



Publication and research integrity: a Wellcome perspective

COPE European Seminar 2017

The changing face and future of publication ethics

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Agenda

- Publication & research ethics
- Wellcome's approach
 - Policies
 - Platforms
- Next steps

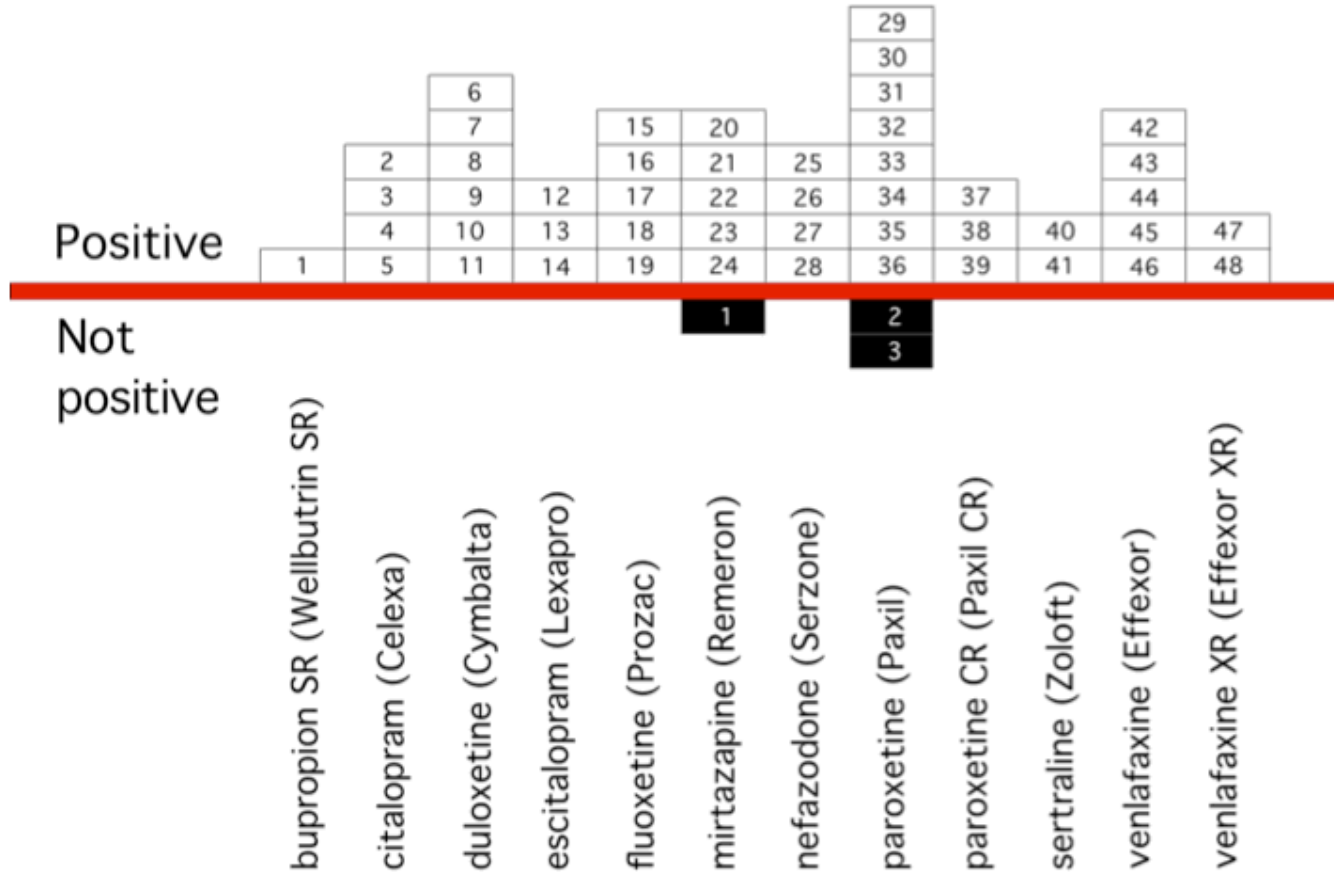


Good research publication practice

- Research publications are:
 - Accessible
 - Published in a timely manner
 - Re-analysable and reproducible
 - Peer reviewed – including PPPR
 - Absent of publication bias
- And one where research assessment is NOT based on venue of publication

