

A PRESENTATION ON INNOVATING WITH eLIFE: MAY 2017

# Accelerating discovery with technology

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Innovation Officer

@eLifeInnovation



## Slides available at

<https://github.com/npscience/eLife-innovation-May2017-presentation>



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## What we'll cover

1. About eLife
2. Driving change through the journal
3. Innovation at eLife
4. Discussion

# About eLife



MAX-PLANCK-GESELLSCHAFT

eLife is a non-profit organisation inspired by research funders and led by scientists

## Motivations

- Overdependence on a limited set of journals
- Legacy of print
- Inefficient and dispiriting processes
- Misdirected incentives
- Progress – and careers – are inhibited

eLIFE

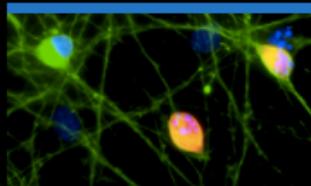
Helping scientists accelerate discovery by  
operating a platform for research communication  
that encourages and recognises the most  
responsible behaviours in science

## What do we mean by “responsible behaviours”?

- Sharing of data, tools, and resources
- Objective and comprehensive reporting
- Cooperation and collaboration
- Constructive feedback and encouragement



# A new twist in the Hippo-YAP pathway

[Read more](#)

RESEARCH ARTICLE

## Regulating stress signaling in neurons

RESEARCH ARTICLE

## Multicellularity in metazoan evolution

### FEATURE ARTICLE

## The fight against tuberculosis

### INSIGHT

T-cell immunology:  
The maths of memory

### INSIGHT

Reward-based learning:  
Subtract and conquer

### INSIGHT

Endosymbiotic algae:  
Gasping for air

# eLIFE

The open-access journal for outstanding research in the life and biomedical sciences

## A selection of recent highlights

### Latest research

UPCOMING

APR

MAY

| ARCHIVE

### Oriented clonal cell dynamics enables accurate growth and shaping of vertebrate cartilage

The clonal oriented cell dynamics enables directional expansion and accurate scaling of sheet-like or rod-like cartilaginous elements and uncouples the mechanisms of elongation from thickness or diameter control.

Marketa Kaucka, Tomas Zikmund, Marketa Tesarova, Daniel Gyllborg, Andreas Hellander, Josef Jaros, Jozef Kaiser, Julian Petersen, Bara Szarowska, Phillip T Newton, Vyacheslav Dyachuk, Lei Li, Hong Qian, Anne-Sofie Johansson, Yuji Mishina, Joshua D Currie, Elly M Tanaka, Alek Erickson, Andrew Dudley, Hjalmar Brismar, Paul Southam, Enrico Coen, Min Chen, Lee S Weinstein, Ales Hampel, Ernest Arenas, Andrei S Chagin, Kaj Fried, Igor Adameyko  
[10.7554/eLife.25902](https://doi.org/10.7554/eLife.25902)

[Research Article](#)[— Developmental Biology and Stem Cells](#)[— Published on April 17, 2017](#)[— Updated on May 4, 2017](#)[View in eLife Lens](#)

### Subjects

[↳ Bioche](#)[↳ Biophys](#)[↳ Cance](#)[↳ Cell Bi](#)[↳ Comp](#)[↳ Develo](#)[↳ Ecol](#)

### PUBLISHING

Priority of discovery in  
the life sciences

### GLOBAL HEALTH

Mapping global  
environmental suitability  
for Zika

### STRUCTURAL BIOLOGY

The regulation of a DNA  
recombination reaction



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## Major subject areas

- Biochemistry
- Biophysics and Structural Biology
- Cancer Biology
- Cell Biology
- Computational and Systems Biology
- Developmental Biology and Stem Cells
- Ecology
- Epidemiology and Global Health
- Genes and Chromosomes
- Genomics and Evolutionary Biology
- Human Biology and Medicine
- Immunology
- Microbiology and Infectious Disease
- Neuroscience
- Plant Biology

# Driving change through the journal

## At eLife (for example):

1. We don't use the impact factor
2. We impose no limit on the number of papers we select for publication
3. We facilitate open discussion among reviewers
4. We help reviewers to gain credit
5. We're exploring reproducibility in cancer research
6. We support early-career researchers

# eLife Early-Career Advisory Group (ECAG)



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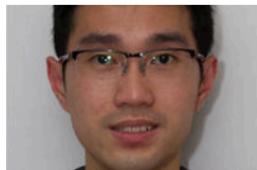
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States)



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University College London  
(United Kingdom)



**Jia-wei Wang**  
Shanghai Institutes for  
Biological Sciences (China)

## eLife's approach to peer review

- Initial decisions are delivered quickly
- Consultative process
- Revision requests are consolidated – only necessary revisions are requested
- Limited rounds of revision
- Active scientists make all decisions

# Editors

Editor-in-Chief **Randy Schekman**, University of California at Berkeley (USA)

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**Detlef Weigel**, Max Planck Institute for Developmental Biology (Germany)

40 Senior Editors

300+ Reviewing Editors

## eLife's approach to peer review

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- Revision requests are consolidated – only necessary revisions are requested
- Limited rounds of revision
- Active scientists make all decisions
- Decisions and responses are available for all to read

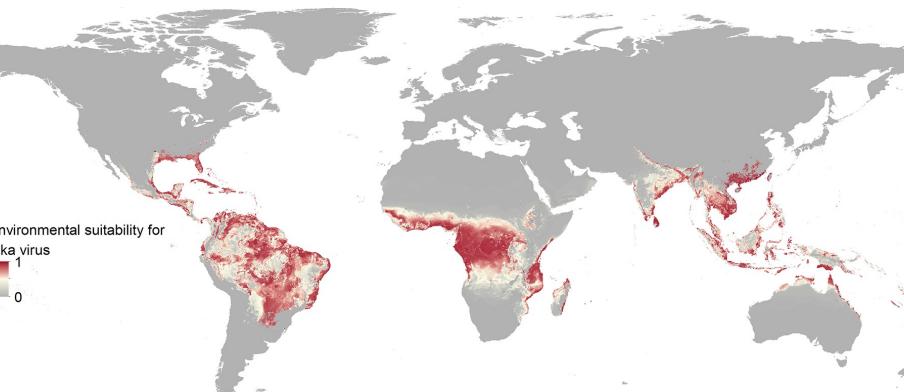
# THE eLIFE EDITORIAL PROCESS

The screenshot shows the eLife article page for the paper "The mesh is a network of microtubule connectors that stabilizes individual kinetochore fibers of the mitotic spindle". The page includes the title, authors (Faye M Nixon, Cristina Gutiérrez-Caballero, Fiona E Hood, Daniel G Booth, Ian A Prior, Stephen J Royle), institutions (Warwick Medical School, United Kingdom), DOI (10.7554/eLife.07635), and a link to the PDF (http://dx.doi.org/10.7554/eLife.07635). The main content area displays the "Decision letter" from Anna Akhmanova, a Reviewing editor at Utrecht University, Netherlands. The letter discusses the article's evaluation and provides feedback. A red box highlights the statement: "The following individuals responsible for the peer review of your submission have agreed to reveal their identity: J Richard McIntosh and Helder Maiato. A further reviewer remains anonymous." To the right, a sidebar titled "Jump to:" lists various sections of the article: Abstract, eLife digest, Main text, Introduction, Results, Discussion, Materials and methods, References, Acknowledgements, Decision letter, Author response, and Leave a comment.

- The decision letter is published, with reviewer identities if they agree, as is the author response
- Making progress toward more reviewers naming themselves

## *Homo naledi*, a new species of the genus *Homo* from the Dinaledi Chamber, South Africa

Lee R Berger , John Hawks, Darryl J de Ruiter, Steven E Churchill, Peter Schmid, Lucas K Delezene, Tracy L Kivell, Heather M Garvin, Scott A Williams, Jeremy M DeSilva, Matthew M Skinner, Charles M Musiba, Noel Cameron, Trenton W Holliday, William Harcourt-Smith, Rebecca R Ackermann, Markus Bastir, Barry Bogin, Debra Bolter, Juliet Brophy, Zachary D Cofran, Kimberly A Congdon, Andrew S Deane, Mana Dembo, Michelle Drapeau, Marina C Elliott, Elen M Feuerriegel, Daniel Garcia-Martinez, David J Green, Alia Gurtov, Joel D Irish, Ashley Kruger, Myra F Laird, Damiano Marchi, Marc R Meyer, Shahed Nalla, Enquye W Negash, Caley M Orr, Davorka Radovcic, Lauren Schroeder, Jill E Scott, Zachary Throckmorton, Matthew W Tocheri, Caroline VanSickle, Christopher S Walker, Pian pian Wei, Bernhard Zipfel



## Intraneuronal stimulation elicits discrimination of textural features by artificial fingertip in intact and amputee humans

