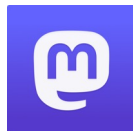


Open access and open science

Journée de la recherche HEP-VS
Marc Robinson-Rechavi



@marc_rr



@marcrr@ecoevo.social



A note on references in this talk

To avoid highlighting journal titles, each reference will be
First author – year – keyword
with a unique result in Google Scholar

e.g. " Liu 2020 positive selection"



The moral case for Open Access



Winners of Open Access

researchers

text mining

start-ups & SMEs

medical doctors

patients

journalists

teachers

amateur scientists

the public (GMOs, vaccines, climate...)



Losers of Open Access

Commercial publishers

Medium rich labs if APC Gold OA

too rich to waive publication costs

too poor to pay for all papers

Researchers in low-income countries if no waivers

Some scientific societies

share profits of publishers



From talk to action



The start: the Public Library of Science

Open Letter

In 2000 Harold Varmus, Patrick Brown, and Michael Eisen circulated an open letter that would eventually be signed by 34,000 scientists from 180 countries and spark the foundation for PLOS

Led to PLOS

I signed on 5 Jan 2001

“

We support the establishment of an online public library that would provide the full contents of the published record of research and scholarly discourse in medicine and the life sciences in a freely accessible, fully searchable, interlinked form. Establishment of this public library would vastly increase the accessibility and utility of the scientific literature, enhance scientific productivity, and catalyze integration of the disparate communities of knowledge and ideas in biomedical sciences.

We recognize that the publishers of our scientific journals have a legitimate right to a fair financial return for their role in scientific communication. We believe, however, that the permanent, archival record of scientific research and ideas should neither be owned nor controlled by publishers, but should belong to the public and should be freely available through an international online public library.

To encourage the publishers of our journals to support this endeavor, we pledge that, beginning in September 2001, we will publish in, edit or review for, and personally subscribe to only those scholarly and scientific journals that have agreed to grant unrestricted free distribution rights to any and all original research reports that they have published, through PubMed Central and similar online public resources, within 6 months of their initial publication date.

Harold Varmus, Patrick Brown, and Michael Eisen
PLOS co-founders

<https://plos.org/open-letter/>

Personal commitment to open access

- All papers open access since 2010
- Preprinting since 2014
- Editorial boards *PLOS One* then *PLOS Computational Biology*
- 2018: resigned from all editorial roles at for-profit publishers
- 2020: *Review Commons* advisory board
- 2021: *bioRxiv* affiliate

Public access	VIEW ALL
1 article	93 articles
not available	available
Based on funding mandates	

<https://tinyurl.com/mrrxiv>



Big Deals Open Access – Swissuniversities

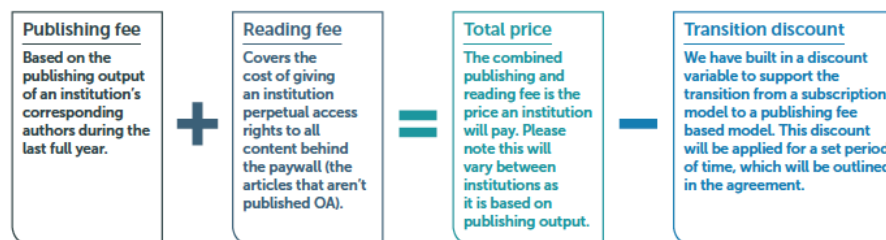
1st round of Big Deal negotiations 2018-2021