Publication bias

Journal version of antidepressant trials



Graphic courtesy of OpenFDA trials, based on data presented <http://www.nejm.org/doi/full/10.1056/NEJMsa065779#t=article>,

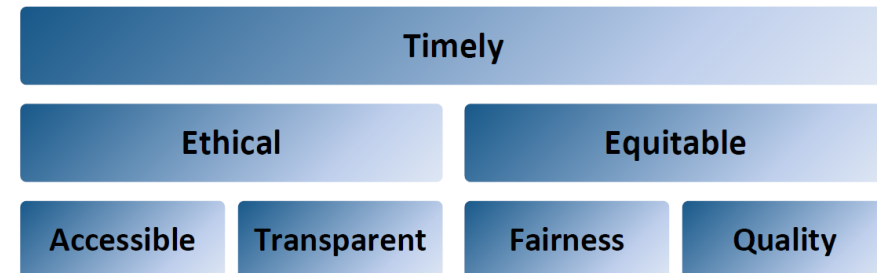
Wellcome policies

Wellcome policies to support good publication practices (1)

- Open access to publications
 - Publisher requirements, include requirements around CRE's, and clear licensing statements
- Data sharing
 - Expectation that researchers should maximise the availability of research data with as few restrictions as possible
 - Data underpinning publication must be made available at time of publication
 - Researchers consider how they will share their outputs at the grant application stage
- Data pertaining to public health emergencies
 - Should be shared as soon as ready (i.e. quality assured) and not wait for publication



Key principles for data sharing in a public health emergency



Wellcome policies to support good publication practices (2)

- Clinical trials
 - Trials must be registered; summary outputs should be shared
 - Run ClinicalStudyDataRequest.com secretariat
 - Looking to develop CDSR to accommodate academic clinical trial data
- Output sharing (draft policy)
 - Looking to expand data sharing policy – to cover all research outputs - including data, software and biological materials



Major research funders and international NGOs to implement WHO standards on reporting clinical trial results

News release

18 MAY 2017 | GENEVA - Some of the world's largest funders of medical research and international non-governmental organizations today agreed on new standards that will require all clinical trials they fund or support to be registered and the results disclosed publicly.



Researcher evaluation

- Pressure to publish – can lead to positive outcome bias from researchers
- In our OA [policy](#) we reaffirm the principle *“that it is the intrinsic merit of the work, and not the title of the journal or the publisher with which an author's work is published, that should be considered in making funding decisions”*
- Stressed in guidance to Panel members
- Mirrored in REF [guidance](#)

Wellcome is a signatory to the [DORA](#) guidelines, so please ensure that you follow these when assessing applicants' CVs. In particular, please note the following points:

- You should focus on the content and quality of publications, rather than their number, or the journals in which they were published.
- The format of research outputs is diverse, and varies between disciplines. Wellcome recognises and supports this diversity and you should take this into account when assessing applications.
- You should be sensitive to legitimate delays in research publication, and personal factors (parental or other types of leave, part-time working and disability) that may have affected the applicant's outputs.

Wellcome guidance to Panel members

➊ How will journal impact factors, rankings or lists, or the perceived standing of publishers be used to inform the assessment of research outputs?

