

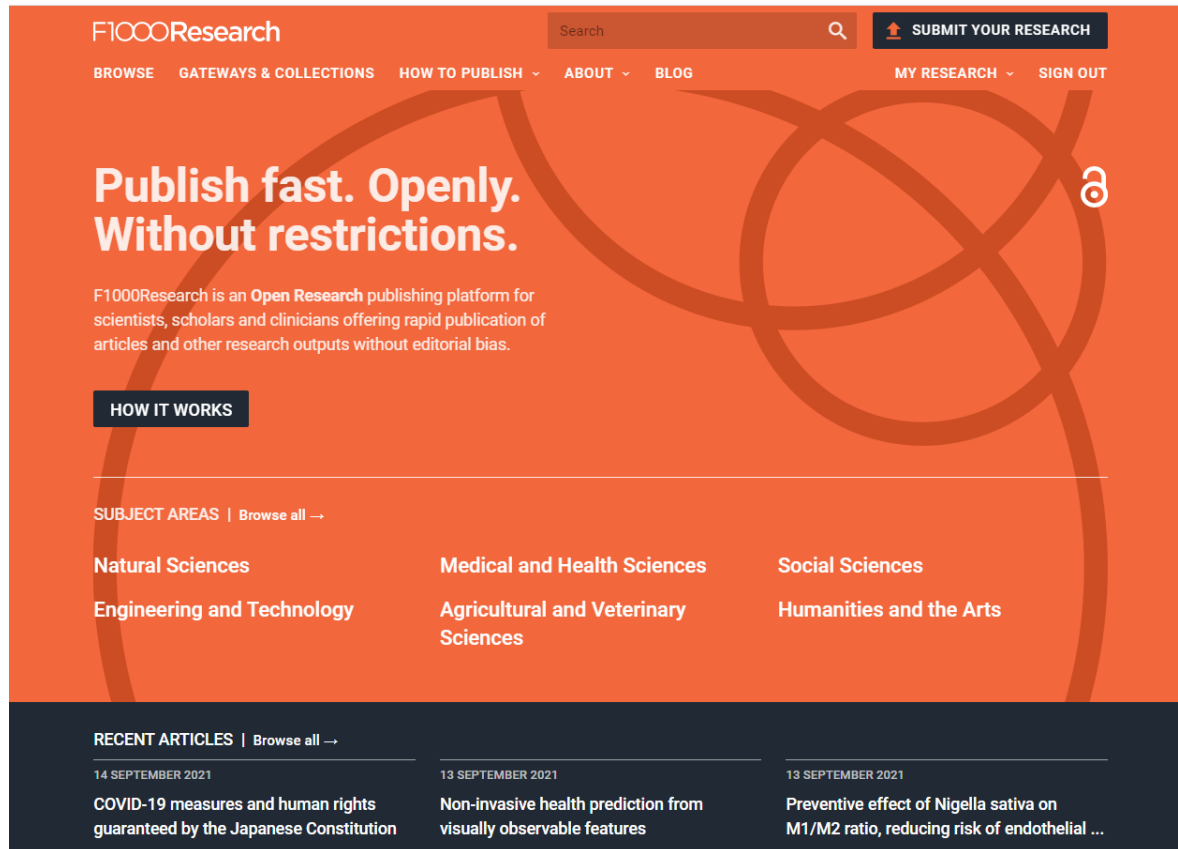
Open Research Practices

Demitra Ellina, Publishing Executive, F1000

20th October 2021, MPDL Open Science Days

F1000

Introducing F1000Research



F1000Research

Search

BROWSE GATEWAYS & COLLECTIONS HOW TO PUBLISH **ABOUT** BLOG MY RESEARCH SIGN OUT

Publish fast. Openly. Without restrictions.

F1000Research is an Open Research publishing platform for scientists, scholars and clinicians offering rapid publication of articles and other research outputs without editorial bias.

HOW IT WORKS

SUBJECT AREAS | Browse all →

- Natural Sciences
- Medical and Health Sciences
- Social Sciences
- Engineering and Technology
- Agricultural and Veterinary Sciences
- Humanities and the Arts

RECENT ARTICLES | Browse all →

- 14 SEPTEMBER 2021
COVID-19 measures and human rights guaranteed by the Japanese Constitution
- 13 SEPTEMBER 2021
Non-invasive health prediction from visually observable features
- 13 SEPTEMBER 2021
Preventive effect of *Nigella sativa* on M1/M2 ratio, reducing risk of endothelial ...

- **Launched in 2013**

- **Aim to rethink and evolve scholarly communication system**

- An Open Research publishing platform where a range of research outputs can be published