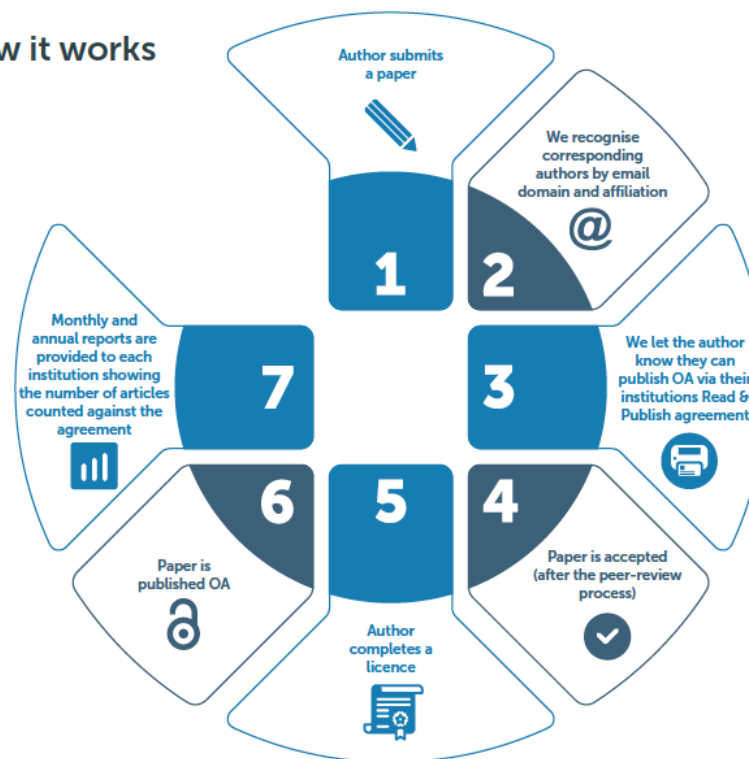
2nd round of Big Deal negotiations 2022-2025



Read & Publish pricing



How it works



Negotiation aims

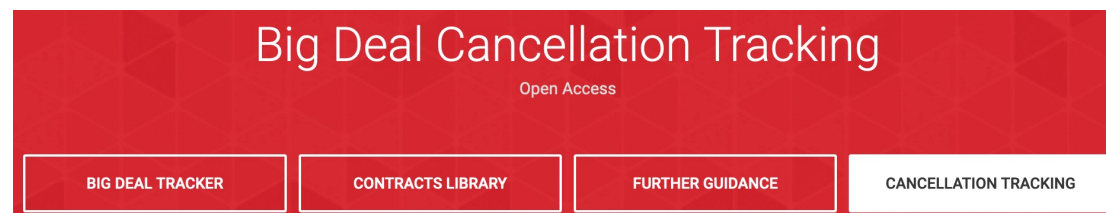
Core provision	<ul style="list-style-type: none"> • Read access rights to journal titles requested by mandating parties Continuing read access to licensed titles after termination of the agreement (post cancellation rights). • Open Access publishing rights for all journal publications, i.e. full publisher portfolio² including prestigious high impact titles (e.g. Nature, Cell, Lancet, etc.) and Gold OA titles and brands (e.g. BioMed Central).
Pricing	<ul style="list-style-type: none"> • Cost neutrality on national level for entire publisher journal portfolio, based on existing spend for transformative agreements, additional licences (Nature journals) and Gold OA. Inflation may have to be accounted for. • Cost control mechanism for Gold Open Access, mandating institutions define their level of central investment. • Price Model for transformative part (Hybrid Open Access) which includes a price point(s) for reading and publishing (Read fee, Publishing fee, or Publish and Read (PAR) fee). • Price Model for publication in Gold Open Access Journals which allows for central and decentral payment of Gold Open Access Article Processing Charges (APCs).

Legal	<ul style="list-style-type: none"> • CC BY licence required as default solution for Open Access publishing, other CC licence types upon request from the author.
	<ul style="list-style-type: none"> • Transformative agreements to be published on conclusion with pricing information on national level only.
Workflow	<ul style="list-style-type: none"> • Institutional and author workflows to follow ESAC-recommendations. If technically feasible for publisher, access via application programming interfaces (API) to resulting publications and publication metadata.

No deal is a possibility

January-June 2020 no deal with Springer.