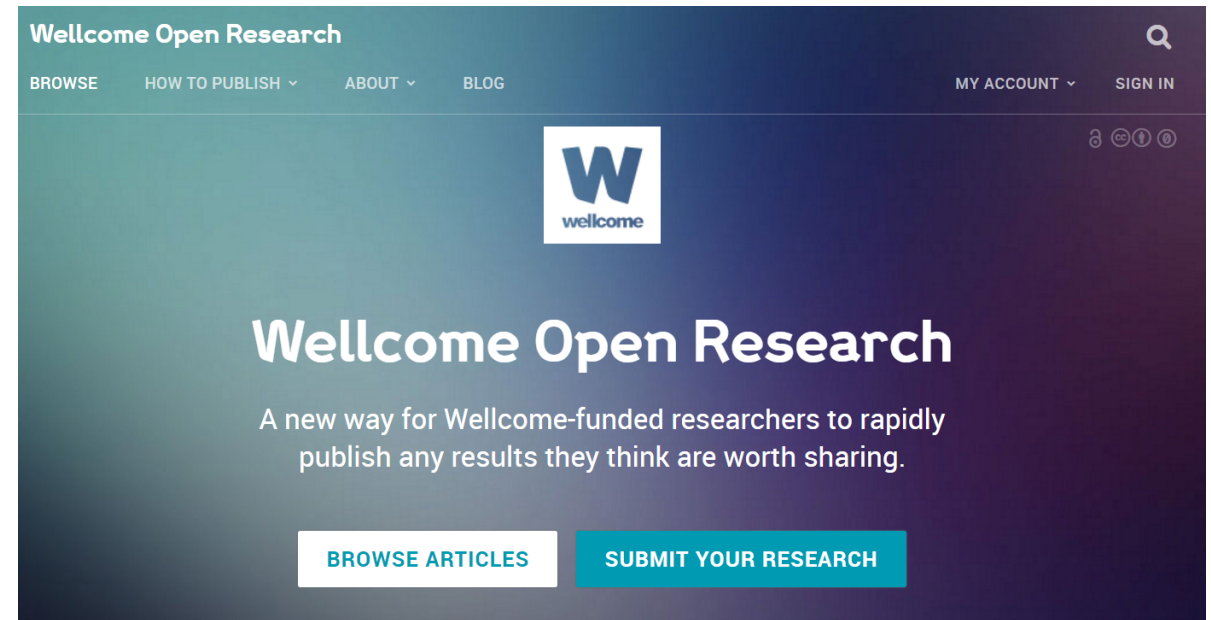
No sub-panel will make any use of journal impact factors, rankings, lists or the perceived standing of publishers in assessing the quality of research outputs. An underpinning principle of the REF is that all types of research and all forms of research outputs across all disciplines shall be assessed on a fair and equal basis.

REF guidance

Platforms

Wellcome Open Research

A new publishing platform where Wellcome-funded researchers can publish any results they think are worth sharing



<http://wellcomeopenresearch.org>

What problem were we seeking to solve?

- Make the sharing of research outputs **faster**
- More **transparent**
 - All reviews are signed and public; everything (one passed initial screening) is published
- Easier for researchers to provide information that supports **reproducibility**
 - all supporting data must be shared (or explanation provided how to access it)
- Encourage the sharing of **all** research outputs
 - Address “file drawer” problem - by publishing negative and non-confirmatory results, as well as protocols, data notes, software notes, case studies etc & remove the bias, where +tive results are more likely to be published
- And keep costs affordable
 - Average APC at WOR is £780; typical average charged to Wellcome is £2044

A model based on post publication peer review

Median time from submission to publication: 19 days

Median time from publication to passing peer review: 31 days



- Approved; ✓✓
- Approved with reservations; ??
- Not approved ✕✕

DATA NOTE



Identifying genes required for respiratory growth of fission yeast [version 1; referees: 4 approved]

Michal Malecki, Jürg Bähler

REFEREES Christopher Herbert; Luis A. Rokeach; Jim Karagiannis; Makoto Kawamukai

FUNDER Wellcome Trust

RESEARCH ARTICLE

AWAITING PEER REVIEW

The LonDownS adult cognitive assessment to study cognitive abilities and decline in Down syndrome [version 1; referees: awaiting peer review]

Carla M. Startin, Sarah Hamburg, Rosalyn Hithersay, Amy Davies, Erin Rodger, Nidhi Aggarwal, Tamara Al-Janabi, André Strydom

REFEREES Invited

FUNDERS Wellcome Trust | Baily Thomas Charitable Fund

RESEARCH ARTICLE



Free serum haemoglobin is associated with brain atrophy in secondary progressive multiple sclerosis [version 1; referees: 1 approved, 1 approved with reservations]

Alex Lewin, Shea Hamilton, Aviva Witkover, Paul Langford, Richard Nicholas, Jeremy Chataway, Charles R.M. Bangham

