

BioRxiv

How I Learned To Stop Worrying And Love The Preprints

Marc Robinson-Rechavi @marc_rr



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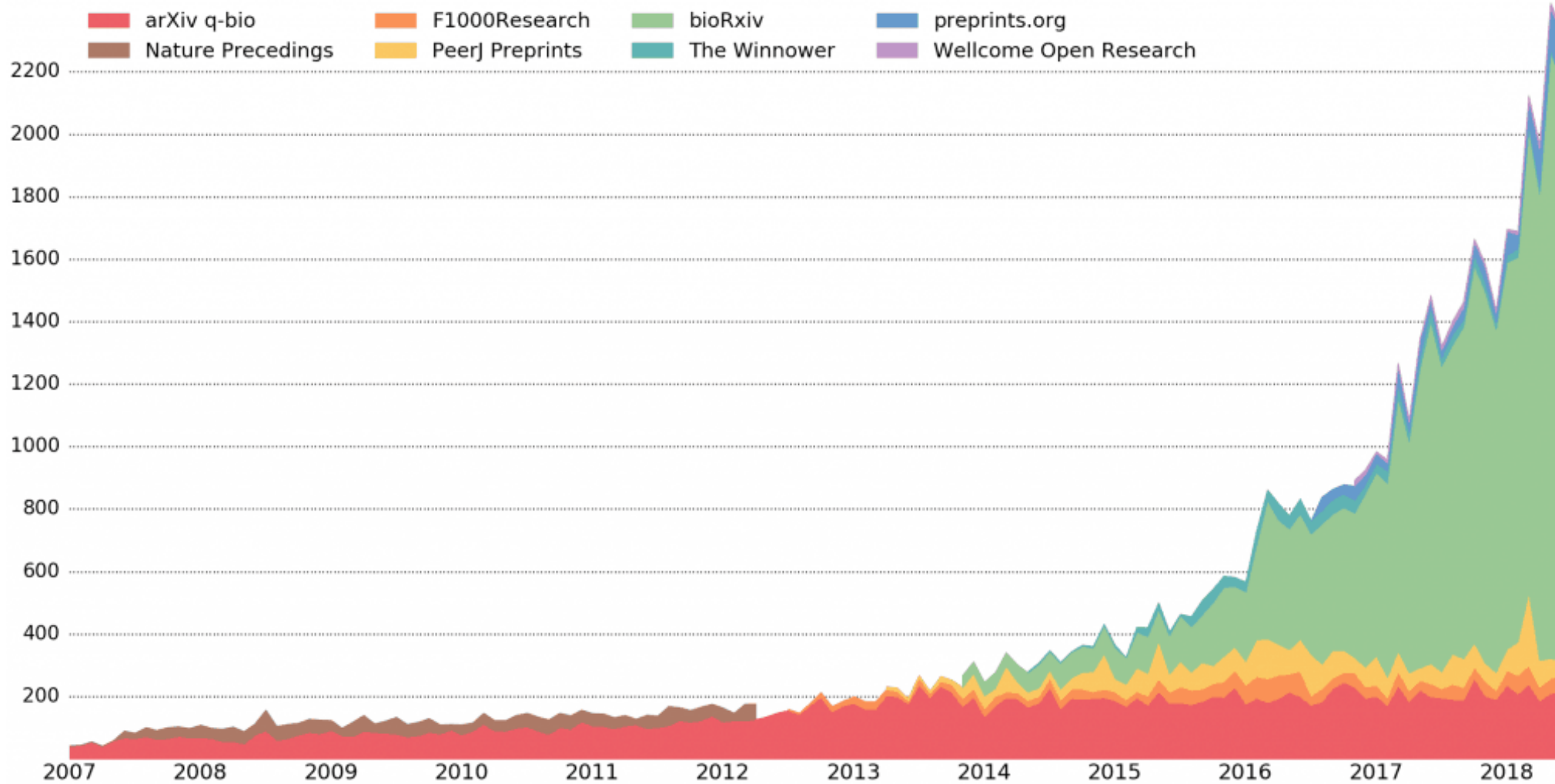
Preprints



