

3. The model of determining causality is far more complex than a model that simply determines location in a space over a period of time.

These differences suggest that there are limits on how strongly you can project your personal experience as a physician into the practice of biology.

Best,
Chris

AMWolfe (A.M. Wolfe) 2018-03-20 16:34:58 UTC #834

I'm glad I let *you* say that instead of trying my hand at it. I was thinking along similar lines, but I appreciate the clarity of your particular presentation. Seems to me there was a false equivalence here.

Jon_Garvey (Jon Garvey) 2018-03-20 17:01:02 UTC #836

> Chris_Falter:
>
> Of course complexity also exists in population genetics, but the fog is much thinner.

Chris. I think you understate the complexity of human origin vis a vis medicine: in both cases we are dealing with multifactorial biological processes, of which we have limited (though increasing) knowledge. Or at the very least, population genetics is a lot closer to medicine than it is to calculating the past orbits of comets (though that itself is surprisingly inexact, if one looks at the actual v predicted times of Halley's comet's appearance over the centuries).

The specific factor to which Joshua himself referred was the uncertainty of mutation rates under the different circumstances operating back then - that was a known unknown, I suppose like the perturbations of Halley's comet's orbit. Some more known - but currently incalculable - unknowns, which also came up in the discussion, are the interactions between the various possible ancestor groups - sapiens, neanderthalis, erectus, at the projected times of the proposed bottlenecks, before and since. Hybridisation events large or small, or other as yet unknown changes around speciation: All decrease certainty.

In the context of the enquiry, that could either change the time of a small bottleneck, or make it more likely, or blow the idea out of the water altogether. All of those would be matters of indifference to me - but the only way to know whether our current "error bars" were correct is by comparison with the real world, just as in the case of projections for Halley's comet back in time - to quote the infallible Wikipedia:

> Researchers in 1981 attempting to calculate the past orbits of Halley by numerical integration starting from accurate observations in the seventeenth and eighteenth centuries could not produce accurate results further back than 837 due to a close approach to Earth in that year. It was necessary to use ancient Chinese comet observations to constrain their calculations.

Even in that simple case of Newtonian gravity, the model was stymied by reality.

Your interfering theologian is not really relevant to the case: this thread *was* a discussion of the science, but on a science-faith site, in which the bigger debate that prompted it is with those who say, on biblical grounds rather stronger than the position of an unnamed comet, that the first humans were a specially created pair. They do have a dog in the fight.

But my point was simply the scientific one that models depend on theories which are often modified by reality - and so the models need to be calibrated by the reality in which they are employed.I'm not sure why that raises any hackles.

Jonathan_Burke (Jon) 2018-03-21 02:55:43 UTC #837

> Jon_Garvey:
>
> But my point was simply the scientific one that models depend on theories which are often modified by reality - and so the models need to be calibrated by the reality in which they are employed.I'm not sure why that raises any hackles.

That didn't raise any hackles. What raised hackles was your unsubstantiated claims about the reliability of specific models, based on nothing more than a version of "You weren't there".

---

gbrooks9 (George Brooks) 2018-03-21 06:49:21 UTC #838

> Jon_Garvey:
>
> Researchers in 1981 attempting to calculate the past orbits of Halley by numerical integration starting from accurate observations in the seventeenth and eighteenth centuries could not produce accurate results further back than 837 due to a close approach to Earth in that year. It was necessary to use ancient Chinese comet observations to constrain their calculations.
>
> Even in that simple case of Newtonian gravity, the model was stymied by reality.

@Jon_Garvey

The example of the comet is a study in the butterfly effect … not an invalidation of the scientific method.

The butterfly effect does not reduce the age of the Earth from 4+ billion years down to 10,000 years… nor does it explain why we have meat from mammoths that is less than 40,000 years old, but not from dinosaurs that are supposed to have drowned 4000 years ago.

Swamidass (Dr. S Joshua Swamidass) 2018-03-22 20:45:42 UTC #839

> Jon_Garvey:
>
> I think you missed the point. When real-world data defy the predictions, the model is proven wrong. If the data is unavailable, as it is for the deep past, the agreement of as many independent models as you like does not “prove” a single one of them. They may only suggest probabilities - but the real world’s certainties have a habit of overturning assessments of probability.

@Jon_Garvey I saw your post on this on your blog: **http://potiphar.jongarvey.co.uk/2018/03/21/do-not-touch-my-anointed/**

The irony here is thick. Both you and @Chris_Falter ***agree*** with the overall conclusions that a recent sole-genetic progenitor is not likely. It seems you both agree with the conclusions I’ve drawn from the data. However the debate continues in an unclear way about our epistemological certainty about this.

I think there is some confusion about how science reasoning works in conjunction with modeling in this area.

The way I see the situation, is that there is data we have collected about human variation. There is, at this time, a wide range of models proposed to account for that data. However, there is not a single model proposed that can account for the data with a single couple origin less than 200 kya, without either (1) inferring ongoing miracles, (2) totally different biology for Adam and Eve (e.g. genetic mosaics), or (3) mutation rates an order of magnitude (or more) higher than we have ever observed in humans.

That is why, based on our current knowledge, we are calling this evidence against a recent bottleneck. Until a model with a shorter time frame is put forward and tested, this is what we think the data is showing us. For those that disagree, they are welcome to put forward a model of their own to test, but failing that there is not really much to dispute.

Generically calling the conclusions into question is not helpful. The best way to unseat the conclusions is to produce a model that accounts for the data in a shorter time span.

However, I think I understand @Jon_Garvey ’s motivation. We do not want to state these claims with too much certainty, as we have just seen a large shift in our understanding here. I’d point, again, to my invitational epistemology as a solution to this paradox. I’ve already pointed out three ways a more recent bottleneck ***might*** be possible:

1. Adam and Eve had totally different biology than us (e.g. genetic mosaics)
2. Ongoing miracles that diversify us more than is possible by natural processes alone.
3. Much higher mutation rates in the distant past than we can imagine or observe in humans (perhaps miraculously?)

All these options require deus ex machina miracles, not attested to in Scripture. So we do not consider them in scientific analysis, even if they could be true. We do however invite all who dispute these findings to propose models of their own to make sense of that data. Until a model is produced that can made sense of the data with a recent bottleneck and no miracles, we are justified in saying: **the data just looks like we do not have a single couple bottleneck before about 500 kya.**

That is the plain reading of human genomes.

Others can dispute those findings, but they better come with a plausible and alternate model with at least as much mathematical rigour as we have done here. Generically casting doubt on the whole exercise does not move us forward. That is not how our understanding progresses.

Argon 2018-03-22 20:55:38 UTC #840

I suspect that a significant burst in the human mutation rates might be noticed in other comparative studies of genetic divergence.

---

jpm (Phil) 2018-03-22 22:10:48 UTC #841

Thank you for such a clear and concise summary of what is a difficult but interesting post for those of us not that familiar with the methods and issues involved.

Swamidass (Dr. S Joshua Swamidass) 2018-03-22 22:21:45 UTC #842

> jpm:
>
> Thank you for such a clear and concise summary of what is a difficult but interesting post for those of us not that familiar with the methods and issues involved.

I just published an article summarizing the current status of the conversation, that might be of interest too.

Reworking the Science of Adam - Peaceful Science

This last year, 2017 till now, we have been Reworking the Science of Adam. This brings us several new ways to think about Adam and Eve in human origins.

Hopefully that is helpful.

---

gbrooks9 (George Brooks) 2018-03-22 22:58:44 UTC #843

> Swamidass:
>
> **The way I see the situation, is that there is data we have collected about human variation. There is, at this time, a wide range of models proposed to account for that data. However, there is not a single model proposed that can account for the data with a single couple origin less than 200 kya, without either**
>
> **(1) inferring ongoing miracles,**
> **(2) totally different biology for Adam and Eve (e.g. genetic mosaics), or**
> **(3) mutation rates an order of magnitude (or more) higher than we have ever observed in humans.**
>
> **That is why, based on our current knowledge, we are calling this evidence against a recent bottleneck. Until a model with a shorter time frame is put forward and tested, this is what we think the data is showing us. For those that disagree, they are welcome to put forward a model of their own to test, but failing that there is not really much to dispute.**

Beautiful summation, @Swamidass !!!

Peter_Wolfe (Peter Wolfe) 2018-03-23 13:38:11 UTC #844

Link not working for me.

Swamidass (Dr. S Joshua Swamidass) 2018-03-23 14:02:04 UTC #845

> Peter_Wolfe:
>
> Link not working for me.

Give it another shot:

Reworking the Science of Adam - Peaceful Science

This last year, 2017 till now, we have been Reworking the Science of Adam. This brings us several new ways to think about Adam and Eve in human origins.

T_aquaticus 2018-03-23 22:05:09 UTC #846

> Swamidass:
>
> However the debate continues in an unclear way about our epistemological certainty about this.

Even that debate is a bit silly when we get down to it. Are we really sure, or are we really, really sure? It's like arguing over the Sun being hot, or really hot, and at the same time trying to deal with another claim that the Sun is actually a ball of ice.

Perhaps the surest conclusion we can make is that there is no scientifically defensible justification for thinking that the data supports the hypothesis of the human lineage winnowing down to two people within the time period covered by the data, models, and tools that we currently have.

Peter_Wolfe (Peter Wolfe) 2018-03-23 22:44:09 UTC #847

👍 works now thanks

Swamidass (Dr. S Joshua Swamidass) 2018-03-24 15:24:47 UTC #848

> T_aquaticus:

> Perhaps the surest conclusion we can make is that there is no scientifically defensible justification for thinking that the data supports the hypothesis of the human lineage winnowing down to two people within the time period covered by the data, models, and tools that we currently have.

I do not think that is the case. It would be better say there is no scientifically justifiable interpretation of the data, ***that we know of***, that has a single couple bottleneck. Of course, if such a model is forthcoming, that would change.

> T_aquaticus:
>
> Even that debate is a bit silly when we get down to it. Are we really sure, or are we really, really sure? It's like arguing over the Sun being hot, or really hot, and at the same time trying to deal with another claim that the Sun is actually a ball of ice.

There is a meaningful reason why it arises. I think this why **@Jon_Garvey** is raising the point.

For a long time, people have presented evidence against a bottleneck ***ever*** in our lineage as a settled finding of population genetics. However, it is not a settled finding, as we have just unsettled it. However, for a long time, questions have been silenced because of the total certainty of that finding. Yet it was wrong.

So how do we avoid that mistake again? I think that is a valid question. I think **@Jon_Garvey** is arguing that we should hold model's loosely, and I agree. The data trumps our conclusions, or at least it should.

I think, however, there is some remaining questions about how constructive dialogue with science could be possible. I've been thinking about that too. I do not think the answer is in generic skepticism. Rather, I think we need some constructive ways of enabling dialogue, and even constructive types of resistance to scientific claims, that can push us all to better knowledge.

Jon_Garvey (Jon Garvey) 2018-03-24 16:33:30 UTC #849

Joshua

The reason I banged on about maintaining healthy uncertainty about even your excellent work in this thread is mainly this: the Christian has another source of information about human origins, which (to put it coarsely, and of course partisanly) is an authoritative eye-witness account from the Holy Spirit. However, like our scientific data its meaning is underdetermined: how are we to relate its teaching to our physical origins?

Each of us who accepts Scripture's authority, and the Church, make our best judgement on interpretation, and even believe we have the Holy Spirit's help. And yet our interpretation must always be held provisionally, with a degree of uncertainty - hoping it will be confirmed or corrected down the line.

If we ignore the uncertainty, and avoid "navel-gazing" by assuming our understanding is the last word, we absolutize our reading of Scripture, and relativize everything else - such as science. That's bigotry.

But the reverse is also true. It's easy to say that the science is as good as it will ever be, and therefore we may as well assume it is true - but that move absolutizes our science, and relativizes Scripture. That's scientism.

So to keep in mind, at all times, that both population genetics and biblical hermeneutics (and whatever other sources of information) are human knowledge, not final truth, we remain open to new insights, which is what I think you are saying in your final sentence.

Jonathan_Burke (Jon) 2018-03-24 18:54:51 UTC #850

> Jon_Garvey:
>
> the Christian has another source of information about human origins, which (to put it coarsely, and of course partisanly) is an authoritative eye-witness account from the Holy Spirit.

Now where have I heard that **before**?

> The point is, the only way we can know for sure how the universe and life were formed is if an infallible eyewitness revealed to us what happened.

> When teaching children, we tell them they should politely ask the question “Were you there?” when talking to someone who believes in millions of years and molecules-to-man evolution. If someone replies by asking the same question, as you have done, we say, “No we weren’t there, but we know Someone who was there, Someone who cannot lie, who knows everything, and has always existed. And this One has revealed to us what happened in the past in His history book called the Bible. Are you interested in reading God’s history book to find out what the Word of One who was there tells us about the true history of the world?”

---

gbrooks9 (George Brooks) 2018-03-25 00:51:06 UTC #851

> Swamidass:
>
> For a long time, people have presented evidence against a bottleneck ever in our lineage as a settled finding of population genetics. However, it is not a settled finding, as we have just unsettled it. However, for a long time, questions have been silenced because of the total certainty of that finding. Yet it was wrong.

@Swamidass ,

It was wrong? Aren’t you quibbling a bit here?

As far as I can tell, for “presenting evidence against a bottleneck ever in our lineage as a settled finding” to be wrong, somebody has to show that evidence that there is evidence **for** a single mating pair bottleneck.

Didn’t we only prove that there could be a bottle neck far enough back that it can’t be detected? And isn’t “far enough back” well beyond the 6000 year range?

So, I would think you should be more “wordy” about what we have proved or not proved. I think we have quite clearly showed that there cannot be a single pair bottleneck within a 10,000 year time frame - - don’t you agree?

Swamidass (Dr. S Joshua Swamidass) 2018-03-25 01:11:52 UTC #852

> gbrooks9:
>
> It was wrong? Aren’t you quibbling a bit here?
>
> As far as I can tell, for “presenting evidence against a bottleneck ever in our lineage as a settled finding” to be wrong, somebody has to show that evidence that there is evidence for a single mating pair bottleneck.

> Didn't we only prove that there could be a bottle neck far enough back that it can't be detected? And isn't "far enough back" well beyond the 6000 year range?
>
> So, I would think you should be more "wordy" about what we have proved or not proved. I think we have quite clearly showed that there cannot be a single pair bottleneck within a 10,000 year time frame - - don't you agree?

The claim that was wrong was that there is solid evidence against a bottleneck of 2 in our lineage, including the time between now and when we diverge from chimps. Some have even argued the evidence goes back 13 million years. That claim about what the evidence showed us was false. It was overstated.

> gbrooks9:
>
> So, I would think you should be more "wordy" about what we have proved or not proved. I think we have quite clearly showed that there cannot be a single pair bottleneck within a 10,000 year time frame - - don't you agree?

Yes, that claim still stands.

---

gbrooks9 (George Brooks) 2018-03-25 01:33:34 UTC #853

> Swamidass:
>
> The claim that was wrong was that there is solid evidence against a bottleneck of 2 in our lineage, including the time between now and when we diverge from chimps. Some have even argued the evidence goes back 13 million years. That claim about what the evidence showed us was false. It was overstated.
>
> **gbrooks9 writes:**
> **So, I would think you should be more "wordy" about what we have proved or not proved. I think we have quite clearly showed that there cannot be a single pair bottleneck within a 10,000 year time frame - - don't you agree?**
>
> Yes, that claim still stands.

@Swamidass , I hope you can see how differently your discussion/conclusion sounds immediately above - - when compared to the much more severe statements you made in the post(s) prior …

> Swamidass:
>
> For a long time, people have presented evidence against a bottleneck ever in our lineage as a settled finding of population genetics. However, it is not a settled finding, as we have just unsettled it. However, for a long time, questions have been silenced because of the total certainty of that finding. Yet it was wrong. So how do we avoid that mistake again?

If someone were to read your quote from post 848, they would no doubt conclude something very different from your clarified comments found in this paragraph: **"The claim that was wrong was that there is solid evidence against a bottleneck of 2 in our lineage, including the time between now and when we diverge from chimps. Some have even argued the evidence goes back 13 million years. That claim about what the evidence showed us was false. It was overstated."**

Jon_Garvey (Jon Garvey) 2018-03-25 11:13:04 UTC #854

https://en.wikipedia.org/wiki/Association_fallacy#Guilt_by_association_as_an_ad_hominem_fallacy

Not for the first time - no doubt not for the last.

Jonathan_Burke (Jon) 2018-03-25 12:16:25 UTC #855

> Jon_Garvey:
>
> Not for the first time - no doubt not for the last.

This is the guilt by association argument.

> Guilt by association as an ad hominem fallacy

> Guilt by association can sometimes also be a type of ad hominem fallacy, **if the argument attacks a person** because of the similarity between the views of someone making an argument and other proponents of the argument.[1]
>
> This form of the argument is as follows:
>
> Source S makes claim C.
> Group G, which is currently viewed negatively by the recipient, also makes claim C.
> Therefore, source S is viewed by the recipient of the claim as associated to the group G and inherits how negatively viewed it is.
> An example of this fallacy would be “My opponent for office just received an endorsement from the Puppy Haters Association. **Is that the sort of person you would want to vote for**?”

I did not make that argument. I didn’t say anything whatsoever about you as a person. I am talking about your argument, not you. How is your argument any different to the argument made by Ken Ham?

Jon_Garvey (Jon Garvey) 2018-03-25 12:56:20 UTC #856

That’s very simple.

Ham says the Holy Spirit was a witness to events (which is orthodox), and inspired history according to Ham’s understanding (which is interpretation), which is therefore a defeater for any other understanding, including evolutionary science (which is fallacy).

I say the Holy Spirit was a witness to events (which is orthodox), and inspired Scripture (which is orthodox), which is therefore authoritative data to bring to the table of understanding, as is evolutionary science.

Different presuppositions, different argument, different conclusion. But superficially similar enough for the careless thinker to confuse them.

Jay313 (Jay Johnson) 2018-03-25 13:07:23 UTC #857

> Jon_Garvey:

> I say the Holy Spirit was a witness to events (which is orthodox), and inspired Scripture (which is orthodox), which is therefore authoritative data to bring to the table of understanding, as is evolutionary science.

To say that the Holy Spirit was a witness to the events of creation is an entirely non-controversial statement, and to say that the Scriptures are inspired and authoritative is equally non-controversial. As well, neither statement espouses or entails a literalist interpretation of Genesis. So, where exactly is the beef, **@Jonathan_Burke** ? Must you argue with every statement that Jon Garvey makes?

Jonathan_Burke (Jon) 2018-03-25 13:10:37 UTC #858

> Jon_Garvey:
>
> I say the Holy Spirit was a witness to events (which is orthodox), and inspired Scripture (which is orthodox), which is therefore authoritative data to bring to the table of understanding, as is evolutionary science.

You don't just say "the Holy Spirit was a witness to events" and "inspired Scripture" (a phrasing designed to make your argument look at least slightly different to Ham's). Like Ham, you say Genesis 1 is "an authoritative eye-witness account from the Holy Spirit" of creation. So you don't just say the Holy Spirit "inspired Scripture", like Ham you say the Holy Spirit inspired an **authoritative eye-witness account of creation**.

And you use that to challenge certain conclusions of evolutionary science, just as he does. So you use the same argument, in the same way.

> Jay313:
>
> To say that the Holy Spirit was a witness to the events of creation is an entirely non-controversial statement, and to say that the Scriptures are inspired and authoritative is equally non-controversial.

If that was all Jon had said, it would indeed have been non-controversial.

> Jay313:
>
> Must you argue with every statement that Jon Garvey makes?

I make about one comment on his posts every month. It's not like I argue the toss with every statement he makes; most of what he posts, I don't even read.

Jon_Garvey (Jon Garvey) 2018-03-25 13:38:25 UTC #859

Jon

I suggest you stop digging. It would be more plausible if your post had set out to refute Ham's argument, or even mine. Instead, it was enough for you to link my name to his, knowing how much weight he carries with the EC community.

I'm out of here.

RichardBuggs (Richard Buggs) 2018-03-25 21:10:42 UTC #861

Hi Joshua,

Reworking the Science of Adam - Peaceful Science

This last year, 2017 till now, we have been Reworking the Science of Adam. This brings us several new ways to think about Adam and Eve in human origins.

Thank you very much for posting this summary; this is a helpful service to us all.

> Swamidass:
>
> However, I think I understand **@Jon_Garvey** 's motivation. We do not want to state these claims with too much certainty, as we have just seen a large shift in our understanding here. I'd point, again, to my invitational epistemology as a solution to this paradox. I've already pointed out three ways a more recent bottleneck might be possible:
>
> Adam and Eve had totally different biology than us (e.g. genetic mosaics)
> Ongoing miracles that diversify us more than is possible by natural processes alone.
> Much higher mutation rates in the distant past than we can imagine or observe in humans (perhaps miraculously?)