REFEREES Hans Lassmann and Simon Hametner; George Harauz and Vladimir V. Bamm

COPE “Journal content must be clearly marked as whether peer reviewed or not”

Open Peer Review

Referee Status:

Invited Referees

Version(s)	1	2	3	4
Version 1 published 15 Nov 2016	 read report	 read report	 read report	 read report

- 1 Christopher Herbert, CEA, CNRS, University Paris-Sud, University Paris-Saclay, France
- 2 Luis A. Rokeach, Université de Montréal, Canada
- 3 Jim Karagiannis, University of Western Ontario, Canada
- 4 Makoto Kawamukai, Shimane University, Japan

All reports (4)

Comments o

All comments (0)

Add a Comment

Journal List > Europe PMC Author Manuscripts > [PMC5133385](#)

Europe PMC Funders Group
Author Manuscript
Accepted for publication in a peer reviewed journal
[SUBMIT A MANUSCRIPT](#)

Wellcome Open Res. Author manuscript; available in PMC 2016 Dec 2. PMID: PMC5133385
Published in final edited form as: Wellcome Open Res. 2016; 1: 12. EMS170609
Published online 2016 Nov 15. doi: [10.12688/wellcomeopenres.9992.1](#)

Identifying genes required for respiratory growth of fission yeast

Michal Malecki^{1,2} and Jürg Bähler^{Ma,1}

Author information ► Copyright and License information ►

Peer Review Summary

Go to:

Review date	Reviewer name(s)	Version reviewed	Review status
2016 Nov 28	Makoto Kawamukai		Approved
2016 Nov 25	Jim Karagiannis		Approved
2016 Nov 24	Luis A. Rokeach		Approved
2016 Nov 21	Christopher Herbert		Approved




Open reviews: critical, helpful and honest

Referee Report 05 Dec 2016	Views 18
Marc Brysbaert , Department of Experimental psychology , Ghent University, Ghent, Belgium	
Approved with Reservation	Comments on study design and data interpretation – Several points require clarification, in our view. <ol style="list-style-type: none">1. There were 140 patients, and 60 controls (3 groups of 20). So the total number is supposed to be 200 serum samples per time point. What are the other 275 samples? The question of sample numbers, both of patients and controls, arises again later when 138 patients are mentioned. Additionally, a valuable control could be a group of patients with another neurodegenerative disease characterised by brain atrophy.2. The 6-month time point was not mentioned in the paragraph describing the study design, and there were no results reported for it.3. For protein profiling by SELDI-TOF mass spectrometry, after the 1:10 serum dilution, one would expect signal
Referee Report 20 Jan 2017	Views 15
Sophie Donnet , University of Paris-Saclay, Paris, France	Cite
Not Approved	
<p>In this paper, the authors claim that the conclusions of several studies would be modified if a statistical models taking into account the variability of the presented stimuli had been considered.</p> <p>Although the problem is interesting, I am not completely convinced by the conclusions and the statistical tools used to assess the results.</p> <p>First of all, the authors argue that, due to the complexity of the new model, the authors can not use the standard numerical tools to perform the statistical inference (R or SAS) and so will prefer a Bayesian inference, making this choice quite opportunist. However, besides the fact that they use a Bayesian inference (including prior distribution), they base their conclusions on frequentist arguments (comparing test statistics). To my point of view, this is quite confusing. If a Bayesian framework is considered, then the hypothesis testings should be perform using Bayes Factor or any other tools taking into account the prior distribution.</p>	

Range of publication types

STUDY PROTOCOL

Effect of tranexamic acid on coagulation and fibrinolysis in women with postpartum haemorrhage (WOMAN-ETAC): protocol and statistical analysis plan for a randomized controlled trial [version 1; referees: 3 approved]




✉ Haleema Shakur ¹,
Olayinka Ogunbode², Taiwo
Roberts¹

+ Author affiliations

+ Grant information

METHOD ARTICLE

UPDATE A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast [version 3; referees: 2 approved]

