

# The Bioconductor channel in F1000Research

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17 ARTICLES [SHOW FILTERS](#)

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**RESEARCH ARTICLE** AWAITING PEER REVIEW

## Bioconductor workflow for microbiome data analysis: from raw reads to community analyses [version 1; referees: awaiting peer review]

Ben J. Callahan, Kris Sankaran, Julia A. Fukuyama, Paul J. McMurdie, Susan P. Holmes

[» Referees: Invited](#)

PUBLISHED 24 JUN 2016

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**SOFTWARE TOOL ARTICLE** AWAITING PEER REVIEW

## From reads to genes to pathways: differential expression analysis of RNA-Seq experiments using Rsubread and the edgeR quasi-likelihood pipeline [version 1; referees: awaiting peer review]

Yunshun Chen, Aaron T. L. Lun, Gordon K. Smyth

[» Referees: Invited](#)

PUBLISHED 20 JUN 2016

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**SOFTWARE TOOL ARTICLE** ✓

## RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR [version 1; referees: 1 approved]


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**ABOUT THIS CHANNEL** [TRACK](#)


This channel highlights **Bioconductor** package-based vignettes, cross-package workflows that guide users through common and important tasks in multi-omic data analysis and integrative bioinformatics, and other articles relating to the Bioconductor project. Please see the accompanying Editorial for the full scope. Bioconductor is an open-source, open-development software project for the analysis and comprehension of high-throughput data in biology. Its aim is to enable interdisciplinary research through collaborative and rapid development of scientific software. The programming and packaging of software is based on the R environment for data analysis

[MORE ABOUT THIS CHANNEL](#)

Channel Advisors

 **Vincent Carey**  
Harvard University  
USA

 **Wolfgang Huber**  
European Molecular Biology  
Laboratory  
Germany



# Bioconductor channel in F1000Research

Started in the autumn of 2015

A place for

- task-oriented end-to-end workflows — these invoke resources from several packages by different authors

as well as

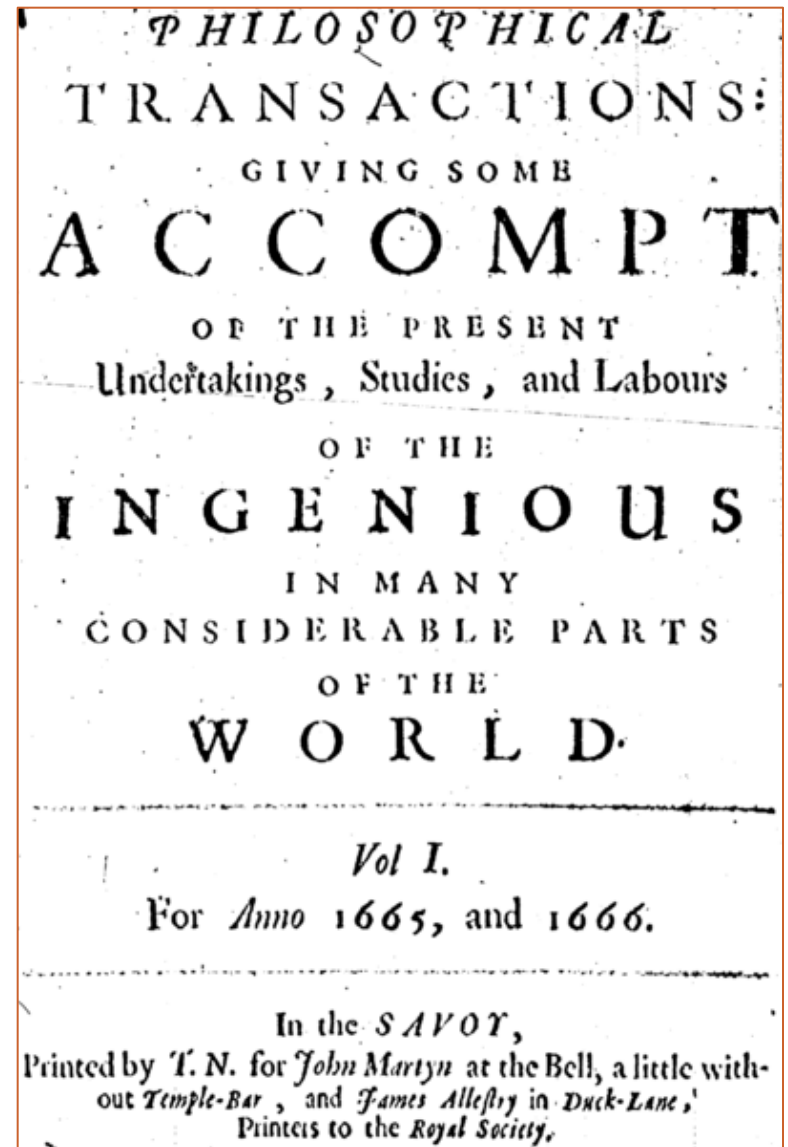
- other articles relating to the Bioconductor project.  
For example software papers on a single package