I agree with you that **@Jon_Garvey** has made valid points, and I respect him for that. We would not want to fall into the trap of attaching too much certainty to any of our claims. This is a very complex field, where direct testing is difficult and sometimes impossible. I have made this point previously in this discussion with reference to the Lenski LTEE experiment.

To my mind, there are three lines of evidence before us now that a bottleneck could not have happened in the last 500,000 years. These are (1) **@glipsnort** 's allele frequency spectrum argument (2) your TMR4A calculations and (3) evidence for introgression from Neanderthals into European and Asian humans.

It is the third one that I think is the strongest argument, as it relies upon archaeological findings that can be dated, as well as sequence data.

However, if someone wanted a more recent Adam and Eve: they could claim (as I think have been claimed previously in this discussion) that Neanderthals were not fully human and not descended from Adam and Eve (perhaps invoking Genesis 6:2). Thus a bottleneck could have occurred in the human lineage even while Neanderthals were co-existing elsewhere. Thinking this through, it has just struck me that your TMR4A argument might also be vulnerable to this argument, if the loci with large TMR4A were also shown to be loci in which there is evidence for polymorphism due to Neanderthal introgression. Is this something that you have thought about?

DennisVenema (Dennis Venema) 2018-03-25 22:47:02 UTC #862

> RichardBuggs:
>
> evidence for introgression from Neanderthals into European and Asian humans.

I assume you mean Neanderthals and Denisovans, correct?

There is also that evidence that the Denisovans have an introgression event into *their* genome to keep in mind - something that would suggest that part of their genome is older than the last common ancestral population of Neanderthals and Denisovans.

One interesting finding from the recent Denisovan paper in Cell is that some human groups in the present day have a *lot* of Denisovan ancestry. I think this makes it problematic to try and excise this ancestry from the discussion. Thoughts?

DennisVenema (Dennis Venema) 2018-03-25 22:50:35 UTC #863

> RichardBuggs:
>
> Thinking this through, it has just struck me that your TMR4A argument might also be vulnerable to this argument, if the loci with large TMR4A were also shown to be loci in which there is evidence for polymorphism due to Neanderthal introgression. Is this something that you have thought about?

My feel for the data is that there is not a lot of Neanderthal DNA left in present-day humans, so it wouldn't have a large effect. There are also really ancient TMRCA values in SS Africa (and thus not due to Neanderthal or Denisovan introgression). That said, in re-skimming the Argweaver paper, I don't see where they tested SS African DNA apart from the entire set (which includes non SSA samples).

DennisVenema (Dennis Venema) 2018-03-25 23:49:58 UTC #864

In case anyone is interested in the data supporting introgression into Denisovans - it comes from **this paper**, and the relevant section is as follows:

> We tested three non-mutually exclusive scenarios that could explain these observations. First, gene flow from the ancestor of Neandertals after the split from Denisovans into the ancestors of all present-day humans would result in more sharing of derived alleles between present-day Africans and Neandertals. However, because gene flow contributes alleles at low frequency the sharing of derived alleles with Neandertals would grow weaker with higher African derived allele frequency (SI 16a), whereas we observe the opposite (Fig. 7). Second, gene flow from the ancestors of present-day humans to Neandertals after their split from Denisovans would also result in more sharing of derived alleles. However, the amount of allele frequency change (genetic drift) that has occurred in present-day Africans since the split from Neandertals is too small to explain the extent of sharing of derived alleles fixed in Africans (SI 16a). Third, we considered a scenario where Denisovans received gene flow from a hominin whose ancestors diverged deeply from the lineage leading to Neandertals, Denisovans and present-day humans. We find that this scenario is consistent with the data, as also suggested by others29, and estimate that 2.7–5.8% (jackknife 95% confidence interval) of the Denisova genome comes from this putative archaic hominin which diverged from the other hominins 0.9–1.4 million years ago (SI 16a). An approximate Bayesian computation30 again supports the third scenario (SI 16b) and estimates that 0.5–8% of the Denisovan genome comes from an unknown hominin which split from other hominins 1.1 and 4 million years ago.
>
> We caution that these analyses make several simplifying assumptions. Despite these limitations we show that the Denisova genome harbors a component that derives from a population that lived prior to the separation of Neandertals, Denisovans and modern humans. This component may be present due to gene flow, or to a more complex population history such as ancient population structure maintaining a larger proportion of ancestral alleles in the ancestors of Denisovans over hundreds of thousands of years.

So, if Denisovans are "in" as it were, then we need to account for the introgression (or ancient population structure) we see in their genomes. This would seem to push the magic date back past 700KYA towards something closer to 1MYA.

This also highlights the problem with deciding on a specific date. I can see new data pushing it further back, but I can't as easily foresee a mechanism to pull it forward. I'll welcome the thoughts of **@RichardBuggs** and **@Swamidass** .

Chris_Falter (Chris Falter) 2018-03-26 00:46:42 UTC #865

> RichardBuggs:
>
> if someone wanted a more recent Adam and Eve: they could claim (as I think have been claimed previously in this discussion) that Neanderthals were not fully human and not descended from Adam and Eve (perhaps invoking Genesis 6:2). Thus a bottleneck could have occurred in the human lineage even while Neanderthals were co-existing elsewhere.

The claim under scrutiny is that a single couple were the *sole* genetic ancestors of all humanity. Or so I thought, until you suggested that the single couple was only the head of one of many genetic lineages for humanity. Is this really a hypothesis you wish to defend? If so, how would you reconcile the hypothesis with the traditional theological concerns of someone like **@agauger** ?

---

gbrooks9 (George Brooks) 2018-03-26 01:45:55 UTC #866

> RichardBuggs:
>
> To my mind, there are three lines of evidence before us now that a bottleneck could not have happened in the last 500,000 years. [The 3rd reason is] . . . evidence for introgression from Neanderthals into European and Asian humans.

How is evidence for introgression an indication of anything? One could assert that the introgression is by a hundreds of random contributions… or by a single mating pair.

The evidence against a bottleneck remains the same in:

(1) **@glipsnort** 's allele frequency spectrum argument; and
(2) **@Swamidass** ' TMR4A calculations .

And the only way to arrive at some other conclusion is **still** the three methods outlined by **@Swamidass** :

> swamidass:
>
> …there is not a single model proposed that can account for the data with a single couple origin less than 200 kya, without either
>
> (1) inferring ongoing miracles,
>
> (2) totally different biology for Adam and Eve (e.g. genetic mosaics), or
>
> (3) mutation rates an order of magnitude (or more) higher than we have ever observed in humans.

No matter how many contributors there may have been to the human genome, the contributors have to participate in a favorably harmonious way with Option (2) or (3), or be completely by-passed by Option (1).

RichardBuggs (Richard Buggs) 2018-03-26 15:20:24 UTC #867

> Jon_Garvey:

> I'm out of here.

Dear moderators,

I would like to note that I think it is very regrettable that **@Jon_Garvey** has apparently been hounded out of this discussion by **@Jonathan_Burke**

@Jon_Garvey 's contributions to this discussion have been erudite, humorous and good natured, and clearly come from his experience of a long career as a physician. He has expressed views that are probably held by many other Christians, and he has defended them well and with good grace.

It appears that he has now left this discussion due to what he (in my view legitimately) feels is an ad hominem attack by **@Jonathan_Burke** .

My understanding of the role of this Biologos forum is to allow debate from people of all perspectives on science and faith. However, it does seem that someone like **@Jon_Garvey** who holds a perspective that perhaps differs from the majority of participants is being unfairly targeted by **@Jonathan_Burke** and this is undermining the purpose of this discussion forum.

best wishes
Richard

Jonathan_Burke (Jon) 2018-03-26 15:25:04 UTC #868

> RichardBuggs:
>
> I would like to note that I think it is very regrettable that **@Jon_Garvey** has apparently been hounded out of this discussion by **@Jonathan_Burke**

He hasn't. He just told me he wasn't going to reply to me.

> RichardBuggs:
>
> However, it does seem that someone like **@Jon_Garvey** who holds a perspective that perhaps differs from the majority of participants is being unfairly targeted by **@Jonathan_Burke** and this is undermining the purpose of this discussion forum.

Nonsense. I made less than a dozen comments over six days, none of which constituted unfair targeting. I note you make absolutely no mention of how Chris Falter and George Brooks have been repeatedly challenging Jon Garvey's perspective on this thread and others.

Swamidass (Dr. S Joshua Swamidass) 2018-03-26 17:00:29 UTC #869

> RichardBuggs:
>
> However, if someone wanted a more recent Adam and Eve: they could claim (as I think have been claimed previously in this discussion) that Neanderthals were not fully human and not descended from Adam and Eve (perhaps invoking Genesis 6:2). Thus a bottleneck could have occurred in the human lineage even while Neanderthals were co-existing elsewhere. Thinking this through, it has just struck me that your TMR4A argument

> might also be vulnerable to this argument, if the loci with large TMR4A were also shown to be loci in which there is evidence for polymorphism due to Neanderthal introgression. **Is this something that you have thought about?**

Yes, I have thought about that! =)

If you allow for interbreeding all bets are off. Adam and Eve could have been 10,000 years ago in the middle east, or 200 kya as the sole-couple progenitors of Homo sapiens, etc. None of the genetic work we have done here has any relevance to the question if interbreeding is allowed.

> RichardBuggs:
>
> To my mind, there are three lines of evidence before us now that a bottleneck could not have happened in the last 500,000 years. These are (1) **@glipsnort** 's allele frequency spectrum argument (2) your TMR4A calculations and (3) evidence for introgression from Neanderthals into European and Asian humans.

That's about right, but do not forget Denisovans.

> RichardBuggs:
>
> It is the third one that I think is the strongest argument, as it relies upon archaeological findings that can be dated, as well as sequence data.

#2 is pretty strong too, as it is very easy to explain to non-experts, and is also very well supported in the data.

> DennisVenema:
>
> There is also that evidence that the **Denisovans have an introgression event into their genome to keep in mind** - something that would suggest that part of their genome is older than the last common ancestral population of Neanderthals and Denisovans.

> DennisVenema:
>
> So, if Denisovans are "in" as it were, then we need to account for the introgression (or ancient population structure) we see in their genomes. This would seem to push the magic date back past 700KYA towards something closer to 1MYA.

That is not really relevant to our question.

We have only 1 Denisovan genome (from a single knuckle, now destroyed), and do not know of we descend directly from this Denisovan. It is possible that Adam and Eve are our sole genetic progenitors, but some Denisovans interbred with another hominem, then subsequently died off without ever contributing to all of us. Unless we can show that those genes appear in humans too, and do not push the TMR4A back, then it does not give us a confident way to push back our date.

They also give an alternate hypothesis:

> DennisVenema:
>
> a more complex population history such as ancient population structure maintaining a larger proportion of ancestral alleles in the ancestors of Denisovans over hundreds of thousands of years.

The issue is that we cannot actually untangle this knot in most cases. In extant scenarios, migration can only measured by getting serial measurements over time and comparing them. Without serial measurements (multiple time points) its not possible to determine the direction of interbreeding events, or distinguish it from incomplete sorting. This, therefore, is just not strong evidence against a bottleneck at 500 kya - 700 kya.

> DennisVenema:
>
> My feel for the data is that there is not a lot of Neanderthal DNA left in present-day humans, so it wouldn't have a large effect. There are also really ancient TMRCA values in SS Africa (and thus not due to Neanderthal or Denisovan introgression). That said, in re-skimming the Argweaver paper, I don't see where they tested SS African DNA apart from the entire set (which includes non SSA samples).

That has never been done. But also we have no way of parsing out what is what that far back.

> DennisVenema:
>
> This also highlights the problem with deciding on a specific date. I can see new data pushing it further back, but I can't as easily foresee a mechanism to pull it forward.

I agree that this will always be subject to revision. However, it is hard to imagine the evidence what would pull the date back earlier than 2 mya. The most likely thing, I would guess, would be trans species variation, having ruled out convergent evolution. To do that, we would need to get a much better census of great ape genetic variation, and do a very careful (and frankly difficult) analysis to make sense of that. Still, it is possible that at a future date a single couple of bottleneck would be ruled out.

Then, however, if we allow for interbreeding (whether it be sanctioned by God or not), all bets are off. We do not think a single-couple origin of our kind needs to correspond with a single couple bottleneck.

> Chris_Falter:
>
> > if someone wanted a more recent Adam and Eve: they could claim (as I think have been claimed previously in this discussion) that Neanderthals were not fully human and not descended from Adam and Eve (perhaps invoking Genesis 6:2). Thus a bottleneck could have occurred in the human lineage even while Neanderthals were co-existing elsewhere.
>
> The claim under scrutiny is that a single couple were the sole genetic ancestors of all humanity. Or so I thought, until you suggested that the single couple was only the head of one of many genetic lineages for humanity. Is this really a hypothesis you wish to defend? If so, how would you reconcile the hypothesis with the traditional theological concerns of someone like **@agauger** ?

As we have shown, if we allow for interbreeding, all bets are off. Adam could be very recent, or at the origin of Homo sapiens, or really any where or time we like.

How would this reconcile with **@agauger** ? Well, that requires theological reflection. If we'd like to change **@agauger** 's view of this, it would probably be best to engage catholic theologians and philosophers (e.g. **@AntoineSuarez**).

Swamidass (Dr. S Joshua Swamidass) 2018-03-26 17:56:01 UTC #870

> RichardBuggs:
>
> I would like to note that I think it is very regrettable that **@Jon_Garvey** has apparently been hounded out of this discussion by **@Jonathan_Burke**

> RichardBuggs:
>
> It appears that he has now left this discussion due to what he (in my view legitimately) feels is an ad hominem attack by **@Jonathan_Burke** .

I agree.

However, this is not the moderators fault. It is more regrettable that an apology from the responsible party is not not forthcoming. We should not interpret **@moderators** inaction as endorsing poor behavior. They may not have seen the exchange, or may be trying to resolve it privately. The best way to bring it to their attention is flagging posts as inappropriate.

Also, **@Jon_Garvey** will be back. He is not banished for good =).

Swamidass (Dr. S Joshua Swamidass) 2018-03-26 17:58:03 UTC #871

> gbrooks9:
>
> No matter how many contributors there may have been to the human genome, the contributors have to participate in a favorably harmonious way with Option (2) or (3), or be completely by-passed by Option (1).

Help me understand that?

Swamidass (Dr. S Joshua Swamidass) 2018-03-26 18:24:23 UTC #872

> RichardBuggs:
>
> To my mind, there are three lines of evidence before us now that a bottleneck could not have happened in the last 500,000 years. These are (1) **@glipsnort** 's allele frequency spectrum argument (2) your TMR4A calculations and (3) evidence for introgression from Neanderthals into European and Asian humans.

We should also remember that these lines are not yet evidence against it, but become so in the future:

1. Trans-species variation
2. HLA exon diversity
3. HLA intron diversity

Those, historically, have been the strongest arguments against a single couple bottleneck, even though we found them wanting. Science, however, progresses. This assessment could change in the future. To this we could also add TMR4A, which could move upwards if we include more extant (or ancient) samples and recompute it in the future.

---

gbrooks9 (George Brooks) 2018-03-26 18:51:37 UTC #873

> Swamidass:
>
> Help me understand that?

Okay… I was wondering if I was going to need to invest more narrative on that point:

> swamidass:
>
> …there is not a single model proposed that can account for the data with a single couple origin less than 200 kya, without either
>
> (1) inferring ongoing miracles,
>
> (2) totally different biology for Adam and Eve (e.g. genetic mosaics), or
>
> (3) mutation rates an order of magnitude (or more) higher than we have ever observed in humans.

Looking at scenario (2) first, if a YEC wants to propose that Neanderthal (or other interbreeding) could change our analysis of possible bottlenecks, he would have to do two things at once:

a) that Neanderthals were an equally legitimate part of the human race per Genesis (I have very rarely found a YEC willing to do so); and

b) having done so, the YEC must somehow show that the Neanderthals introduced a completely different biology - - all the while being on par with the view that they are equivalent to Sapiens.

As for Option ©, it's the same kind of issue… but instead of arguing for a different biology, the YEC has to simultaneously equate the contributors as "on par" with the rest of humanity … and yet also dramatically speed up mutation rates that the conventional analysis assumes for humanity.

Whenever we discuss how the scenarios could be changed, we really need to validate the proposed change with the likelihood that a Young Earth Creationist would tolerate the scenario change. Nothing important is accomplished to argue that **there can be a single pair bottleneck one million years back in time** when we can't find any Creationist who accepts a million year time frame.

And if we find a creationist who *says* he endorses a million year time frame, the next logical question is how does he justify a million year time frame (and thus **Rejecting** the premise of 6 days of creation) while at the same time insisting on Special Creation a million years ago? This kind of creationist is neither Fish nor Fowl, and will be repulsed by Evolutionists (because of the feature of Special Creation) **and** by Creationists (because of the rejection of 6 days of creation).

Rather than making the BioLogos "spin" more palatable, it makes it likely that we will double our opposition, or at least double the apathy of a vast swath of our potential audience.

DennisVenema (Dennis Venema) 2018-03-26 20:23:34 UTC #874

> Swamidass:
>
> Those, historically, have been the strongest arguments against a single couple bottleneck, even though we found them wanting. Science, however, progresses. This assessment could change in the future. To this we could also add TMR4A, which could move upwards if we include more extant (or ancient) samples and recompute it in the future.

I don't think we yet have a comprehensive picture of extant human variation in sub-Saharan Africa. In fact, I'm certain that we don't - the question is merely *how much* a comprehensive picture would shift the TMR4A, etc. There's only one way it will shift, based on new variants being discovered - it will shift to larger values, not smaller ones.

Another potential finding is new hominin remains we can get DNA out of. That could show us introgression events into *Homo sapiens* that could also push the date back.

Let me also push just a bit on that evidence for ancient DNA in Denisovans, and you can tell me what you think. Even if that ancient variation is not in present-day humans (and it is, as far as I know, in Oceanic peoples at least - why wouldn't it be?) - but even if we assume it is not, if Denisovans are "in" then this is evidence that they interbred with another hominin. If that other hominin is also "in", then the time for a last sole genetic couple gets pushed back. If that hominin is "not in", then there is a introgression problem (interbreeding between humans and non-humans). I don't see another option. Thoughts?

DennisVenema (Dennis Venema) 2018-03-26 20:30:25 UTC #875

> DennisVenema:
>
> why wouldn't it be?

Of course, it could be selected against. Neanderthal variation was selected against…

Don't forget the Denisovan DNA we have is fairly recent (last 100,000 years or less).

I'm going to go read that paper again…

T_aquaticus 2018-03-27 14:54:45 UTC #876

> Swamidass:
>
> For a long time, people have presented evidence against a bottleneck ever in our lineage as a settled finding of population genetics. However, it is not a settled finding, as we have just unsettled it. However, for a long time, questions have been silenced because of the total certainty of that finding. Yet it was wrong.

There were two implied conditions that often don't get mentioned. First, there was the implied assumption that we were talking about the last 10,000 years or at most the last 200,000 years which corresponds to anatomically modern humans. The second, and related, assumption was that we were talking about the time period covered by the statistical confidence in the measurements and models themselves. If the 2 person bottleneck crowd has to retreat to time periods where population models are necessarily ambiguous then we go back to the burden of proof problem inherent in that bottleneck hypothesis. In order to work past the null hypothesis you have to have models that will detect a bottleneck if there was one. If the models and data do not allow you to reject the null hypothesis, then you stay with the null hypothesis.

> Swamidass:
>
> I think, however, there is some remaining questions about how constructive dialogue with science could be possible. I've been thinking about that too. I do not think the answer is in generic skepticism. Rather, I think we need some constructive ways of enabling dialogue, and even constructive types of resistance to scientific claims, that can push us all to better knowledge.

My favorite way of tackling these issues is to just treat it as an interesting scientific question separate from any cultural or religious implications. Such research is probably not appropriate for scientists spending their official time on if they are being funded by other sources (e.g. NIH), but I think people can still approach this from an agnostic position and see where it leads.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 15:42:16 UTC #877

> T_aquaticus:
>
> There were two implied conditions that often don't get mentioned. First, there was the implied assumption that we were talking about the last 10,000 years or at most the last 200,000 years which corresponds to anatomically modern humans.

Except that is precisely the assumption i'm challenging as absurd and unwarranted. It such a departure from our current understanding it cannot be justified and should certainly not be implicit.

> T_aquaticus:
>
> The second, and related, assumption was that we were talking about the time period covered by the statistical confidence in the measurements and models themselves.

That also is an unwarranted assumption. It is a scientific error to just assume this to be true of measurements.

> T_aquaticus:
>
> If the 2 person bottleneck crowd has to retreat to time periods where population models are necessarily ambiguous then we go back to the burden of proof problem inherent in that bottleneck hypothesis. In order to work past the null hypothesis you have to have models that will detect a bottleneck if there was one. If the models and data do not allow you to reject the null hypothesis, then you stay with the null hypothesis.