Calogero Maria Oddo , Stanisa Raspopovic, Fiorenzo Artoni, Alberto Mazzoni, Giacomo Spigler, Francesco Petrini, Federica Giambattistelli, Fabrizio Vecchio, Francesca Miraglia, Loredana Zollo, Giovanni Di Pino, Domenico Camboni, Maria Chiara Carrozza, Eugenio Guglielmelli, Paolo Maria Rossini, Ugo Faraguna, Silvestro Micera 

Scuola Superiore Sant'Anna, Italy; École Polytechnique Fédérale de Lausanne, Switzerland; Università Campus Bio-Medico di Roma, Italy; IRCCS San Raffaele Pisana, Italy; Catholic University of The Sacred Heart, Italy; Azienda Ospedaliero-Universitaria Pisana, Italy; IRCCS Stella Maris Foundation, Italy; Università di Pisa, Italy

DOI: <http://dx.doi.org/10.7554/eLife.09148>

Published March 8, 2016

Cite as eLife 2016;5:e09148



## Mapping global environmental suitability for Zika virus

Jane P Messina , Moritz UG Kraemer, Oliver J Brady, David M Pigott, Freya M Shearer, Daniel J Weiss, Nick Golding, Corrine W Ruktanonchai, Peter W Gething, Emily Cohn, John S Brownstein, Kamran Khan, Andrew J Tatem, Thomas Jaenisch, Christopher JL Murray, Fatima Marinho, Thomas W Scott, Simon I Hay 

University of Oxford, United Kingdom; University of Washington, United States; University of Melbourne, United Kingdom; University of Southampton, United Kingdom; Harvard Medical School, United Kingdom; University of Toronto, Canada; St Michael's Hospital, Canada; Flowminder Foundation, Sweden; Heidelberg University Hospital, Germany; Heidelberg partner site, Germany; Ministry of Health Brazil, Brazil; University of California Davis, United States

DOI: <http://dx.doi.org/10.7554/eLife.15272>

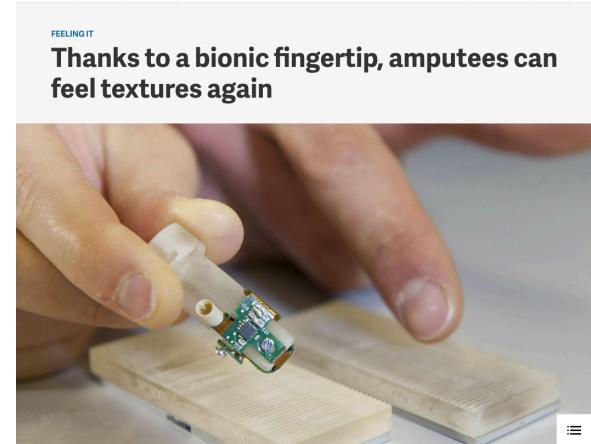
Published April 19, 2016

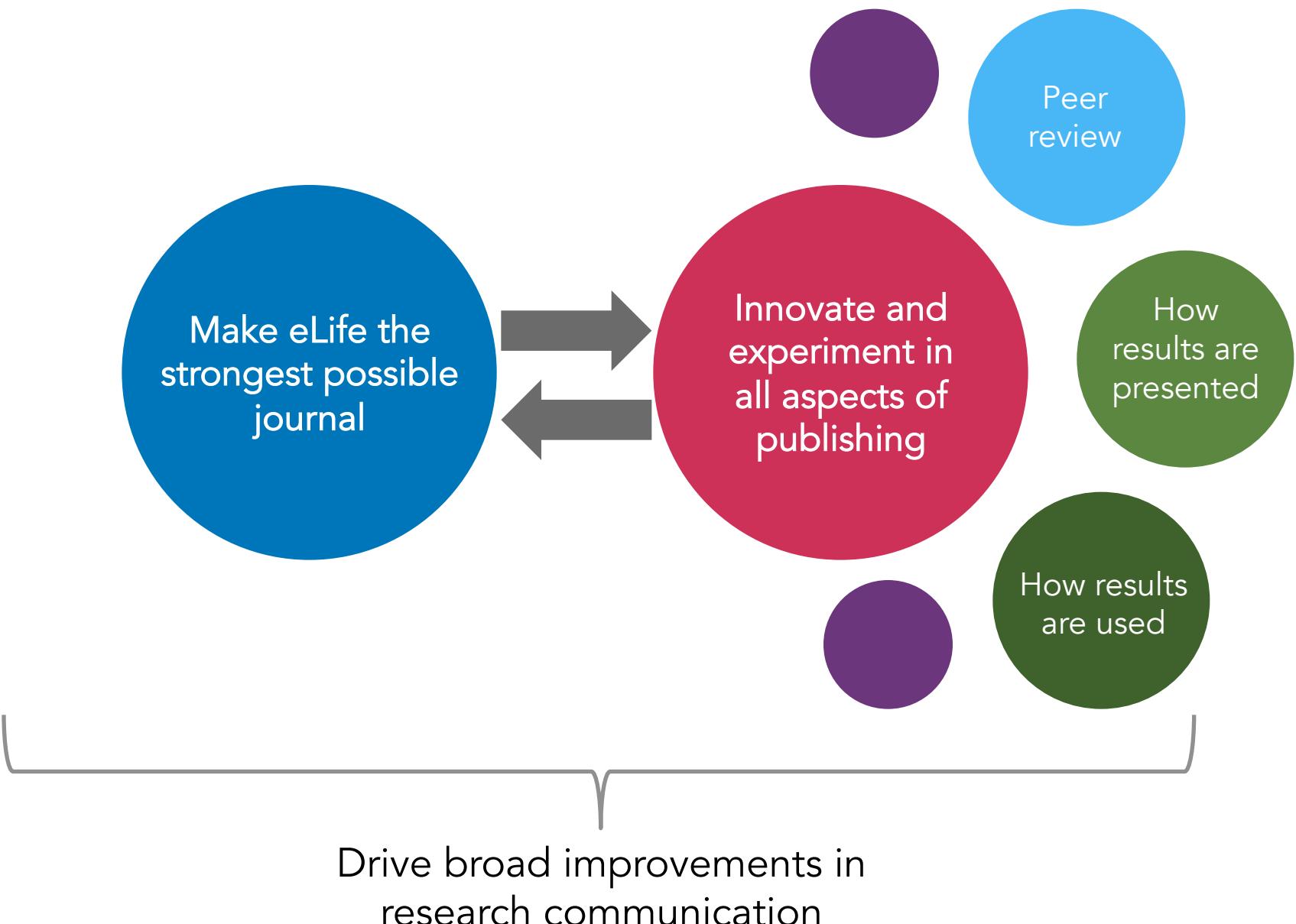
Cite as eLife 2016;5:e15272

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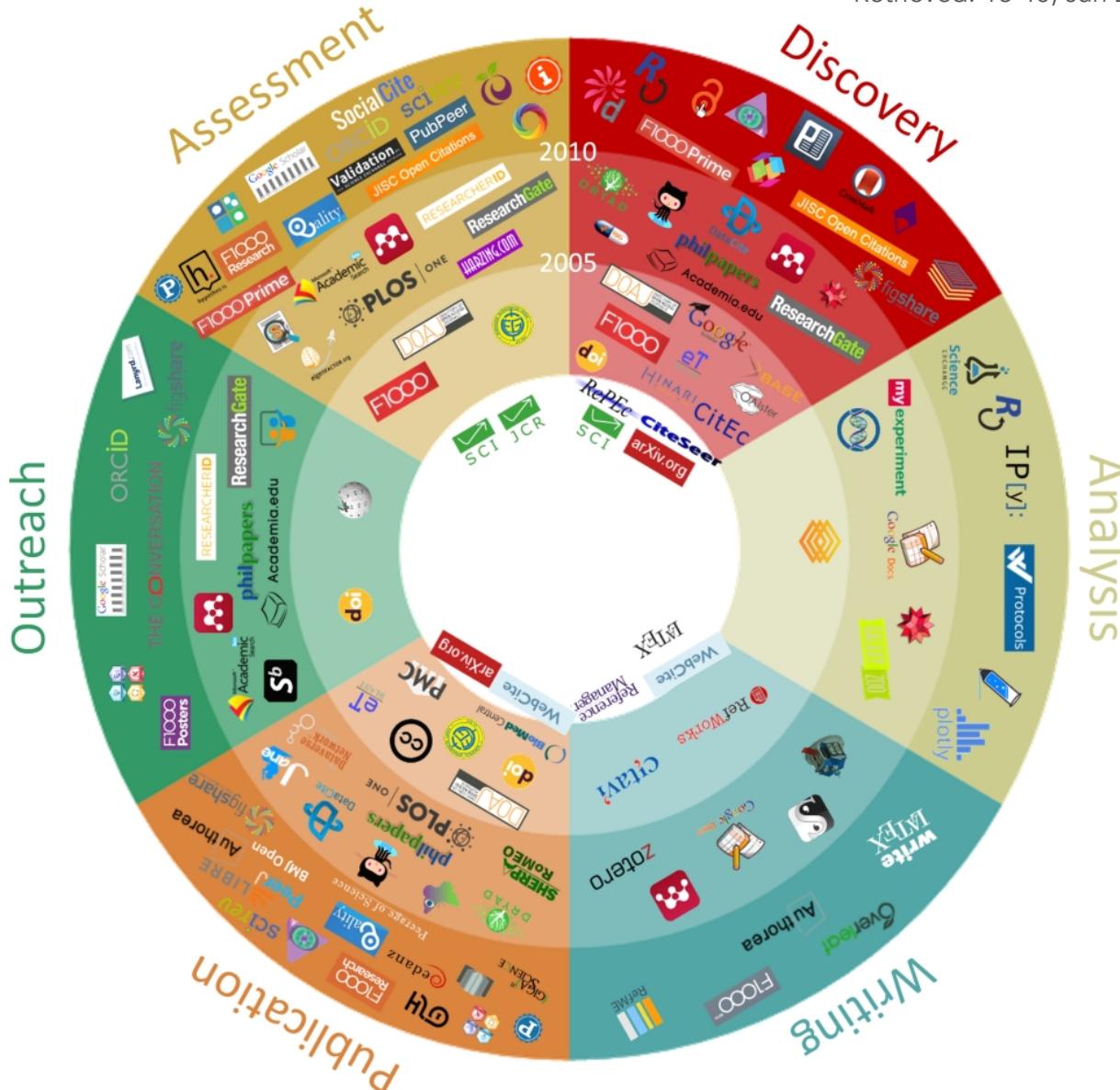