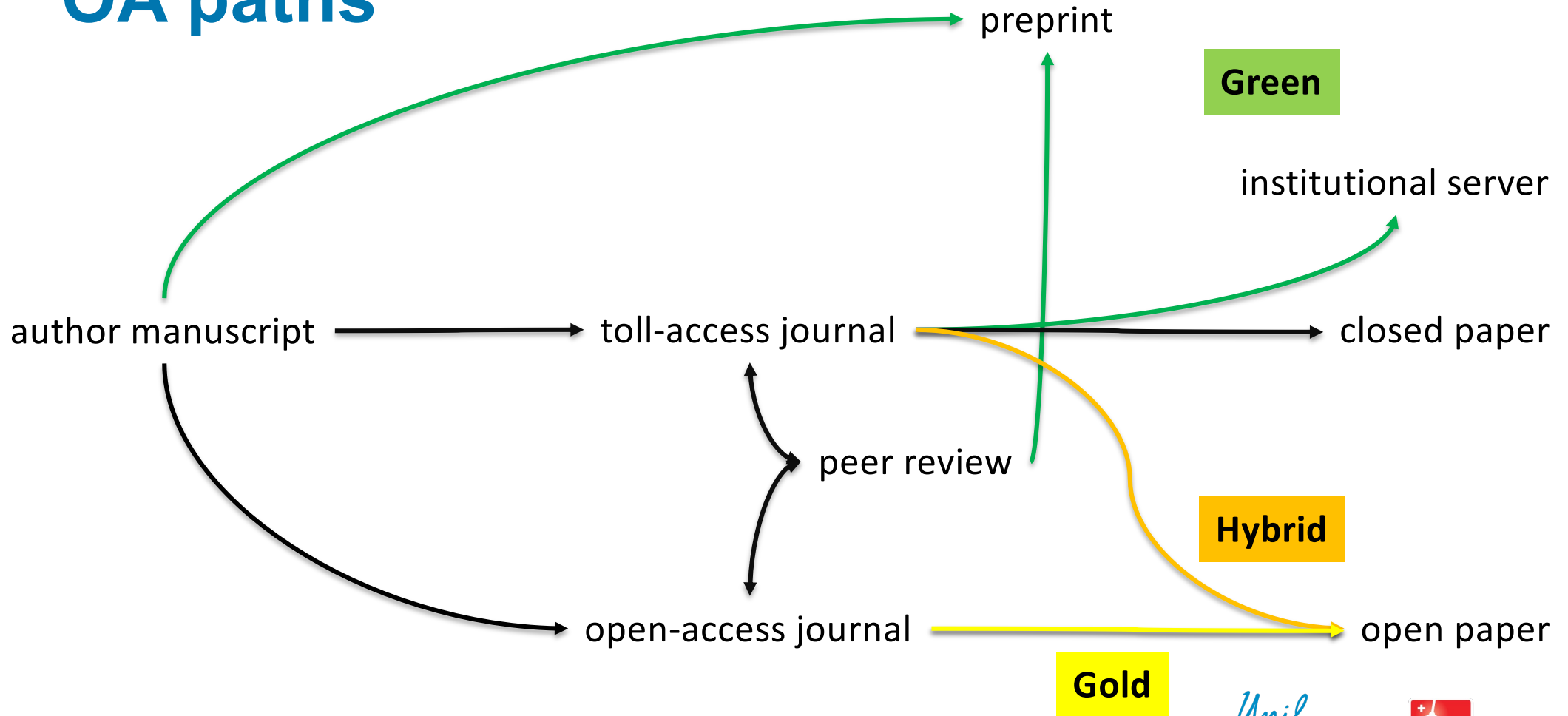
Since January 2022 no deal with OUP.