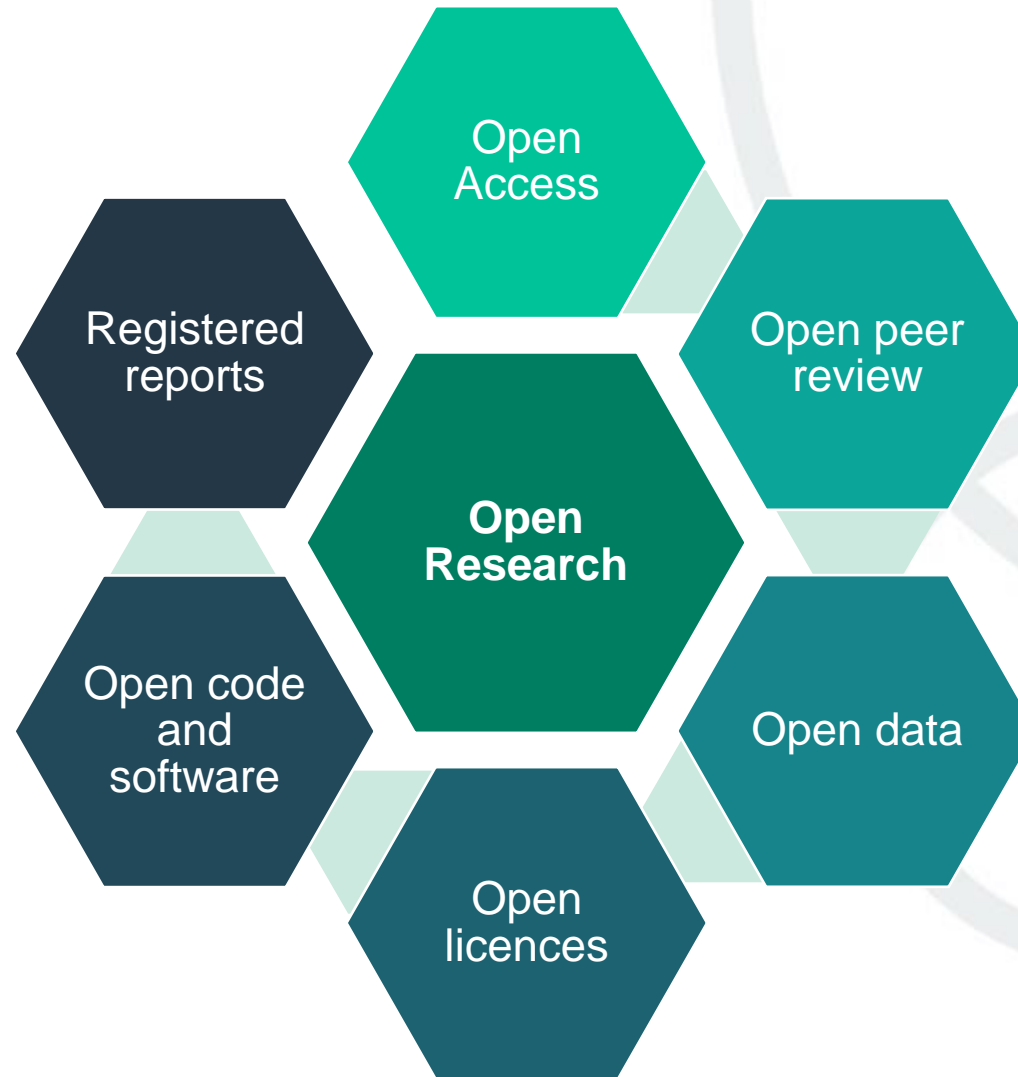
<https://f1000research.com/>

What is Open Research?

*“The practice of science in such a way that others can collaborate and contribute, where research data, lab notes and other research processes are **freely available**, under terms that **enable reuse, redistribution and reproduction** of the research and its underlying data and methods.”*

Foster Open Science

What are the facets of Open Research publishing?



Open Access

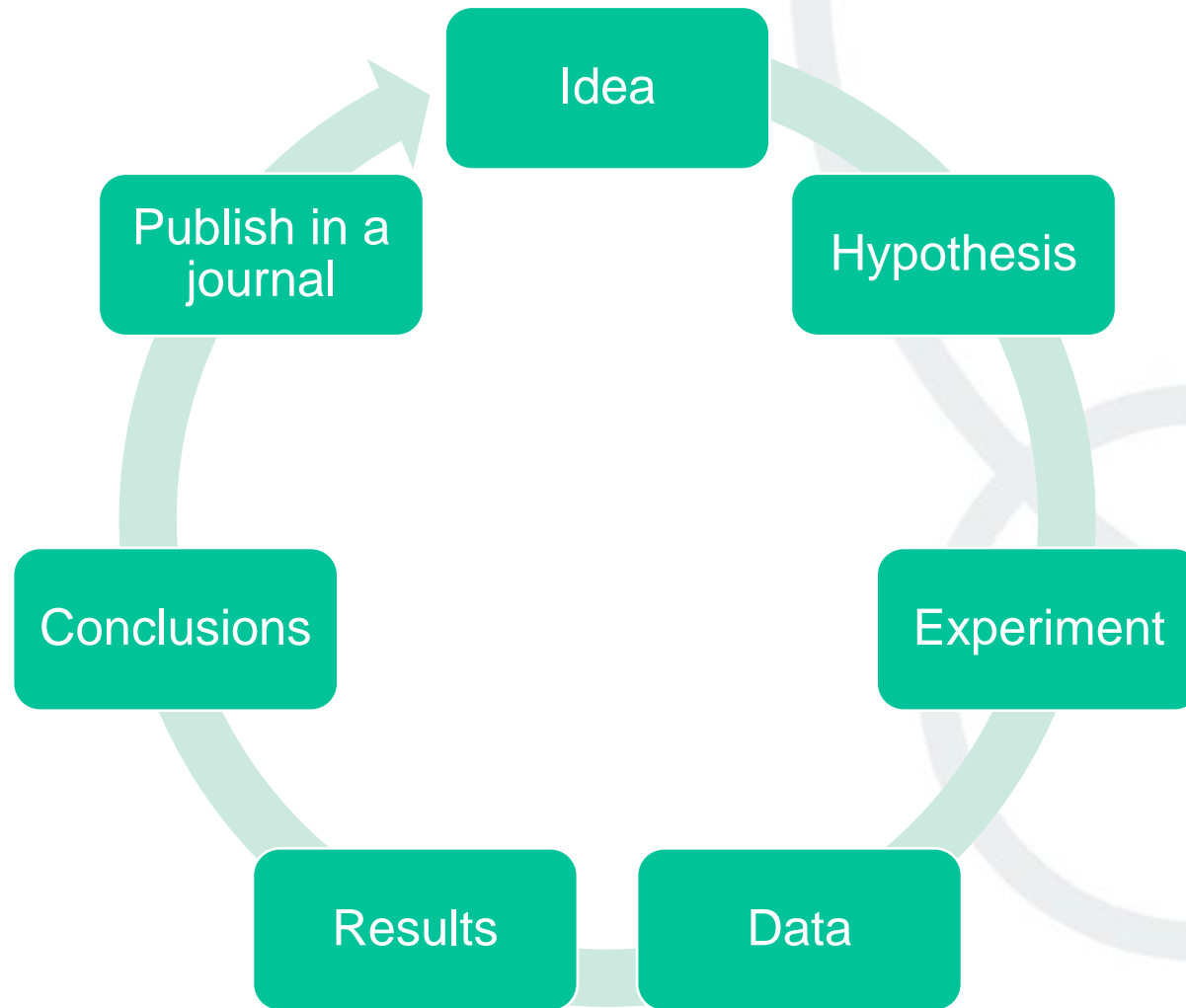
Online access to scientific information that is free of charge to the user and that is re-usable