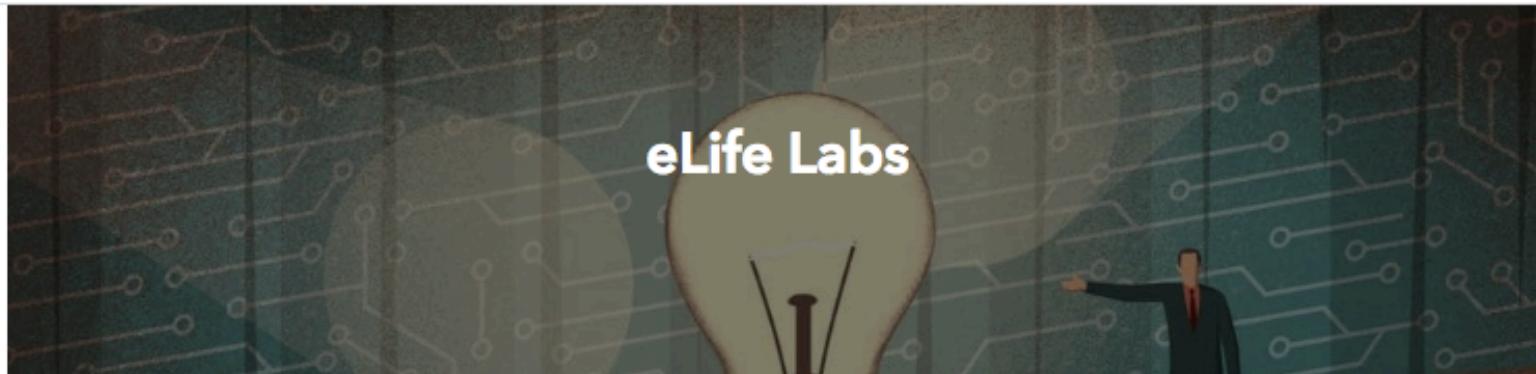


# Innovation at eLife

## eLife Innovation Initiative

We invest in open source technologies, tools and processes that improve the way cutting-edge research is discovered, shared, consumed and evaluated





Exploring open-source solutions at the intersection of research and technology. Learn more about [innovation at eLife](#), or follow us on [Twitter](#).

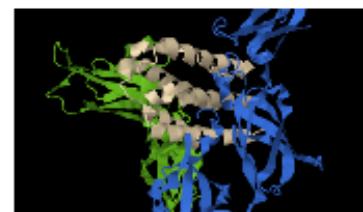
## Latest



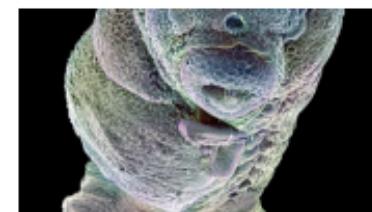
Composing reproducible manuscripts using R Markdown



Hack Cambridge Recurse entries: eXplore, Knowledge Direct, SciChat



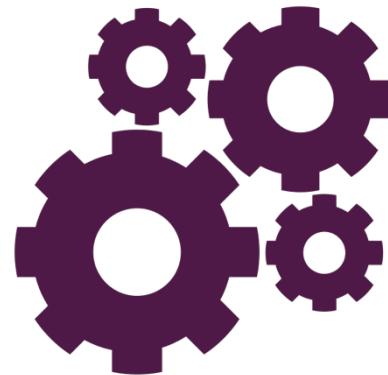
Proteopedia for sharing macromolecule concepts online



The International Image Interoperability Framework (IIIF) for science publishers

# Improving the publishing infrastructure

## INNOVATION & EXPERIMENTATION



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from Noun Project

## eLife Continuum

eLife's open-source, continuous open-access publication platform

# Accelerating discovery

## Simplifying submission



Download the eLife LaTeX template from  
[bit.ly/elife-author-guide](https://bit.ly/elife-author-guide)

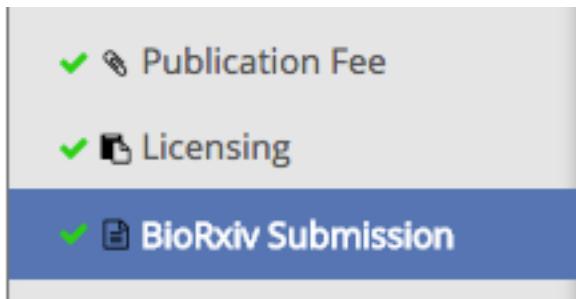


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## Preprints

We encourage authors to preprint their work to accelerate the communication of important results — submit straight to eLife from bioRxiv

and now you can submit straight to bioRxiv from eLife:

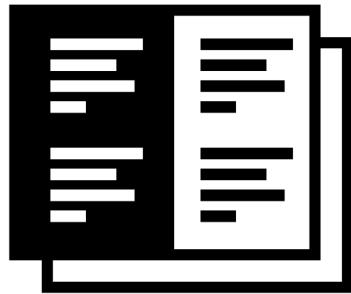


The screenshot shows a vertical list of submission steps. The first two steps, 'Publication Fee' and 'Licensing', have green checkmarks next to them. The third step, 'BioRxiv Submission', is highlighted with a blue bar at the bottom and has a green checkmark next to it. To the right of this list is a question: 'Would you like to also submit your paper to bioRxiv?'. Below the question are two radio buttons: 'Yes' (selected) and 'No'.

Would you like to also submit your paper to bioRxiv?

Yes  No

# Improving the reading experience



Created by Alex Tai  
from Noun Project

# Lens

eLife's open-source, online reading tool

# Dual leucine zipper kinase-dependent PERK activation contributes to neuronal degeneration following insult

Martin Larhammar Sarah Huntwork-Rodriguez Zhiyu Jiang Hilda Solanoy  
 Arundhati Sengupta Ghosh Bei Wang Joshua S Kaminker Kevin Huang  
 Jeffrey Eastham-Anderson Michael Siu Zora Modrusan Madeline M Farley  
 Marc Tessier-Lavigne Joseph W Lewcock Trent A Watkins

RESEARCH ARTICLE APR 25 2017

DOI: 10.7554/eLife.20725

## Abstract

The PKR-like endoplasmic reticulum kinase (PERK) arm of the Integrated Stress Response (ISR) is implicated in neurodegenerative disease, although the regulators and consequences of PERK activation following neuronal injury are poorly understood. Here we show that PERK signaling is a component of the mouse MAP kinase neuronal stress response controlled by the Dual Leucine Zipper Kinase (DLK) and contributes to DLK-mediated neurodegeneration. We find that DLK-activating insults ranging from nerve injury to neurotrophin deprivation result in both c-Jun N-terminal Kinase (JNK) signaling and the PERK- and ISR-dependent upregulation of the Activating Transcription Factor 4 (ATF4). Disruption of PERK signaling delays neurodegeneration without reducing JNK signaling. Furthermore, DLK is both sufficient for PERK activation and necessary for

## Abstract

### Introduction

### Results

- ISR-related expression changes in both PNS and CNS models of axonal damage
- Acute neuronal insults activate PERK
- The ISR influences the mRNA levels of ATF4 target genes after nerve injury
- DLK/JNK signaling is required for PERK activation
- Axonal JNK signaling contributes to PERK activation upon neuronal stress
- Profiling of ISR-dependent gene expression changes following NGF deprivation
- The ISR contributes to neurodegeneration in vitro
- DLK- and PERK-dependent activation of the ISR following optic nerve crush
- PERK signaling contributes to neurodegeneration after axon injury