Paths to open access



OA paths



Preprints



Principle of preprints

Manuscripts available as early as possible, before journal publication

DOI, publication date

- stable, citable

Dedicated servers:

- arXiv.org in physics, maths, CS... **since 1991**
- biorXiv.org in biology in 2013
- **EdArXiv, PsAarXiv**, MedArXiv, ChemrXiv, paleorXiv, engrXiv, SocArXiv, AgriXiv, EarthArXiv, PhilArchive, ESSOAr, AfricArxiv...
- Mixed model preprint + OA journal: F1000, eLife



Advantages of preprints

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





Guillaume Bourque @guilbourque 2d

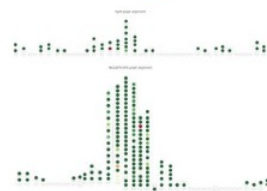
Can I just say that I think [@biorxivpreprint](#) is the greatest thing since sliced bread? Within a week, lots of feedback and even a new collaboration! So much better than waiting for months for 2-3 reviews that are sometimes uneven in terms of quality...

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/10.1101/2020.08.11.300000](https://www.biorxiv.org/content/10.1101/2020.08.11.300000)



Green Open Access with preprints

Preprint then publication in toll-access journal

But final version might differ

But copyright to editor

© 2019 Elsevier Ltd. All rights reserved.

SPRINGER NATURE

© 2019 Springer Nature Publishing AG



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 (sometimes)





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).

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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



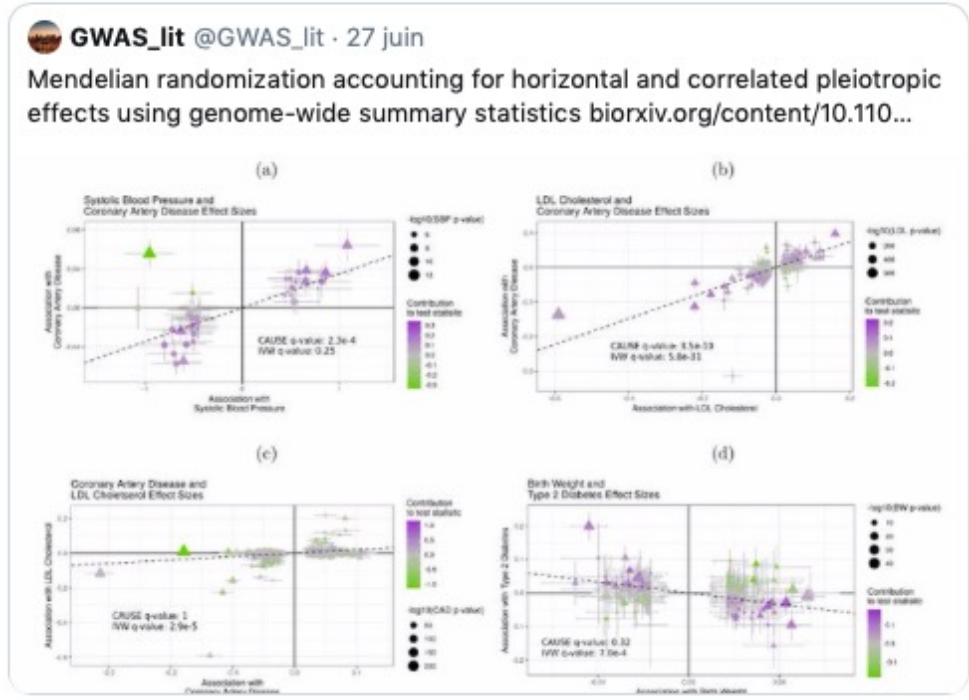


Zoltan Kutalik
@zkutalik



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

[Traduire le Tweet](#)



Highly competitive fields use preprints

- Human genetics GTEx consortium: 32 in biorXiv
- 22'028 "Covid19" in medRxiv
- Pharmaceutical industry uses preprints
 - Roche + Sanofi + Novartis = 56% (Subramanian et al 2021 industry preprints)



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



Sherpa Romeo publisher policies

e.g. Science

Published Version	✗ Not Permitted	+
Accepted Version [pathway a]	⌛ None ☰ 📁 Institutional Repository, Author's Homepage	-
⌛ Embargo	No Embargo	
© Copyright Owner	Authors	
📁 Location	Author's Homepage Institutional Repository	
☰ Conditions	Published source must be acknowledged with DOI Set statement must accompany post-print (see policy) Must link to publisher version Can not be deposited until publication by AAAS	
Accepted Version [pathway b]	📁 🌐 6m ☰ 📁 PMC, Funder Designated Location	+
Accepted Version [pathway c]	📁 ⌛ None 📄 CC BY 📁 Any Website, +2	+
Submitted Version	⌛ None ☰ 📁 arXiv, bioRxiv, ChemRxiv, medRxiv, +1	+