Principle of preprints

- Manuscripts available as early as possible, before journal publication
- DOI, publication date
 - stable, citable
- Dedicated websites:
 - arXiv.org in physics, maths, CS... **since 1991**
 - **biorXiv.org** in biology in 2013
 - MedArXiv, ChemRxiv, paleoRxiv, engrXiv, SocArXiv, PsyArXiv, AgriXiv, EarthArXiv, PhilArchive, ESSOAr, AfricArxiv, EdArXiv...
 - <https://en.wikipedia.org/wiki/Preprint>
 - Mixed model preprint + OA journal: PeerJ, F1000

Preprints per Month



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Advantages of preprints

- You the researcher chose when to publish
- Free (as in beer) for authors and readers

Green Open Access with preprints

- Preprint then publication in toll-access journal
- But final version might differ
- But copyright to editor

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SPRINGER NATURE

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Not convinced?




Some practical points

- Updates possible with versioning
- Supplementary materials can be included
 - and probably should
- At publication, link to journal version
- Direct submission preprint to journal
 - 166 journals from bioRxiv

New Results

1 comment

Adaptive evolution of animal proteins over development: support for the Darwin selection opportunity hypothesis of Evo-Devo

 Jialin Liu,  Marc Robinson-Rechavi

doi: <https://doi.org/10.1101/161711>

Now published in *Molecular Biology and Evolution* doi: [10.1093/molbev/msy175](https://doi.org/10.1093/molbev/msy175)

Abstract

Full Text

Info/History

Metrics

 Preview PDF

ARTICLE INFORMATION

doi <https://doi.org/10.1101/161711>

History August 7, 2018.

ARTICLE VERSIONS

Older version (July 10, 2017 - 15:03).

Older version (July 12, 2017 - 07:03).

Older version (January 24, 2018 - 19:26).

You are viewing the most recent version of this article.

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Actually a bit worried?



But scooping?

- Results public with official date stamp
- Yes ideas can be used without citation
 - Like for papers
 - Not legally forbidden, but poor practice
- Risk exists during anonymous peer review
- You are in control



Zoltan Kutalik
@zkutalik



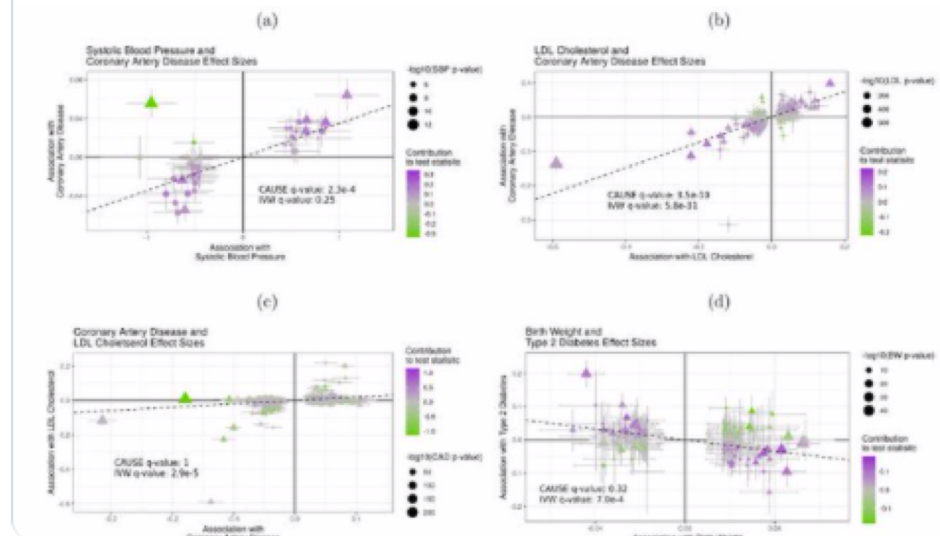
...and we have just been scooped! Needless to say, it's a really great idea. :)