### Discussion

### Materials and methods

- Mouse models
- Antibodies and inhibitors
- In vivo nerve injury models
- ISRib dosing in adult mice
- Intravitreal injection of adeno-associated viral (AAV) vectors
- Assessment of RGC survival
- Primary neuron culture and NGF withdrawal
- Microarray analysis
- Quantitative RT-PCR (qPCR) analysis
- High-throughput RNA sequencing
- RNA-Seq alignment
- RNA-seq differential gene expression

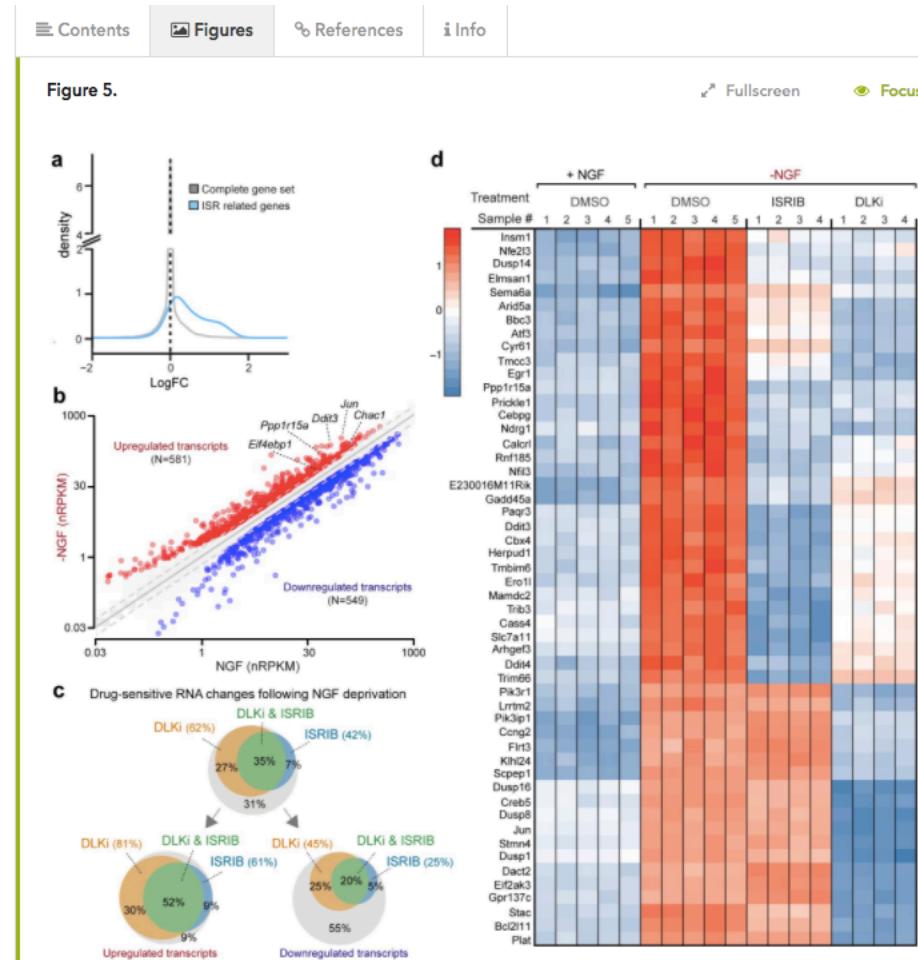
control of ATF4 implied by ISRIB sensitivity and suggest that DLK does not control activation of the ISR primarily through c-Jun-mediated transcriptional changes.

## Profiling of ISR-dependent gene expression changes following NGF deprivation

The preceding data argues that ISR activation by PERK represents a previously unappreciated general feature of the DLK-mediated stress response that is more commonly associated with MAP kinase stress signaling. To more broadly examine the relative contribution of DLK/ISR signaling, we performed high-throughput RNA sequencing (RNA-seq) on NGF-deprived cultures of embryonic DRG sensory neurons in the presence of either ISRIB or DLKi (Figure 5).

First, we assessed whether global expression analysis supports the hypothesis that SNC, ONC, and NGF deprivation share the ISR as a common feature. Cross-model analysis showed less broad commonality in expression patterns when comparing SNC to NGF deprivation (Figure 5—figure supplement 1) or when comparing ONC to NGF deprivation (Figure 5—figure supplement 2) than we observed when comparing SNC to ONC (Figure 1b). Nevertheless, we found that, as in the ONC and SNC models, an ISR-related gene set representing putative ATF4-dependent transcripts (Lange et al., 2008) is enriched in this neuronal stress model (Figure 5a). We further examined the ISR genes that we had previously evaluated by qPCR, confirming that *Chac1*, *Eif4ebp1*, *Ppp1r15a*, *Ddit3* were, along with *Jun*, among a group of 1130 mRNAs that reached a strict criterion ( $>1.5$  fold, adjusted  $p < 0.001$ ) for expression change following NGF deprivation (Figure 5b and Figure 5—source data 1).

We next examined this group of expression changes for DLK-dependence, finding that about two-thirds were significantly reduced in the presence of DLKi (Figure 5c and Figure 5—source data 1). Further analysis revealed that the DLK-dependence is particularly enriched among upregulated RNAs, with over 80% of the 581 upregulated RNAs exhibiting DLKi sensitivity that reached statistical significance (Figure 5c). Together these findings argue that DLK-mediated stress signaling following NGF deprivation contributes more prominently to induction of stress responsive genes than to downregulation of neuronal gene expression (e.g., the transcription factor *Pou4f2*), distinct from the influential role of DLK in both up- and down-regulated mRNAs previously observed in ONC (Watkins et al., 2013).



### RNA-seq reveals ISRIB- and DLK inhibitor-sensitive expression changes following NGF deprivation.

(a–b) Global expression analysis indicates an enrichment in ISR-related genes upregulated 4.5 h after NGF withdrawal from embryonic DRG cultures in the presence of DMSO vehicle (n = 5/condition). (a) Density plot showing 'ISR-related' genes (blue, see Materials and methods) are more frequently upregulated compared to the distribution of all mRNAs expression changes ('complete gene set') ( $p < 1 \times 10^{-5}$ , one-tailed Student's t-test). (b) Scatterplot of gene expression levels (nRPKM) in NGF-containing and NGF-deprived samples.



# ScienceFair

The screenshot shows a mobile application window titled "sciencefair". At the top, there is a search bar with a magnifying glass icon and the placeholder text: "type # to access tagged papers, or \*keyword to search local collection". Below the search bar, the main screen features a large, bold text "Search for a paper.". At the bottom of the screen, there is a dark footer bar containing several status indicators: "offline", "0 results", "18 saved", "1 datasources", and a small upward-pointing arrow icon.

Credit: Richard Smith-Unna; Source: <https://github.com/codeforscience/sciencefair>

 crispr

Enhanced homology-directed human genome engineering by controlled timing of CRISPR/Cas9 delivery

*Lin et al.*

2014

Intrinsic sequence specificity of the Cas1 integrase directs new spacer acquisition

*Rollie et al.*

2015

Making better CRISPR libraries

*Zhu and Wei*

2016

Functional CRISPR screening identifies the ufmylation pathway as a regulator of SQSTM1/p62

*DeJesus et al.*

2016

CRISPR/Cas9 mutagenesis invalidates a putative cancer dependency targeted in on-going clinical trials

*Lin et al.*

2017

Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation

*Horbeck et al.*

2016

Selection of chromosomal DNA libraries using a multiplex CRISPR system

*Ryan et al.*

2014

Concerning RNA-guided gene drives for the alteration of wild populations

*Esveld et al.*

2014

An oxygen-insensitive Hif-3 $\alpha$  isoform inhibits Wnt signaling by destabilizing the nuclear  $\beta$ -catenin complex

*Zhang et al.*

2016

RNA-programmed genome editing in human cells

*Jinek et al.*

2013

offline

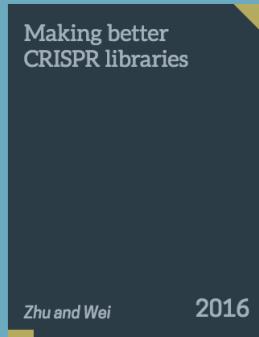
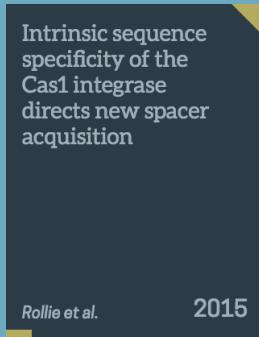
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Credit: Richard Smith-Unna; Source: <https://github.com/codeforscience/sciencefair>

🔍 crispr

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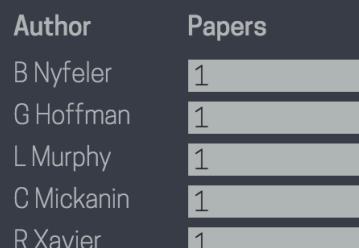
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Credit: Richard Smith-Unna; Source: <https://github.com/codeforscience/sciencefair>

DNA cleavage in eukaryotic cells are of great interest.