<https://v2.sherpa.ac.uk/id/publication/11114?template=romeo>

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

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 Re... Article usage: June 2017 to November 2017

doi: https://doi.org/10.1101/181111

This article is a part of

Show by month	Abstract	Pdf
total	7,340	2,164

Abstract



- 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...
be passe...
gamete f...
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:

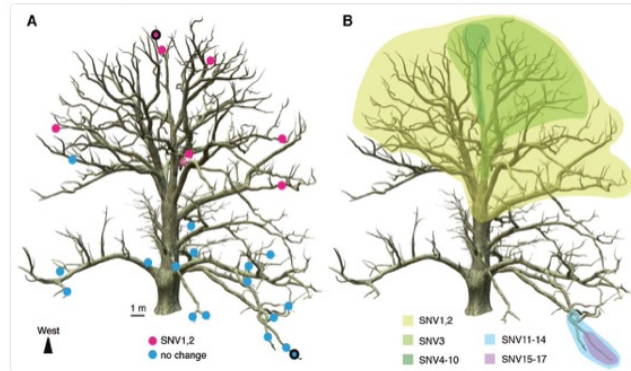
Casey Bergman @caseybergman
@mike_schatz @notSoJunkDNA @ewanbirney @embl @wolfgangkhuber @Eileen_Furlong
Indeed, something like this! <https://t.co/InppB7cyNp>
22 Sep 2017

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/181111>
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/901111111)

À l'origine en anglais



17:11 - 13 juin 2017

208 Retweets 290 J'aime



6 comments 208 retweets 290 likes



1

New Results

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

Namrata Sarkar, Emanuel Schmid-Siegert, Christian Iseli, Sandra Caldeyron, Caroline Gouhier, Jacqueline Chrast, Pietro Cattaneo, Frederic Schutz, Laurence Farinelli, Marco Pagni, Michel Scuderi, Jeremie Voumard, Michel Jaboyedoff, Christian Fahlhäusser, Christian S. Hardtke, Laurent Keller, Alexandre Roussel, and Heidi Ledford
Article usage: June 2017 to November 2017
doi: <https://doi.org/10.1101/164111>

This article is a preprint of [Low Rate of Somatic Mutations in a Long-Lived Oak Tree](#) published in *Nature* on 19 June 2017. To view the published version, please visit [https://doi.org/10.1038/nature21056](#).

Abstract

2

Abstract

Because the tree's genome is so large, it is expected that it would have accumulated many mutations over its long life. However, we find that the mutations that do occur perfectly follow the tree's shape, with a high density in the stem and a low density in the branches. This suggests that the tree's genome is being protected from mutations, possibly by a mechanism that is specific to long-lived trees.



- Picked up by 2 news outlets
- Blogged by 2
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- The Daily Scan from GenomeWeb, 21 Jun 2017

Tweets referencing this article:

Casey Bergman @caseybergman
@mike_schatz @notSoJunkDNA @ewanbirney @embl @wolfgangkhuber
Indeed, something like this! <https://t.co/1nppB7cyNp>
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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

Search

3



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.

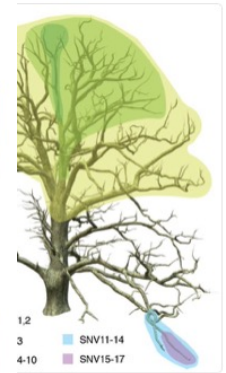
Heidi Ledford
19 June 2017 (preprint 13 June)

PDF Rights & Permissions



The 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.

old oak tree has
use 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, Jérémie 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/10.1101/161111>

This article is a preprint. [Show by month](#)

Month	Abstract
Total	7,340

Abstract



Abstract

Because of the way they pass on their genome, somatic mutations could be found in trees.