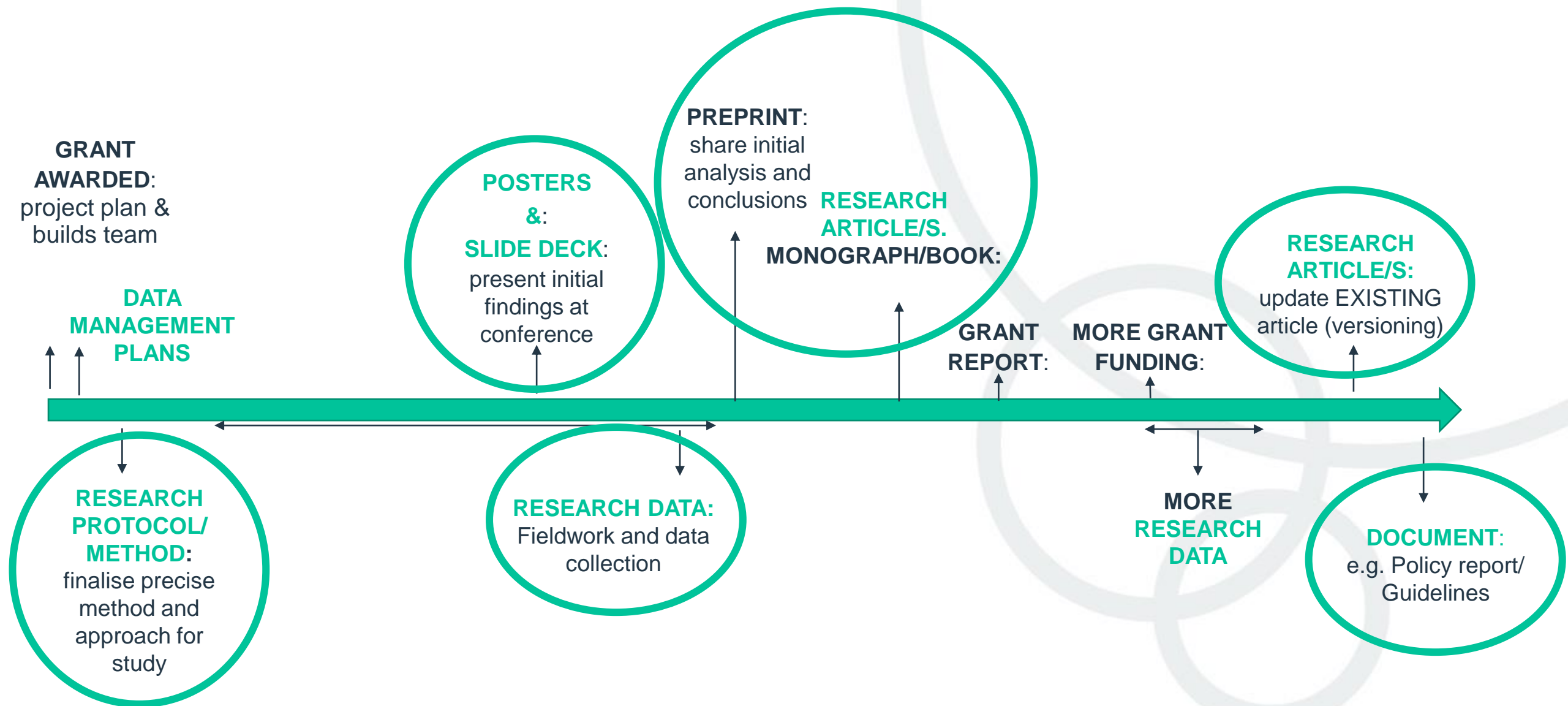
- Accelerates discovery and citations
- Public access and engagement
- Education and re-use outside of research
- Estimates say at least 28% of the scholarly literature is Open Access
- Over 13,000 Open Access journals are listed in DOAJ
- Growing number of research organisations and funders have OA policies/mandates



Moving from Open Access to Open Research



F1000Research: supporting the research journey



A diversity of research articles types

Research outputs come in a variety of shapes. So do our article types.



**Method
articles**



**Study
protocols**



**Software
tools**



**Systematic
reviews**



**Data
articles**



**Brief
reports**



Reviews



**Opinion
articles**



**Case
studies**



**Registered
reports**

F1000Research publishing: a diversity of output

Original research publishing
Peer reviewed

F1000Research
Open for Science

Home » Browse » Benchmarking of long-read assemblers for prokaryote whole genome sequencing

RESEARCH ARTICLE

UPDATE Benchmarking of long-read assemblers for prokaryote whole genome sequencing [version 2; peer review: 4 approved]

Ryan R. Wick¹, Kathryn E. Holt^{1,2}

Author details

Abstract

Background: Data sets from long-read sequencing platforms (Oxford Nanopore Technologies and Pacific Biosciences) allow for most prokaryote genomes to be completely assembled – one contig per chromosome or plasmid. However, the high per-read error rate of long-read sequencing necessitates different approaches to assembly than those used for short-read sequencing. Multiple assembly tools (assemblers) exist, which use a variety of algorithms for long-read assembly.

Methods: We used 500 simulated read sets and 120 real read sets to assess the performance of seven long-read assemblers (Canu, Flye, Miniasm/Minipolish, NECAT, Raven, Redbean and Shasta) across a wide variety of genomes and read parameters. Assemblies were assessed on their structural accuracy/completeness, sequence identity, contig circularisation and computational resources used.