This is in error. The choice of null hypothesis is subjective and is being used here to shift burden of proof. The right answer is that we do not know from the evidence. Any one who makes confident claims one way or another adopts the burden of proof, but the no bottleneck position is not epistemologically privileged.

> T_aquaticus:
>
> My favorite way of tackling these issues is to just treat it as an interesting scientific question separate from any cultural or religious implications. Such research is probably not appropriate for scientists spending their official time on if they are being funded by other sources (e.g. NIH), but I think people can still approach this from an agnostic position and see where it leads.

That is a good approach. Most opposition to this inquiry has come from those theologically motivated agains Adam theology.

T_aquaticus 2018-03-27 16:10:29 UTC #878

> Swamidass:

> Except that is precisely the assumption i'm challenging as absurd and unwarranted. It such a departure from our current understanding it cannot be justified and should certainly not be implicit.

But those assumptions were implicit in many of the debates prior to this one. That's the point. It isn't fair to suddenly change the parameters of the debate and expect older arguments to hold up. Remember, we are talking about a debate that is heavily influenced by young Earth creationism.

> Swamidass:
>
> This is in error. The choice of null hypothesis is subjective and is being used here to shift burden of proof. The right answer is that we do not know from the evidence. Any one who makes confident claims one way or another adopts the burden of proof, but the no bottleneck position is not epistemologically privileged.

It isn't subjective at all. The hypothesis is that there was a bottleneck down to two people in the direct human lineage somewhere in the past. If your models and measurements are incapable of differentiating between a 2 person bottleneck and a continuous large population then you can't differentiate between the hypothesis and null hypothesis. This is straightforward statistics and hypothesis testing. You could say that the choice of alpha (i.e. p values) is subjective, but even then it is splitting hairs.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 17:48:44 UTC #879

> T_aquaticus:
>
> But those assumptions were implicit in many of the debates prior to this one. That's the point. It isn't fair to suddenly change the parameters of the debate and expect older arguments to hold up. Remember, we are talking about a debate that is heavily influenced by young Earth creationism.

It is certainly fair to point out when conclusions depend on unwarranted and hidden assumptions. No one forced people to make those errors or to claim the evidence was on their side, when it was not.

> T_aquaticus:
>
> It isn't subjective at all. The hypothesis is that there was a bottleneck down to two people in the direct human lineage somewhere in the past. If your models and measurements are incapable of differentiating between a 2 person bottleneck and a continuous large population then you can't differentiate between the hypothesis and null hypothesis. This is straightforward statistics and hypothesis testing. You could say that the choice of alpha (i.e. p values) is subjective, but even then it is splitting hairs.

That is not correct.

There are two hypothesis:

1. No bottleneck in our lineage, ever.
2. At least one bottleneck in our lineage.

We do not have the data, yet, it seems to distinguish these two hypothesis. The right answer is "we do not know" not "heliocentric certainty for H1".

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 18:25:43 UTC #880

> DennisVenema:
>
> Let me also push just a bit on that evidence for ancient DNA in Denisovans,

Please do. Let's get the evidence straight.

> DennisVenema:
>
> Even if that ancient variation is not in present-day humans (and it is, as far as I know, in Oceanic peoples at least - why wouldn't it be?) -

As far as i know, we cannot find the ***entire*** Neandertal genome in human variation, just a small portion of it. Neither can we find the ***entire*** Denisovan genome in human variation either, just a tiny fraction of it. That means we do not expect any specific portion of the Denisovan genome, e.g. that tiny portion which was inherited *possibly* from an ancient hominin, to be in human variation. As far as I can tell, that portion of the genome is not found in extant humans.

Moreover, it only seems that a portion of the Homo sapien genome (i.e. loci) shows signs of interbreeding. Is that not correct?

If I misunderstand that status of the evidence. If I do, by all means please correct me. It is important to get this straight.

> DennisVenema:
>
> but even if we assume it is not, if Denisovans are "in" then this is evidence that they interbred with another hominin.

I do not know if the sole-*genetic* progenitor model specifies what happens to "humans" that do not ultimately contribute to extant humans. There are several shades of gray…

1. Are genealogical ancestors that are not genetic ancestors allowed to descend from other lines?
2. Are descendents of Adam and Eve that do not become ancestors of extant humans allowed to interbreed? (e.g. as put forth in ***all*** AIG models because of Nephilim)
3. And as we have already covered, is interbreeding that contributes to extant humans allowed? (e.g. genealogical Adams)

Unless we can show that the variation from a 1 mya hominin appears in extant humans, and this is not incomplete sorting, then #2 and #1 are live possibilities. It would mean that there could be a bottleneck of a single couple in our lineage. Keep in mind also that we have no idea if that *specific* Denisovan was in our lineage or not. All we know is that there some fragments of human variation that seems to match that knuckle. As far as I can tell, there are severals ways this could have happened, not all of which would rule out sole-genetic progentiorship within the last 700 kya.

Of course, please do correct me if I am wrong or missed something important here.

> DennisVenema:
>
> the question is merely how much a comprehensive picture would shift the TMR4A, etc.

True, and that is why I've pointed out 700 kya as a date that might stand the test of time, and also 2 mya. Conversely, 500 kya might ultimately be too early, even if we cannot definitively rule it out at this point.

As for what ultimately happened, and what the evidence will ultimately show, we can make guesses and take bets, but we should start by explaining honestly what the data shows us right now.

Of course it is also possible I misunderstood something in the introgression data (see above). Please do correct me if that is the case.

DennisVenema (Dennis Venema) 2018-03-27 18:30:53 UTC #881

> Swamidass:
>
> The right answer is “we do not know” not “heliocentric certainty for H1”.

@Swamidass

I thought we had already covered this pretty thoroughly. I did not claim “heliocentric certainty for H1" in Adam and the Genome. Perhaps this is not what you are referring to, and I’ve missed a part of the conversation.

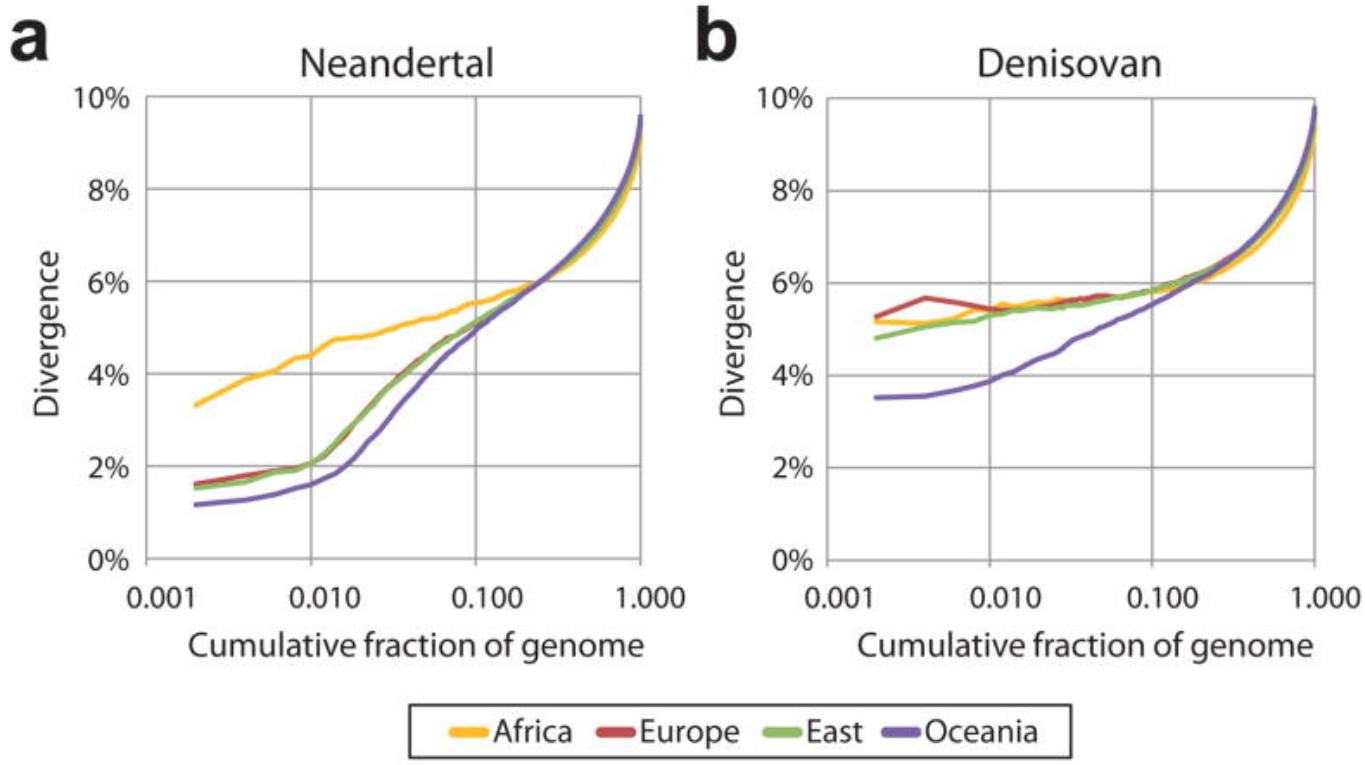
Swamidass (Dr. S Joshua Swamidass) 2018-03-27 18:38:36 UTC #882

> DennisVenema:
>
> I thought we had already covered this pretty thoroughly. I did not claim “heliocentric certainty for H1" in Adam and the Genome. Perhaps this is not what you are referring to, and I’ve missed a part of the conversation.

True. But you did claim very high certainty. You also retracted that claim. So I am not holding your feet to the fire on that one. Certainly there are other people making that claim, even now.

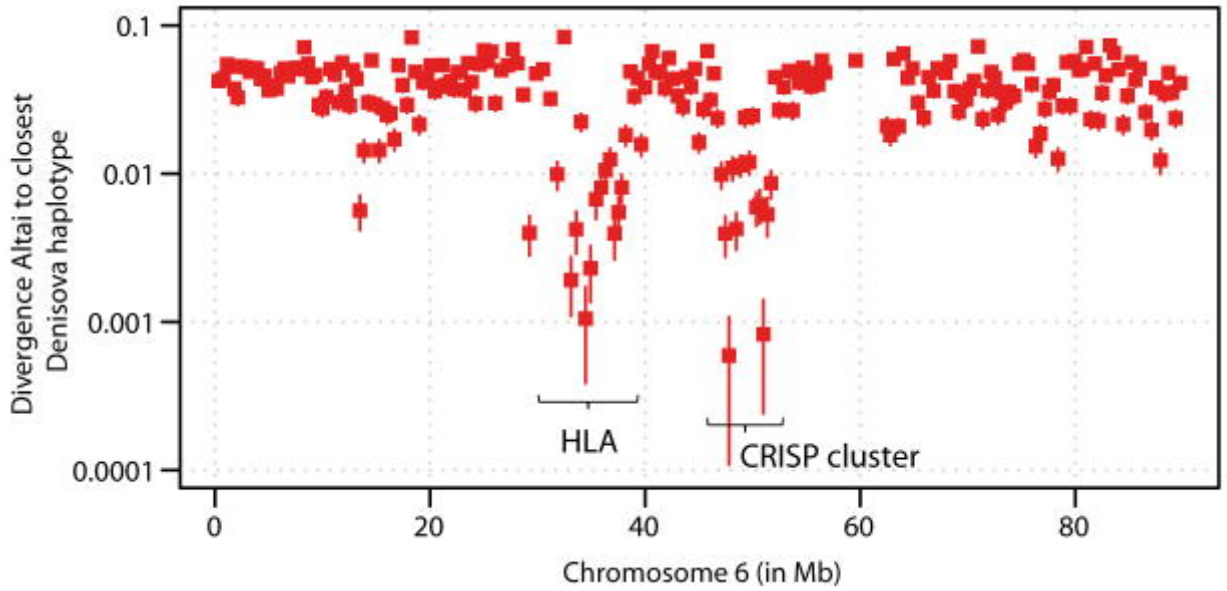
> Swamidass:
>
> As far as i know, we cannot find the entire Neandertal genome in human variation, just a small portion of it. Neither can we find the entire Denisovan genome in human variation either, just a tiny fraction of it. That means we do not expect any specific portion of the Denisovan genome, e.g. that tiny portion which was inherited possibly from an ancient hominin, to be in human variation. As far as I can tell, that portion of the genome is not found in extant humans.

This graph from the paper seems to support my understanding. Looks like there is only weak evidence of less than 1%-3% of the genome showing interbreeding (contrast that with the higher certainty for Neandertal)…



https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4031459/

But there is a critical failure point in this analysis too. A large proportion of the data is in HLA and other immunity related genes. It is possible this might be convergent evolution too. I'm not entirely sure how important this wrinkle is, and it will take some effort to process. However, if convergent evolution was not tested for, and we do not see introgression evidence more widespread, that does weaken the claim.



https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4031459/

That being said, I do think Neanderthals and Denisovans (and other hominins) interbred with *Homo sapiens*. Though, I'd resist using introgression claims two or three steps removed as evidence against a bottleneck.

DennisVenema (Dennis Venema) 2018-03-27 18:40:51 UTC #883

> Swamidass:
>
> I do not know if the sole-genetic progenitor model specifies what happens to “humans” that do not ultimately contribute to extant humans. There are several shades of gray…
>
> Are genealogical ancestors that are not genetic ancestors allowed to descend from other lines?
> Are descendents of Adam and Eve that do not become ancestors of extant humans allowed to interbreed? (e.g. as put forth in all AIG models because of Nephilim)
> And as we have already covered, is interbreeding that contributes to extant humans allowed? (e.g. genealogical Adams)
>
> Unless we can show that the variation from a 1 mya hominin appears in extant humans, and this is not incomplete sorting, then #2 and #1 are live possibilities. It would mean that there could be a bottleneck of a single couple in our lineage. Keep in mind also that we have no idea if that specific Denisovan was in our lineage or not. All we know is that there some fragments of human variation that seems to match that knuckle. As far as I can tell, there are severals ways this could have happened, not all of which would rule out sole-genetic progentiorship within the last 700 kya.

These are the correct questions to ask, and I guess it would fall to those investigating a sole genetic progenitor model (**@RichardBuggs** **@agauger** , others?) to say what their preference is. My understanding of the motivations (which might be incorrect) is that the idea of getting back to a sole pair is so that you can have *unique* genealogical and genetic descent from that point on. If so, then introgression into the Denisovans becomes relevant. But I’ll wait to hear what **@RichardBuggs** and **@agauger** might have to say about these issues.

DennisVenema (Dennis Venema) 2018-03-27 18:44:39 UTC #884

> Swamidass:
>
> True. But you did claim very high certainty. You also retracted that claim. So I am not holding your feet to the fire on that one. Certainly there are other people making that claim, even now.

Ah - but as you phrased it in that quote, it’s at any point in our lineage. Well, our lineage is 3.5 billion years old, plus or minus, just like every other living thing on the planet. That’s a long time, and I certainly don’t claim certainty that there has never been a bottleneck to 2 in that entire time.

DennisVenema (Dennis Venema) 2018-03-27 18:49:06 UTC #885

> Swamidass:
>
> As far as i know, we cannot find the entire Neandertal genome in human variation, just a small portion of it. Neither can we find the entire Denisovan genome in human variation either, just a tiny fraction of it.

Yes, this is correct. But, we have found human remains that have a lot more Neandertal DNA in them than present humans do. At the point of hybridization, the first generation would have had the entire Neandertal set as one of their haploid sets. The same would apply to first generation hybrids of Homo sapiens and Denisovans. So, at some point in our prehistory, we had individuals that (most likely) did have that ancient Densiovan DNA in their genomes, even if it was later lost. Are those individuals “in” or “out”? That’s the question.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 18:51:58 UTC #886

> DennisVenema:
>
> Ah - but as you phrased it in that quote, it's at any point in our lineage. Well, our lineage is 3.5 billion years old, plus or minus, just like every other living thing on the planet. That's a long time, and I certainly don't claim certainty that there has never been a bottleneck to 2 in that entire time.

Yes yes, that's right.

I think in the past (and you do not say this now), you have said **going back 13 mya**, or at least before we diverge from chimps. In the past too, I've agreed with that conclusion, but always had less certainty. A lot of people have made that mistake.

And you have retracted that any ways. So I was not calling you out. I was more pointing out it is totally fair to make that correction in the first place.

> DennisVenema:
>
> Yes, this is correct. But, we have found human remains that have a lot more Neandertal DNA in them than present humans do. At the point of hybridization, the first generation would have had the entire Neandertal set as one of their haploid sets. The same would apply to first generation hybrids of Homo sapiens and Denisovans. So, at some point in our prehistory, we had individuals that did have that ancient Densiovan DNA in their genomes, even if it was later lost. Are those individuals "in" or "out"? That's the question.

Sort of. That hybrid was more neanderthal than human (25/75), but point taken. Regarding the Denisovan, you missed my point. It is possible that the Denisovans that interbred with Homo sapiens did not have DNA or ancestry with that ancient hominin. In that case, our lineage would never have to account for them.

Keep in mind, however, that that ancient intebreeding even it is highly speculative. The authors write:

> The evidence **suggestive** of gene flow into Denisovans from an unknown hominin is interesting. The estimated age of 0.9 to 4 million years for the population split of this unknown hominin from the modern human lineage is compatible with that it contributed its mtDNA to Denisovans since the Denisovan mtDNA diverged from the mtDNA of the other hominins about 0.7–1.3 million years ago41. The estimated population split time is also compatible with the possibility that this unknown hominin was what is known from the fossil record as Homo erectus. This group started to spread out of Africa around 1.8 million years ago42, but Asian and African H. erectus populations may have become finally separated only about one million years ago43. **However, further work is necessary to establish if and how this gene flow event occurred.**

DennisVenema (Dennis Venema) 2018-03-27 18:55:20 UTC #887

I also agree that the HLA data is very interesting. I think that introgression and selection makes a lot more sense than convergent evolution in this case, for the following reasons:

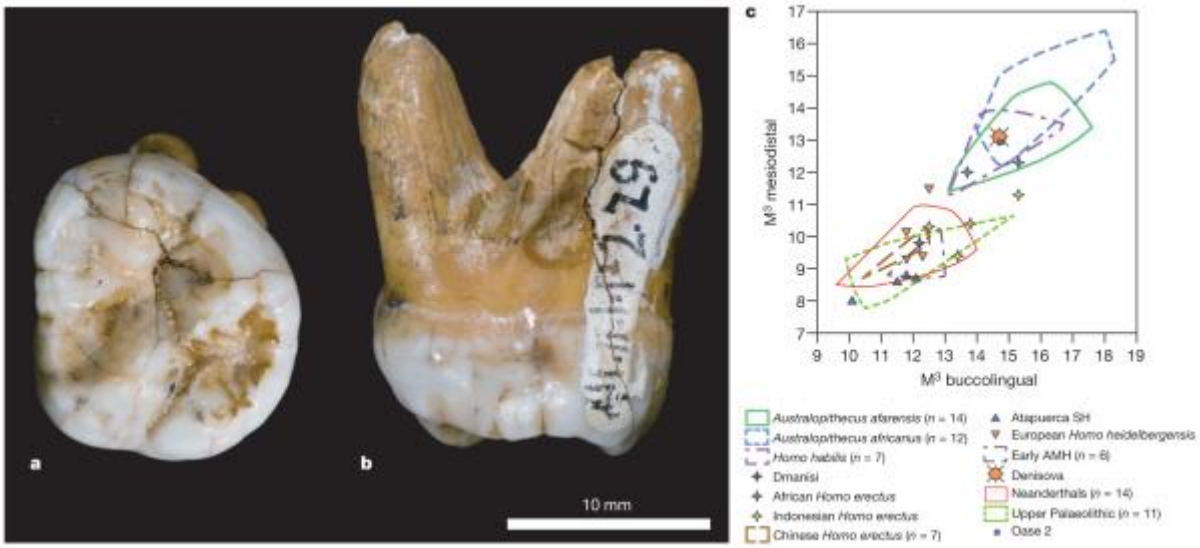
- we know that Neandertals and Denisovans had certain HLA alleles, which are generally under strong selection, and it makes sense that they would have had time for their alleles to come under selection in their local environments outside of Africa since they were there longer than humans have been.

- we know introgression took place, from the DNA evidence. As such, it is likely that those alleles entered Homo sapiens from these events
- since there is good reason to suspect that those same alleles would be adaptive for Homo sapiens in those same environments, it's not surprising that they were retained.
- the alternative hypothesis, of convergent evolution, is possible, but it would take longer to act. I would also expect more molecular differences if ti was convergence, but I haven't looked at it too closely.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 18:55:54 UTC #888

> Swamidass:
>
> that knuckle

And I do believe it is a tooth, not a knuckle. Is that right?



https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4306417/

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 18:59:21 UTC #889

> DennisVenema:
>
> I also agree that the HLA data is very interesting. I think that introgression and selection makes a lot more sense than convergent evolution in this case, for the following reasons:

That is possible but needs to be quantitatively tested. The qualitative arguments do not work here. Notice also how the divergence is extremely high? That appears to be because of very high rates of sequencing errors and DNA degradation. Inferences from sequences with this much error need to be made very carefully.