<http://f1000research.com/channels/bioconductor>

**What is F1000Research?**

## PUBLISHING AND PEER REVIEW

- First scientific journals were not peer reviewed.
- Peer review was introduced later, and developed as a method to select what is fit to print in limited available space.
- Journals as gatekeepers.
- Current popular system of peer review dates from mid-twentieth century.



# PAINFUL PUBLISHING



Published online 27 April 2011 | *Nature* **472**, 391 (2011) | doi:10.1038/472391a

Column: World View

## End the wasteful tyranny of reviewer experiments



Peer review of scientific papers in top journals is bogged down by unnecessary demands for extra lab work, argues Hidde Ploegh.

Hidde Ploegh

Submit a biomedical-research paper to *Nature* or other high-profile journals, and a common recommendation often comes back from

“...what is in the paper is fundamentally the responsibility of the authors, not of the reviewers.”

**Nobel Laureate Robert Horvitz**

*Science* 4 July 2008:  
Vol. 321 no. 5885 p. 36  
DOI: 10.1126/science.321.5885.36a

### LETTERS

## Painful Publishing

Biomedical science has never been more exciting or productive. Research tools have become increasingly powerful, and progress continues to accelerate. Yet, these are stressful times for many biomedical scientists, because competition for grant support, job publishing in the most prestigious journals is also accelerating. The stress associated with publishing experimental results—a process that can take as long as obtaining the results in the first place—can rob much of the joy from practicing science.



Comment  
**Are we training pit bulls to review our manuscripts?**  
Virginia Walbot

## *Open Science Publishing Platform*

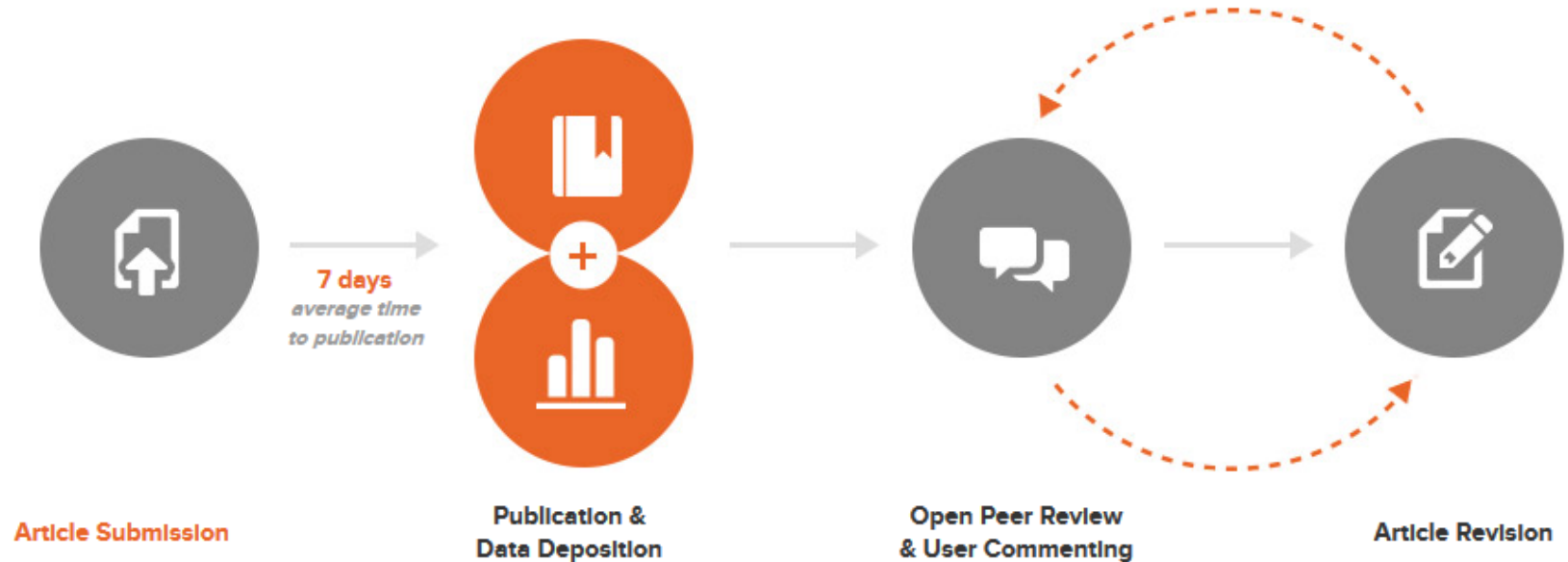
**Scope:** all research – big and small – across the life sciences and medicine