- Picked up by 2 news outlets
- Blogged by 2
- Tweeted by 352
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21 Aug 2017

Search

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.

The towering 234-year-old 'Napoleon' oak has weathered storms both meteorological and human. Its genome has remained largely — and surprisingly — unchanged. *Nature Plants* 3, 926–929 (2017) | [Download Citation](#)

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



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

33



Swiss Institute of Bioinformatics

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



SNSF, EU, and other funders accept preprints

Preprints used in "Current state of own research" in October 2021 SNSF application:

- Djordjevic et al. *Dynamics of sex-biased gene expression over development in the stick insect Timema californicum*. bioRxiv. 2021; 2021.01.23.427895
- Jaron et al. *Convergent consequences of parthenogenesis on stick insect genomes*. bioRxiv. 2020; 2020.11.20.391540
- Laloum & Robinson-Rechavi. *Why is the expression of so many genes rhythmic? Energetic cost explains protein rhythmicity and expression noise control explains mRNA rhythmicity*. bioRxiv. 2021; 2021.04.15.439944



Open science, beyond OA



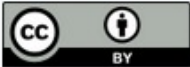


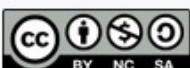



Different open for different stuff

- Open access
- Open source
- Open data

Open: **free** as in beer and **free** as in freedom

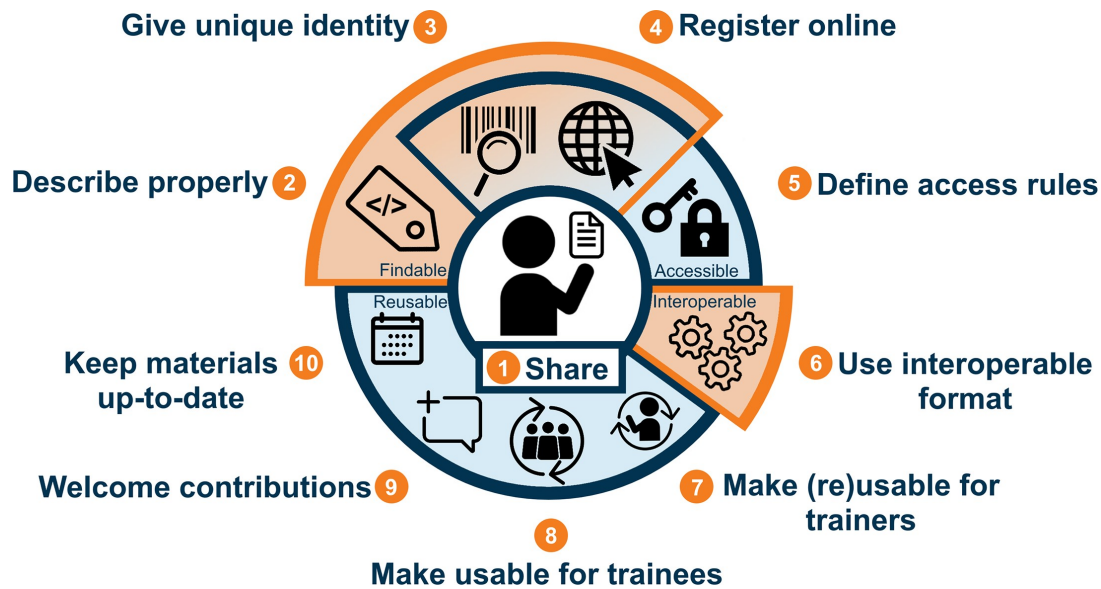


Creative Commons Licenses

License name	Abbreviation	Icon	Attribution required	Allows remix culture	Allows commercial use	Allows Free Cultural Works	Meets the OKF 'Open Definition'
Attribution	BY		Yes	Yes	Yes	Yes	Yes
Attribution-ShareAlike	BY-SA		Yes	Yes	Yes	Yes	Yes
Attribution-NonCommercial	BY-NC		Yes	Yes	No	No	No
Attribution-NonCommercial-ShareAlike	BY-NC-SA		Yes	Yes	No	No	No
Attribution-NoDerivatives	BY-ND		Yes	No	Yes	No	No
Attribution-NonCommercial-NoDerivatives	BY-NC-ND		Yes	No	No	No	No
"No Rights Reserved"	CC0		No	Yes	Yes	Yes	Yes