Results: Canu v1.9 produced moderately reliable assemblies but had the longest runtimes of all assemblers tested. Flye v2.7 was more reliable and did particularly well with plasmid assembly. Miniasm/Minipolish v0.3 and NECAT v20200119 were the most likely to produce clean contig circularisation. Raven v0.0.8 was the most reliable for chromosome assembly, though it did not perform well on small plasmids and had circularisation issues. Redbean v2.5 and Shasta v0.4.0 were computationally efficient but more likely to produce incomplete assemblies.

Conclusions: Of the assemblers tested, Flye, Miniasm/Minipolish and Raven performed best overall. However, no single tool performed well on all metrics, highlighting the need for continued development on long-read assembly algorithms.

Open Peer Review

Reviewer Status **✓✓✓✓**

Reviewer Reports

	1	2	3	4
Version 2 (update) 22 Apr 20				
Version 1 23 Dec 19	✓ read	✓ read	✓ read	✓ read

Invited Reviewers

- Aleksey Zimin, Johns Hopkins University, Baltimore, USA
- Steven I. Salzberg, Johns Hopkins University School of Medicine, Baltimore, USA; Whiting School of Engineering, Johns Hopkins University, Baltimore, USA; Bloomberg School of Public Health, Johns Hopkins University, Baltimore, USA
- Robert Vaser, University of Zagreb, Zagreb, Croatia
- Mile Šikić, University of Zagreb, Zagreb, Croatia; Genome Institute of Singapore, A*STAR, Singapore
- Mikhail Kolmogorov, University of California San Diego, La Jolla, USA
- Olin Silander, Massey University Auckland, North Shore, New Zealand

Other research-based content
Not peer reviewed

Documents

Building Knowledge Systems in Agriculture
Five Key Areas for Mobilising the Potential of Extension and Advisory Services

Position Paper
June 2012

Logos: IFPRI, CGIAR, International Food Policy Research Institute, etc.

Implementation of the Robson classification of births, Dasht-e-Barchi Hospital, Afghanistan

Ghahis Bak, Mukhtar W, Fotheringham C, Omar MP, Hameed H, Azizi F, Deslandes D, Morton N, Adat E

Background and Aims

Methods

Results and Discussion

Conclusion

This audit has identified a population at significantly increased risk of adverse perinatal outcomes, those with breech presentation.

Posters

Maastricht University *Leading in Learning!*

Maastricht Brain Imaging Center

Multi-Parameter Quantitative Brain Anatomy at 7 Tesla
Roy A.M. Haast¹, Dimo Ivanov¹, Giancarlo Valente¹, Elsa Formisano¹ and Kamil Ulasog¹

¹Department of Cognitive Neuroscience, Faculty of Psychology and Neuroscience, Maastricht University, Maastricht, Netherlands

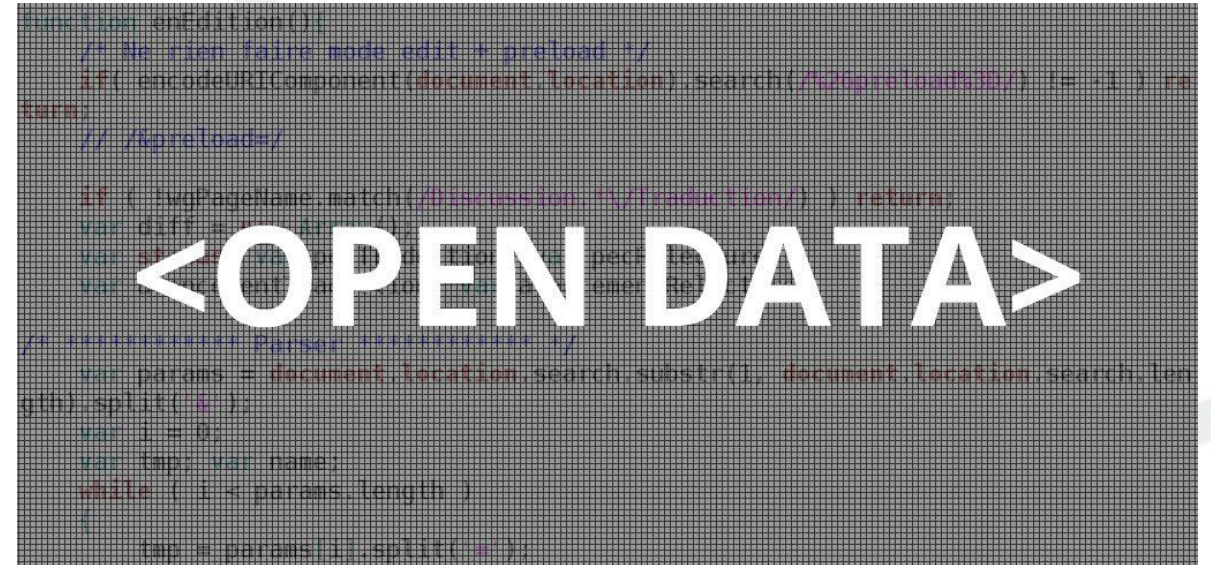
Slide Decks

Open Data

Open data

As open as possible, as closed as necessary

- We endorse the FAIR data principles alongside our own open data policies
- Our part in ensuring the research published on our platforms is reproducible
- Data Notes promote the reuse of datasets by providing a detailed description of a dataset; making it easier for other researchers to interpret