[Traduire le Tweet](#)



GWAS_lit @GWAS_lit · 27 juin

Mendelian randomization accounting for horizontal and correlated pleiotropic effects using genome-wide summary statistics [biorxiv.org/content/10.1101...](https://www.biorxiv.org/content/10.1101/2019.06.27.171111)



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Other concerns

- Will journals reject because of preprint?
 - Most accept
 - Others can change policy when demands
- Less quality?
 - Do you want to attach your name publicly to poor work?
- Makes coordinated submissions easier

Search - Publisher copyright policies & self-archiving

English | [Español](#) | [Magyar](#) | [Nederlands](#) | [Português](#)

One journal found when searched for: **0028-0836**

Journal:	Nature (ISSN: 0028-0836, EISSN: 1476-4687)
RoMEO:	This is a RoMEO yellow journal
Author's Pre-print:	<input checked="" type="checkbox"/> author can archive pre-print (ie pre-refereeing)
Author's Post-print:	<input checked="" type="checkbox"/> subject to Restrictions below , author can archive post-print (ie final draft post-refereeing)
Restrictions:	<ul style="list-style-type: none"> 6 months embargo
Publisher's Version/PDF:	<input checked="" type="checkbox"/> author cannot archive publisher's version/PDF
General Conditions:	<ul style="list-style-type: none"> Research articles only On author's personal website, institutional repository and funder designated repository Publisher's version/PDF cannot be used Authors retain copyright Must link to publisher version Published source must be acknowledged and DOI cited Post-prints are subject to Springer Nature re-use terms
Mandated OA:	Compliance data is available for 24 funders
Notes:	<ul style="list-style-type: none"> Applies to Research articles only
Copyright:	Pre-print policy - Self-archiving policy - Post-print re-use terms
Updated:	20-Sep-2018 - Suggest an update for this record
Link to this page:	http://sherpa.ac.uk/romeo/issn/0028-0836/
Published by:	Nature Research (part of Springer Nature) - Yellow Policies in RoMEO

This summary is for the journal's *default* policies, and changes or exceptions can often be negotiated by authors.
All information is correct to the best of our knowledge but should not be relied upon for legal advice.

Search again?

Journal titles or ISSNs
 Publisher names

0028-0836

Exact phrase only
 All keywords
 Any

[Advanced Search](#)

RoMEO Colour	Archiving policy
Green	Can archive pre-print <i>and</i> post-print or publisher's version/PDF
Blue	Can archive post-print (ie final draft post-refereeing) or publisher's version/PDF
Yellow	Can archive pre-print (ie pre-refereeing)
White	Archiving not formally supported

[More on colours and restrictions](#)

or [View all publishers](#)

<http://www.sherpa.ac.uk/romeo/index.php>



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Stories & Use cases





Guillaume Bourque @guilbourque 2d

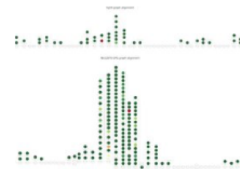
Can I just say that I think [@biorxivpreprint](#) is the greatest thing since sliced bread? Within a week, lots of feedback and even a new collaboration! So much better than waiting for months for 2-3 reviews that are sometimes uneven in terms of quality...

Guillaume Bourque @guilbourque

Linear genomes are so 2000s... Say hello to graph genomes for epigenomic data! Check out this ChIP-seq peak that would have been missed otherwise...

Very excited about our new paper on this:

[biorxiv.org/content/10.1101/2023.03.15.532111](https://doi.org/10.1101/2023.03.15.532111)



Not every paper
should be a
preprint

Discussion of

Ganna et al 2019

Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior

Science 365: eaat7693



Stephen B Montgomery @sbmontgom · 8h

Was this paper ever a preprint? (I may just be having trouble searching for it)



1



Steve Reilly

@ReillyLikesIt

En réponse à @sbmontgom @marc_rr et 4 autres

I don't think so. Especially after the reaction at ASHG, I think the authors were smart and responsible in the specific case of not doing a preprint before peer review.

