BioRχiv

How I Learned To Stop Worrying And Love The Preprints

Marc Robinson-Rechavi @marc_rr

Preprints

Principle of preprints

- Manuscrits 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

Jordan Anaya, prepubmed.org

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

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/10.110...

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

. . . opening access to research

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

Journal:	Nature (ISSN: 0028-0836, ESSN: 1476-4687)
RoMEO:	This is a RoMEO **yellow** journal
Author's Pre-print:	✓ author **can** archive pre-print (ie pre-refereeing)
Author's Post-print:	**subject to Restrictions below**, author **can** archive post-print (ie final draft post-refereeing)
Restrictions:	• 6 months embargo
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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**

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White	Archiving not formally supported
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http://www.sherpa.ac.uk/romeo/index.php

Stories & Use cases

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

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.

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doi: https://do

This article is a p

Abstract

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Article usage: June 2017 to November 2017

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Tweeted by **352**
On **5** Facebook pages
Mentioned in **1** Wikipedia entries

14 readers on Mendeley

Abstract

Because
be passe
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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 @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.…

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…

À l'origine en anglais

17:11 - 13 juin 2017

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6 208 290

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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)

PDF | Rights & Permissions

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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.

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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

Nature Plants **3**, 926–929 (2017) | Download Citation

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 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 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

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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 Frochaux, 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)

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

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

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

@marc_rr