If convergent evolution has not been tested in the literature, we cannot rule it out unless we are willing to do the test ourselves. Given the extremely high rate of convergent evolution in HLA, I'm not convinced this is going to bear out.

The evidence for Neanderthals, however, is stronger, because it seems to be lower error data, from more individuals, and also include a greater portion of the genome. We also have direct evidence in the form of that 25/75 individual. The evidence for Denisovan interbreeding is just much weaker on several fronts.

gbrooks9 (George Brooks) 2018-03-27 19:00:58 UTC #890

> Swamidass:
>
> There are two hypothesis:
>
> No bottleneck in our lineage, ever.
> At least one bottleneck in our lineage.
>
> We do not have the data, yet, it seems to distinguish these two hypothesis. The right answer is “we do not know” not “heliocentric certainty for H1”.

@Swamidass

Do you write these things… just so you can get my reaction?

You have left out one last hypothesis, and it is the most crucial:

There are Three `[two]` hypothesis:

1] No bottleneck in our lineage, ever.
2] At least one bottleneck in our lineage, at any time. Or, most importantly,
3] At least one bottleneck in our lineage within the last 10,000 years.

The third one is the only one that matters… and I concur that we know that the hypothesis has been disproven to the same level of certainty I have for a heliocentric solar system.

DennisVenema (Dennis Venema) 2018-03-27 19:01:09 UTC #891

> Swamidass:
>
> Sort of. That hybrid was more neanderthal than human (25/75), but point taken. Regarding the Denisovan, you missed my point. It is possible that the Denisovans that interbred with Homo sapiens did not have DNA or ancestry with that ancient hominin. In that case, our lineage would never have to account for them.

Hmm - the hybrid I was thinking of was more human than Neanderthal - let me see if I can dig up the paper.

Yes, the evidence for introgression into the Denisovans is tentative. I’m just pointing out the evidence is there, and that folks who are happy to camp out at 700KYA might keep it in mind. I’ll go out on a limb here and say that in the next decade, we will find more evidence for introgression events between different hominin species, and that it will further cloud the conversation about sole genetic progenitorship. The other thing to keep in mind is that I see the data progressively pushing us further back in time, not pulling us forward in time.

There is also some good evidence that there were introgression events into sub-Saharan Africans. If we ever find hominin remains with matching DNA that could shake things up as well. Too bad SSA is such a lousy location for obtaining preserved hominin DNA.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 19:02:40 UTC #892

> DennisVenema:

> The other thing to keep in mind is that I see the data progressively pushing us further back in time, not pulling us forward in time.

Um…the data just pulled us *forward* in time. =)

> DennisVenema:
>
> Yes, the evidence for introgression into the Denisovans is tentative. I'm just pointing out the evidence is there, and that folks who are happy to camp out at 700KYA might keep it in mind. I'll go out on a limb here and say that in the next decade, we will find more evidence for introgression events between different hominin species, and that it will further cloud the conversation about sole genetic progenitorship.

That is possible. We will see. At the moment, we need to give an accurate acount of what we know now.

> DennisVenema:
>
> Hmm - the hybrid I was thinking of was more human than Neanderthal - let me see if I can dig up the paper.

Please do.

DennisVenema (Dennis Venema) 2018-03-27 19:03:38 UTC #893

> Swamidass:
>
> Please do.

Here you are: **link**

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 19:05:44 UTC #894

> gbrooks9:
>
> **The third one is the only one that matters… and I concur that we know that the **
>
> hypothesis has been disproven to the same level of certainty I have for a heliocentric solar system

As I've already stated, this depends on several assumptions about God's action in human origins.

> Swamidass:
>
> The way I see the situation, is that there is data we have collected about human variation. There is, at this time, a wide range of models proposed to account for that data. However, there is not a single model proposed that can account for the data with a single couple origin less than 200 kya, without either (1) inferring ongoing miracles, (2) totally different biology for Adam and Eve (e.g. genetic mosaics), or (3) mutation rates an order of magnitude (or more) higher than we have ever observed in humans.

Relaxing those assumptions we cannot know for sure. It is not science at this point, but we cannot know for sure. I certainly do not know as certainly as I know that the earth moves around the sun.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 19:07:55 UTC #895

> Swamidass:
>
> Sort of. That hybrid was more neanderthal than human (25/75), but point taken. Regarding the Denisovan, you missed my point. It is possible that the Denisovans that interbred with Homo sapiens did not have DNA or ancestry with that ancient hominin. In that case, our lineage would never have to account for them.

> DennisVenema:
>
> Hmm - the hybrid I was thinking of was more human than Neanderthal - let me see if I can dig up the paper.

> DennisVenema:
>
> Here you are: link

You are right **@DennisVenema** . I was in error. It looks, instead, like it was about 9% Neandertal and 91% Sapien, like he had 1 great-grandparent neandertal.

DennisVenema (Dennis Venema) 2018-03-27 19:08:31 UTC #896

> Swamidass:
>
> If convergent evolution has not been tested in the literature, we cannot rule it out unless we are willing to do the test ourselves. Given the extremely high rate of convergent evolution in HLA, I'm not convinced this is going to bear out.

I think it was tested, but I don't recall offhand. Time to re-read more papers. 🙂

---

gbrooks9 (George Brooks) 2018-03-27 19:10:42 UTC #897

I will agree to your 3 points of stiupulation … if you will agree to include the 10,000 year time frame (at least once each time) in your future summaries of the options.

Every time you list the options without including at least one that respects the 10,000 year time frame, you are materially contributing to confusion in minds of at least one segment of the readership, and inevitably recreating the requirement to more clearly explain what you meant some time down the road…

DennisVenema (Dennis Venema) 2018-03-27 19:10:54 UTC #898

> Swamidass:
>
> like he had 1 great-grandparent neandertal.

Yes, the paper is a really cool one because the data indicate really recent Neandertal ancestry for that individual. It also shows that the hybrid great-grandparent seems to have interbred with Homo sapiens, and so on, down to this individual. I.e. the hybrid and his or her later offspring were accepted within the Homo sapiens group.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 19:18:38 UTC #899

> DennisVenema:
>
> Yes, the paper is a really cool one because the data indicate really recent Neandertal ancestry for that individual. It also shows that the hybrid great-grandparent seems to have interbred with Homo sapiens, and so on, down to this individual. I.e. the hybrid and his or her later offspring were accepted within the Homo sapiens group.

And I suppose my point is that this is very strong evidence. We do not have comparable evidence for Denisovans. We do not even know for sure if they looked more like an ape or a human. Their teeth were certainly very ancient looking.

---

glipsnort (Steve Schaffner) 2018-03-27 19:25:31 UTC #900

> Swamidass:
>
> As far as i know, we cannot find the entire Neandertal genome in human variation, just a small portion of it.

I believe that a least a third of the Neandertal genome can be found somewhere in today's human population.

> Swamidass:
>
> Moreover, it only seems that a portion of the Homo sapien genome (i.e. loci) shows signs of interbreeding. Is that not correct?

That is correct. Gene-rich regions are less likely to show interbreeding, suggesting the action of purifying selection.

---

glipsnort (Steve Schaffner) 2018-03-27 19:26:40 UTC #901

> Swamidass:
>
> And I do believe it is a tooth, not a knuckle. Is that right?

As the linked abstract states, the finger bone provided the genome, while the tooth contributed mtDNA.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 20:02:05 UTC #902

> glipsnort:
>
> I believe that a least a third of the Neandertal genome can be found somewhere in today's human population.

Do you know a reference for that? It would be great to have it.

> glipsnort:
>
> That is correct. Gene-rich regions are less likely to show interbreeding, suggesting the action of purifying selection.

Except HLA and CRISP gene regions are included. Once again, does raise the specter of convergen-evolution in these regions. Though that is not all the regions for neandertal.

> glipsnort:
>
> As the linked abstract states, the finger bone provided the genome, while the tooth contributed mtDNA.

Well there you go. Thanks.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 20:03:33 UTC #903

> gbrooks9:
>
> I will agree to your 3 points of stiupulation … if you will agree to include the 10,000 year time frame (at least once each time) in your future summaries of the options.
>
> Every time you list the options without including at least one that respects the 10,000 year time frame, you are materially contributing to confusion in minds of at least one segment of the readership, and inevitably recreating the requirement to more clearly explain what you meant some time down the road…

It is pretty clear where I stand here:

Reworking the Science of Adam - Peaceful Science

This last year, 2017 till now, we have been Reworking the Science of Adam. This brings us several new ways to think about Adam and Eve in human origins.

I might occasionally speak in shorthand, where in context it is clear what I mean. I have no problem taking to task people who quote mine me as supporting a YEC position.

AMWolfe (A.M. Wolfe) 2018-03-27 20:36:37 UTC #904

> RichardBuggs:
>
> I look forward to your responses to the objections I have raised to your use of: (1) the example of the Tasmanian Devils, (2) PSMC analysis, (3) the linkage disequilibrium study by Tenesa and colleagues, and (4) incomplete lineage sorting.

Hi **@DennisVenema** ,

Honest question from a complete amateur here. I hope it's pertinent. In your **Evolution Basics posts** on BioLogos that I read some years ago, I found the arguments from incomplete lineage sorting to be lucid, persuasive, and interesting. The very idea that there might be analogous genetic variation across different species, even through *complete* lineage

sorting, was mindblowing to me (and intuitive, once I thought about it). Are we now saying that a bottleneck of two — even millions of years ago, shortly after the chimp-human split — can accommodate lineage sorting data without postulating these miraculous, so-called mosaic genomes?

Please forgive me if this is an elementary question covered elsewhere in this 892-comment thread. It would be wonderful if you could give me a link and say, “I already explained that here: [link].” Fwiw, I did a search for Incomplete Lineage Sorting and it only brought up a single snippet — the one above from Richard in post #12. Unfortunately, searching for “ILS” gives me dozens of posts with the word “detaILS” in it. 🙂

Thanks for any response you may have time to give. I suppose it would be great to hear from any of the other biologists on the thread, too, but I’m directing the question to Dennis because it’s something he’s written a good bit about and I’m confused why it no longer seems to be relevant to the bottleneck question.

T_aquaticus 2018-03-27 20:52:46 UTC #905

> Swamidass:
>
> It is certainly fair to point out when conclusions depend on unwarranted and hidden assumptions. No one forced people to make those errors or to claim the evidence was on their side, when it was not.

I guess the point I was trying to make is that very often they weren’t hidden assumptions. They were part of the creationist argument.

> Swamidass:
>
> That is not correct.
>
> There are two hypothesis:
>
> No bottleneck in our lineage, ever.
> At least one bottleneck in our lineage.
>
> We do not have the data, yet, it seems to distinguish these two hypothesis. The right answer is “we do not know” not “heliocentric certainty for H1”.

It might be helpful go back a little bit in the conversation. This is what I had to say before:

“If the 2 person bottleneck crowd has to retreat to time periods where population models are necessarily ambiguous ***then we go back to the burden of proof problem inherent in that bottleneck hypothesis***. In order to work past the null hypothesis you have to have models that will detect a bottleneck if there was one. If the models and data do not allow you to reject the null hypothesis, then you stay with the null hypothesis.”

I was talking about the bottleneck hypothesis, and the null hypothesis that goes with it. The point I was trying to make is that if you start with the evidence there is no reason that you would never get to a conclusion of a bottleneck. The evidence simply doesn’t lead there.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 20:54:49 UTC #906

> T_aquaticus:

> I was talking about the bottleneck hypothesis, and the null hypothesis that goes with it. The point I was trying to make is that if you start with the evidence there is no reason that you would never get to a conclusion of a bottleneck. The evidence simply doesn't lead there.

Sure, but the same could be said of the hypothesis against a bottleneck. It is very symmetric ignorance we have here.

> T_aquaticus:
>
> I guess the point I was trying to make is that very often they weren't hidden assumptions. They were part of the creationist argument.

Not really. YEC scientsits almost uniformly hold that the genus Homo is human, not just sapiens.

The insistence that "human = Homo sapiens" seems to be disproportionately common amongst EC writers. It is very out of step with current thinking in the field.

T_aquaticus 2018-03-27 21:11:31 UTC #907

> Swamidass:
>
> Sure, but the same could be said of the hypothesis against a bottleneck. It is very symmetric ignorance we have here.

It is asymmetric with respect to the last 200,000 years. There is strong evidence (i.e. strong statistical significance) for a large continuous human population over that time period and no evidence for a 2 person bottleneck during that time. For the periods that our models and evidence can give us a reliable answer it doesn't support a 2 person bottleneck.

> Swamidass:
>
> Not really. YEC scientsits almost uniformly hold that the genus Homo is human, not just sapiens.

That simply isn't true. Here is a chart mapping out the diversity of opinions among YECs:

Creationist Classifications of Hominid Fossils

Specimen		Cuozzo (1998)	Gish (1985)	Mehlert (1996)	Bowden (1981) Menton (1988) Taylor (1992) Gish (1979)	Baker (1976) Taylor and Van Bebber (1995)	Taylor (1996) Lubenow (1992)
	ER 1813 (510 cc)	Ape	Ape	Ape	Ape	Ape	Ape
	Java (940 cc)	Ape	Ape	Human	Ape	Ape	Human
	Peking (915-1225 cc)	Ape	Ape	Human	Ape	Human	Human
	ER 1470 (750 cc)	Ape	Ape	Ape	Human	Human	Human
	ER 3733 (850 cc)	Ape	Human	Human	Human	Human	Human
	WT 15000 (880 cc)	Ape	Human	Human	Human	Human	Human

reference

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 21:20:02 UTC #908

> T_aquaticus:
>
> It is asymmetric with respect to the last 200,000 years. There is strong evidence (i.e. strong statistical significance) for a large continuous human population over that time period and no evidence for a 2 person bottleneck during that time. For the periods that our models and evidence can give us a reliable answer it doesn't support a 2 person bottleneck.

Of course I agree with that.

> T_aquaticus:
>
> That simply isn't true. Here is a chart mapping out the diversity of opinions among YECs:

Love the chart. Where did you get it from?

Nonetheless, they usually put Neandertals with Homo sapiens as "humans" too. Everything on the table here appears to be at the border of Homo genus. There is debate about what is in Homo and what isn't, and that is well known about YECs. It is also strong evidence that there is not sharp dividing line (or else why would they argue about it?).

The confusion about defining Homo, however, is different than claiming “human = Homo sapiens” which I do not think *any* of the listed people here make that claim.

YECs can believe a lot of crazy things, as can we all, but “human = Homo sapiens” does not appear to be one of the beliefs we can pin on them. That appears to be more of an EC failing.

---

gbrooks9 (George Brooks) 2018-03-27 21:31:21 UTC #909

> Swamidass:
>
> YECs can believe a lot of crazy things, as can we all, but “human = Homo sapiens” does not appear to be one of the beliefs we can pin on them. That appears to be more of an EC failing.

@T_aquaticus

Its been my experience that YECs are very quick to call Neanderthal “Homo sapiens with arthritis”.
And if pushed, they would probably call the other variants recently uncovered as more adaptations than evolutions…

T_aquaticus 2018-03-27 21:34:46 UTC #910

> Swamidass:
>
> Love the chart. Where did you get it from?
>
> Nonetheless, they usually put Neandertals with Homo sapiens as “humans” too. Everything on the table here appears to be at the border of Homo genus. There is debate about what is in Homo and what isn’t, and that is well known about YECs. It is also strong evidence that there is not sharp dividing line (or else why would they argue about it?).
>
> The confusion about defining Homo, however, is different than claiming “human = Homo sapiens” which I do not think any of the listed people here make that claim.
>
> YECs can believe a lot of crazy things, as can we all, but “human = Homo sapiens” does not appear to be one of the beliefs we can pin on them. That appears to be more of an EC failing.

At times it can feel like a constantly moving target, the purpose of which is to keep beliefs from being pinned down. Prior to all of the work that has gone into human genetic diversity I doubt you would have found very many people in the ID/creationist community who would have been on board with Adam and Eve being part of H. erectus with all of its ape-like features. It would be very interesting to poll the readership at ENV and see if they are ok with a 2 person bottleneck (i.e. genetic Adam and Eve) at 500,000 years ago within the H. erectus species.

T_aquaticus 2018-03-27 21:39:14 UTC #911

> gbrooks9:
>
> Its been my experience that YECs are very quick to call Neanderthal “Homo sapiens with arthritis”.

It’s been a while since I saw that old YEC chestnut. The first Neanderthal fossil did appear to have rickets which YECs misinterpreted as rickets being responsible for all of the physical differences between Neanderthals and modern

humans. The truth is that the specimen may have had rickets AS WELL AS many non-rickets associated features that differentiated it from modern humans.

---

gbrooks9 (George Brooks) 2018-03-27 21:46:01 UTC #912

> T_aquaticus:
>
> It's been a while since I saw that old YEC chestnut. The first Neanderthal fossil did appear to have rickets which YECs misinterpreted as rickets being responsible for all of the physical differences between Neanderthals and modern humans. The truth is that the specimen may have had rickets AS WELL AS many non-rickets associated features that differentiated it from modern humans.

@T_aquaticus , yes, of course it had rickets. And of course it is not Homo sapiens.

Old, "mostly" inaccurate positions are a specialty of that community… YEC's minimize the importance of differences between Homo [something] at the drop of a hat. If there is evidence of genetic sharing … they **will definitely** erase any distinctions. It's their methodology.

… even if we were to show we had genes from Homo erectus!

T.j_Runyon (T J Runyon) 2018-03-27 22:42:41 UTC #913

For what's it's worth I know of some researchers who consider the Dali specimen as a possible Denisovan (it's brow is also very similar to the Broken Hill Specimen. Though it's face is different). But of course we can't know without their DNA. Just thought this could lead to some interesting research for you.

DennisVenema (Dennis Venema) 2018-03-27 22:48:32 UTC #914

> T_aquaticus:
>
> Prior to all of the work that has gone into human genetic diversity I doubt you would have found very many people in the ID/creationist community who would have been on board with Adam and Eve being part of H. erectus with all of its ape-like features.

When I debated Georgia Purdom at LeTourneau university back around 2011 (?) she was fine with *Homo erectus* as human. Interestingly, when I debated Nathaniel Jeanson last year at SEBTS, he was trying to avoid the Neanderthal data. Part of the motivation was that he was trying to say present-day mitochondrial variation can be traced back to three women (the wives of Noah's sons). If you add Neandertal or Denisovan mtDNA to that mix it of course just doesn't work, and when I pressed him on that he claimed that Neandertal mtDNA was "too degraded" to be certain of its sequence. That's wrong, of course.

So, what exactly AiG thinks about erectus, Neandertals and Denisovans is a bit up in the air.

---

agauger (Ann Gauger) 2018-03-27 23:04:27 UTC #915

> DennisVenema:
>
> These are the correct questions to ask, and I guess it would fall to those investigating a sole genetic progenitor model (**@RichardBuggs** **@agauger** , others?) to say what their preference is.

Here are some quotes from the past: : Hössjer O, Gauger A, Reeves C (2016) Genetic modeling of human history part 1: comparison of common descent and unique origin approaches. BIOComplexity 2016 (3):1–15. doi:10.5048/BIO-C.2016.3

Out of Africa replacement
adherents also use various common descent assumptions (such as the divergence time of humans and chimps) and genetic diversity estimates between humans and archaic hominins, to predict a split between them about 500,000 years ago or earlier [28,75,76,77]. If this is true, it is remarkable that two populations, after such a long time of separation, were still able to get fertile offspring [78]. But even if this would be possible, because of the long separation, it is reasonable to believe that the offspring had low fitness, since our archaic ancestors had, most likely, accumulated many alleles which are deleterious for humans, before the admixture took place.
The large fraction of archaic DNA among present-day humans seems in view of this more reconcilable with a unique origin model in which Neanderthals and Denisovans are descendants of the first founding couple, and hence our fully human ancestors. Indeed, sequencing of mitochondrial DNA suggests that the diversity among Neanderthals is much smaller than among humans [79]. As a possible explanation, they could have been quite early descendants of the first man and woman.
And the close genetic resemblance between Neanderthals, Denisovans and people of today suggests that the morphological differences are mostly explained by changed gene expression due either to mutations of regulatory DNA or to epigenetic changes [80].

And from Science and Human Origins (2012) Chapter 13 Casey Luskin does not argue for a first pair, but he does argue for a “Big Bang” origin of the genus Homo.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 23:10:19 UTC #916

> T_aquaticus:
>
> At times it can feel like a constantly moving target, the purpose of which is to keep beliefs from being pinned down.

If that is true, then its all the more important to appropriately qualify scientific conclusions, rather than injecting silent assumptions into them. It leave them open to being overturned, as we have already seen here.