- Immediate publication
- Transparent refereeing
- No editorial bias
- All source data included
- Indexed in PubMed



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## F1000RESEARCH: POST-PUBLICATION PEER REVIEW



- Author-driven process: *F1000Research* articles are published online after an in-house pre-refereeing check
- Peer review and revisions are open
- Invited referees judge whether the work is scientifically sound
- Articles with sufficient positive referee reports are indexed in PubMed

# POST-PUBLICATION PEER REVIEW

F1000Research » Articles



SOFTWARE TOOL ARTICLE

## FORGE: A tool to discover cell specific enrichments of GWAS associated SNPs in regulatory regions [v1; ref status: awaiting peer review, <http://f1000r.es/4ze>]

Ian Dunham, Eugene Kulesha, Valentina Iotchkova, Sandra Morganello, Ewan Birney

Author affiliations

Grant information

### Abstract

Genome Wide Association Studies (GWAS) provide an unbiased discovery mechanism for numerous human diseases. However, a frustration in the analysis of GWAS is that the majority of variants discovered do not directly alter protein-coding genes. We have developed a simple analysis approach that detects the tissue-specific regulatory component of a set of GWAS SNPs by identifying enrichment of overlap with DNase I hotspots from diverse tissue samples. Functional element Overlap analysis of the Results of GWAS Experiments (FORGE) is available as a web tool and as standalone software and provides tabular and graphical summaries of the enrichments. Conducting FORGE analysis on SNP sets for 260 phenotypes available from the GWAS catalogue reveals numerous overlap enrichments with tissue-specific components reflecting the known aetiology of the phenotypes as well as revealing other unforeseen tissue involvements that may lead to mechanistic insights for disease.

Corresponding author: Ian Dunham

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### Open Peer Review

Referee Status: *AWAITING PEER REVIEW*

### Discuss this article

Comments (0)

Add a Comment

### Articles that may interest you

RESEARCH ARTICLE



**REVISED** From zebrafish heart jogging genes to mouse and human orthologs: using Gene Ontology to investigate mammalian heart development. [v2; ref status: indexed, <http://f1000r.es/2ys>]

SOFTWARE TOOL ARTICLE



Enrichment Map – a Cytoscape app to visualize and explore OMICs pathway enrichment results [v1; ref status: indexed, <http://f1000r.es/3qs>]



# TRANSPARENT PEER REVIEW

The screenshot shows a peer review interface with several callout boxes:

- Referee Report 09 May 2014**
- Referee names are visible**: Points to the reviewer's name and affiliation: **Christine Mummy**, Department of Anatomy and Embryology, Leiden University Medical Center, Leiden, Netherlands.
- View count shows how many people read the referee report**: Points to a **Views** box showing **638**.
- Referee reports are citable with a DOI**: Points to a **Cite** button.
- Referee reports and author comments are visible to anyone**: Points to the entire review content area.

**Approved** (with a green checkmark icon)

The authors describe their attempt to reproduce a study in which it was claimed that mild acid treatment was sufficient to reprogramme postnatal splenocytes from a mouse expressing GFP in the oct4 locus to pluripotent stem cells. The authors followed a protocol that has recently become available as a technical update of the original publication.

They report obtaining no pluripotent stem cells expressing GFP driven over the same time period of several days described in the original publication. They describe observation of some green fluorescence that they attributed to autofluorescence rather than GFP since it coincided with PI positive dead cells. They confirmed the absence of oct4 expression by RT-PCR and also found no evidence for Nanog or Sox2, also markers of pluripotent stem cells.

• • •

**I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.**

**Competing Interests:** No competing interests were disclosed. [Close](#)

Author Response 12 May 2014  
**Kenneth Lee**, School of Biomedical Sciences, Chinese University of Hong Kong, Hong Kong  
Professor Mummy has provided some excellent suggestions for changes to improve the paper. We will try our best and accommodate her requests 1-3 by doing some new additional experiments.