[Traduire le Tweet](#)

11:48 PM · 1 sept. 2019 · [Twitter for iPhone](#)

1 J'aime



Stephen B Montgomery @sbmontgom · 7h

En réponse à @ReillyLikesIt @marc_rr et 4 autres

Thanks! I could see some pluses and minuses there. It is interesting if potentially controversial papers might shy away from preprints. They are in part designed to get broad scientific community feedback.



2



Steve Reilly @ReillyLikesIt · 7h

I for one am happy that early versions I saw are not out there, public, forever.




The preprint, the oak tree, and the blue bird



1

New Results

Low Rate of Somatic Mutations in a Long-Lived Oak Tree

Namrata Sarkar, Emanuel Schmid-Siegert, Christian Iseli, Sandra Calderon, Caroline Gouhier-Darimont, Jacqueline Chrast, Pietro Cattaneo, Frederic Schutz, Laurent Farinelli, Marco Pagni, Michel Schneider, Jeremie Voumard, Michel Jaboyedoff, Christian Fankhauser, Christian S. Hardtke, Laurent Keller, John R. Pannell, Alexandre Reymond, Marc Robinson-Rechavi, Ioannis Xenarios,  Philippe Reymond

doi: <https://doi.org/10.1101/149203>

This article is a preprint and has not been peer-reviewed [what does this mean?].

Abstract

Info/History

Metrics

Supplementary material

 Preview PDF

Abstract

Because plants do not possess a proper germline, deleterious somatic mutations can be passed to gametes and a large number of cell divisions separating zygote from gamete formation in long-lived plants may lead to many mutations. We sequenced the genome of two terminal branches of a 234-year-old oak tree and found few fixed somatic single-nucleotide variants (SNVs), whose sequential appearance in the tree could be traced along nested sectors of younger branches. Our data suggest that stem cells of shoot meristems are robustly protected from accumulation of mutations in trees.

1

New Results

Low Rate of Somatic Mutations in a Long-Lived Oak Tree

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Article usage: June 2017 to November 2017

doi: <https://doi.org/10.1101/161111>

This article is a preprint

Show by month

Abstract

Pdf

2



See more details

- Picked up by 2 news outlets
- Blogged by 2
- Tweeted by 352
- On 5 Facebook pages
- Mentioned in 1 Wikipedia entries
- 14 readers on Mendeley

Abstract

Abstract

Because
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genome
somatic :
could be
stem cell
in trees.

Blog posts linking to this article:

the Node, 05 Jul 2017

Our latest monthly trawl for developmental biology (and other cool) preprints. See last year's introductory post for background...

The Daily Scan from GenomeWeb, 21 Jun 2017

Tweets referencing this article:



Casey Bergman

@caseybergman

@mike_schatz @notSoJunkDNA @ewanbirney @embl @wolfganghuber @Eileen_Furlong
Indeed, something like this? <https://t.co/1nppB7cyNp>

22 Sep 2017



Richard Cronn

@rcronn1

RT @marc_rr: Fun cool science: a 234 year old oak tree has few somatic mutations, and those we find perfectly follow tree shape. <https://t.co/1nppB7cyNp>