> T_aquaticus:
>
> Prior to all of the work that has gone into human genetic diversity I doubt you would have found very many people in the ID/creationist community who would have been on board with Adam and Eve being part of H. erectus with all of its ape-like features.

That is false. The motivation for including Homo erectus starts from the fossil record, not genetics. There is strong evidence that they are more human-like than ape-like. YEC's have, for a long time, incorporated that into their model by saying the whole Homo genus is fully human and easily distinguishable from apes. Whether that is true or not is another question, but it is just flat out wrong to say that they have been constantly changing the bar on this one.

The more likely question is that EC writers fixated on the 6 kya date, and ignored the rest of YECs were saying. They probably just were not listening closely enough.

> DennisVenema:
>
> So, what exactly AiG thinks about erectus, Neandertals and Denisovans is a bit up in the air.

Not really. He is saying they are human, but we can't measure the mtDNA correctly.

> T_aquaticus:
>
> It's been a while since I saw that old YEC chestnut. The first Neanderthal fossil did appear to have rickets which YECs misinterpreted as rickets being responsible for all of the physical differences between Neanderthals and modern humans. The truth is that the specimen may have had rickets AS WELL AS many non-rickets associated features that differentiated it from modern humans.

That's about right.

> DennisVenema:
>
> When I debated Georgia Purdom at LeTourneau university back around 2011 (?) she was fine with Homo erectus as human. Interestingly, when I debated Nathaniel Jeanson last year at SEBTS, he was trying to avoid the Neanderthal data. Part of the motivation was that he was trying to say present-day mitochondrial variation can be traced back to three women (the wives of Noah's sons). If you add Neandertal or Denisovan mtDNA to that mix it of course just doesn't work, and when I pressed him on that he claimed that Neandertal mtDNA was "too degraded" to be certain of its sequence. That's wrong, of course.

It will be really interesting to see how Jeanson handles the TMR4A data. It is identical to his mtDNA analysis, but with far more data and much much better measures of mutation rate. MtDNA mutation rate is nearly impossible to measure directly, in contrast with autosomal DNA, which we can measure and have measured very precisely. That data, however, falsifies his position. I wonder if he will try and respond…

Also, I'll say that some theologians have really appreciated TMR4A because it is easy to understand, and makes space for their position at an earlier date.

DennisVenema (Dennis Venema) 2018-03-27 23:22:40 UTC #917

> Swamidass:
>
> Not really. He is saying they are human, but we can't measure the mtDNA correctly.

Agreed. It was surprising to me, based on my conversation with Georgia, that Neandertals would even be an issue. I expected that Jeanson would argue that their mtDNA variation would fit within his model, but he went a different direction, saying it was too degraded to use.

Denisovans are even a worse problem for Jeanson, since their mtDNA divergence is even greater.

Swamidass (Dr. S Joshua Swamidass) 2018-03-27 23:38:40 UTC #918

> agauger:
>
> And the close genetic resemblance between Neanderthals, Denisovans and people of today suggests that the morphological differences are mostly explained by changed gene expression due either to mutations of regulatory DNA or to epigenetic changes

The same could be said of the differences between human and chimp. =)

---

agauger (Ann Gauger) 2018-03-27 23:52:25 UTC #919

> Swamidass:
>
> The same could be said of the differences between human and chimp. =)

Indeed. But more of them between humans and chimps than between humand and Neanderthals.

DennisVenema (Dennis Venema) 2018-03-28 00:47:17 UTC #920

Ann (**@agauger**) - if I'm reading you correctly, introgression of ancient hominin DNA into Denisovans would then be problematic in your view, unless that unknown hominin population also descended from Adam and Eve?

Or, in the alternative view, if it's due to ancient population structure, you'd be ok with moving the TMR4A back to match the data? Just curious how this evidence plays into your thinking.

DennisVenema (Dennis Venema) 2018-03-28 00:58:38 UTC #921

> AMWolfe:
>
> Hi **@DennisVenema** ,
>
> Honest question from a complete amateur here. I hope it's pertinent. In your Evolution Basics posts on BioLogos that I read some years ago, I found the arguments from incomplete lineage sorting to be lucid, persuasive, and interesting. The very idea that there might be analogous genetic variation across different species, even through complete lineage sorting, was mindblowing to me (and intuitive, once I thought about it). Are we now saying that a bottleneck of two — even millions of years ago, shortly after the chimp-human split — can accommodate lineage sorting data without postulating these miraculous, so-called mosaic genomes?
>
> Please forgive me if this is an elementary question covered elsewhere in this 892-comment thread. It would be wonderful if you could give me a link and say, "I already explained that here: [link]." Fwiw, I did a search for Incomplete Lineage Sorting and it only brought up a single snippet — the one above from Richard in post #12. Unfortunately, searching for "ILS" gives me dozens of posts with the word "detaILS" in it. 🙂
>
> Thanks for any response you may have time to give. I suppose it would be great to hear from any of the other biologists on the thread, too, but I'm directing the question to Dennis because it's something he's written a good bit about and I'm confused why it no longer seems to be relevant to the bottleneck question.

Great question. The short answer is that we can observe ILS even with small numbers of alleles that could be, in theory, transmitted through a bottleneck - or even with single alleles. In other words, even if a really severe bottleneck did happen, we still would expect to observe ILS.

The ILS data gives us an opportunity to “check in” on our lineage at various time points along the way, prior to species divergence. We can use it to estimate the common ancestral population of two present-day species. The human, chimp common ancestral population comes in at around 50,000 or so, as do the (human, chimp, gorilla) and (human, chimp, gorilla, orang-utan) populations. After two lineages diverge, the technique is not informative for ruling out bottlenecks after that time point. For that, we look to other techniques - PSMC, MSMC, ancestral recombination graphs (ARGs), and so as we have been discussing in this thread.

Now, ILS is also fantastic evidence for common ancestry, and it’s a line of evidence I’ve not seen adequately addressed by any anti-evolutionary source. **IDers even go so far as to claim it’s an ad-hoc attempt to explain away problems for evolution**, but that is just silly for anyone for knows the field. We expect it, and we predicted it in advance before we sequenced chimps, gorillas and orangs.

---

glipsnort (Steve Schaffner) 2018-03-28 01:35:51 UTC #922

> Swamidass:
>
> Do you know a reference for that? It would be great to have it.

This paper reconstructs more than 1 Gb of Neandertal haplotype in modern humans. **This one** identifies 20% of the Neanderthal genome, but reports simulation results suggesting that 35% - 70% persists in modern humans.

> Swamidass:
>
> Except HLA and CRISP gene regions are included. Once again, does raise the specter of convergen-evolution in these regions. Though that is not all the regions for neandertal.

I’m not sure what you’re suggesting. Convergent evolution causes greater similarity, and therefore greater difficulty in detecting introgression? In any case, this is a broad effect across the genome, which is not at all what I would expect from convergent evolution.

---

glipsnort (Steve Schaffner) 2018-03-28 01:46:48 UTC #923

> Swamidass:
>
> Sure, but the same could be said of the hypothesis against a bottleneck. It is very symmetric ignorance we have here.

For me, that depends on what question you’re asking and (to some extent) on what your approach is to hypothesis testing. I’m a Bayesian at heart (at least on Tuesdays), so I’m fine with explicitly incorporating background knowledge into one’s prior. In this case, if you are posing a purely *scientific* question about whether a largish mammal underwent a population collapse to single pair followed by a massive increase in population size, I would place a very small prior probability on that scenario. It would be a very odd situation in which such a crash would not lead to extinction, whereas more or less stable population sizes are quite common. (Note that a small founder population during range expansion is a different scenario, and a more plausible one. But that would not meet the conditions required here.)

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 02:10:04 UTC #924

> glipsnort:
>
> I'm not sure what you're suggesting. Convergent evolution causes greater similarity, and therefore greater difficulty in detecting introgression? In any case, this is a broad effect across the genome, which is not at all what I would expect from convergent evolution.

I agree. This is just a question about Denisovans, not Neandertals. Denisovans have a much smaller amount of their genomes similar to us.

DennisVenema (Dennis Venema) 2018-03-28 02:30:11 UTC #925

> glipsnort:
>
> if you are posing a purely scientific question about whether a largish mammal underwent a population collapse to single pair followed by a massive increase in population size, I would place a very small prior probability on that scenario. It would be a very odd situation in which such a crash would not lead to extinction, whereas more or less stable population sizes are quite common.

Not only does it not lead to extinction, the conditions are such that *exponential* population growth occurs immediately after the crash. I asked earlier for **@RichardBuggs** to speculate what might have led to these remarkable events, but I didn't see a reply.

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 02:48:06 UTC #926

> DennisVenema:
>
> exponential population growth

Why is that so hard to believe? Whenever you are below carrying capacity, growth is exponential.

DennisVenema (Dennis Venema) 2018-03-28 02:55:53 UTC #927

> Swamidass:
>
> Why is that so hard to believe? Whenever you are below carrying capacity, growth is exponential.

What caused the catastrophic decline prior to the expansion?

DennisVenema (Dennis Venema) 2018-03-28 02:57:26 UTC #928

> glipsnort:
>
> I'm a Bayesian at heart (at least on Tuesdays

What's your prior for that? 😄

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 02:57:45 UTC #929

> DennisVenema:
>
> What caused the catastrophic decline prior to the expansion?

Natural disaster? Act of God?

There does not need to be a catastrophic decline any ways. Geographic isolation. Cultural isolation. Etc.

DennisVenema (Dennis Venema) 2018-03-28 03:02:04 UTC #930

> Swamidass:
>
> Natural disaster? Act of God?
>
> There does not need to be a catastrophic decline any ways. Geographic isolation. Cultural isolation. Etc.

If a natural disaster occurred, it was very widespread - Hominins are spread out all over Africa, Asia, Europe… how could an event occur that would wipe out all of them except two? Not seeing it.

Geographical isolation? Permanently? How?

Cultural isolation? Suddenly, with no genetic exchange? Not following you here either.

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 03:10:28 UTC #931

> DennisVenema:
>
> Cultural isolation? Suddenly, with no genetic exchange? Not following you here either.

Imagine a context where this is the first couple with symbolic thought and a theory of mind. It is the first couple with language. That could be enough to keep their kids from interbreeding with those around them, even if they were biologically compatible. They would not be able to see the others as one of them.

Also there is a genetic interference as a possibility too.

Taking theology into account, maybe they are the first with souls and know it. Maybe they see the others around them as non-human, and do not want to interbreed with them. Who knows.

Maybe all hominids die across the globe and God resurrects two of them. Who knows. Not science, but possible and not ruled out by evidence.

> DennisVenema:
>
> If a natural disaster occurred, it was very widespread - Hominins are spread out all over Africa, Asia, Europe… how could an event occur that would wipe out all of them except two?

Does not have to be global. All it has to be is a natural disaster that locally reduces a population to a single couple. As long as there is enough time to sufficiently differentiated, and they become the only surviving lineage, that would do it.

I'm not arguing that any of these events happened. But there are several scenarios that could be possible.

DennisVenema (Dennis Venema) 2018-03-28 03:30:15 UTC #932

Ok, but I thought we were asking for scientifically plausible events. Suddenly acquired discontinuous characteristics, first souls, and God resurrecting two hominins don't fit in that category.

Geographic isolation with no genetic exchange isn't plausible either. You yourself have modelled this. If Tasmania can be reached, as you've argued, there isn't anywhere on the African or Eurasian continents that we can reasonably expect to stay isolated for any length of time.

DennisVenema (Dennis Venema) 2018-03-28 03:32:59 UTC #933

> Swamidass:
>
> Not science, but possible and not ruled out by evidence.

The idea that the first two hominins on the planet were dropped off by visiting aliens (Star Trek, anyone?) is also possible and not ruled out by evidence. So are any number of other ideas. I don't see those criteria as particularly helpful.

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 03:33:04 UTC #934

> DennisVenema:
>
> Ok, but I thought we were asking for scientifically plausible events.

Strong genetic interference can do it too, especially if it is selectively advantageous.

It is possible, also, that there were jumps or leaps in abilities. That is a live possibility. We do not know exactly how a theory of mind arose, at it has only arisen once.

Though I agree, many of those scenarios are inferring something special about that bottleneck couple.

T.j_Runyon (T J Runyon) 2018-03-28 03:34:36 UTC #935

An intergalactic space stork?

DennisVenema (Dennis Venema) 2018-03-28 03:35:53 UTC #936

Star Trek tries to retroactively explain why so many species resemble humans through some sort of DNA mumbo-jumbo. I thought it might be fun to riff on that idea a bit. 😉

Edit: here you go. Star Trek's **ancient hominin panspermia**.

Christy (Christy Hemphill) 2018-03-28 03:51:24 UTC #937

> Swamidass:
>
> Not really. YEC scientsits almost uniformly hold that the genus Homo is human, not just sapiens.

But that is just part and parcel of denying the fossil record and insisting there is no such thing as “cavemen”, not an actual reasoned to position based on facts or “current thinking in the field.” It’s completely irrelevant to the discussion at hand, where consensus timelines are being assumed.

Christy (Christy Hemphill) 2018-03-28 04:07:36 UTC #938

> Swamidass:
>
> It is the first couple with language.

How is this even possible? “Language” is not a concrete thing one possesses or doesn’t possess like the knowledge of how to make fire. Language development surely happened on a continuum that moved from a simpler verbal/gestural semiotic system to a more complex one. It was surely communicated socially from one generation to the next. Deciding exactly when this semiotic system qualified as a full-fledged language would be an arbitrary designation and there wouldn’t be much difference between how the parents talked and how the children talked. Language has to be acquired as a baby/child from a caregiver. You’re talking about it like some couple somewhere invented human verbal communication de novo and then had no one else to talk to except their own children. This sounds utterly ridiculous to me from a linguistic perspective. You should strike this “maybe” from your list.

AMWolfe (A.M. Wolfe) 2018-03-28 04:07:53 UTC #939

> DennisVenema:
>
> After two lineages diverge, the technique is not informative for ruling out bottlenecks after that time point.

Thank you for the helpful explanation! That makes sense.

It seems to me that if you had a situation with multiple alleles where the number of alleles was greater than four and all of them were observable in chimpanzees, this would be a serious challenge for the bottleneck of two. But what I’m reading between the lines is that perhaps the vast majority of genes don’t have that many alleles. This is the kind of fact that’s probably patently obvious to anyone who’s worked with genetics, but not obvious to a complete layman like me. 🙂

Thanks again!
AMW

DennisVenema (Dennis Venema) 2018-03-28 04:13:04 UTC #940

> AMWolfe:
>
> It seems to me that if you had a situation with multiple alleles where the number of alleles was greater than four and all of them were observable in chimpanzees, this would be a serious challenge for the bottleneck of two. But what I’m reading between the lines is that perhaps the vast majority of genes don’t have that many alleles.

You've got it. We have examples of complete lineage sorting (i.e. the same alleles in two species) with up to four alleles - but, four alleles could possibly pass through 2 people (two different alleles in each person). If we ever do observe more - and it could happen, because we don't have a decent survey of chimpanzee or gorilla variation - we would have a situation where those alleles could not have passed through 2 people. The remaining fallback position here would be convergent evolution - that the excess allele(s) arose independently in the two lineages after the bottleneck.

DennisVenema (Dennis Venema) 2018-03-28 04:18:00 UTC #941

> Christy:
>
> How is this even possible? "Language" is not a concrete thing one possesses or doesn't possess like the knowledge of how to make fire. Language development surely happened on a continuum that moved from a simpler verbal/gestural semiotic system to a more complex one.

Even the knowledge of how to control fire and eventually produce it from scratch was probably gradually obtained. But the idea that there was a first couple with language and that isolated them from their previous population is even more of a stretch. If it was so discontinuous, how did two hominins - and only two - acquire this ability de novo?

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 04:41:09 UTC #942

> DennisVenema:
>
> > How is this even possible? "Language" is not a concrete thing one possesses or doesn't possess like the knowledge of how to make fire. Language development surely happened on a continuum that moved from a simpler verbal/gestural semiotic system to a more complex one.
>
> Even the knowledge of how to control fire and eventually produce it from scratch was probably gradually obtained. But the idea that there was a first couple with language and that isolated them from their previous population is even more of a stretch. If it was so discontinuous, how did two hominins - and only two - acquire this ability de novo?

We do not know how quickly these things progressed. Do we? You are putting forward rationale for why it might be gradual, but there is rationale for why it might not be gradual too, at least at points. As far as a I know, from evidence, we cannot discriminate which one is correct.

I understand you are working with a mental model of fine-grain gradualism, but there is at times saltations in evolutionary processes.

I'm not asking you to change your mental model, but to just see things from a different view for just a moment. Even from a secular point of view, there are evolutionary biologists that have posited sharp breaks or saltations in the evolution of the human mind (see **here**). Even Wallace, the equal co-discoverer of evolution with Darwin, wondered about the need for a leap in the evolution of the human mind. None of this means non-natural processes are required, but the insistence on fine-grained gradualism is not a requirement of the data.

As to why just two, maybe it was luck or maybe providence. Varki puts forward in the link above that perhaps a full theory of mind is improbable to evolve because awareness of one's own death is profoundly non-adaptive. Maybe it required two people evolving it at the same moment to be able to be adaptive; and that is very unlikely, but that is the

most likely way to cross that barrier. Varki, to be clear, is not writing from a Christian point of view, but in an entirely scientific speculation.

There are mysteries about the details of our origins. Rather than insisting our personal instincts are correct, its better to just say “we do not know.”

DennisVenema (Dennis Venema) 2018-03-28 04:58:26 UTC #943

> Swamidass:
>
> evolutionary biologists that have posited sharp breaks or saltations in the evolution of the human mind

I haven’t read the book, but from the reviews that describe it, it seems that there author is working within a population, and that a theory of mind (TOM) was gradual, not a sharp break. The idea that two individuals discontinuously achieve TOM in the absence of their contemporaries doesn’t seem to be what is being advanced here. Am I reading this correctly?

DennisVenema (Dennis Venema) 2018-03-28 05:00:49 UTC #944

> Swamidass:
>
> Rather than insisting our personal instincts are correct, its better to just say “we do not know.”

As a scientist, I’m trained to be skeptical and seek plausible explanations. I’m not insisting that my instincts are correct. What I am interested in is the best possible case for a 2-person bottleneck. These issues arise out of that interest. I’m especially interested in what folks who favour a 2-person bottleneck have to say about it. Paging **@RichardBuggs** and **@agauger** once more…

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 05:15:51 UTC #945

> DennisVenema:
>
> As a scientist, I’m trained to be skeptical and seek plausible explanations.

That is not what scientists do, as far as I know.

Instead, we look to test hypotheses with data, and we are very careful not go beyond what the data tells us when making scientific claims. Plausibility, after all, is in the eye of beholder. Skepticism as you are using it is selective. The same skepticism could and should be directed to all positions, including yours.

I’ve already said that the evidence is not going to tell us one way or another. I do not think there is a strong evidential case for a bottleneck, or against it. Science is not good with singular events in the distant past. So this should be no surprise.

> DennisVenema:
>
> I haven’t read the book, but from the reviews that describe it, it seems that there author is working within a population, and that a theory of mind (TOM) was gradual, not a sharp break. The idea that two individuals

> discontinuously achieve TOM in the absence of their contemporaries doesn't seem to be what is being advanced here. Am I reading this correctly?

You are not reading it correctly. (no suprise because you are not reading it)

Varki is arguing that there may have been largely smooth development of the human mind, but at some point there was a very difficult to cross barrier. The indirect evidence he marshals to this point is that there are no other animals with a full theory of mind. None of our cousin species seem to have achieved it, so it must be hard to achieve. If it is so adaptive too, why is that? His resolution is that there is a difficult barrier when it first arises that usually ends it before it can become adaptive. It is a very unlikely event.

That is a reasonable theory. Very difficult to test, but its just as "plausible" as yours. And if this is the case, central to thesis is that there is a sharp difference between before and after in our minds. A sharp difference that can easily account for the absence of interbreeding. He even explains this at length, all from a secular point of view.

DennisVenema (Dennis Venema) 2018-03-28 05:34:39 UTC #946

You're saying that he posits this happening to just an individual? or a pair? and not to the rest of those individuals' contemporaries?

Edit: it's not a theory. It's at best a hypothesis.

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 05:48:14 UTC #947

> DennisVenema:
>
> You're saying that he posits this happening to just an individual? or a pair? and not to the rest of those individuals' contemporaries?

He argues that it happens many times in individuals, but usually ends in that individuals failure to reproduce. Then in one rare case in a single individual it persists, because s/he is so unlikely to have simultanuosly evolved the capacity for reality denial. This get's him/her over the barrier of knowing his/her mortality, but not letting this become non-adaptive.

A critical feature of this model is that there is a sharp transition in the evolution of the human mind, which you do not seem to allow for.

I'm suggesting that one other way it's possible that the barrier (if it exists) could be crossed is if two individuals (a mating couple) are so unlikely as to simultaneously evolve the capacity for a theory of mind at the same time. Perhaps their companionship and ability to connect gets them over. That is my innovation for the purpose of putting forward an alternate reason for why something so profoundly adaptive only appear to have evolved one time in all history.