Request 4 ... [Continue reading](#)

[Respond or Comment](#)

## REFEREE SCORES



• Approved



• Approved with reservations



• Not approved

Articles with sufficient positive evaluations are indexed in PubMed, Scopus, and Embase



or



Articles that haven't yet reached this threshold can be revised and re-reviewed (no time limit)

### Open Peer Review

Referee Status:

#### Invited Referees

	1	2	3
<b>REVISÉD</b> version 3 published 14 Nov 2013			 report
		↑	↑
<b>REVISÉD</b> version 2 published 01 Nov 2013	 report	 report	 report
	↑		
version 1 published 25 Sep 2013	 report		

- 1 Maximiliano Gutierrez, MRC National Institute for Medical Research, UK
- 2 Yoshiko Takahashi, Kyoto University, Japan
- 3 Tom Gillis, Louisiana State University School of Medicine, USA

[Read the reports \(6\), Responses \(1\)](#)

#### Discuss this article

[Comments \(0\)](#)

[Add a Comment](#)

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## VERSIONS: LIVING ARTICLES

*F1000Research* articles can always be updated, even after being indexed.

Amended papers have one of two possible labels:

**REVISED**

Authors amended their article in response to referee or community feedback

**UPDATE**

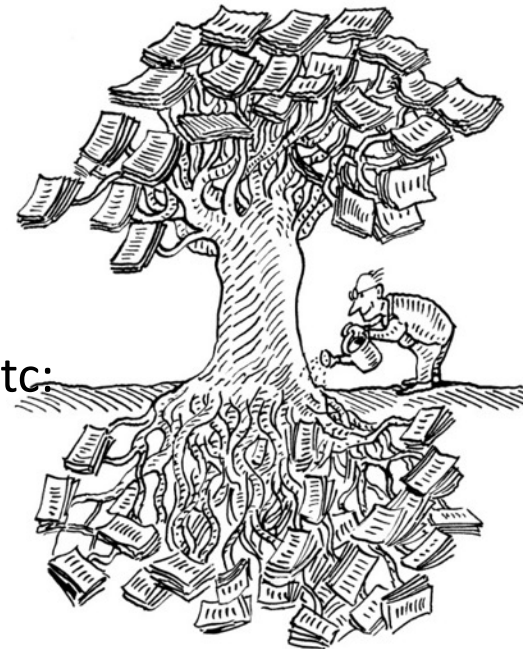
Authors updated the article following minor developments (e.g. software updates)

Especially useful for software tools, systematic reviews, etc:  
ensures article remains up-to-date;  
better reflects the pace of research