Research into genome defense mechanisms in bacteria showed that CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)/Cas (CRISPR-associated) loci encode RNA-guided adaptive immune systems that can destroy foreign DNA ([Bhaya et al., 2011](#); [Terns and Terns, 2011](#); [Wiedenheft et al., 2012](#)).

The Type II CRISPR/Cas systems require a single protein, Cas9, to catalyze DNA cleavage ([Sapranauskas et al., 2011](#)). Cas9 generates blunt DSBs at sites defined by a 20-nucleotide guide sequence contained within an associated CRISPR RNA (crRNA) transcript ([Gasiunas et al., 2012](#); [Jinek et al., 2012](#)). Cas9 requires both the guide crRNA and a trans-activating crRNA (tracrRNA) that is partially complementary to the crRNA for site-specific DNA recognition and cleavage ([Deltcheva et al., 2011](#); [Jinek et al., 2012](#)). Recent experiments showed that the crRNA:tracrRNA complex can be redesigned as a single transcript (single-guide RNA or sgRNA) encompassing the features required for both Cas9 binding and DNA target siterecognition ([Jinek et al., 2012](#)). Using sgRNA, Cas9 can be programmed to cleave double-stranded DNA at any site defined by the guide RNA sequence and including a GG protospacer-adjacent (PAM) motif ([Sapranauskas et al., 2011](#); [Jinek et al., 2012](#)). These findings suggested the exciting possibility that Cas9:sgRNA complexes might constitute a simple and versatile RNA-directed system for generating DSBs that could facilitate site-specific genome

Contents

Figures

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Info

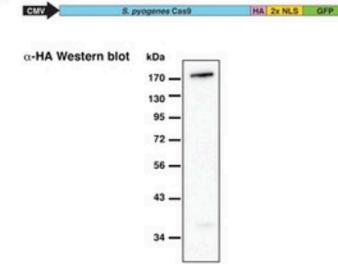


Figure 1.

Fullscreen

Focus

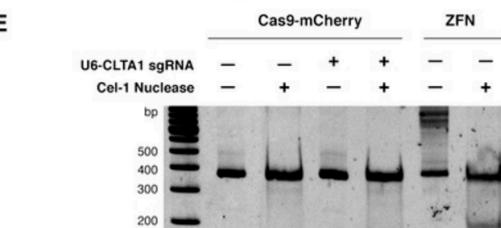
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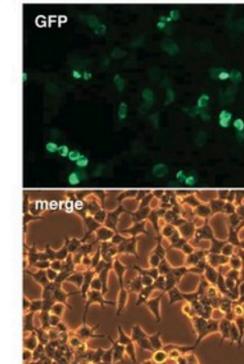
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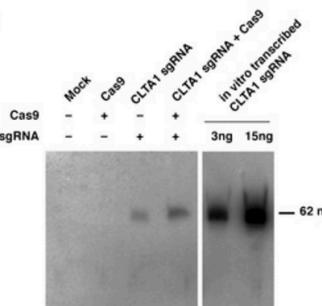
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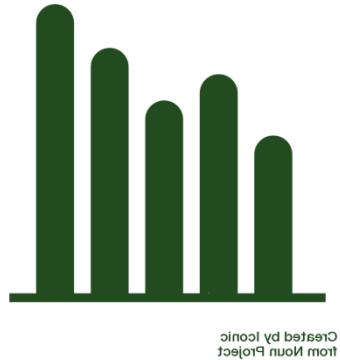
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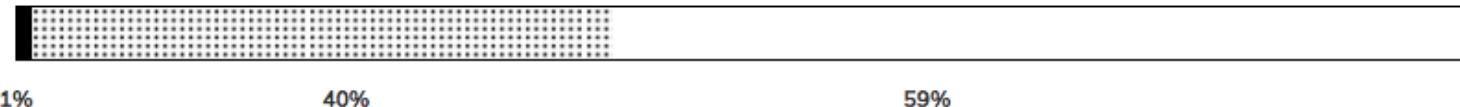
# Improving research evaluation



# Exposing the data behind the impact factor to highlight its limitations

PREPRINT: Lariviere et al., “A simple proposal for the publication of journal citation distributions”

How many citations are open today?



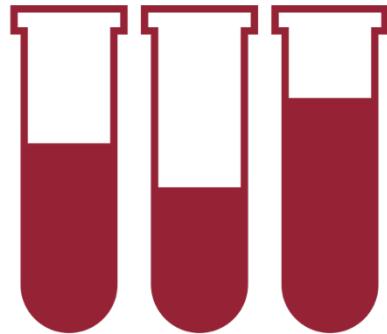
As of March 2017, the fraction of publications with open references has grown from 1% to more than 40% out of the nearly 35 million articles with references deposited with Crossref (to date).

Six organizations collaborated to form I4OC:



The creation of I4OC was spearheaded by: [Jonathan Dugan](#), [Martin Fenner](#), [Jan Gerlach](#), [Catriona MacCallum](#), [Daniel Mietchen](#), [Cameron Neylon](#), [Mark Patterson](#), [Michelle Paulson](#), [Silvio Peroni](#), [David Shotton](#), and [Dario Taraborelli](#).

# Addressing research reproducibility



Created by Alex Auda Samora  
from Noun Project

## Reproducibility Project: Cancer Biology

Attempting to replicate key findings in 50 top cancer studies from 2010-2012

## Cancer reproducibility project releases first results

An open-science effort to replicate dozens of cancer-biology studies is off to a confusing start.

**Monya Baker & Elie Dolgin**

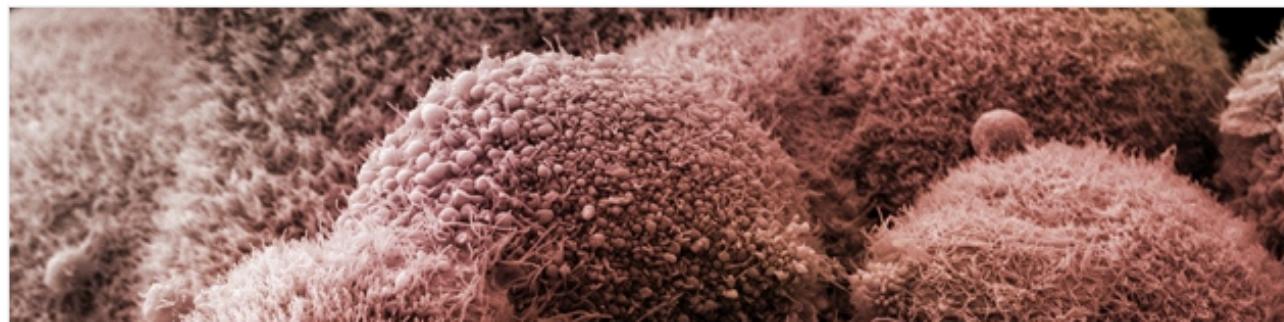
18 January 2017

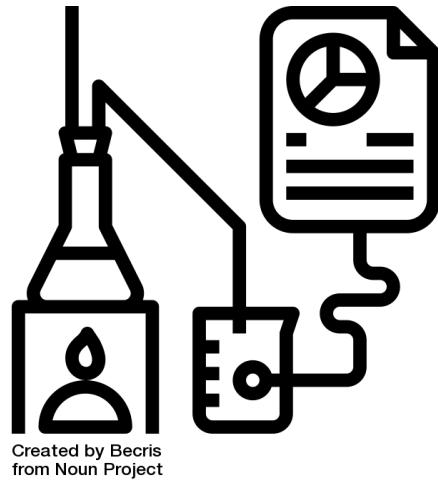


[PDF](#)



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## Research reproducibility

We encourage comprehensive publication of methods



## eLIFE

Protocol title	Link to original paper
Evaluation of Muscle Performance in Mice by Treadmill Exhaustion Test and Whole-limb Grip Strength Assay	Sep 2016
Gene Expression Analysis of Sorted Cells by RNA-seq in <i>Drosophila</i> Intestine	Jun 2016
The Object Context-place-location Paradigm for Testing Spatial Memory in Mice	Jun 2016
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## Longest post onset detection of Zika RNA in semen in multiple case studies

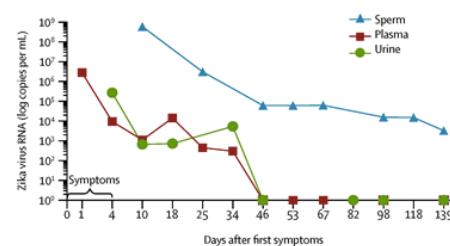
Christa Osuna

Type of test and sample	Results			
	Day 12*	Day 93*	Day 134*	Day 188*
ZIKV real-time RT-PCR serum	Neg	Neg	Neg	NT
ZIKV real-time RT-PCR urine	Neg	Pos (Ct 36.3)	Neg	NT
ZIKV real-time RT-PCR saliva	Neg (Ct 36.4)	Pos (Ct 36.4)	Neg	NT
ZIKV real-time RT-PCR semen	NT	Pos (Ct 29.6)	Pos (Ct 32.5)	Pos (Ct 30.2)
IFA ZIKV IgM titre	1:60	1:40	1:20	1:20
IFA ZIKV IgG titre	1:60	1:20	1:20	1:40
MNT antibody titre	1:60	at 320	at 320	NT

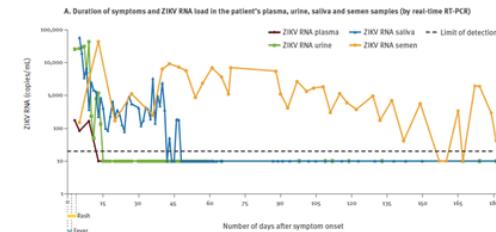
\*Number of days after symptom onset.