✉ María Rodríguez-López ¹, Cristina Cotobal ¹, Oscar Fernández-Sánchez¹,
Natalia Borbarán Bravo ¹, Risky Oktriani¹, Heike Abendroth¹, Dardan Uka¹, Mimoza Hoti¹, Jin
Wang¹, Mikel Zaratiegui², ✉ Jürg Bähle

SOFTWARE TOOL ARTICLE

Neopeptide Analyser: A software tool for neopeptide discovery in proteomics data [version 1; referees: 2 approved]

Data and software availability

Data availability

Sequence data used for analysis in this study is publicly archived at the European Nucleotide Archive (ENA) under accession code [ERR1898537](#). Files contain high quality sequence data, as well as associated alignment data.

Data availability

ALSPAC data used for this submission will be made available on request to the ALSPAC Executive via this website, which also provides full details and distributions of the ALSPAC study variables:

<http://www.bristol.ac.uk/alspac/researchers/access/>. The ALSPAC data management plan (available here:

<http://www.bristol.ac.uk/alspac/researchers/data-access/documents/alspac-data-management-plan.pdf>) describes in detail the policy regarding data sharing. A sampler set of similar data containing relevant ALSPAC variables is available from the European Genome-phenome Archive (accession number: EGAS00001000090):

<https://www.ebi.ac.uk/ega/studies/EGAS00001000090>.

Software availability

SeqPlots is distributed as user-friendly stand-alone applications for Mac and Windows or Linux, and is available as an R programming language package from the Bioconductor repository. SeqPlots can be also deployed as a server application, which is useful for data sharing within laboratories, collaborative usage and remote work. SeqPlots is an open source and open development project: source code wiki, bug tracker and pull requests are available via GitHub.

Software is available from:

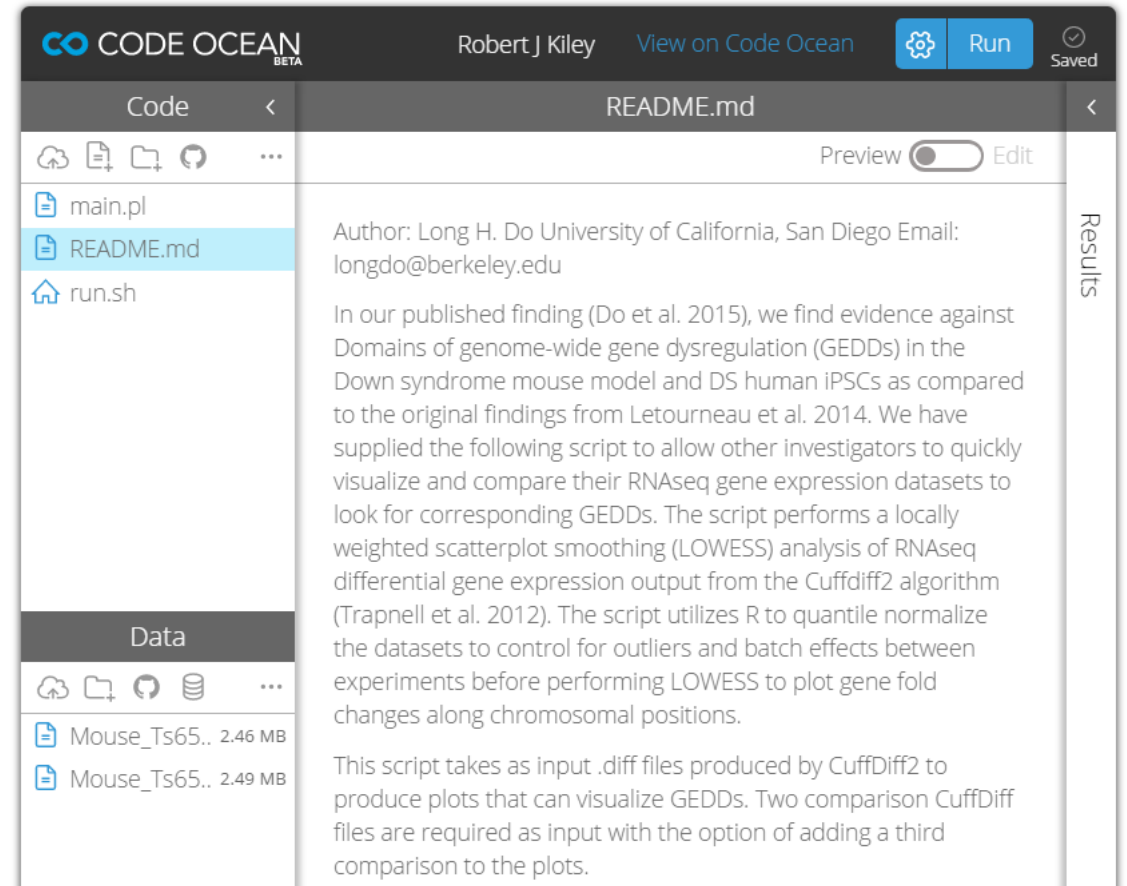
- <http://przemol.github.io/seqplots> (Mac, Windows, Linux, full documentation)
- <http://bioconductor.org/packages/seqplots> (R/Bioconductor)
- <http://przemol.github.io/seqplots/#installation--server-deployment> (server deployment)