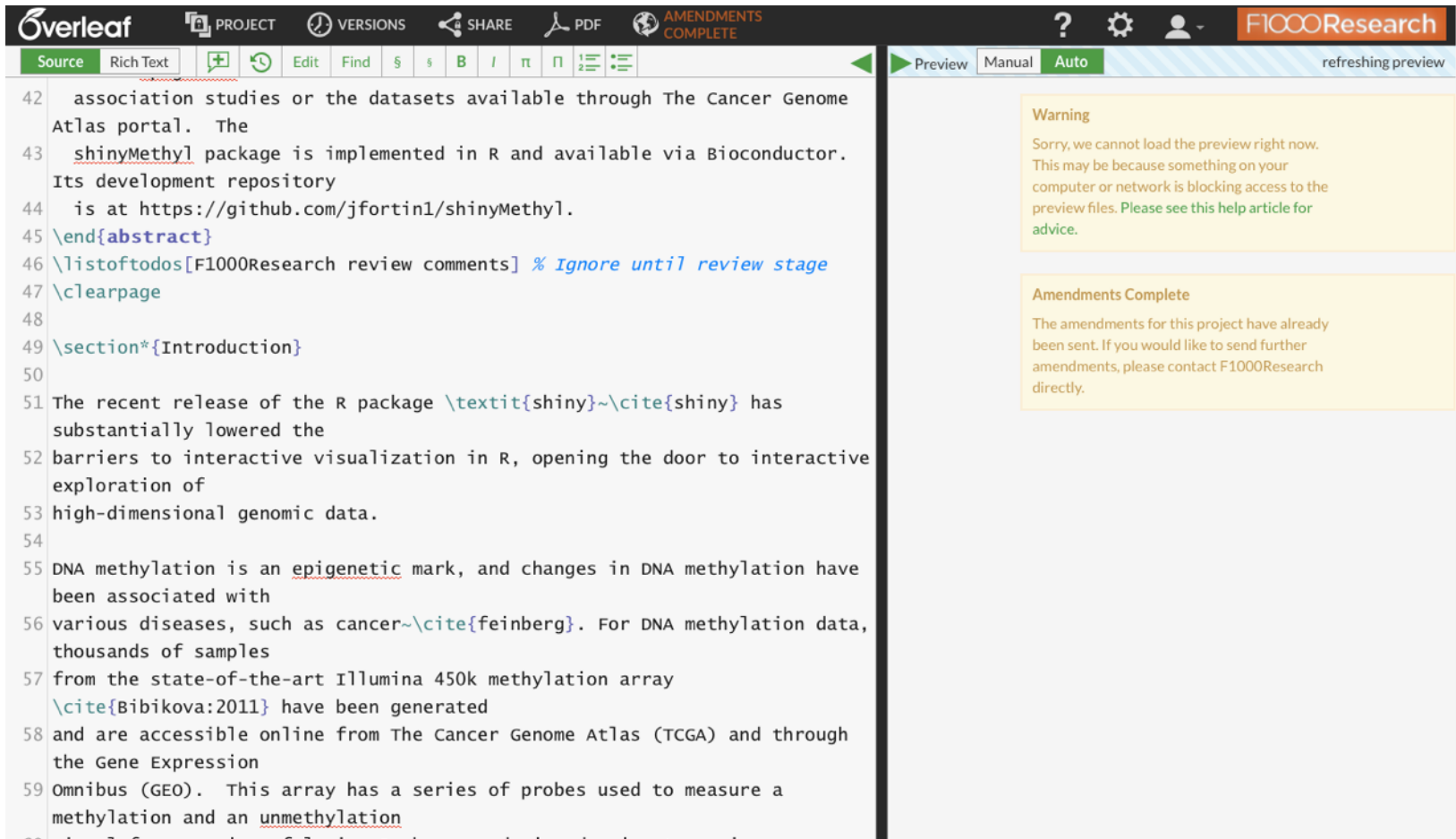
Each version is independently citable yet linked

All versions indexed in PubMed, PubMed Central, etc (if article passed review)

‘Track’ option



# OVERLEAF: Online Latex editor (working on process for workflows)



The screenshot displays the Overleaf online LaTeX editor interface. The top navigation bar includes the Overleaf logo, a 'PROJECT' button, 'VERSIONS', 'SHARE', 'PDF', and 'AMENDMENTS COMPLETE' status. The right side of the top bar shows a user profile, a settings gear, and the 'F1000Research' logo. Below the navigation bar, there are tabs for 'Source' (selected) and 'Rich Text', and a 'Preview' section with 'Manual' and 'Auto' options. The 'Source' pane shows LaTeX code for an abstract and a section introduction. The 'Preview' pane shows a warning message and an 'Amendments Complete' notification.

```
42 association studies or the datasets available through The Cancer Genome
43 Atlas portal. The
44 shinyMethyl package is implemented in R and available via Bioconductor.
45 Its development repository
46 is at https://github.com/jfortin1/shinyMethyl.
47 \end{abstract}
48 \listoftodos[F1000Research review comments] % Ignore until review stage
49 \clearpage
50 \section*{Introduction}
51 The recent release of the R package \textit{shiny}~\cite{shiny} has
52 substantially lowered the
53 barriers to interactive visualization in R, opening the door to interactive
54 exploration of
55 high-dimensional genomic data.
56 DNA methylation is an epigenetic mark, and changes in DNA methylation have
57 been associated with
58 various diseases, such as cancer~\cite{feinberg}. For DNA methylation data,
59 thousands of samples
60 from the state-of-the-art Illumina 450k methylation array
61 \cite{Bibikova:2011} have been generated
62 and are accessible online from The Cancer Genome Atlas (TCGA) and through
63 the Gene Expression
64 Omnibus (GEO). This array has a series of probes used to measure a
65 methylation and an unmethylation
```

**Warning**  
Sorry, we cannot load the preview right now. This may be because something on your computer or network is blocking access to the preview files. [Please see this help article for advice.](#)

**Amendments Complete**  
The amendments for this project have already been sent. If you would like to send further amendments, please contact F1000Research directly.

# Call for Contributions