21 Aug 2017



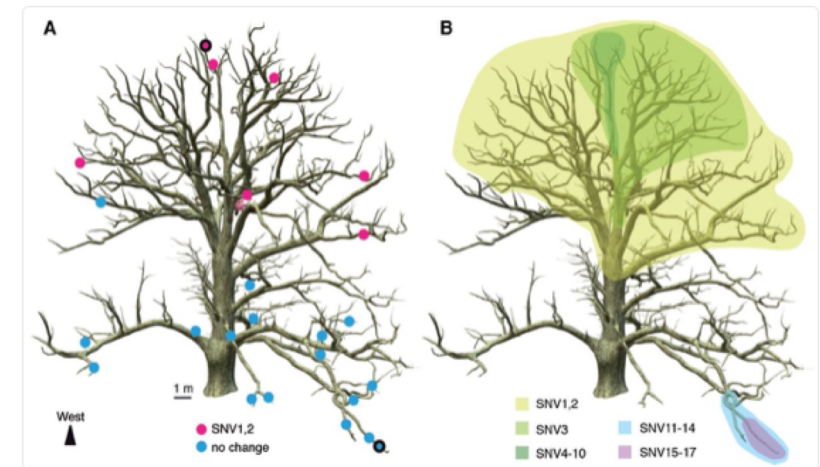
Marc RobinsonRechavi

@marc_rr

Fun cool science: a 234 year old oak tree has few somatic mutations, and those we find perfectly follow tree shape.

[twitter.com/c_s_hardtke/st...](https://twitter.com/c_s_hardtke/status/874111111111111111)

À l'origine en anglais



17:11 - 13 juin 2017

208 Retweets 290 J'aime



6

208

290



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1

New Results

Low Rate of Somatic Mutations in a Long-Lived Oak Tree

Namrata Sarkar, Emanuel Schmid-Siegert, Christian Iseli, Sandra Calderon, Caroline Gouhier, Jacqueline Chrast, Pietro Cattaneo, Frederic Schutz, Laurent Farinelli, Marco Pagni, Michel Scerif, Jeremie Voismard, Michel Jaboyedoff, Christian Fankhauser, Christian S. Hardtke, Laurent Keller, Alexandre Roy
Article usage: June 2017 to November 2017
doi: <https://doi.org/10.1101/168111>

This article is a preprint. It has not been certified by peer review and should not be used to guide clinical practice.

Show by month	Abstract
Total	7,340

Abstract

2



See more details

- Picked up by 2 news outlets
- Blogged by 2
- Tweeted by 352
- On 5 Facebook pages
- Mentioned in 1 Wikipedia entries
- 14 readers on Mendeley

Abstract

Because of its ability to pass on its genome through gametes, the somatic mutations found in trees can be passed on to their offspring.

Blog posts linking to this article:

- the Node, 05 Jul 2017
Our latest monthly trawl for developmental biology (and other cool) preprints. So far, we've found a lot of interesting preprints for background reading.
- The Daily Scan from GenomeWeb, 21 Jun 2017

Tweets referencing this article:



Casey Bergman

@caseybergman

@mike_schatz @notSoJunkDNA @ewanbirney @embl @wolfgangkhub Indeed, something like this? <https://t.co/1nppB7cyNp>

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Richard Cronn

@rcronn1

RT @marc_rr: Fun cool science: a 234 year old oak tree has few somatic mutations. The mutations we find perfectly follow tree shape. <https://t.co/1nppB7cyNp>

21 Aug 2017

3

nature International weekly journal of science

Home | News & Comment | Research | Careers & Jobs | Current Issue | Archive | Audio & Video | For Authors

Archive | Volume 546 | Issue 7659 | News | Article

NATURE | NEWS

Ancient oak's youthful genome surprises biologists

DNA of 234-year-old tree has few mutations, giving weight to idea that plants protect their stem cells.

Heidi Ledford

19 June 2017 (preprint 13 June)

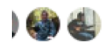
PDF | Rights & Permissions



The 'Napoleon' oak has few single-letter mutations in its genome.

The towering 234-year-old 'Napoleon' oak on the campus of the University of Lausanne in Switzerland has weathered storms both meteorological and political. The tree was young when Napoleon's troops passed through town in 1800, and has grown into a majestic city landmark. But through it all, its genome has remained largely — and surprisingly — unchanged.

...d oak tree has ...
...se we find



1

New Results

Low Rate of Somatic Mutations in a Long-Lived Oak Tree

Namrata Sarkar, Emanuel Schmid-Siegert, Christian Iseli, Sandra Calderon, Caroline Gouhier, Jacqueline Chrast, Pietro Cattaneo, Frederic Schutz, Laurent Farinelli, Marco Pagni, Michel Schneider, Jeremie Voumard, Michel Jaboyedoff, Christian Fankhauser, Christian S. Hardtke, Laurent Keller, Alexandre Reymond, Philippe Reymond
Article usage: June 2017 to November 2017
doi: <https://doi.org/10.1101/171111>

This article is a preprint. It has not been certified by peer review and should not be used to guide clinical practice.