Reproducible code

- F1000Research added Code Ocean widgets to articles
- [Code Ocean](#) is a cloud-based platform that makes the computational code used in research both accessible and usable. Researchers and software engineers can now share and run code with a single click
- Look to extend functionality to WOR

RNAseq data from hFibro-L, hiPSCs-L, and hiPSCs-H were downloaded from the Sequence Read Archive (SRP039348, SRP032928) and uploaded to Illumina BaseSpace for mapping (BaseSpace App v1.0, TopHat v2) and differential gene analysis (BaseSpace App v1.1, CuffLinks v2.1.1). PCA was performed using R (v3.1.0) from normalized gene count values (FPKM). Overall Spearman correlation values were calculated from locally weighted scatterplot smoothing (LOWESS) with 30% bandwidth between log2 (FC) gene expression of comparison samples, ordered by genes along each chromosome and plotted using R and custom scripts.



The screenshot displays the Code Ocean interface. At the top, the user is identified as Robert J Kiley, with options to 'View on Code Ocean' and a 'Run' button. The main area shows a file explorer on the left with files: main.pl, README.md (selected), and run.sh. Below this is a 'Data' section with two files: Mouse_Ts65.. (2.46 MB) and Mouse_Ts65.. (2.49 MB). The main content area displays the README.md file, which includes the author's name (Long H. Do), affiliation (University of California, San Diego), and email (longdo@berkeley.edu). The text describes a published finding (Do et al. 2015) and provides a detailed description of the script used for RNAseq analysis, including the use of Cuffdiff2, R, and LOWESS. A 'Results' sidebar is visible on the right.

Preprints

- Wellcome also supporting the adoption of preprints

We now accept preprints in grant applications

🕒 News / Published: 10 January 2017

🔗 [Open access](#)

As of January 2017, we will permit researchers to cite preprints, or pre-peer reviewed manuscripts, in their grant applications and end-of-grant review reports.

A preprint is a complete and public draft of a scientific document, yet to be certified by peer review.