https://en.wikipedia.org/wiki/Creative_Commons_license#Four_rights

FAIR



To be Findable:

- F1. (meta)data are assigned a globally unique and persistent identifier
- F2. data are described with rich metadata (defined by R1 below)
- F3. metadata clearly and explicitly include the identifier of the data it describes
- F4. (meta)data are registered or indexed in a searchable resource

To be Accessible:

- A1. (meta)data are retrievable by their identifier using a standardized communications protocol
 - A1.1 the protocol is open, free, and universally implementable
 - A1.2 the protocol allows for an authentication and authorization procedure, where necessary
- A2. metadata are accessible, even when the data are no longer available

To be Interoperable:

- I1. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
- I2. (meta)data use vocabularies that follow FAIR principles
- I3. (meta)data include qualified references to other (meta)data

To be Reusable:

- R1. meta(data) are richly described with a plurality of accurate and relevant attributes
 - R1.1. (meta)data are released with a clear and accessible data usage license
 - R1.2. (meta)data are associated with detailed provenance
 - R1.3. (meta)data meet domain-relevant community standards

"as open as possible and as closed as necessary"

H2020 guidelines

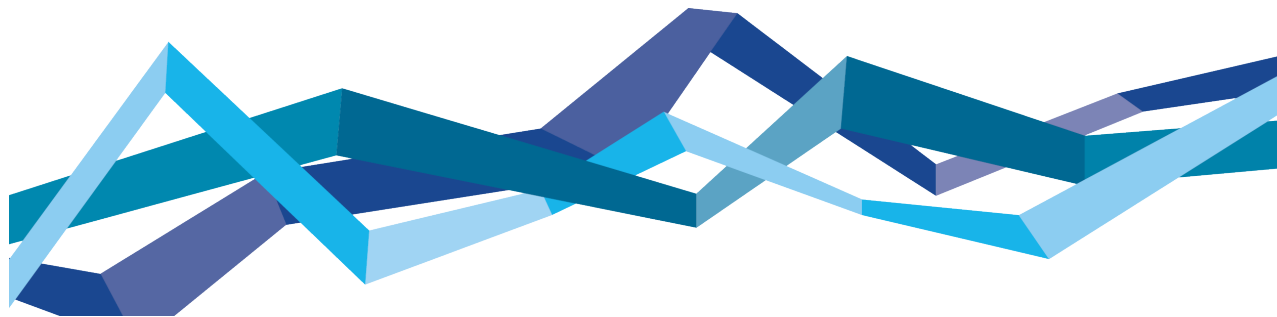
Research evaluation is adapting



Agreement signed by Swissuniversities and SNSF

— AGREEMENT ON REFORMING RESEARCH ASSESSMENT

20 July 2022





Evaluation criteria

- Focus research assessment criteria on quality.
 - Reward the originality of ideas, the professional research conduct, and results beyond the state-of-the-art.
- Consider also the full range of research outputs
 - such as scientific publications, data, software, models, methods, theories, algorithms, protocols, workflows, exhibitions, strategies, policy contributions, etc.
- Abandon inappropriate uses in research assessment of journal- and publication-based metrics, in particular inappropriate uses of Journal Impact Factor (JIF) and h-index



SNSF: Major scientific achievements

Most important scientific achievements.

In addition to scientific publications, any other relevant information, such as a knowledge transfer event, a software, database, prototype, etc. may be provided here. Describe for each achievement the applicant's specific contribution and the overall impact of the work.



"When will 'open science' become simply 'science'?"