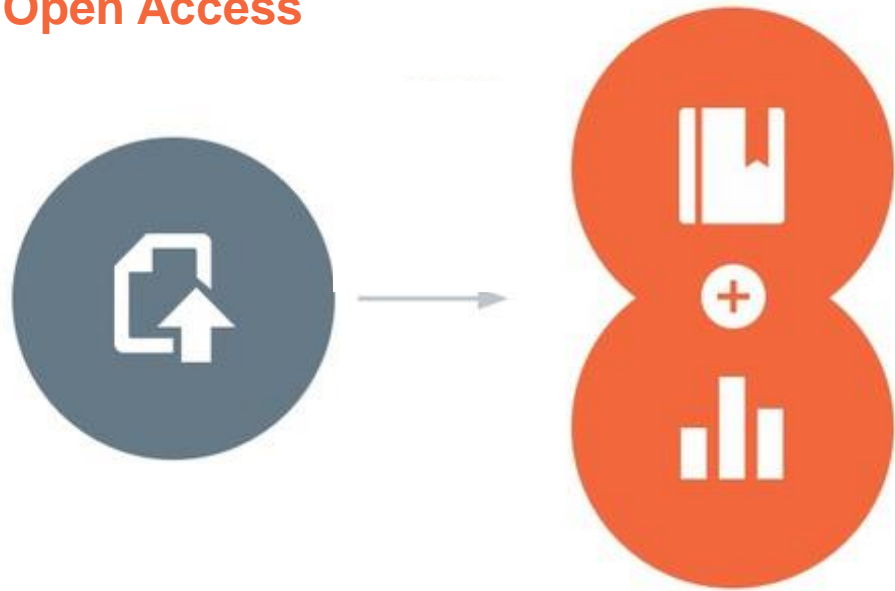
Your go-to guide to making your data Findable, Accessible, Interoperable, and Reusable:

https://f1000researchdata.s3.amazonaws.com/resources/FAIR_Open_Guide.pdf

F1000Research publishing: how does it work?

For original research articles

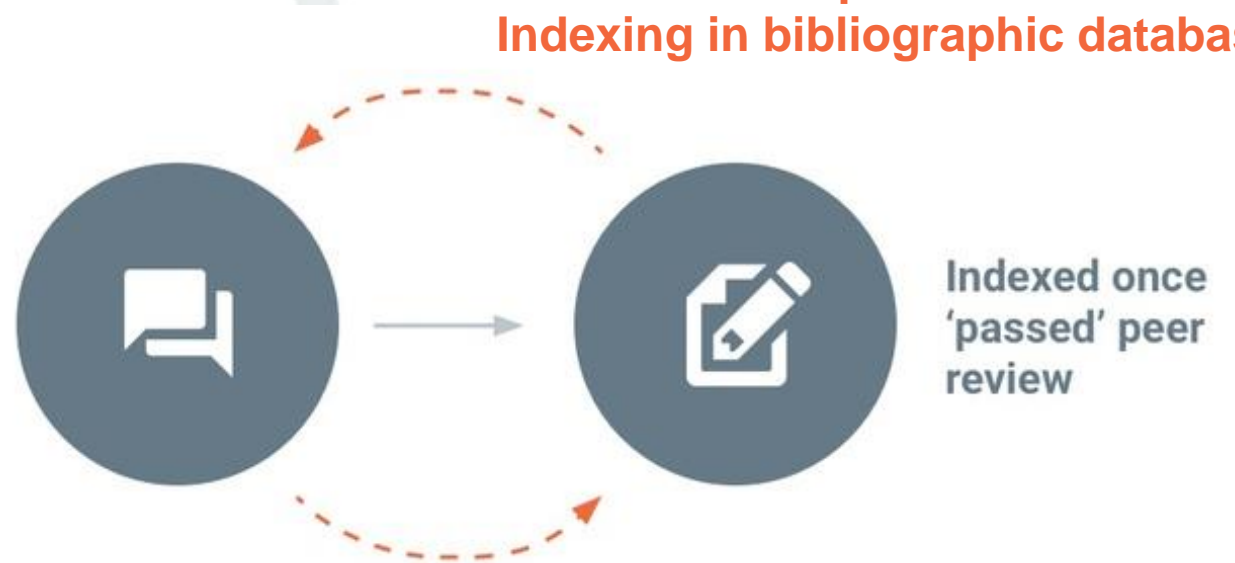
Submission and preprint-like stage
Open Access



Article
submission

Publication &
data deposition

Formal invited peer review
Indexing in bibliographic databases



Open peer review &
user commenting

Article
revision

Articles are immediately indexed (as preprints) in Google Scholar and Europe PMC.

Once an article passes peer review it will be indexed in PubMed, PubMed Central, MEDLINE, Scopus and more

The peer review process is open and transparent



Home » Browse » [bwimage: A package to describe image patterns in natural structures](#)

SOFTWARE TOOL ARTICLE

[EDIT VERSION](#)

 Check for updates

REVISED bwimage: A package to describe image patterns in natural structures [version 3; peer review: 2 approved]

 [Carlos Biagolini-Jr.](#) ¹, [Regina H. Macedo](#)²

[+ Author details](#)

REVISED Amendments from Version 1

Implementation:

- Clarified the arguments surrounding Figure 1 for a new method of calculating log gene expression ratios for scRNAseq data and updated the figure.
- Removed Figure 2 and the related text, as it was erroneously proposing filters that violated assumptions of false discovery rate control.
- Improved methods section for functions implementing differential expression testing methods in scClustViz, including highlighting the option to pass user-defined DE testing results to scClustViz.
- Updated description of underlying data object generated by the setup step of scClustViz to reflect adoption of a formal S4 class.

Operation:


- Added a section explaining scClustViz incorporation into existing clustering pipelines for improved reproducibility.
- Added note concerning Shiny app functionality from remote R sessions in system requirements.

Cell set comparisons:

- Added volcano plots to the set of figures designed to explore individual cluster comparisons. All figures were updated after implementation of a new function designed to reduce label overlap.