Wither its a theory or a hypothesis, its not clear how to rule it in or out with evidence. We just do not know.

DennisVenema (Dennis Venema) 2018-03-28 05:55:56 UTC #948

> Swamidass:
>
> A critical feature of this model is that there is a sharp transition in the evolution of the human mind, which you do not seem to allow for.

I'd be happy to consider evidence for it. These ideas, while interesting, are not evidence. They're speculation, and I don't see an easy way to test the idea.

Taking this speculation further, that this happened simultaneously to two individuals in close proximity and that it became reproductively isolating for them… again, this is speculation, and I see no way to even begin to test it.

---

agauger (Ann Gauger) 2018-03-28 06:16:31 UTC #949

> DennisVenema:
>
> Or, in the alternative view, if it's due to ancient population structure, you'd be ok with moving the TMR4A back to match the data? Just curious how this evidence plays into your thinking.

@DennisVenema , I am OK with moving the TMR4A back. I have said based on fossils it could go back to the origin of Homo. I know this puts it well beyond what most would consider Adam and Eve, but then that was true for 500-700 kya anyway.

---

agauger (Ann Gauger) 2018-03-28 06:31:12 UTC #950

@Christy
Have you seen this paper? These are some pretty big names, and they see no evidence for the gradual emergence of language.

> **The mystery of language evolution**
>
> Understanding the evolution of language requires evidence regarding origins and processes that led to change. In the last 40 years, there has been an explosion of research on this problem as well as a sense that considerable progress has been made. ...

DennisVenema (Dennis Venema) 2018-03-28 06:34:47 UTC #951

> agauger:
>
> I am OK with moving the TMR4A back. I have said based on fossils it could go back to the origin of Homo. I know this puts it well beyond what most would consider Adam and Eve, but then that was true for 500-700 kya anyway.

Thanks for clarifying. I guess the real question then is why you see a divide between Homo and the australopithecines, but that's a conversation for another day.

DennisVenema (Dennis Venema) 2018-03-28 06:47:43 UTC #952

> agauger:
>
> Have you seen this paper? These are some pretty big names, and they see no evidence for the gradual emergence of language.

I skimmed the paper, and I'm not seeing how you draw this conclusion. Can you elaborate?

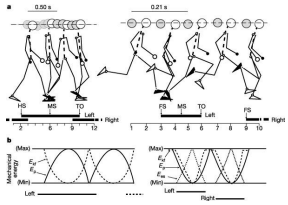
They also take a view that language is specific to Homo sapiens - not even Neandertals have it, etc. How would that square with your preference to include Neandertals, Denisovans, and possibly H. erectus as the descendants of Adam and Eve if they lacked language (to accept their claims for the sake of argument)?

---

agauger (Ann Gauger) 2018-03-28 06:51:42 UTC #953

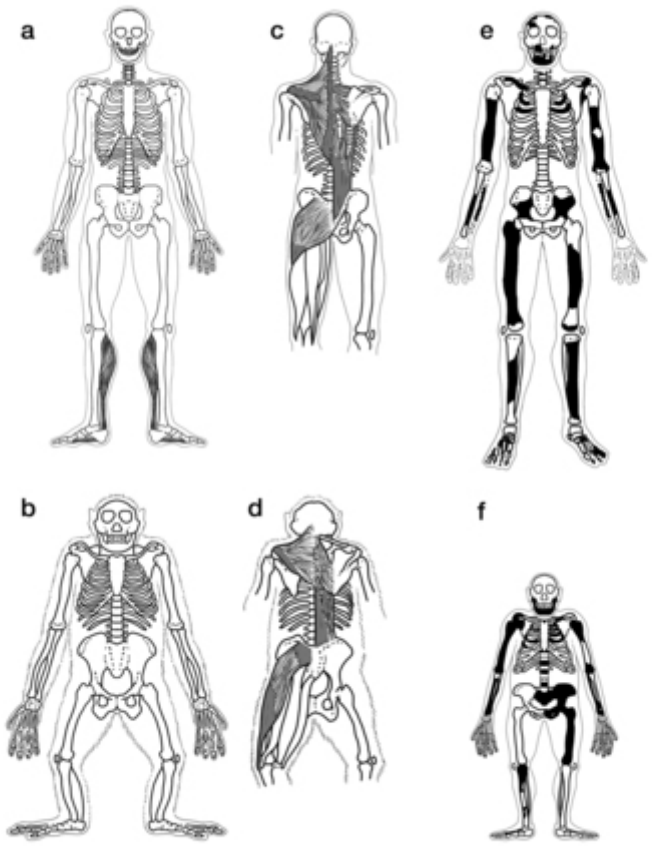
> DennisVenema:
>
> but that's a conversation for another day.

It's almost another day here. So this is a graphical image of why I see a divide between Homo and other hominins. a and c are human, e is Homo erectus. b and d are chimp and f is Austalopithecus (Lucy) Homo erectus emerges in Africa with precious few potential intermediates, but with a very different skeleton. He rapidly dispersed throughout Europe and Asia, with even some evidence that he sailed (!) to distant islands. Did he have a theory of mind? If he built boats and sailed them I would imagine that took cooperation, which I would propose requires a theory of mind. The figure by the way is a copy of one from Bramble and Lieberman.



Endurance running and the evolution of Homo

Endurance running and the evolution of Homo



DennisVenema (Dennis Venema) 2018-03-28 06:59:30 UTC #954

> agauger:
>
> It's almost another day here.

Yep, here too.

How does habilis fit into your thinking? Or nadeli? Or sediba?

agauger (Ann Gauger) 2018-03-28 07:25:21 UTC #955

@DennisVenema

> DennisVenema:
>
> How does habilis fit into your thinking? Or nadeli? Or sediba?

For habilis it's tricky because not everyone agrees where they group. I would place them as closer to Australopithecines than Homo. As to naledi, they are an oddball species, ape-like in their rib cages and arms, probably an offshoot of a non-Homo hominin. I know people argue they had intelligence because of how they were buried (buried themselves?). I

think we need more data. Lee Berger, who found naledi, is something of a sensationalist and controversial among paleoanthropologists. He is also responsible for claiming sediba as ancestral. Lots of disagreement there.

The record is really sparse between 3 and 2 mya. And hotly contested. There is no clear tree of ancestry leading to Homo. If anything it's a thicket with a gap.

Gaps can be filled, I acknowledge. But it's a pretty big gap from Lucy to Homo erectus.

Signing off.

T.j_Runyon (T J Runyon) 2018-03-28 07:40:03 UTC #956

I would like to see your reasons why for assigning Habilis closer to the Australopithecines than Homo. Naledi is very human like in the hands, feet and ankles. Long legs. I think naledi fits in the adaptive grade of Homo quite well. Also, I think its very premature to seriously discuss moving habilis out of homo. People like Wood who push this idea focus way too much on brain and body size. We need more post cranial remains before I think we can really consider something like that. Also, I think you have Lee wrong. Every time I've had the pleasure of meeting and speaking with him he came off very tentative. Especially with naledi (im aware of the various news reports and comments by those like Tim White).

DennisVenema (Dennis Venema) 2018-03-28 07:42:41 UTC #957

Thanks for sharing your thoughts, Ann. Goodnight!

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agauger (Ann Gauger) 2018-03-28 07:44:14 UTC #958

@Christy
It's late and it would take too long to go through each section. They begin by describing what it is about language and language acquisition we must explain. Then at every turn they say something like this:

The question of interest is whether these seemingly modest claims about animal signals help us understand the evolution of our capacity to represent words, including not only their referentiality but their abstractness, their composition via phonology and morphology, and their syntactic roles. Our simple answer is No, for five specific reasons: for animals, (i) acquisition of the entire lexicon is complete by the end of the early juvenile period, and for most species, the sounds or gestures are innately specified; (ii) those sounds and gestures refer, at best, to directly observable objects or events, with great uncertainty about the precise meaning, and no evidence for signals that map to abstract concepts that are detached from sensory experiences; (iii) with a few rare exceptions, individuals only produce single utterances or gestures, never combining signals to create new meaning based on new structures; (iv) utterances are holistic, with no evidence of complex syntactic composition derived from an inventory of discrete morphological elements; (v) the utterances or gestures are not marked by anything remotely resembling grammatical classes, agreement, etc. **Given these differences, it is not possible to empirically support a continuity thesis whereby a nonhuman animal form served as a precursor to the modern human form.**

They go through the fossil record, concluding that language developed after Neanderthals. I have seen other opinions, at least concerning the intellectual abilities of Neanderthals. Bottom line fossils can't tell us about the evolution of language.

Molecular biology and neurobiology: We don't know nearly enough.

Modelling: not grounded in experiment or the internal and external processes that are necessary for language to work.

They close with this:

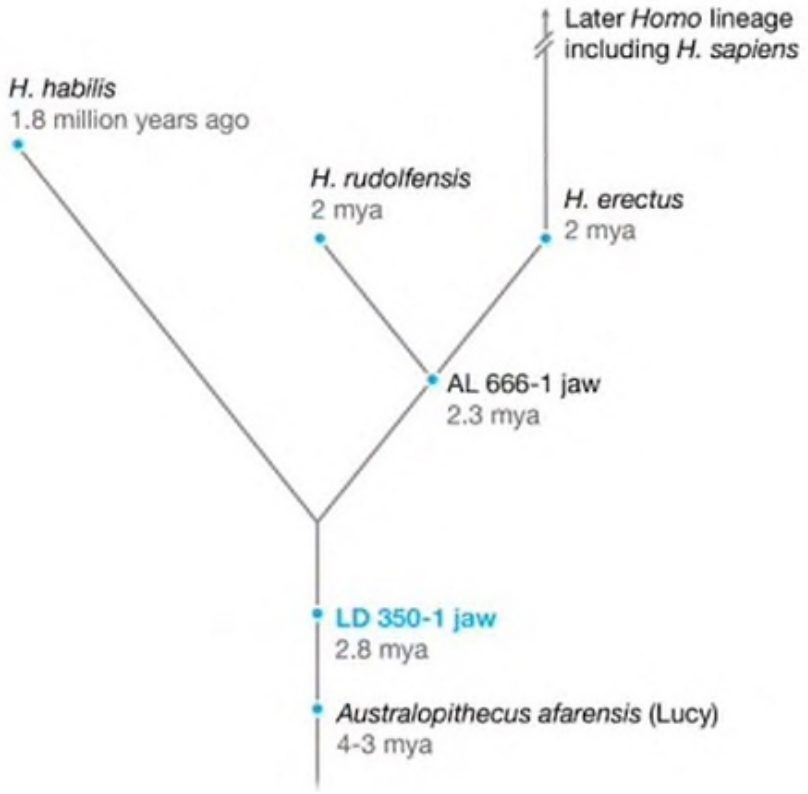
Should such discoveries from comparative animal behavior, paleontology, neurobiology, and archaeology be made, along with greater depth of understanding of gene-phenotype mapping, it would open the door to more relevant genomics and modeling. **These are all big IFs about the nature and possibility of future evidence.** Until such evidence is brought forward, understanding of language evolution will remain one of the great mysteries of our species.

They don't see any evidence. They believe that's what happened but can't find evidence of it.

Going to bed now, she said, while herding the dogs to the kennel and then turning out the light.

T.j_Runyon (T J Runyon) 2018-03-28 08:24:35 UTC #959

I defintely agree with you that the record is sparse between 3 and 2mya. But I would like your thoughts on LD-350-1



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glipsnort (Steve Schaffner) 2018-03-28 11:57:11 UTC #960

> Swamidass:
>
> Why is that so hard to believe? Whenever you are below carrying capacity, growth is exponential.

But it is rarely explosive growth, as required here. Rabbits, sure, but not hominins.

T.j_Runyon (T J Runyon) 2018-03-28 12:15:26 UTC #961

I don't think the gap is a big as you think it is. Let's say LD 350-1 is Homo, which I think it is. That's Homo at 2.8mya. Not too long after afarensis. There is also some debate over sediba. Australopithecine or Homo? What if it's Homo?

Well there's another Homo at 2 mya. So yes, more data would be fantastic but it's not a big of a gap potentially as some make it out to be. Habilis we need to withhold judgement right now. I think there is too much variation is Habilis to be one species so I take the position that it should be divided into two. H. habilis and H. rudolfensis. We just need more post cranial elements to make that decision. For instance if we found a limb bone of H. rudolfensis and it was like those of H. ergaster that would support keeping them in Homo

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Swamidass (Dr. S Joshua Swamidass) 2018-03-28 13:57:23 UTC #962

> glipsnort:
>
> But it is rarely explosive growth, as required here. Rabbits, sure, but not hominins

Why does it have to be explosive?

Christy (Christy Hemphill) 2018-03-28 14:16:17 UTC #963

> Swamidass:
>
> We do not know how quickly these things progressed. Do we? You are putting forward rationale for why it might be gradual, but there is rationale for why it might not be gradual too, at least at points. As far as a I know, from evidence, we cannot discriminate which one is correct.

There are better and worse models for language evolution, it's not guesswork and imagination. I'm just letting you know that you are speaking outside your area of expertise and what you are saying sounds ignorant. We aren't talking about a "rationale," we are talking about what we know about human language. We know a lot about child language acquisition, diachronic language change, and the cognitive psychology of language use. This knowledge is evidence based and allows us to create models of how languages develop, change, and are transmitted in communities. Throwing out a "we weren't there, so we can't know for sure" to license any old fantastical guess is as silly in this situation as it is in flood geology.

> Swamidass:
>
> I understand you are working with a mental model of fine-grain gradualism, but there is at times saltations in evolutionary processes.

What I know about biological evolutionary processes is irrelevant here, (and if it were just about evolution, I would be much less confident I know what I'm talking about) we are talking about linguistic evolution. How much have you actually looked into the specific topic of the evolution of language? Nothing you have said makes me think you have studied it.

> Swamidass:
>
> Even from a secular point of view, there are evolutionary biologists that have posited sharp breaks or saltations in the evolution of the human mind (see here).

Somehow equating the evolution of the human mind with language sounds completely unwarranted to me, because language is inherently a *socially* transmitted construct, not an intellectual capability. Every individual who speaks a

language was taught the language socially, it's not like geometry. No one just "figures it out" because they are smarter than the next guy.

> Swamidass:
>
> Rather than insisting our personal instincts are correct, its better to just say "we do not know."

But it's not my "personal instinct," Josh. It's basic facts I know about the field I work in and have two master's degrees in. I was doing you a favor by letting you know what you are proposing is laughable to people in my field. If you honestly just want to tell linguists that they need to ignore the consensus of their field and open their minds to imaginative scenarios with no basis in observed reality, well that sounds familiar, but it's not usually the kind of argument I'd expect from a scientist. 😉

> agauger:
>
> Have you seen this paper? These are some pretty big names, and they see no evidence for the gradual emergence of language.

Claiming the origins of human language are still a mystery is not the same thing as saying they see no evidence for the gradual emergence of human language. I only read the abstract, but where in this paper does anyone claim anything close to "language probably emerged with a discontinuous group"?

---

glipsnort (Steve Schaffner) 2018-03-28 14:41:06 UTC #964

> Swamidass:
>
> Natural disaster? Act of God?

I know of no natural disaster that would be widespread enough to reduce a large population and yet leave ideal conditions for subsequent rapid growth. What do you have in mind?

> Swamidass:
>
> There does not need to be a catastrophic decline any ways. Geographic isolation. Cultural isolation. Etc.

We have lots of examples of geographic and cultural isolation. None of them involve complete genetic isolation except when there is complete geographic isolation, which is not in view here.

> Swamidass:
>
> Imagine a context where this is the first couple with symbolic thought and a theory of mind. It is the first couple with language. That could be enough to keep their kids from interbreeding with those around them, even if they were biologically compatible. They would not be able to see the others as one of them.

I find that extremely implausible. Based on all historical evidence, humans will attempt to mate with just about anything that looks remotely human. They also have quite a strong aversion to incest (as do apes in general), which further discourages mating within a single family. This looks like an ad hoc hypothesis with no scientific motivation.

Jay313 (Jay Johnson) 2018-03-28 14:41:44 UTC #965

> Swamidass:
>
> YECs can believe a lot of crazy things, as can we all, but “human = Homo sapiens” does not appear to be one of the beliefs we can pin on them. That appears to be more of an EC failing.

You consistently confuse “human” as used in scientific literature and “human” as used in everyday discourse. Word meanings are determined by usage, not by fiat. In everyday usage, “human” is exactly equal to *H. sapiens*, which is not confusing at all to the average person since we are the only living example of the genus *Homo*. In scientific discourse, where many extinct examples of *Homo* must be taken into consideration, “human” takes on a different meaning. Constantly insisting that everyone use “human” in its scientific sense is a waste of time and energy, as well as a hindrance to actual communication.

> Swamidass:
>
> Imagine a context where this is the first couple with symbolic thought and a theory of mind. It is the first couple with language.

Chimps have theory of mind on the order of human children below the age of 5. (Yes, I used human in its colloquial sense.) This is presupposed by the fact that chimps practice deception. I can supply a citation, if you like.

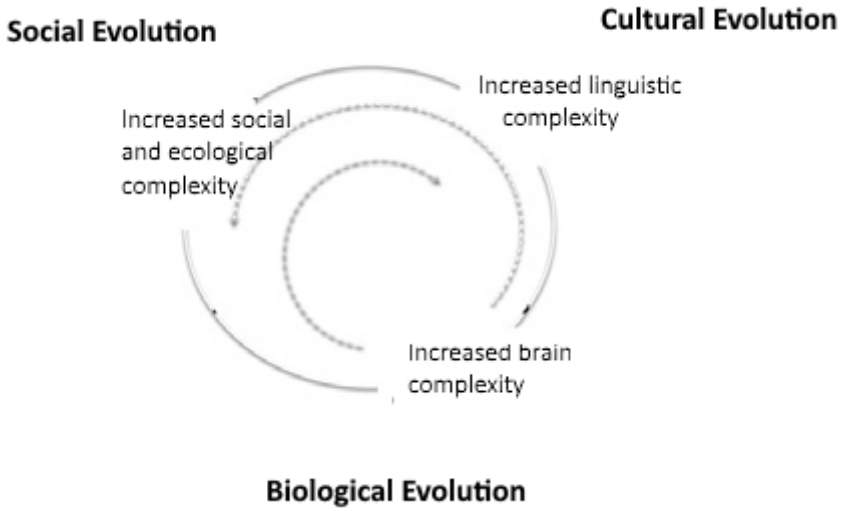
Language requires a population of speakers. It is as unlikely for two people to invent a language as it is for a single breeding pair to give rise to a species. The rest of your post is a long list of “maybe this, maybe that, maybe *maybe* **maybe**.”

> DennisVenema:
>
> They also take a view that language is specific to Homo sapiens - not even Neandertals have it, etc. How would that square with your preference to include Neandertals, Denisovans, and possibly H. erectus as the descendants of Adam and Eve if they lacked language (to accept their claims for the sake of argument)?

I don’t have time to read the paper right now, but I suspect the distinction is between full-blown “modern” language – with fully modern grammar – versus a “proto-language.” Proto-language can be of varying complexity, beginning from gestures and simple one-word communications, which do not require symbolicity. Proto-language most likely began with *erectus*, and Neanderthal certainly possessed an advanced form of it, although not fully modern language. Hope that helps.

> Christy:
>
> Somehow equating the evolution of the human mind with language sounds completely unwarranted to me, because language is inherently a socially transmitted construct, not an intellectual capability.

It was a spiral process.



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glipsnort (Steve Schaffner) 2018-03-28 14:42:41 UTC #966

> Swamidass:
>
> Why does it have to be explosive?

Because you've been looking for two-person bottlenecks that could escape detection – that won't be detected by PSMC, that don't reduce heterozygosity too much. A prolonged small population would not escape detection.

Jay313 (Jay Johnson) 2018-03-28 14:49:12 UTC #967

> glipsnort:
>
> This looks like an ad hoc hypothesis with no scientific motivation.

I find a whole lot of this going on. Check out the definition of an *ad hoc* auxiliary hypothesis in *Cladistics and the Origin of Birds*, p. 27 (emphasis mine):

An ad-hoc auxiliary hypothesis is one that has been formulated for the specific purpose of restoring agreement between a hypothesis and falsifying observations; **it serves no independent explanatory function and does not entail any significant, independently testable implications** (e.g., Hempel 1966, Popper 2002). Although ad-hoc auxiliary hypotheses are often used to protect favored hypotheses (Kuhn 1970), and **although they may be empirically valid, they actually interfere with testability** (Hempel 1966, Popper 2002) **by increasing the range of observations with which a hypothesis is compatible.** If the introduction of ad-hoc auxiliary hypotheses were considered legitimate, they could be used to **explain away all falsifying observations, rendering a favored hypothesis immune to any criticism.** Repeatedly obtained observations that contradict a hypothesis should be accepted as falsifying observations rather than explained away. **http://www.bio.fsu.edu/James/Ornithological%20Monographs%202009.pdf**

The "favored hypothesis," in this case, is that *ha'adam* ("the man") was an actual individual.