Laboratory findings related to Zika virus infection in a traveller returning from Haiti to Italy, Feb-July 2016

Nicostri et al  
Eurosurveillance



Zika virus in semen and spermatozoa  
Mansuy et al  
Lancet Infectious Diseases



Clinical and laboratory findings in a patient returning from Haiti to Italy, Jan 2016  
Barzon et al  
Euro Surveillance



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# Circuit mechanisms encoding odors and driving aging-associated behavioral declines in *Caenorhabditis elegans*

Sarah G Leinwand, Claire J Yang, Daphne Bazopoulou, Nikos Chronis, Jagan Srinivasan, Sreekanth H Chalasani

University of California, San Diego, United States; Salk Institute for Biological Studies, United States;

RESEARCH ARTICLE Dec 12, 2015

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## Abstract

Chemosensory neurons extract information about chemical cues from the environment. How is the activity in these sensory neurons transformed into behavior? Using *Caenorhabditis elegans*, we map a novel sensory neuron circuit motif that encodes odor concentration. Primary neurons, AWC<sup>ON</sup> and AWA, directly detect the food odor benzaldehyde (BZ) and release insulin-like peptides and acetylcholine, respectively, which are required for odor-evoked responses in secondary neurons, ASEL and AWB. Consistently, both primary and secondary neurons are required for BZ attraction. Unexpectedly, this combinatorial code is altered in aged animals: odor-evoked activity in secondary, but not primary, olfactory neurons is reduced. Moreover, experimental manipulations increasing neurotransmission from primary neurons rescues aging-associated neuronal deficits. Finally, we correlate the odor responsiveness of aged animals with their lifespan. Together, these results show how odors are encoded by primary and secondary neurons and suggest reduced neurotransmission as a novel mechanism driving aging-associated sensory neural activity and behavioral declines.

DOI: <http://dx.doi.org/10.7554/eLife.10181.001>



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# Circuit mechanisms encoding odors and driving aging-associated behavioral declines in *Caenorhabditis elegans*

Sarah G Leinwand, Claire J Yang, Daphne Bazopoulou, Nikos Chronis, Jagan Srinivasan, Sreekanth H Chalasani et al.

University of California, San Diego, United States; Salk Institute for Biological Studies, United States

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## Abstract

Chemosensory neurons extract information about chemical cues from the environment. How is the activity in these sensory neurons transformed into behavior? Using *Caenorhabditis elegans*, we map a novel sensory neuron circuit motif that encodes odor concentration. Primary neurons, AWC<sup>ON</sup> and AWA, directly detect the food odor benzaldehyde (BZ) and release insulin-like peptides and acetylcholine, respectively, which are required for odor-evoked responses in secondary neurons, ASEI and AWB. Consistently, both primary and secondary neurons are required for BZ attraction. Unexpectedly, this combinatorial code is altered in aged animals: odor-evoked activity in secondary, but not primary, olfactory neurons is reduced. Moreover, experimental manipulations increasing neurotransmission from primary neurons rescues aging-associated neuronal deficits. Finally, we correlate the odor responsiveness of aged animals with their lifespan. Together, these results show how odors are encoded by primary and secondary neurons and suggest reduced neurotransmission as a novel mechanism driving aging-associated sensory neural activity and behavioral declines.

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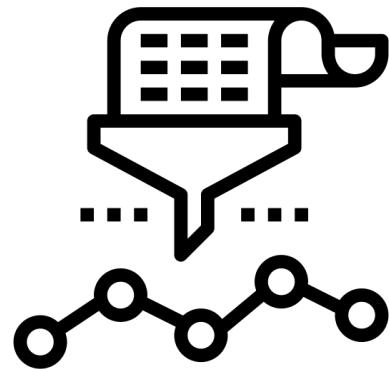
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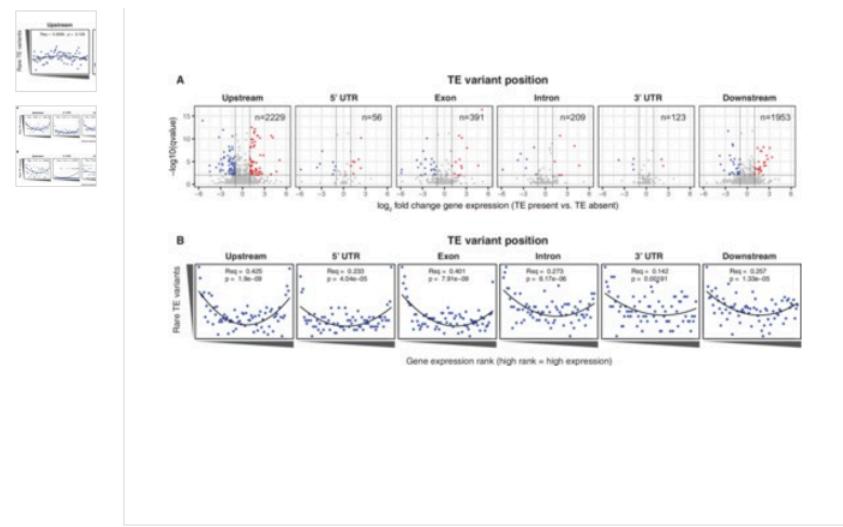
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**Figure 4.**

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Differential transcript abundance associated with TE variant presence/absence.

(A) Transcript abundance differences for genes associated with TE insertion variants at different positions, indicated in the plot titles. Genes with significantly different transcript abundance in accessions with a TE insertion compared to accessions without a TE insertion are colored blue (lower transcript abundance in accessions containing TE insertion) or red (higher transcript abundance in accessions containing TE insertion). Vertical lines indicate  $\pm 2$  fold change in FPKM. Horizontal line indicates the 1% false discovery rate. (B) Relationship between rare TE variant counts and gene expression rank. Cumulative number of rare TE variants in equal-sized bins for gene expression ranks, from the lowest-ranked accession (left) to the highest-ranked accession (right). Lines indicate the fit of a quadratic model.

DOI: <http://dx.doi.org/10.7554/eLife.20777.025>

**Figure 4—source data 1.**

Differentially expressed genes associated with TE presence/absence.

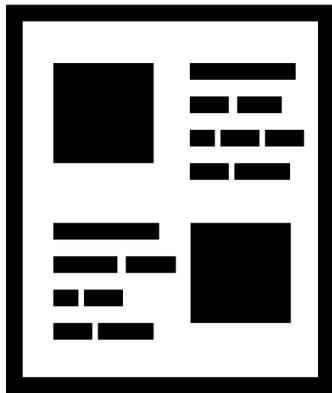
List of genes differentially expressed dependent on the presence/absence of nearby TE variants.

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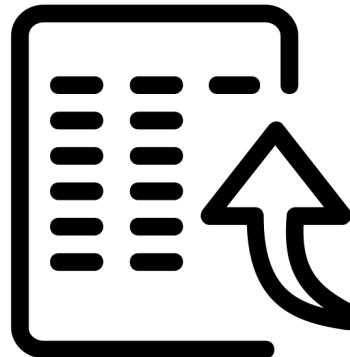
eLife 2016;5:e20777

# Can we bring the data closer to the narrative?



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## The interactive figure

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# Data-driven, interactive science, with d3.js plots and IPython Notebooks

---

Alberto Pepe  
Nathan Jenkins  
Matteo Cantiello

## 1 Javascript, d3.js, and d3po.js

4

Javascript offers many ways to create data-driven graphics. A popular solution is [D3.js](#), a JavaScript library to create and control web-based dynamic and interactive graphical forms. A gallery of some beautiful d3.js plots can be found [here](#).

Authorea now supports most Javascript-based data visualization solutions. The example below - Figure 1 - is a plot generated using [D3po.js](#) which is a javascript extension of d3.js. D3po allows anyone with no special data visualization skills, to make an interactive, publication-quality figure that has staged builds and linked brushing through scatter plots. What's even cooler is that the plot below is based on actual data (astrophysics data, yay!). The figure describes how metallicity affects color in cool stars. It is based on work of graduate student Elizabeth Newton and others ([Newton 2014](#)). Try clicking and dragging in the scatter plots to understand the power of linked brushing in published figures.