See the authors' detailed response to the review by [Michael Steinbaugh](#)

See the authors' detailed response to the review by [Martin Hemberg](#) and [Tallulah Andrews](#)


 **ALL METRICS**


574
VIEWS

78
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 Cite

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Open Peer Review

Reviewer Status   

Reviewer Reports

Invited Reviewers

1 2

Version 3

(revision)

14 Apr 20

Version 2

(revision)

29 Oct 19

Version 1

23 Jul 19



read

↑



read



read

1. **Francesco Chianucci** , The Council for Agricultural Research and Economics (CREA) - Research Centre for Forestry and Wood, Arezzo, Italy
2. **Roy Francis**, Uppsala University, Uppsala, Sweden; National Bioinformatics Infrastructure Sweden, Uppsala, Sweden

Alongside their report, reviewers assign a status to the article:

 **APPROVED**

The paper is scientifically sound in its current form and only minor, if any, improvements are suggested

 **APPROVED WITH RESERVATIONS**

Key revisions are required to address specific details and make the paper fully scientifically sound

 **NOT APPROVED**

Fundamental flaws in the paper seriously undermine the findings and conclusions

animal, ecology methods, field, image analyses, image processing, vegetation patterns

Open Peer Review creates a constructive dialogue

Authors response

Responses (1)

AUTHOR RESPONSE 02 Apr 2019

Matthieu Schapira, SGC, Toronto, Canada

1) **Secrecy.** In the introduction, reasons are suggested for why scientists may keep results secret. We would suggest that there are two important reasons that are not explicitly mentioned: i) that the scientist may want to patent something, and ii) that the scientist cannot be bothered to work out how to release research using atypical means. The first point is alluded to where mention is made of ownership, and the second point is alluded to by the mention of "paper" but we would argue these two factors are significant enough that they should be made explicit.

Points well taken. The following statement was added to the Introduction "...and can be compounded by constraints associated with patent protection procedures or the absence of clear mechanism to make one's data publicly available."

2) **Careers.** We'd be interested in whether there is a justification for the statement "Many believe that openly sharing work online will limit career opportunities." If there is none, then perhaps rephrase this more as a possibility?

This was not clear. The sentence was replaced as follows:

"Many believe that the chances of getting scooped before one publishes their work in a peer-reviewed journal increase when openly sharing their work online [9]"

3) **Grants.** The statement "Grant applications that highlight the use of open lab notebooks are being viewed positively" may be true (one hopes it is), but the evidence presented doesn't support that statement (the grants may have been funded because the science was so good, regardless of the dissemination plan), so again, this probably needs to be made more aspirational.

This was revised as follows:

Reviewer Report


06 Feb 2019 | for Version 1

19 Views

Cite this report

Responses (1)

Matthew H. Todd , School of Pharmacy, University College London (UCL), London, UK

Edwin Tse , University of Sydney, Sydney, Australia

Marat Korsik, University of Sydney, Sydney, Australia

Mathamsanqa Bhebhe, University of Sydney, Sydney, Australia

? APPROVED WITH RESERVATIONS 

This opinion piece is on a timely, important topic and is clearly and engagingly written. Anecdotally, we find that many of our colleagues in science are unaware that open lab notebooks exist. This article will help.

The authors identify several important advantages and challenges associated with the near-immediate deposition of results into the public domain, online. They use examples from their own research to highlight the possibilities.

The refereeing team behind this review are seasoned users of open lab notebooks, and so are in a good position to judge the piece. We judge it to have cleared peer review from our perspective, once the following comments and suggestions have been acted upon. There are a number, which should be read not as criticism but as testament to our shared enthusiasm for this subject and its importance in the future of research.

1) **Secrecy.** In the introduction, reasons are suggested for why scientists may keep results secret. We would suggest that there are two important reasons that are not explicitly mentioned: i) that the scientist may want to patent something, and ii) that the scientist cannot be bothered to work out how to release research using atypical means. The first point is alluded to where mention is made of ownership, and the second point is alluded to by the mention of "paper" but we would argue these two factors are significant enough that they should be made explicit.

2) **Careers.** We'd be interested in whether there is a justification for the statement "Many believe that openly sharing work online will limit career opportunities." If there is none, then perhaps rephrase this more as a possibility?