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 14:52:35 UTC #968

> glipsnort:
>
> Because you've been looking for two-person bottlenecks that could escape detection – that won't be detected by PSMC, that don't reduce heterozygosity too much. A prolonged small population would not escape detection.

The math and simulations we are doing show it's just fine to double every generation. With each couple having 4 kids. That is an annual growth rate of 1.2%, far lower that the ~3% inferred for long time spans amoung native americans. At that rate it is well beyond coallescent methods to detect.

---

glipsnort (Steve Schaffner) 2018-03-28 15:05:22 UTC #969

> Swamidass:
>
> The math and simulations we are doing show it's just fine to double every generation. With each couple having 4 kids. That is an annual growth rate of 1.2%,

I consider that explosive growth.

> Swamidass:
>
> far lower that the ~3% inferred for long time spans amoung native americans.

I'm not familiar with this estimate. Reference?

Jonathan_Burke (Jon) 2018-03-28 15:18:20 UTC #970

> Christy:
>
> Throwing out a "we weren't there, so we can't know for sure" to license any old fantastical guess is as silly in this situation as it is in flood geology.

This is very quotable.

Jonathan_Burke (Jon) 2018-03-28 15:21:24 UTC #971

> Jay313:
>
> Check out the definition of an ad hoc auxiliary hypothesis in Cladistics and the Origin of Birds, p. 27 (emphasis mine):

That's incredibly useful, thanks.

T_aquaticus 2018-03-28 15:37:44 UTC #972

> Swamidass:

> That is false. The motivation for including Homo erectus starts from the fossil record, not genetics. There is strong evidence that they are more human-like than ape-like. YEC's have, for a long time, incorporated that into their model by saying the whole Homo genus is fully human and easily distinguishable from apes. Whether that is true or not is another question, but it is just flat out wrong to say that they have been constantly changing the bar on this one.
>
> The more likely question is that EC writers fixated on the 6 kya date, and ignored the rest of YECs were saying. They probably just were not listening closely enough.

I would certainly like to be proven wrong. Can you cite any pre-2000's examples of creationists putting forward the idea that Adam and Eve were part of H. erectus in a time period of 200,000+ years before present? I am unaware of any such reference, but I hardly have a handle on all of the literature that exists from that time period.

Also, I doubt any YECs are putting forward the idea that any species existed 200,000 years ago.

T_aquaticus 2018-03-28 15:50:48 UTC #973

> agauger:
>
> Gaps can be filled, I acknowledge. But it's a pretty big gap from Lucy to Homo erectus.

It's a gap that has already been partially filled by A. sediba. At one time, there was a massive gap filled by no hominid fossils. Now we have many different hominid transitional species that fill those gaps. It would seem that the demarcation between Homo and Australopithecus is a subjective and arbitrary one that is a product of our ignorance more than knowledge.

---

agauger (Ann Gauger) 2018-03-28 15:55:48 UTC #974

> Christy:
>
> Claiming the origins of human language are still a mystery is not the same thing as saying they see no evidence for the gradual emergence of human language. I only read the abstract, but where in this paper does anyone claim anything close to **"language probably emerged with a discontinuous group"**?

@Christy ,
In fact, I did not say that they said "language probably emerged with a discontinuous group." I said they find no evidence for it. They have very strict requirements for what language is and what must be accounted for in any evolutionary explanation. This is described in a fairly lengthy section. And nothing they see in current research comes close to explaining it.

---

agauger (Ann Gauger) 2018-03-28 16:09:00 UTC #975

> T_aquaticus:
>
> It would seem that the demarcation between Homo and Australopithecus is a subjective and arbitrary one that is a product of our ignorance more than knowledge.

I agree. Where the line is drawn is influenced to some extent by point of view.

agauger (Ann Gauger) 2018-03-28 16:17:18 UTC #976

@T.j_Runyon ,

I'd like to see references about LD 350-1. I have no problems with Homo at 2 mya. Does sediba differ much in morphology from erectus or could they be variants of the same species? From what I read, early erectus had considerable variation in its skull, for example. What do you think of the fossils found at Dminisi?

---

agauger (Ann Gauger) 2018-03-28 16:26:32 UTC #977

> Jay313:
>
> Chimps have theory of mind on the order of human children below the age of 5. (Yes, I used human in its colloquial sense.) This is presupposed by the fact that chimps practice deception. I can supply a citation, if you like.

@Jay313 , I have read that but don't remember where. Can you give me the citation please?

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 17:17:55 UTC #978

> T_aquaticus:
>
> I would certainly like to be proven wrong. Can you cite any pre-2000's examples of creationists putting forward the idea that Adam and Eve were part of H. erectus in a time period of 200,000+ years before present? I am unaware of any such reference, but I hardly have a handle on all of the literature that exists from that time period.
>
> Also, I doubt any YECs are putting forward the idea that any species existed 200,000 years ago.

Of course they do not take that position, because they think everything is less than 10 ky old. Rather, they do usually think that Homo genus is "human". That is very well established, even by links you've offered here.

> agauger:
>
> > Claiming the origins of human language are still a mystery is not the same thing as saying they see no evidence for the gradual emergence of human language. I only read the abstract, but where in this paper does anyone claim anything close to "language probably emerged with a discontinuous group"?
> > **@Christy** ,
>
> In fact, I did not say that they said "language probably emerged with a discontinuous group." I said they find no evidence for it. They have very strict requirements for what language is and what must be accounted for in any evolutionary explanation. This is described in a fairly lengthy section. And nothing they see in current research comes close to explaining it.

This is an open question about which there are strong opinions and little evidence. Strong opinions are not findings. We'd do better to just say we do not know for sure, even though we are opinionated about it.

> agauger:

> > It would seem that the demarcation between Homo and Australopithecus is a subjective and arbitrary one that is a product of our ignorance more than knowledge.
>
> I agree. Where the line is drawn is influenced to some extent by point of view.

Agreed. Another case of strong opinions and little evidence.

> agauger:
>
> > Chimps have theory of mind on the order of human children below the age of 5. (Yes, I used human in its colloquial sense.) This is presupposed by the fact that chimps practice deception. I can supply a citation, if you like.
>
> **@Jay313** , I have read that but don't remember where. Can you give me the citation please?

I do not know if there is a good recent citation to it. I though the great ape language experiments put that hypothesis to bed a long time ago. Even 1 year old children can have more advanced language than a chimp (both articulated and comprehension). Yes, chimps can practice deception, but so can 1 year olds; that is not an indicator of a full theory of mind. Chimps cannot even use sign language in full sentences or handle counterfactuals, but at least some 1 year olds can. It seems to have become well established that there is very large differences between the human mind and that of all other animals. Of course, there are similarities, but there are also large differences.

> Christy:
>
> Claiming the origins of human language are still a mystery is not the same thing as saying they see no evidence for the gradual emergence of human language

You are reading me incorrectly. I never said that, nor do I believe that. My point is exactly the opposite.

> Christy:
>
> How much have you actually looked into the specific topic of the evolution of language? Nothing you have said makes me think you have studied it.

Quite a bit. I think you are misreading me.

> Christy:
>
> Throwing out a "we weren't there, so we can't know for sure" to license any old fantastical guess is as silly in this situation as it is in flood geology.

That in no way is what I have said. I would hope you would be able to draw distinctions between Ken Ham and me should possible. If that is really the comparison you think is appropriate, I suppose there is not really any place for continued engagement.

T_aquaticus 2018-03-28 17:33:45 UTC #979

> Swamidass:
>
> Of course they do not take that position, because they think everything is less than 10 ky old. Rather, they do usually think that Homo genus is “human”. That is very well established, even by links you’ve offered here.

Actually, there is a pretty wide array of positions on that matter within the YEC community. This is what Answers in Genesis has to say on the subject:

"The Javan and Peking forms of erectus in particular came under considerable attack by creationists in the 1970s and 1980s.8-10 The thrust of these critiques was that all erectus forms were extremely ape-like and even possibly fraudulent."

Homo erectus Modern Man: Evolution or Human Variability?

An interesting change is taking place in creationist circles in respect of the status of the taxon Homo erectus and its relationship to Homo sapiens sapiens.

I think it would be fair to say that attitudes towards H. erectus have changed quite a bit over time.

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 17:35:37 UTC #980

> T_aquaticus:
>
> Actually, there is a pretty wide array of positions on that matter within the YEC community. This is what Answers in Genesis has to say on the subject

Yes that is true.

> T_aquaticus:
>
> I think it would be fair to say that attitudes towards H. erectus have changed quite a bit over time.

However, right now, among YECs that are scientists trying to formulate their view, they almost uniformly say Homo genus = human. They do not say human = sapiens. In that one point, they are more aligned with the Natural History museum than EC writers.

The article you site, keep in mind is from 1994, nearly 25 years ago. That change happened, past tense.

T_aquaticus 2018-03-28 17:40:10 UTC #981

> Swamidass:
>
> However, right now, among YECs that are scientists trying to formulate their view, they almost uniformly say Homo genus = human. They do not say human = sapiens. In that one point, they are more aligned with the Natural History museum than EC writers.

That is part of the equation. The other part is putting Adam and Eve 250,000+ years in the past as part of a population that was entirely H. erectus. AiG and other YECs are arguing that H. erectus is essentially H. sapiens, and that they were all part of the same population as recently as 4,000 years ago. I'm not sure how that can be squared with the model that others are putting forward.

Jay313 (Jay Johnson) 2018-03-28 17:42:07 UTC #982

> agauger:
>
> Can you give me the citation please?

Here are two:

Humans aren't the only great apes that can 'read minds'

Soap opera experiment suggests chimps, bonobos, and orangutans can predict what others are thinking

HIGHER-ORDER THEORY OF MIND AND SOCIAL COMPETENCE IN SCHOOL-AGE CHILDREN

What Swamidass seems to miss is that ToM involves more than one layer of understanding. The first is understanding false beliefs, i.e. I know you believe something that is false. From the second article:

The consensus of such studies is that, through a progression of stages starting at around 2 years, normally developing children have acquired full competence on first-order ToM tasks by 5 years of age (WELLMAN et al., 2001).

Researchers working on adults, however, have developed more demanding tasks by probing recursive ToM understanding (second level: inferences about a belief about a belief; third level: inferences about a belief about a belief about a belief, and so on, up to fifth or in one case, eighth, level; KINDERMAN, DUNBAR, and BENTALL, 1998; STILLER and DUNBAR, in press). Such tasks involve reading or hearing multi-character stories, and inferring what one character believes about another character's belief, etc. Most adults perform much better than chance up to fourth level, but the error rate increases dramatically above this point (KINDERMAN et al., 1998).

Edit:

> Swamidass:
>
> I though the great ape language experiments put that hypothesis to bed a long time ago. Even 1 year old children can have more advanced language than a chimp (both articulated and comprehension). Yes, chimps can practice deception, but so can 1 year olds; that is not an indicator of a full theory of mind. Chimps cannot even use sign language in full sentences or handle counterfactuals, but at least some 1 year olds can.

Okay, I see the confusion. You are mixing up language development with Theory of Mind. Second-, third-, and fourth-order ToM virtually requires recursive language, but first-order ToM does not. Again, in order to practice deception, which chimps do every day as part of their social order, a chimp must understand false belief, even if it cannot express the concept.

Chris_Falter (Chris Falter) 2018-03-28 17:44:12 UTC #983

> agauger:
>
> If he built boats and sailed them I would imagine that took cooperation, which I would propose requires a theory of mind.

If cooperation implies the existence of a theory of mind, then many mammals, including non-primates, possess a theory of mind.

EDIT: Ravens, which practice deception, seem to possess a theory of mind as well.

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 17:51:51 UTC #984

> Jay313:
>
> Okay, I see the confusion. You are mixing up language development with Theory of Mind.

No. You are mistaking a theory of mind, for a full theory of mind, which is often thought to presuppose language. The two are intertwined.

Moreover, there is a pervasive equivocation between the development of language and the ontogeny of language.

Chris_Falter (Chris Falter) 2018-03-28 17:56:57 UTC #985

> Swamidass:
>
> I though the great ape language experiments put that hypothesis to bed a long time ago. Even 1 year old children can have more advanced language than a chimp (both articulated and comprehension). Yes, chimps can practice deception, but so can 1 year olds; that is not an indicator of a full theory of mind. Chimps cannot even use sign language in full sentences or handle counterfactuals, but at least some 1 year olds can

Hi Joshua, could you provide some references? I would love to read further.

Best,
Chris

Jay313 (Jay Johnson) 2018-03-28 17:59:09 UTC #986

> Swamidass:
>
> The two are intertwined.

Not in the way you think. But, I've said enough for now. Sorry for steering you in the right direction … haha. Enjoy the journey!

Christy (Christy Hemphill) 2018-03-28 18:11:11 UTC #987

> Swamidass:

> That in no way is what I have said.

You said:

> Swamidass:
>
> Imagine a context where this is the first couple with symbolic thought and a theory of mind. It is the first couple with language.

And then you went on to say we can't know anything for sure.

"The first couple with symbolic thought and a theory of mind; the first couple with language" is not plausible based on any definition of language that I am aware of. There is just no such thing as a "theoretical first couple with language" unless your "theories" about how language works are wacky. It's not a plausible "maybe." You should strike it from your list. I'm really pretty amused that you are sticking by it.

Swamidass (Dr. S Joshua Swamidass) 2018-03-28 18:59:32 UTC #988

> Chris_Falter:
>
> > I though the great ape language experiments put that hypothesis to bed a long time ago. Even 1 year old children can have more advanced language than a chimp (both articulated and comprehension). Yes, chimps can practice deception, but so can 1 year olds; that is not an indicator of a full theory of mind. Chimps cannot even use sign language in full sentences or handle counterfactuals, but at least some 1 year olds can
>
> Hi Joshua, could you provide some references? I would love to read further.

For this conversation, this article is an excellent must read. Notably, its authors include the great Noam Chomsky, essentially making the main point I've been making here. Likewise, acquisition of language does not necessarily mirror the origin of language. **There is a great deal of mystery in the origin of language, very little evidence, and a lot of ungrounded but strong opinions.**

> **The mystery of language evolution**
>
> Understanding the evolution of language requires evidence regarding origins and processes that led to change. In the last 40 years, there has been an explosion of research on this problem as well as a sense that considerable progress has been made. ...

Regarding the failure of the great apes in language experiments, this article is really good, quantitative and recent. A key point is that they cannot even achieve the point of forming sentences, but only two word phrases. My son at 12 months was *far* beyond Nim Chimpsky in acquisition of language, knowing at least 125 words (like chimpsky) but also putting them together occasionally into 5 word sentences (he was advanced). It also took *much* less effort for my son to acquire this competency than Chimpsky.

> **Ontogeny and phylogeny of language**

> How did language evolve? A popular approach points to the similarities between the ontogeny and phylogeny of language. Young children's language and nonhuman primates' signing both appear formulaic with limited syntactic combinations, thereby...

No matter how you cut it, chimps are quantitatively and qualitatively ***very*** far from human language. I had the privilege of talking about this with Ajit Varki on stage at UCSD a couple years back too. I wrote an article up about it, but the video is worth watching too.

More Than Just Apes - Peaceful Science

Scientifically speaking, humans appear to be genetically-modified apes. But are we just apes? Or are we more? Follow the conversation with Dr. Ajit Varki.

Regarding theory of mind, it was a common theme in my january Veritas forums.

Veritas Forums the Week Dad Died (January 2018)

So last part of January I did a whirlwind of 7 events in 2 universities, in just 3 days. As crazy as this was to plan for, the Saturday before, late at night, I received a phone call. My father was in the ER, without a pulse. He had just had a heart...

Reading time: 2 mins Likes: 5 ❤

In particular, the talk I gave at UCSB with a grief counselor, just following the mudslides in SB, on how humans grieve differently than animals is germaine to this conversation. Grief is one area the distinctions between human and animals is incomparable, partly because we have a full theory of mind, and they do not.

As for the surprising resistance to explaining the limits of scientific knowledge, it's remarkable how quickly things devolve…

> Christy:
>
> And then you went on to say we can't know anything for sure.

(I did not say that).

> Jonathan_Burke:
>
> > Throwing out a "we weren't there, so we can't know for sure" to license any old fantastical guess is as silly in this situation as it is in flood geology.
>
> This is very quotable.

(no, I am not making Ken Ham's argument)

> glipsnort:
>
> This looks like an ad hoc hypothesis with no scientific motivation.

(just like is the case for all scientific theories, **https://en.wikipedia.org/wiki/Duhem–Quine_thesis**)

> Christy:
>
> Somehow equating the evolution of the human mind with language sounds completely unwarranted to me, because language is inherently a socially transmitted construct, not an intellectual capability.

(yet we have been unable to socially transmit language or theory of mind to the great apes)

> Christy:
>
> What I know about biological evolutionary processes is irrelevant here, (and if it were just about evolution, I would be much less confident I know what I'm talking about) we are talking about linguistic evolution.

(no, we are talking about linguistic origin, *not* linguistic evolution, which is intertwined with biological evolution)

It is ironic that the first time I was similarly accused of pseudoscience and other such things on this forum was almost exactly a year ago, about genealogical science and the genealogical Adam. I ended up making my case in spades on that one.

Perhaps consider backing off the heated rhetoric, and realize that I've solidly justified several theses that, on face value, seemed absurd to this forum. I have a track record of demonstrating surprising things like this. Maybe lets not accuse me of total ignorance from the get go. Moreover, as a professor at a secular institution, I have much more at stake here than does almost everyone else (with some notable exceptions). I would not make claims here I could not justify thoroughly to my secular colleagues.

Jonathan_Burke (Jon) 2018-03-28 19:37:05 UTC #989

> Swamidass:
>
> I have a track record of demonstrating surprising things like this.

Right now you're throwing out half a dozen theses which you haven't demonstrated, and which you say may not be demonstrable at all. You're explicitly saying "Maybe", "We don't know", and "I'm not arguing that any of these events happened". So I doubt you're going to be demonstrating any of these "surprising things" any time soon, especially since you say you are not actually arguing for them.

You are very concerned about communication and how your readers "hear" you, so you need to consider what they hear when they read statements such as this.

- "We do not know how quickly these things progressed. Do we? You are putting forward rationale for why it might be gradual, but there is rationale for why it might not be gradual too, at least at points. As far as a I know, from evidence, we cannot discriminate which one is correct."

- “Taking theology into account, maybe they are the first with souls and know it. Maybe they see the others around them as non-human, and do not want to interbreed with them. Who knows.”
- “Maybe all hominids die across the globe and God resurrects two of them. Who knows. Not science, but possible and not ruled out by evidence.”
- “Does not have to be global. All it has to be is a natural disaster that locally reduces a population to a single couple. As long as there is enough time to sufficiently differentiated, and they become the only surviving lineage, that would do it.”
- “It is possible, also, that there were jumps or leaps in abilities. That is a live possibility. We do not know exactly how a theory of mind arose, at it has only arisen once.”
- “**I’m saying that it looks like we share common ancestry, not that we actually do. Taking into account God’s action we cannot be sure**.” [emphasis mine]

It should be clear to you that more than one person has “heard” these statements as ad hoc arguments aimed at supporting a specific concordist reading of Scripture. Ironically (given yesterday’s performance), Christy herself even “heard” you as advancing the same argument as Ken Ham.

The fact that several individuals sharing different views (including different views on Adam; I believe in a historical Adam less than 10,000 years ago, for example), are “hearing” the same message from what you write, should give you pause to consider how effectively you’re communicating.

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agauger (Ann Gauger) 2018-03-28 19:45:56 UTC #990

@Chris_Falter

See **@Jay313** ’s clarification on theory of mind, above. We face much the same difficulty in language studies. Animals have been represented as having rudimentary language, but when compared to what even two year old humans are capable of, it is clear there are significant gaps. A distinctive feature of both language and theory of mind is recursiveness, it would seem. David Premack, now deceased eminent psychologist, gave this example of recursiveness in human language:

> “Language evolved, it is conjectured, at a time when humans or protohumans were hunting mastodons… Would it be a great advantage for one of our ancestors squatting alongside the embers to be able to remark, Beware of the short beast whose front hoof Bob cracked when, having forgotten his own spear back at camp, he got in a glancing blow with the dull spear he borrowed from Jack”? He goes on to say, “Human language is an embarrassment for evolutionary theory because it is vastly more powerful than one can account for in terms of selective fitness.”

Quoted in Pinker, The Language Instinct, 387

Thank goodness no one usually speaks or writes like that, but we are capable of handling it, just as adults can follow the beliefs of characters about other characters to the fourth level.