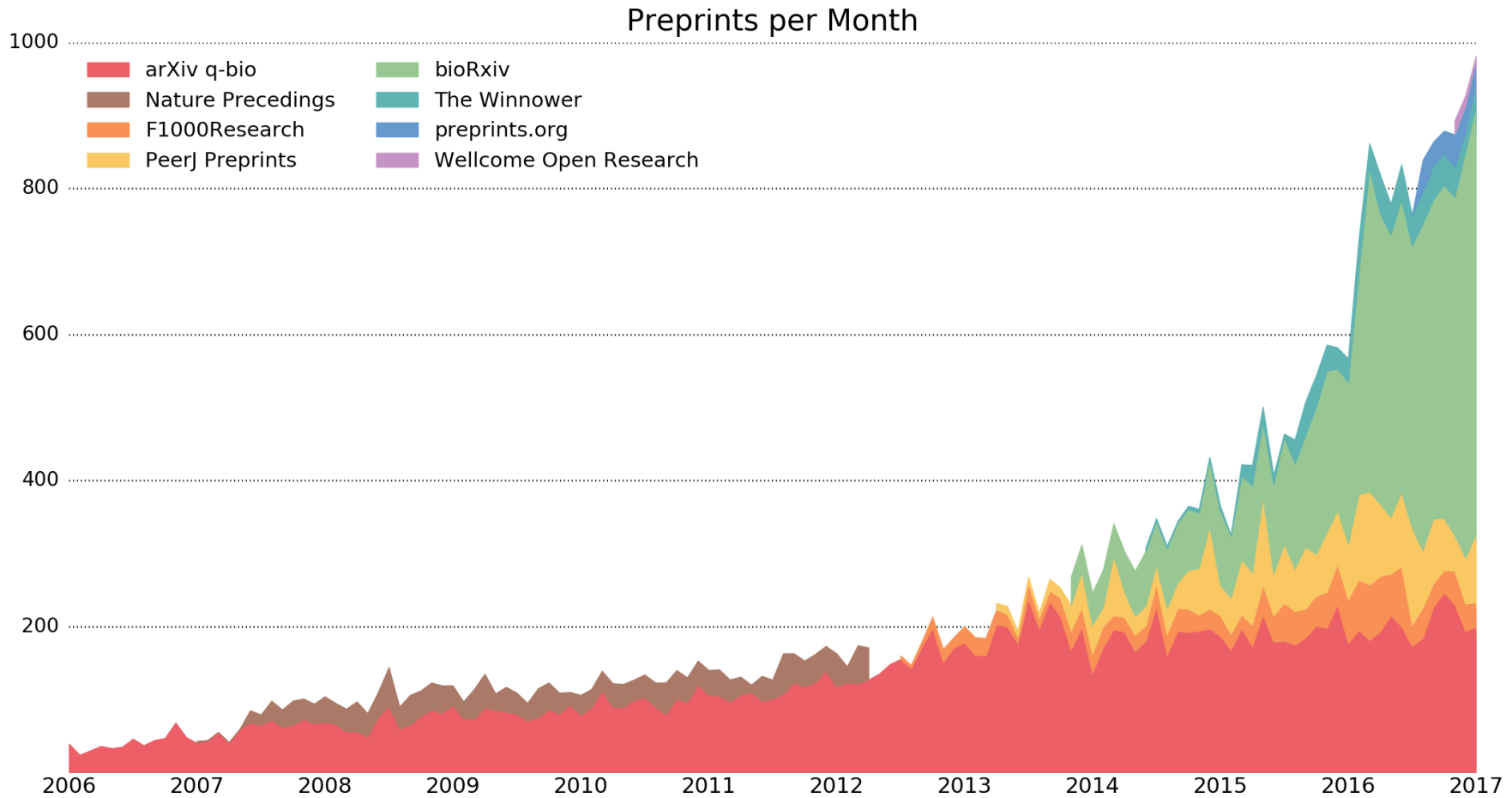
This change will help us (and those reviewing grant applications) to get a more up-to-date picture of researchers' work.

Preprints: we're supporting calls for a Central Service

🕒 Explainer / Published: 13 February 2017

🔗 [Data sharing](#), [Open access](#)

Preprints in biology are growing...



Next steps?

Next steps?

- Encouraging publishers to develop data sharing policies
- PLOS and Springer/Nature good exemplars
- As a minimum publishers should:
 - publish a data sharing policy
 - develop a data availability statement (and make that a mandatory part of the submission – just like a Col)
- Encouraging data citations
 - Exploring “data authorship”

• Mandatory • Optional ○ Not Required

Feature	Explanation	Type 1	Type 2	Type 3	Type 4
Data sharing via repositories supported	Details of sharing via repositories is referred to in journal guide to authors	•	•	•	•
Data citation permitted	Journal style guide permits authors to cite publicly available datasets in reference lists	•	•	•	•
Publisher helpdesk	Helpdesk contact details included in journal information for authors	◐	◐	◐	◐
Public data deposition and dataset identifier checks for specific types of data	Data deposition checked as part of the publishing process where there is an established research community mandate	○	◐	•	•

Questions