Reviewers names and affiliations

Status

Reviewers comments

Open Peer Review

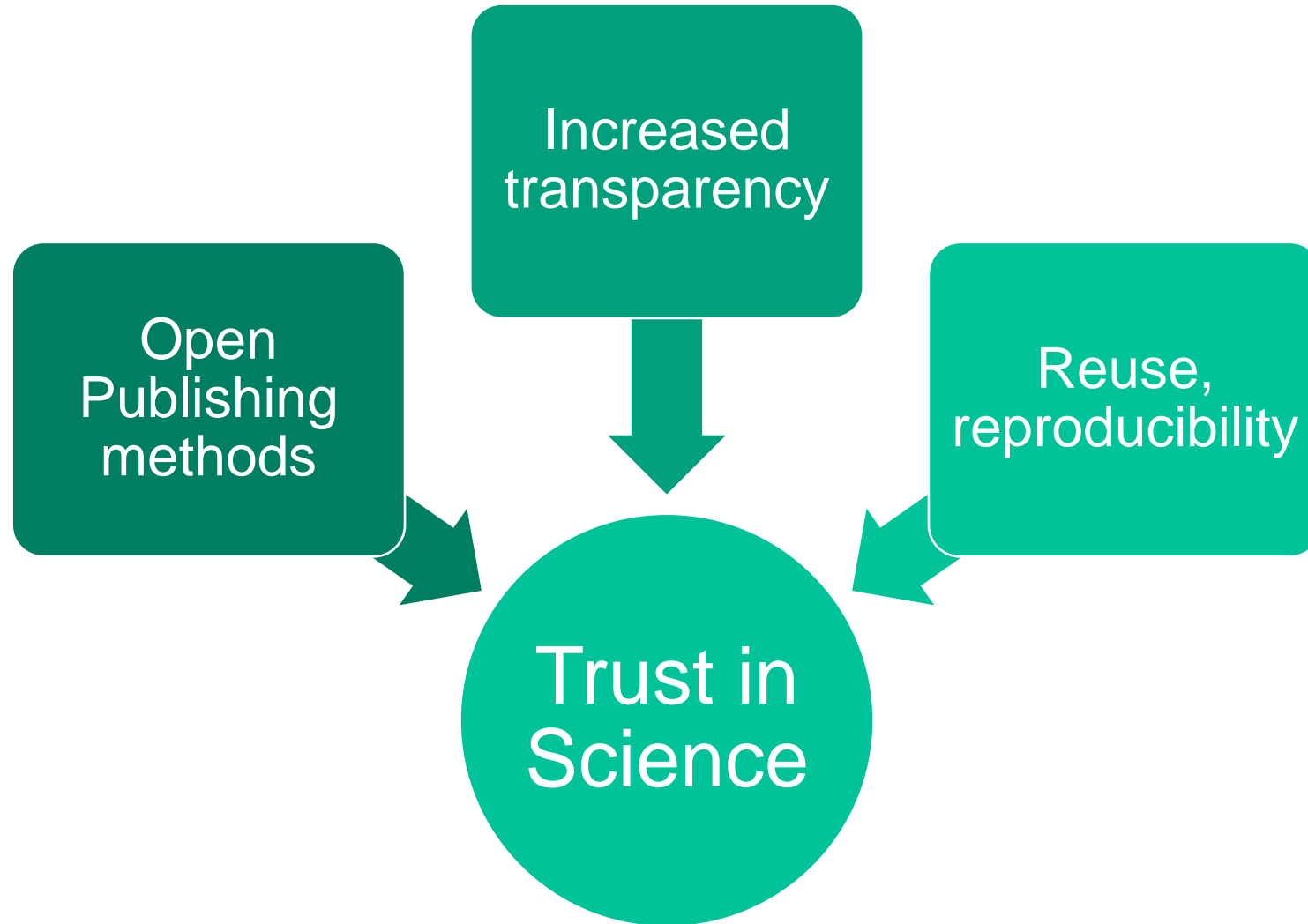


Open peer
review

Why this model?

- Minimising bias - reviewers publicly stand by their comments
- Constructive dialogue
- Useful info in reports
- Credit for referees

How does it fit together?



Funder-based publishing platforms

Testing new approaches to improve science & its impact:

- accelerate access & sharing of findings & data
- reduce waste & support reproducibility
- alternative OA model - access, transparency, cost

Enable researchers get credit & recognition for a wider range of research outputs

Play a leading role as a funder in researcher evaluation - help shift the needle and inform new policies on researcher assessment, move away from IF

The image displays four panels, each representing a different funder-based publishing platform. Each panel includes a logo, a description of the target audience, the platform name, and a 'SUBMIT' button.

- Wellcome Open Research:** Logo: Wellcome (W). Description: For Wellcome-funded researchers. Button: SUBMIT.
- Gates Open Research:** Logo: Gates Foundation (Gf). Description: For Gates Foundation-funded researchers. Button: SUBMIT.
- HRB Open Research:** Logo: HRB. Description: For HRB-funded researchers. Button: SUBMIT.
- AAS Open Research:** Logo: AAS. Description: For researchers funded by AAS or AESA programs. Button: SUBMIT.

Immediate & Transparent Publishing

A new way for Wellcome-funded researchers to rapidly publish any results they think are worth sharing

[SUBMIT YOUR RESEARCH](#)

[BROWSE ARTICLES](#)

Wellcome Open Research

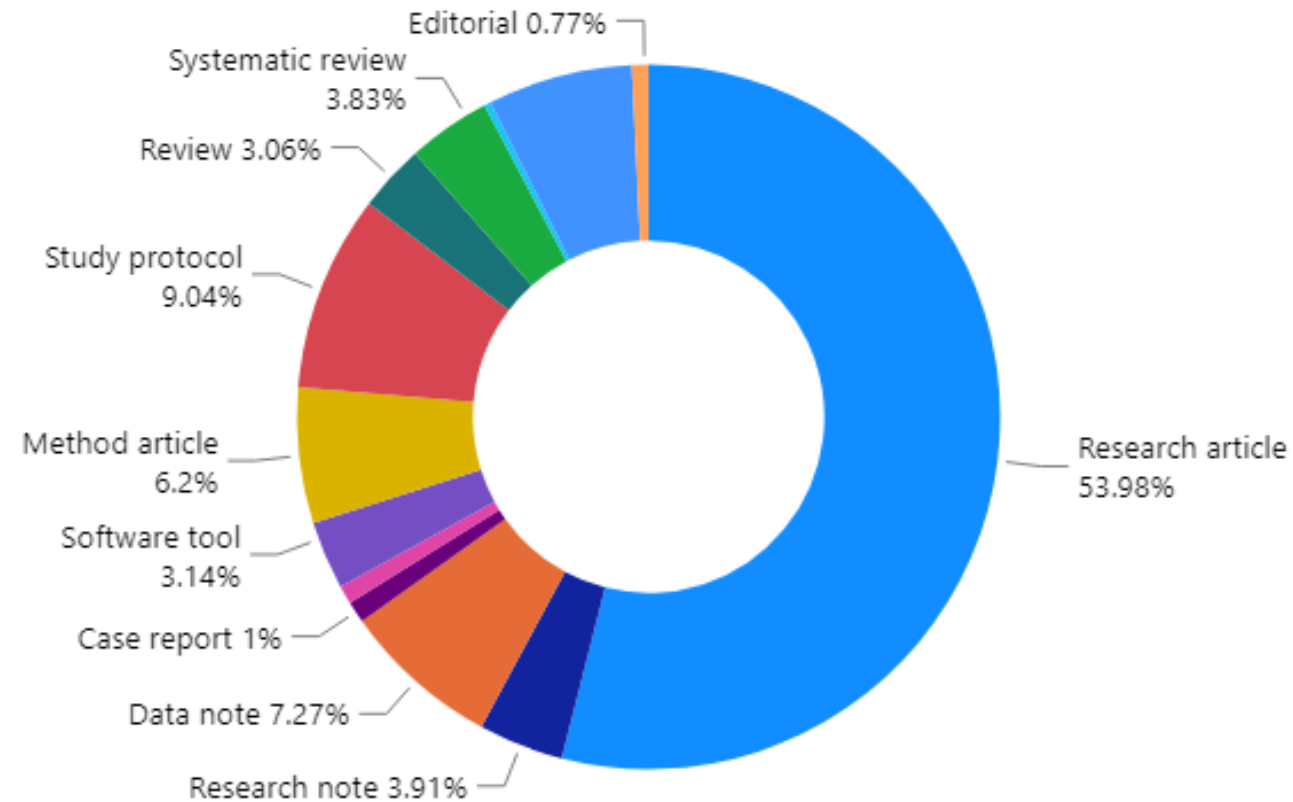


Powered by
F1000

How's Wellcome Open Research performing?