Abstract	Total	Abstract
	255	7,340

2



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- On 5 Facebook pages
- Mentioned in 1 Wikipedia entries
- 14 readers on Mendeley

Abstract

Because the genome of a 234-year-old oak tree has few somatic mutations, we find that the mutations that do occur perfectly follow the tree's shape.

Blog posts linking to this article:

- the Node, 05 Jul 2017
- Our latest monthly trawl for developmental biology (and other cool) preprints. So far, we've found a few interesting ones. Here's a post for background...
- The Daily Scan from GenomeWeb, 21 Jun 2017

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Casey Bergman @caseybergman
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21 Aug 2017

3

nature International weekly journal of science

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Archive | Volume 546 | Issue 7659 | News | Article

NATURE | NEWS

Ancient oak's youthful genome surprises biologists

DNA of 234-year-old tree has few mutations, giving weight to idea that plants protect their stem cells.

Heidi Ledford

19 June 2017

(preprint 13 June)

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4

nature plants

Brief Communication | Published: 04 December 2017

Low number of fixed somatic mutations in a long-lived oak tree

Emanuel Schmid-Siegert, Namrata Sarkar, Christian Iseli, Sandra Calderon, Caroline Gouhier-Darimont, Jacqueline Chrast, Pietro Cattaneo, Frédéric Schütz, Laurent Farinelli, Marco Pagni, Michel Schneider, Jérémie Voumard, Michel Jaboyedoff, Christian Fankhauser, Christian S. Hardtke, Laurent Keller, John R. Pannell, Alexandre Reymond, Marc Robinson-Rechavi, Ioannis Xenarios & Philippe Reymond

The towering 234-year-old 'Napoleon' oak has weathered storms both meteorological and human. It passed through town in 1800, and has a genome that has remained largely — and surprisingly — unchanged.

old oak tree has few mutations we find



Key role of Twitter in preprint success





B. Arman Aksoy
@armish

A 6-year old project from my graduate days has just got published (i.e. peer-reviewed to be worthy) so here is a cautionary tale for y'all and how [@biorxivpreprint](#) can save your career (1/n)



B. Arman Aksoy
@armish

Long story short: I graduated, started interviewing for jobs, and got to meet with lots of people whom I wouldn't if it wasn't for the preprint. I even had a chance to shake hands with [@cshperspectives](#) after presenting my work and giving a shoutout to [@biorxivpreprint](#) (9/n)



B. Arman Aksoy @armish 21h

Six years after the deposit, the paper was still waiting for my former PI's blessings but this time he, for some reason, got really interested in getting this paper published. Of course, I was asked to revive the project, run new analyses, revise the paper... (10/n)

1 1 3 ...



B. Arman Aksoy @armish 21h

And I refused; new people got involved and now it was being led by people who weren't really into the preprint idea. All the analysis code was publicly available, intermediate data archived, and the preprint was a well-written one so I didn't feel guilty about quitting (11/n)

1 1 4 ...



B. Arman Aksoy @armish 21h

But boy -- it got nasty. Another long story short: I was now on bad terms with two prolific/big-wig PIs. Eventually, they got it published without me doing anything but they still have me as a co-author to honor my earlier efforts (12/n)

1 1 2 ...