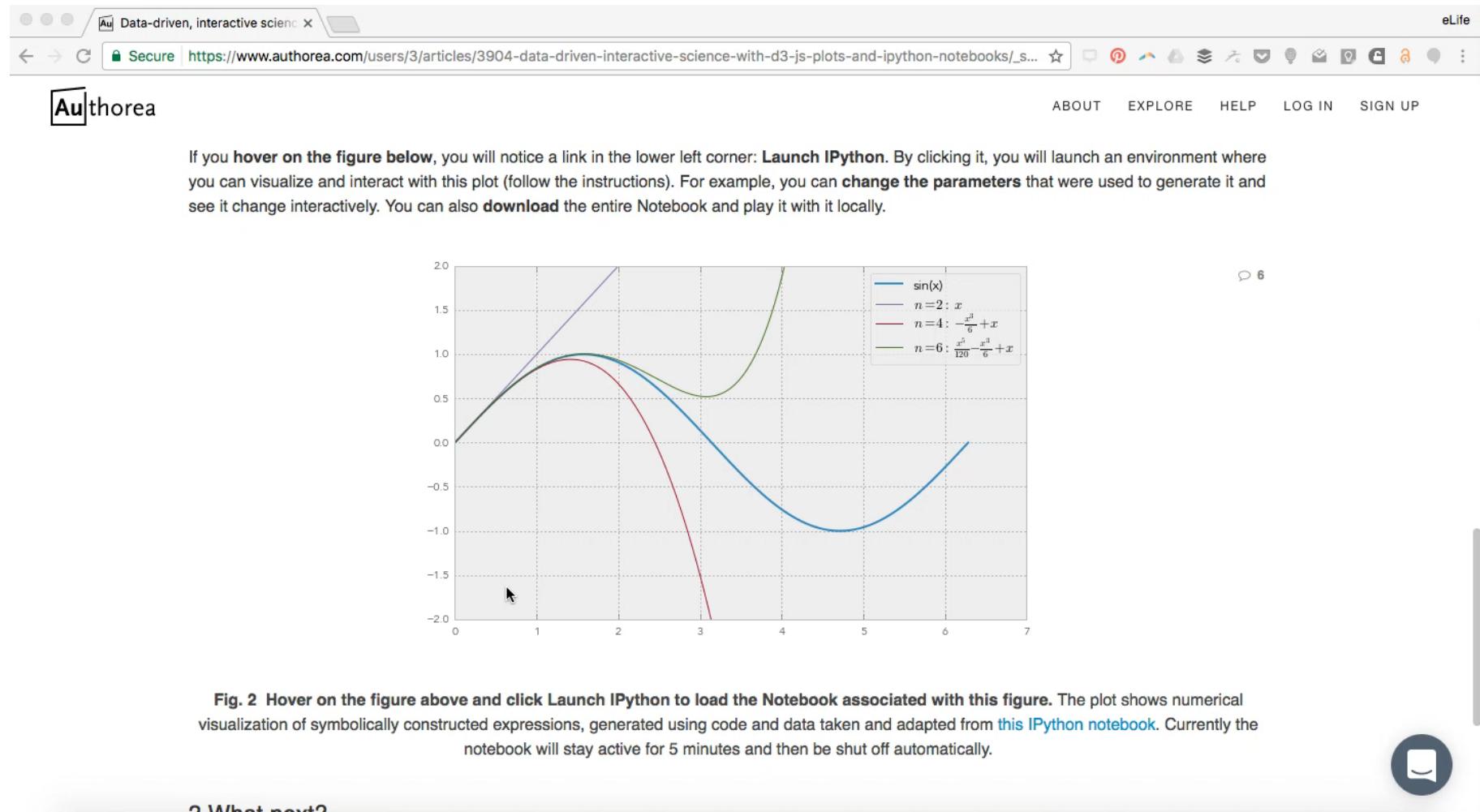
You should know that this entire visualization is running within Authorea. The Javascript, HTML, CSS and all the data associated with this image are all part of this blog post. They are individual files which can be found by clicking on the folder icon on the top left corner of this page.

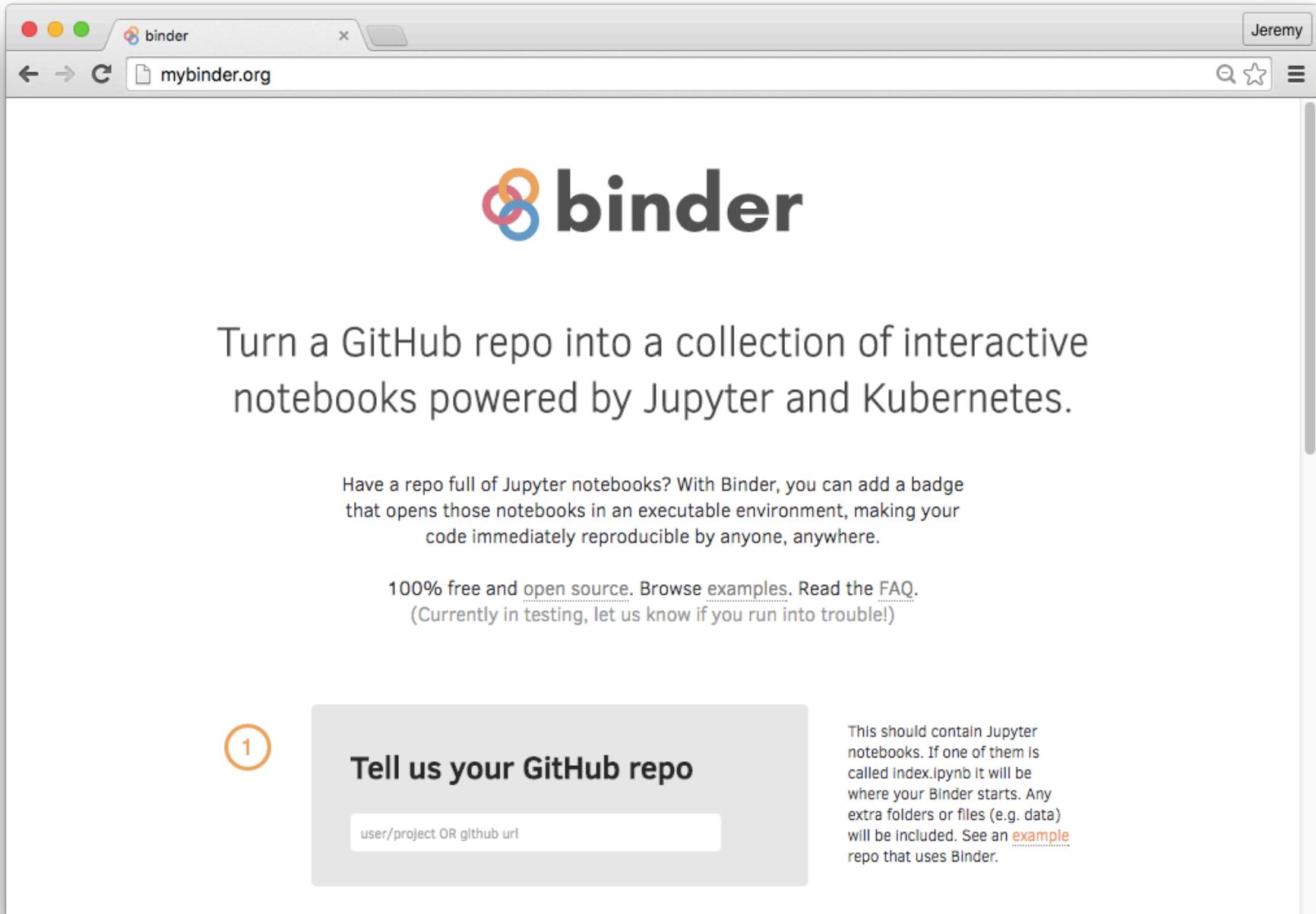
1

# The executable figure

Credit: Authorea

**Some steps removed and sequences shortened**





A screenshot of a web browser window titled "binder". The address bar shows "mybinder.org". The page content features the Binder logo (three overlapping circles in red, blue, and orange) and the text: "Turn a GitHub repo into a collection of interactive notebooks powered by Jupyter and Kubernetes." Below this, a paragraph explains that with Binder, you can add a badge that opens Jupyter notebooks in an executable environment, making code immediately reproducible. It also states that Binder is 100% free and open source, with links to browse examples and read the FAQ. A call-to-action box prompts users to enter their GitHub repo URL.

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Have a repo full of Jupyter notebooks? With Binder, you can add a badge that opens those notebooks in an executable environment, making your code immediately reproducible by anyone, anywhere.

100% free and open source. Browse examples. Read the FAQ.  
(Currently in testing, let us know if you run into trouble!)