I submit that such a quantum level jump in language, theory of mind, and abstract thought requires guided evolution *at a minimum* to explain things, or the possibility of sudden jumps, also guided. But not testable at this time, if ever. Maybe it will come down to models, as they discuss in the Hauser et al paper. Wouldn’t that be interesting–population genetics models that cannot rule out a first pair, language and theory of mind models that can’t rule out a jump, and inconclusive fossil evidence. Let’s work toward positive evidence.

But I submit, though this discussion is limited to scientific materialism, that nonmaterial explanations may be what we are left with. That's the elephant in the room in this discussion. When material explanations have failed, but we have a nonmaterial cause known to be able to produce the phenomena in question, it is a reasonable inference to make. The inference would be held in the same manner as all scientific hypotheses, that is, provisionally, and always subject to revision.

Given that this is BioLogos and most people are Christian (yes?) is this such an impossible answer?

Don't all jump on me at once.🙂

AMWolfe (A.M. Wolfe) 2018-03-28 19:50:55 UTC #991

Hello Joshua,

I hope all is well with you.

First of all, let me say, I don't actually like piling on. And I can agree with you that it's hard to say anything about the origin of language definitively, because language doesn't leave fossils, and we can't experiment with a Neanderthal called Neanderm Neandersky. 🙂

That said, you should know that quoting Hauser and Chomsky (and particularly calling him "great") is probably going to lose you ground with a lot of linguists, right out of the gate. You probably are aware that lead author **Hauser was disgraced for scientific misconduct some years back**. And Chomsky's linguistic theorizing is considered very poor-quality science by a great many linguists (not just Dan Everett of recent Forum mention). Folks in the functionalist-typological school (or working in Cognitive Linguistics or construction grammar), and anyone at, for instance, the Max Planck Institute, are generally much more solid scientifically, despite what Chomskian linguists may tell you to the contrary. Now, you can continue to quote Hauser and Chomsky, but just know that there will be lots of folks in the back snickering and wondering when you might get around to quoting linguists who do real science. Sorry… Just being honest, again, not particularly wanting to pile on. And perhaps the paper is quite relevant and error-free. I didn't actually spend time in the article. But sources matter.

> Swamidass:
>
> [Christy] Somehow equating the evolution of the human mind with language sounds completely unwarranted to me, because language is inherently a socially transmitted construct, not an intellectual capability.
>
> (yet we have been unable to socially transmit language or theory of mind to the great apes)

Pardon me, but this is a non sequitur of a comment. The development of language was (at least) a two-step process. First, we had to develop the capacity for language. Then, we had to develop language itself. You're saying that creatures that are without the capacity for language can't develop (or learn) language when we teach it to them. How is this germane? You might as well say that we've been unable to transmit language to rabbits, or lichen. The question is how language first developed among hominins with highly developed brains, not among Pan or Gorilla or Pongo.

I sometimes agree with your detractors here, but I appreciate your voice and trust you'll continue to stick it out here. It's helpful for all of us when we have contrarian voices in the mix.

Peace,
AMW

Jonathan_Burke (Jon) 2018-03-28 19:57:39 UTC #992

> agauger:
>
> When material explanations have failed, but we have a nonmaterial cause known to be able to produce the phenomena in question, it is a reasonable inference to make.

Yes. But first we must demonstrate all material explanations have failed. Medieval Christian writers made this point repeatedly. Behold their methodological naturalism.

Adelard of Bath.

> “Adelard’s emphasis on the use of reason is rather remarkable. His message is clear. He firmly believed that God was the creator of the world, and that God provided the world with a rational structure and a capacity to operate by its own laws. In this well-ordered world, natural philosophers must always seek a rational explanation for phenomena. **They must search for a natural cause and not resort to God, the ultimate cause of all things, unless the secondary cause seems unattainable**.”, Grant, ‘God and Reason in the Middle Ages’, (2001), 72.

Gerald of Wales.

> “The spectacle of leaping salmons in the rivers of Wales and Ireland was dissected in similar fashion, Gerald observing that this behaviour may seem hard to believe **but it is from the nature (ex natura) of this fish** to perform such feats. He was also reluctant to accept the beliefs of Welsh villagers who held that the groaning of a lake in winter was miraculous. Dismissing their claims, **Gerald offered an alternative physical explanation**, ascribing the noises to air trapped beneath its frozen surface and being violently released.", Watkins, ‘History and the Supernatural in Medieval England’ (2007), 30.

William of Conches.

> “**William thought it improper to invoke God’s omnipotence as an explanation for natural phenomena**. Like all natural philosophers in the Middle Ages, William of Conches believed that God was the ultimate cause of everything, but, like Adelard of Bath, he believed that **God had empowered nature to produce effects and that one should therefore seek the cause of those effects in nature**.”, Grant, ‘God and Reason in the Middle Ages’ (2001), 73.

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agauger (Ann Gauger) 2018-03-28 19:58:27 UTC #993

@Jonathan_Burke

Agreed

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gbrooks9 (George Brooks) 2018-03-28 19:59:45 UTC #994

> Jonathan_Burke:
>
> William of Conches.
>
> “William thought it improper to invoke God’s omnipotence as an explanation for natural phenomena. Like all natural philosophers in the Middle Ages, William of Conches believed that God was the ultimate cause of everything, but,

> like Adelard of Bath, he believed that God had empowered nature to produce effects and that one should therefore seek the cause of those effects in nature.", Grant, 'God and Reason in the Middle Ages' (2001), 73.

A very excellent quote and sentiment!

Jonathan_Burke (Jon) 2018-03-28 20:01:31 UTC #995

> gbrooks9:
>
> A very excellent quote and sentiment!

Methdological naturalism is a very old Christian tradition. It was one of Christianity's greatest contributions to the modern Western scientific continuum.

AMWolfe (A.M. Wolfe) 2018-03-28 20:08:29 UTC #996

> agauger:
>
> When material explanations have failed, but we have a nonmaterial cause known to be able to produce the phenomena in question, it is a reasonable inference to make. The inference would be held in the same manner as all scientific hypotheses, that is, provisionally, and always subject to revision.

Hi Ann,

Hope you're well today.

The problem, frankly, is that as long as all we're looking at is Chomsky, Hauser, Pinker, et al., we're not going to get very far. They will always say that "material explanations have failed." Always.

Here's the thing: Chomsky is committed to a deeply modular view of the linguistic faculty. He believes in a sort of linguistic "black box" in the brain where language acquisition and processing is done, and that language is a completely separate faculty from everything else the brain does.

This is no longer accepted by a growing number of linguists, who see the principles that govern the linguistic faculty as being pervasive throughout human cognition, not limited to language. It would take me some time to do justice to this train of thought, so I won't really elaborate further here, but will just humbly recommend you do some reading of cognitive linguists who are among Chomsky's detractors.

The reason I encourage you in this vein is that Chomsky's entire research program is very cozy with Intelligent Design. It says, essentially, the black box is the way it is because that's how it's designed! This style of explanation is utterly circular, and because Chomskian linguistics is doggedly committed to continuing to use this circular reasoning, it is blinded from seeing the way that language is largely governed by factors external to it: considerations of cognitive processing and communicative efficiency and categorization, functional and pragmatic factors of the situational context, etc. etc.

So as long as you're reading Chomskian folks, you're reading stuff that will reinforce your presuppositions. If you want to challenge your presuppositions, read his detractors. And don't mistake "Chomskian linguists believe material explanations have failed" for "material explanations have failed." There is a world of difference here. 🙂

Have a great day —
AMW

agauger (Ann Gauger) 2018-03-28 20:13:07 UTC #997

@AMWolfe

Thanks for the thoughtful response. I'll take it on board.

AMWolfe (A.M. Wolfe) 2018-03-28 20:20:30 UTC #999

…and if I come across a good pithy article on this from a non-Chomskian linguist, I'll be sure to share it. It's not something I'm currently reading about, but if I stumble across something, I'll send it your way!

Incidentally, while we're on the topic, I find it curious that the premiere organization of Christian field linguists, **SIL International**, leans largely non-Chomskian (with some exceptions). One might expect an organization with an American Evangelical base to lean toward the theoretical framework that resonates with ID… yet it doesn't. And, ironically, it takes a fair amount of flak for that by Chomskian linguists in the secular academy. Quite a bit of irony there!

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jpm (Phil) 2018-03-28 23:02:13 UTC #1000

5 posts were merged into an existing topic: **What about embodied cognition?**

DennisVenema (Dennis Venema) 2018-03-29 00:33:16 UTC #1001

> glipsnort:
>
> I'm not familiar with this estimate. Reference?

I'd like to see it as well. I've not noticed that (though it is a big field, so not surprising that I haven't).

Christy (Christy Hemphill) 2018-03-29 01:17:22 UTC #1002

> Swamidass:
>
> Notably, its authors include the great Noam Chomsky, essentially making the main point I've been making here.

Could you please clarify what point you are making that you believe this article supports? Do you think it supports the idea that language could plausibly have emerged discontinuously in a single mating pair?

> Swamidass:
>
> Christy:
>
> And then you went on to say we can't know anything for sure.
>
> (I did not say that).

Okay, that was my summary of your response to Dennis when you said:

> Swamidass:

> We do not know how quickly these things progressed. Do we? You are putting forward rationale for why it might be gradual, but there is rationale for why it might not be gradual too, at least at points. As far as a I know, from evidence, we cannot discriminate which one is correct (…) There are mysteries about the details of our origins. Rather than insisting our personal instincts are correct, its better to just say “we do not know.”

and again when you said:

> Swamidass:
>
> I’ve already said that the evidence is not going to tell us one way or another.

There is a difference between saying we cannot disprove that two individuals invented language de novo because the origin of language is a mystery and saying we cannot discriminate between plausible models of how language emerged in human communities and implausible models.

Fine, we can’t disprove the idea that two people invented language de novo and consequently geographically isolated themselves because they felt so different/superior with their new abilities that they didn’t want their children associating with the rest of their social group anymore. In my humble opinion, it’s still laughably implausible, and it doesn’t make sense to assert it as a real possibility under consideration by anyone who theorizes about these things. If you never meant to make it sound like that was what you were arguing, then sorry for misunderstanding your argument.

I was not trying to somehow insult you by pointing out it sounded like a creationist argument to me. I was just trying to get you to clarify what you were actually claiming, because “the evidence is not going to tell us one way or another” sure sounded to me like a pretty lame defense of your contention that maybe there was a two person bottleneck because of geographic isolation caused by two people inventing language and not wanting their kids to interbreed with anyone around them. The challenge wasn’t meant to be hostile in any way, just an invitation to make your presentation of options better. It seems like you don’t really appreciate that kind of feedback though and are just going to double down on how it really does make lots of sense, so I’m happy to drop the subject. 🙂 I’m on vacation and I’m not trying to pick fights with anyone.

> Swamidass:
>
> (yet we have been unable to socially transmit language or theory of mind to the great apes)

I don’t understand what significance this piece of information has in your mind. So what? The issue is when has human language ever been transmitted non-socially?

> Swamidass:
>
> (no, we are talking about linguistic origin, not linguistic evolution, which is intertwined with biological evolution)

To me that is like saying that what we know about how genes work in the here and now has no bearing on studying the origin of our species. Yes, what we know about how languages are acquired and evolve in the here and now have bearing on what we theorize about how language worked at it’s origin. For language to qualify as language it has to function in certain predictable ways that we understand based on our study of contemporary languages and historical linguistics.

> Swamidass:
>
> Perhaps consider backing off the heated rhetoric,

It's not heated rhetoric. It's a conversation with someone who doesn't think you have a good argument on one minor point. That's what we do on this forum, we discuss stuff and occasionally disagree. Please relax a little.

Swamidass (Dr. S Joshua Swamidass) 2018-03-29 02:28:24 UTC #1003

> DennisVenema:
>
> > I'm not familiar with this estimate. Reference?
>
> I'd like to see it as well. I've not noticed that (though it is a big field, so not surprising that I haven't).

There was an error i made there, I misremembered the figure. THe paper to which I was referring:

Prehistoric hunter–gatherer population growth rates rival those of...

Among the many useful yardsticks of evolutionary success, trajectory of population growth is perhaps the most telling, and it is the focus on this metric that makes the contribution by Zahid et al. (1) in PNAS so compelling. They document...

> t suggests a trajectory of continuous, long-term Wyoming-Colorado hunter–gatherer population growth of 0.041% from 13,000–6,000 cal BP, doubling roughly every 1,700 y, within which there were **short-term fluctuations during which growth rates were sometimes more than an order of magnitude larger** (i.e., r > 0.4%), doubling in less than 200 y.

A couple points I would make:

1. Hunter gatherer growth rates can be about the same as agriculturalists. Counterintuitively, the main difference might be in carrying capacity, not growth rate.
2. Rate is going to be inversely related with distance from carrying capacity. Smaller populations can grow percentagewise much faster than larger populations.
3. Doubling every generation for a few generations (when very far below carrying capacity) does not seem implausible. So, going from 2 -> 4 -> 8 -> 16 -> 32 -> 64 etc. over a 150 to 200 year period (4 children for each couple) does not seem implausible, even if the long term rate moves lower once there are, say, over 100 or 1000 individuals.
4. Though I do agree that is faster than what was observed in North American hunter gatherers. What I said earlier was in error.

So thanks for pressing me on that reference. It was important to get that straight, especially for some of the simulations we have been doing.

Chris_Falter (Chris Falter) 2018-03-28 20:48:52 UTC #1004

> AMWolfe:
>
> And Chomsky's linguistic theorizing is considered very poor-quality science by a great many linguists (not just Dan Everett of recent Forum mention).

Chomsky famously has refused to acknowledge any value in probabilistic language models. Meanwhile, Google Translate and Bing Translate use them to great effect.

EDIT: iirc, Alexa is more accurate in listening to and transcribing language on the fly than the average adult. And probabilistic models are behind that capability, of course.

What about embodied cognition?

AntoineSuarez (Antoine Suarez) 2018-03-29 12:17:05 UTC #1005

> agauger:
>
> Animals have been represented as having rudimentary language, but when compared to what even two year old humans are capable of, it is clear there are significant gaps.

It seems to me you are searching for a feature capable of sharply distinguishing between human Image Bearers, and non-human animals.

But then why do you not refer to writing?

Notice that writing is motivated by the need of registering marriages, arranging contracts, and enacting laws. Therefore it reveals awareness of personal identity, moral responsibility and accountability.

A.Suarez's Treatment on a Pope's Formulation for Original Sin's Transmission!

AMWolfe (A.M. Wolfe) 2018-03-29 12:48:38 UTC #1006

> AntoineSuarez:
>
> But then why do you not refer to writing?

For what purpose are you suggesting referring to writing, may I ask?

Writing is a *very* recent phenomenon in the history of H. sapiens, and does not extend to many human contexts and languages even today. Are you suggesting (perish the thought) that these peoples are somehow less human??

I'm not sure I get where you're going with this.

Bill_II 2018-03-29 14:18:27 UTC #1007

> AntoineSuarez:
>
> Notice that writing is motivated by the need of registering marriages, arranging contracts, and enacting laws.

Writing is motivated by the need to record the verbal agreements that resulted in marriage, contracts, and laws. Social behavior predates writing. Antoine what you should be looking for are indications of group behavior that would lead to language that would lead to cities that would lead to writing.

Christy (Christy Hemphill) 2018-03-29 14:23:19 UTC #1008

> AMWolfe:
>
> Incidentally, while we're on the topic, I find it curious that the premiere organization of Christian field linguists, SIL International, leans largely non-Chomskian (with some exceptions).

True. I've never met anyone personally who uses transformational grammar to describe minority languages. One critique I commonly hear is that it tends to see all languages through an "English as normal," indo-european-centric lens, which introduces all sorts of complications when you are doing descriptive linguistics of languages that function very differently than English. Everyone I know uses Role and Reference Grammar or Lexical-Functional Grammar.

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glipsnort (Steve Schaffner) 2018-03-29 15:12:56 UTC #1009

> Swamidass:
>
> t suggests a trajectory of continuous, long-term Wyoming-Colorado hunter–gatherer population growth of 0.041% from 13,000–6,000 cal BP, doubling roughly every 1,700 y, within which there were short-term fluctuations during which growth rates were sometimes more than an order of magnitude larger (i.e., r > 0.4%), doubling in less than 200 y.
>
> A couple points I would make:
>
> Hunter gatherer growth rates can be about the same as agriculturalists. Counterintuitively, the main difference might be in carrying capacity, not growth rate.
>
> Rate is going to be inversely related with distance from carrying capacity. Smaller populations can grow percentagewise much faster than larger populations.
>
> Doubling every generation for a few generations (when very far below carrying capacity) does not seem implausible. So, going from 2 -> 4 -> 8 -> 16 -> 32 -> 64 etc. over a 150 to 200 year period (4 children for each couple) does not seem implausible, even if the long term rate moves lower once there are, say, over 100 or 1000 individuals.
>
> Though I do agree that is faster than what was observed in North American hunter gatherers. What I said earlier was in error.
>
> So thanks for pressing me on that reference. It was important to get that straight, especially for some of the simulations we have been doing.

To be clear, what you're postulating is very much what I would call explosive growth. So back to my question: what kind of natural disaster are you postulating that would leave the environment intact enough for explosive growth to occur immediately afterwards?

> Swamidass:

> Also there is a genetic interference as a possibility too.

Again, what are you actually proposing? What kind of genetic interference creates a bottleneck of two in mammals? What examples are there?

> Swamidass:
>
> (just like is the case for all scientific theories, **https://en.wikipedia.org/wiki/Duhem–Quine_thesis**)

No. Just no. Sure, there are an infinite number of possible hypotheses that can explain any set of data. No, science does not treat all hypotheses equally – it has heuristics that let scientists drastically restrict the set of hypotheses that they actually consider.

Remember, my claim was that “abrupt bottleneck of size two” and “slowly varying population size” should not be treated as equally valid *scientific* hypotheses. You haven’t given me any reason to change my view.

AntoineSuarez (Antoine Suarez) 2018-03-29 15:36:02 UTC #1010

> AMWolfe:
>
> For what purpose are you suggesting referring to writing, may I ask?

In order to single out a criterion allowing us to *sharply* establishing when God makes Humanity to a community of people in the Image of God.

I have the impression is what Ann Gauger is looking for after all, isn’t she?

> AMWolfe:
>
> Writing is a very recent phenomenon in the history of H. sapiens

The beginnings of *Homo sapiens* as an *evolving* biological taxon is a matter of arbitrary definition and are therefore necessarily fuzzy.

So what matters here is not “the history of *evolving Homo sapiens*” but establishing the beginning of the *history of Humanity* as community of Image Bearers.

> AMWolfe:
>
> and does not extend to many human contexts and languages even today. Are you suggesting (perish the thought) that these peoples are somehow less human??

Not at all!

Consider those in this thread who propose language as the criterion for distinguishing humans from animals:

Are they suggesting that new-born babies or hydranencephalic childs “are somehow less human”?

No. Their argument amounts to establish the time T when language appears, and then infer: all creatures exhibiting a human body after time T cannot be considered animals.

Similarly I argue:

The time when writing appears at about 3500 BC marks the moment when God makes the first humans in His Image: It is the moment referred to in Genesis 1:27. After the Flood all the extant human-like animals are made to Image Bearers: It is the moment referred to in Genesis 9:6; in the wording of **@Bill_II** one could say: at this moment the percentage of Image Bearers among human-like animals becomes 100%. In the time between this percentage increased both, by children generation and by further direct creation by God of "sons of God", according to Genesis 6:1-4.

Since the moment referred to in Genesis 9:6 the percentage of Image Bearers among humans is 100% forever, independently of they write or not.

This thread is showing that "language" is highly controversial as a cut-off criterion. So it may be worth to try with writing.

> AMWolfe:
>
> I'm not sure I get where you're going with this.

I hope it is now clearer. If not, I will be pleased answering further comments.

Christy (Christy Hemphill) 2018-03-29 15:42:49 UTC #1011

> AntoineSuarez:
>
> But then why do you not refer to writing?
>
> Notice that writing is motivated by the need of registering marriages, arranging contracts, and enacting laws. Therefore it reveals awareness of personal identity, moral responsibility and accountability.

Thousands of languages/cultures today do not have writing systems. Are they less image bearers, or less moral? Isn't it problematic that writing was specific to relatively few societies until modern times?

A.Suarez's Treatment on a Pope's Formulation for Original Sin's Transmission!

AMWolfe (A.M. Wolfe) 2018-03-29 16:36:19 UTC #1012

> AntoineSuarez:
>
> After the Flood all the extant human-like animals are made to Image Bearers: It is the moment referred to in Genesis 9:6; in the wording of **@Bill_II** one could say: at this moment the percentage of Image Bearers among human-like animals becomes 100%.

To me this is an utterly bizarre interpretation of Genesis 9:6, but I am willing to be shown wrong. By chance are you aware of any scholarly commentaries that take this approach to that verse, namely that this moment of bestowing God's image in this verse refers to a separate moment in time from humanity's initial creation?

Forgive me if you've covered this in the other long thread with your name in the title. I have not been following that conversation at all.

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