B. Arman Aksoy
@armish

I wouldn't consider it as my paper/work anymore, but thanks to that [@biorxivpreprint](#) preprint, I already got what I wanted out of the original effort: lots of fun, a few citations, two job offers, new friends, and, the last but not the least, another chance to rant 😊 (13/n)



Make your life simpler



More open, less stress

- Easy to provide reference for a talk / poster
- Lab members don't worry about sharing
- OK to share manuscript you're reviewing

Use in grants



27 Results for author "robinson-rechavi"

Items/Page 10 Order by Newest First



An evolutionary conservation based benchmark of seven methods detecting nycthemeral rhythms in gene expression shows that only strong rhythmic signals are reliably detected

David Laloum, Marc Robinson-Rechavi

bioRxiv 730937; doi: <https://doi.org/10.1101/730937>

+ Add to Selected Citations

Phylogenetic comparative methods are problematic when applied to gene trees with speciation and duplication nodes: correcting for biases in testing the ortholog conjecture

Tina Begum, Marc Robinson-Rechavi

bioRxiv 719336; doi: <https://doi.org/10.1101/719336>

+ Add to Selected Citations

Selection against expression noise explains the origin of the hourglass pattern of Evo-Devo

Jialin Liu, Michael Frochoux, Vincent Gardeux, Bart Deplancke, Marc Robinson-Rechavi

bioRxiv 700997; doi: <https://doi.org/10.1101/700997>

+ Add to Selected Citations

Enabling Semantic Queries Across Federated Bioinformatics Databases

Ana Claudia Sima, Tarcisio Mendes de Farias, Erich Zbinden, Maria Anisimova, Manuel Gil, Heinz Stockinger, Kurt Stockinger, Marc Robinson-Rechavi, Christophe Dessimoz

bioRxiv 686600; doi: <https://doi.org/10.1101/686600>

+ Add to Selected Citations

Sex-biased gene expression is repeatedly masculinized in asexual females

Darren J. Parker, Jens Bast, Kirsten Jalvingh, Zoé Dumas, Marc Robinson-Rechavi, Tanja Schwander

bioRxiv 553172; doi: <https://doi.org/10.1101/553172>

+ Add to Selected Citations

Identifying gene function and module connections by the integration of multi-species expression compendia

Hao Li, Daria Rukina, Fabrice P.A. David, Terytty Yang Li, Chang-Myung Oh, Arwen W. Gao, Elena Katsyuba, Maroun Bou Sleiman, Andrea Komljenovic, Qingyao Huang, Robert W. Williams, Marc

Proposal SNSF October 2016: preprints used in "Current state of own research"

1. Daub et al *Detection of pathways affected by positive selection in primate lineages ancestral to humans* (published Feb 2017)
2. Kryuchkova-Mostacci & Robinson-Rechavi *Tissue-specificity of gene expression diverges slowly between orthologs, and rapidly between paralogs vertebrates* (published Dec 2016)
3. Roux et al *Selective constraints on coding sequences of nervous system genes are a major determinant of duplicate gene retention in vertebrates* (published Nov 2017)



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<https://tinyurl.com/mrrxiv>

29

Linked papers



Cross-cite papers

- Submit papers 1 and 2 as preprint
- Get DOIs
- Update papers 1 and 2 to cite each others DOIs
- *Et voilà !*

- Also works for large consortia






Of the importance of being wrong

Attacked on bioRxiv!

- Dec 2016: paper published with my student
- March 2017: preprint saying we are wrong
 - they have a point
 - they missed some stuff
- Started work to improve on their approach
- Invited to discuss at their department

Contradictory Results

Pairwise comparisons across species are problematic when analyzing functional genomic data

 Casey W Dunn,  Felipe Zapata,  Catriona Munro,  Stefan Siebert,  Andreas Hejnol

doi: <https://doi.org/10.1101/107177>

Now published in PNAS doi: [10.1073/pnas.1707515115](https://doi.org/10.1073/pnas.1707515115)

Posted August 02, 2019

Contradictory Results

[Comment on this paper](#)

Phylogenetic comparative methods are problematic when applied to gene trees with speciation and duplication nodes: correcting for biases in testing the ortholog conjecture

 Tina Begum,  Marc Robinson-Rechavi

doi: <https://doi.org/10.1101/719336>

This article is a preprint and has not been peer-reviewed [what does this mean?].



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If it's not communicated, it's not science

@marc_rr



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