Head to our blog for more information...

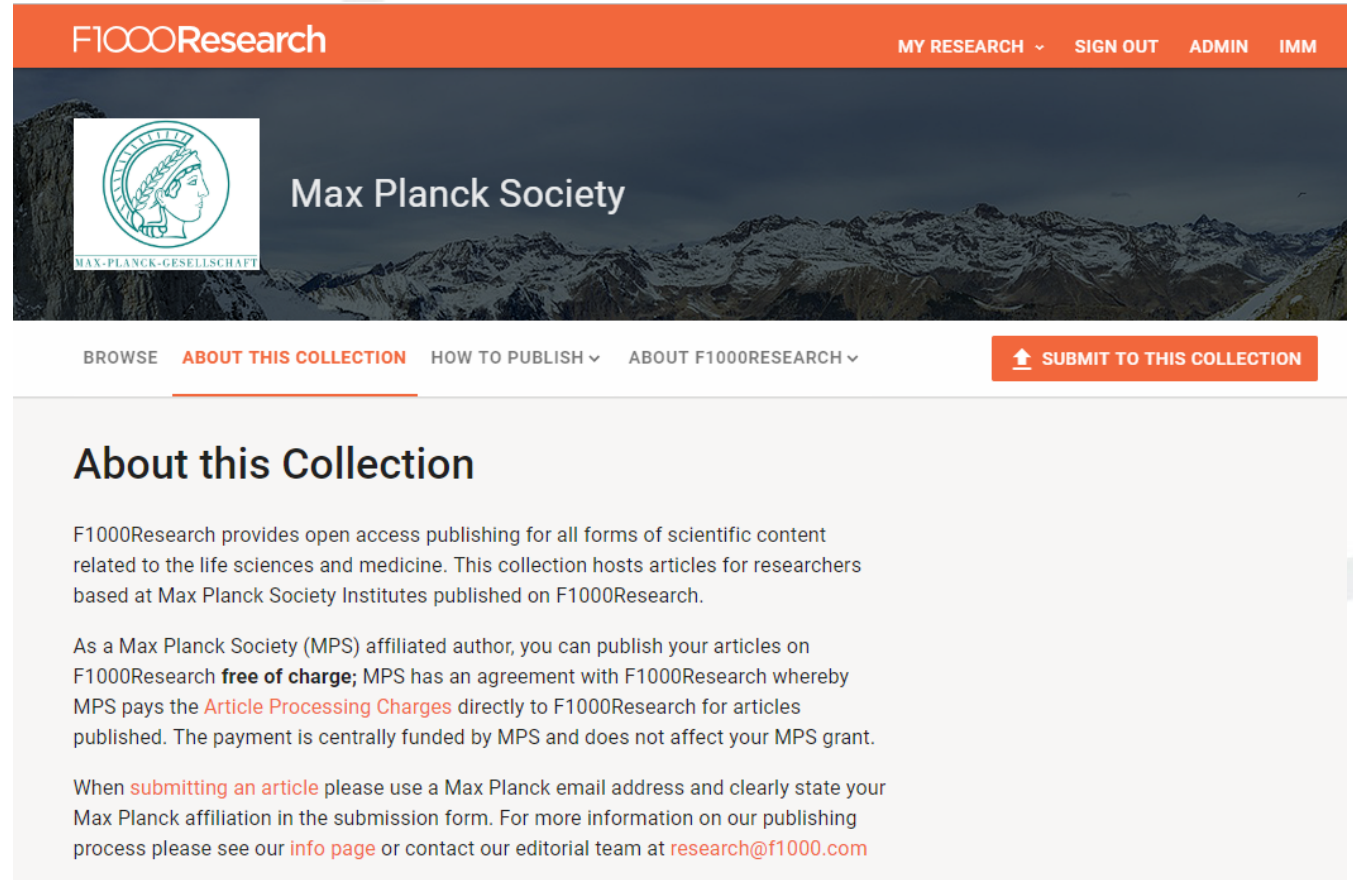
- Over 1000 articles published
- 29 days (median) from submission to publication
- 70 days (median) from publication to indexed
- Over 5,300 authors from across over 1,600 institutions



<https://blog.wellcomeopenresearch.org/2021/02/08/wellcome-open-research-a-summary-of-year-4/>

The Max Planck Society Collection

- Reduces administrative burden
- Promotes open research
- Experience our publishing model
- Open access publishing that is compliant with funder mandates, including Plan S



The screenshot shows the F1000Research website interface. At the top, there is an orange navigation bar with the F1000Research logo on the left and links for 'MY RESEARCH', 'SIGN OUT', 'ADMIN', and 'IMM' on the right. Below this is a dark banner featuring the Max Planck Society logo (a profile of Minerva) and the text 'Max Planck Society'. A secondary navigation bar contains links for 'BROWSE', 'ABOUT THIS COLLECTION' (which is highlighted), 'HOW TO PUBLISH', and 'ABOUT F1000RESEARCH'. A prominent orange button on the right says 'SUBMIT TO THIS COLLECTION'. The main content area is titled 'About this Collection' and contains the following text:

F1000Research provides open access publishing for all forms of scientific content related to the life sciences and medicine. This collection hosts articles for researchers based at Max Planck Society Institutes published on F1000Research.

As a Max Planck Society (MPS) affiliated author, you can publish your articles on F1000Research **free of charge**; MPS has an agreement with F1000Research whereby MPS pays the **Article Processing Charges** directly to F1000Research for articles published. The payment is centrally funded by MPS and does not affect your MPS grant.

When **submitting an article** please use a Max Planck email address and clearly state your Max Planck affiliation in the submission form. For more information on our publishing process please see our **info page** or contact our editorial team at research@f1000.com

<https://f1000research.com/collections/maxplansociety/>

Any questions?

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