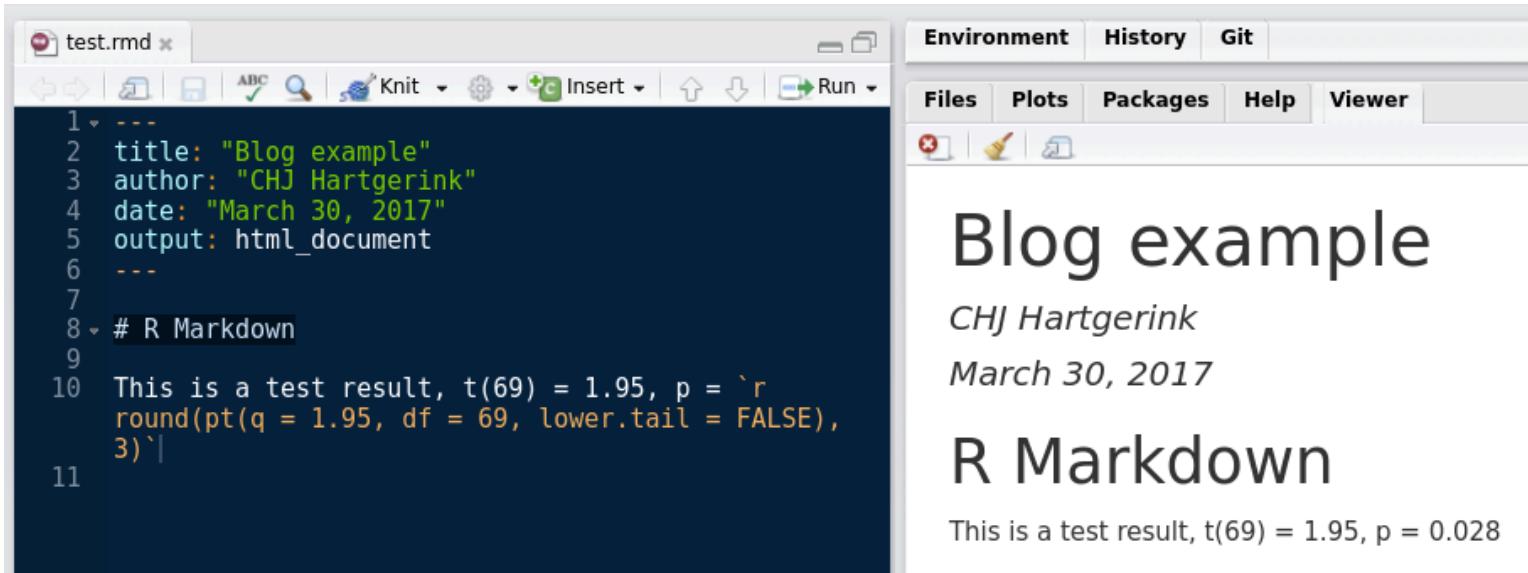
1

Tell us your GitHub repo

user/project OR github url

This should contain Jupyter notebooks. If one of them is called index.ipynb it will be where your Binder starts. Any extra folders or files (e.g. data) will be included. See an [example](#) repo that uses Binder.

# The reproducible document



The screenshot shows the RStudio interface. On the left, the code editor displays an R Markdown file named "test.rmd". The code includes YAML front matter and an R code chunk. On the right, the preview pane shows the rendered output: a blog post titled "Blog example" by "CHJ Hartgerink" on "March 30, 2017". The R code chunk output is also visible in the preview.

```
1 ---  
2 title: "Blog example"  
3 author: "CHJ Hartgerink"  
4 date: "March 30, 2017"  
5 output: html_document  
6 ---  
7  
8 # R Markdown  
9  
10 This is a test result, t(69) = 1.95, p = `r  
round(pt(q = 1.95, df = 69, lower.tail = FALSE),  
3)`|  
11
```

Blog example  
CHJ Hartgerink  
March 30, 2017  
**R Markdown**  
This is a test result, t(69) = 1.95, p = 0.028

"It took me a couple of hours to...  
REPRODUCE EXACTLY the analysis presented in the manuscript...  
With few more hours, I **was able to modify the authors' code**  
to change a linear scale for a log scale for their Fig. 4."

Christophe Pouzat, reviewer  
GigaScience blog: <http://gigasciencejournal.com/blog/qa-on-dynamic-documents>

# Challenges

- Static version of peer-reviewed article
- Persistence and accuracy



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3



9

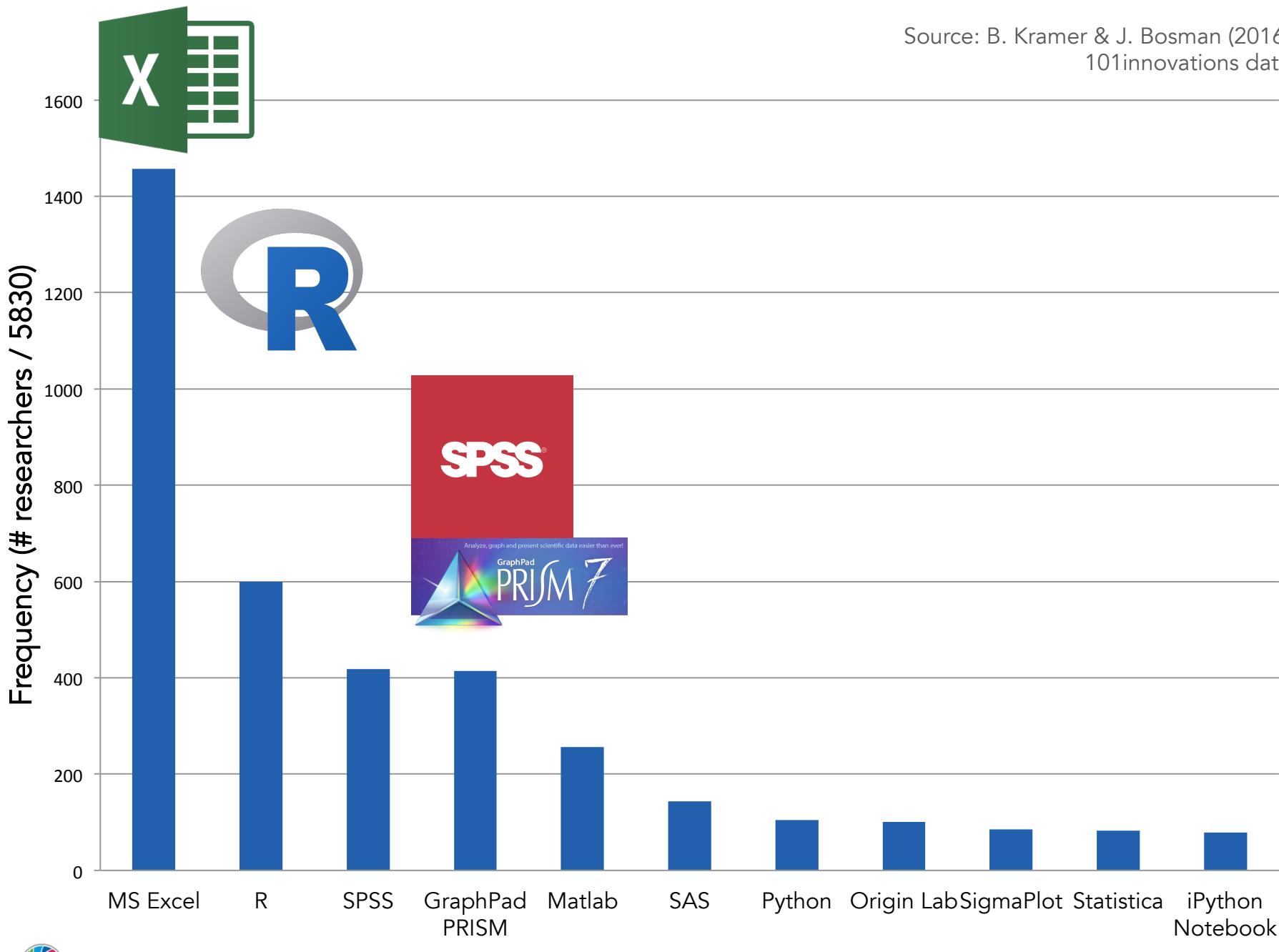


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# Challenges

- Static version of peer-reviewed article
- Persistence and accuracy
- Who stores? Who hosts? Who computes?
- Computational analyses and methods are not widespread



# Incentives

- “No time or funding” to learn new tools, document data well
- “No benefit” to sharing data openly



Van den Eynden, Veerle et al. (2016)  
Towards Open Research: Practices,  
experiences, barriers and  
opportunities. Wellcome Trust. <https://dx.doi.org/10.6084/m9.figshare.4055448>

# Take-home messages

Science publishing is on the brink of change

We are exploiting new technologies to improve how research is recorded, shared, consumed, and reused

eLife can help bring new tools to the users (**you**) to improve the experience of research communication

# What ideas do you have?

Naomi Penfold  
Innovation Officer  
[@eLifelnnovation](https://twitter.com/eLifelnnovation)  
[innovation@elifesciences.org](mailto:innovation@elifesciences.org)

## Discussion points

- What frustrates you in your research life?
- How can we best serve you?
- In which new technologies do you see promise?

**“The **impact** we cherish is  
**discovery** in science”**

Randy Schekman, eLife Editor-in-Chief