

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

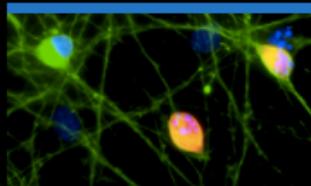
Helping scientists accelerate discovery by  
operating a platform for research communication  
that encourages and recognises the most  
responsible behaviours in science

## 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](#)[↳ Cancer](#)[↳ 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

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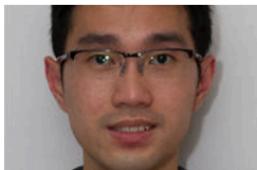
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Singapore (Singapore)



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(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)

Deputy Editors **Eve Marder**, Brandeis University (USA)

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

Senior Editors **40** including

Kevin Struhl, Aviv Regev, Arup Chakraborty, Prabhat Jha

Reviewing Editors **>300** including

David Knipe, Wade Harper, David Ginty, Jon Clardy, Karen Adelman

## eLife's approach to peer review

- Initial decisions are delivered quickly
- 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

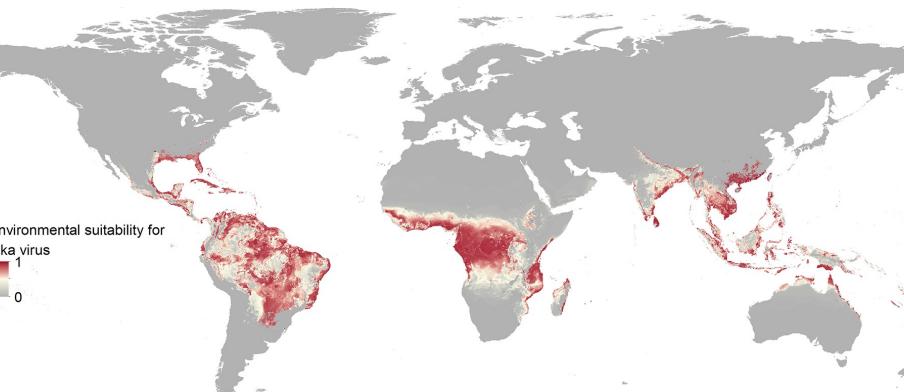
# THE eLIFE EDITORIAL PROCESS

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>

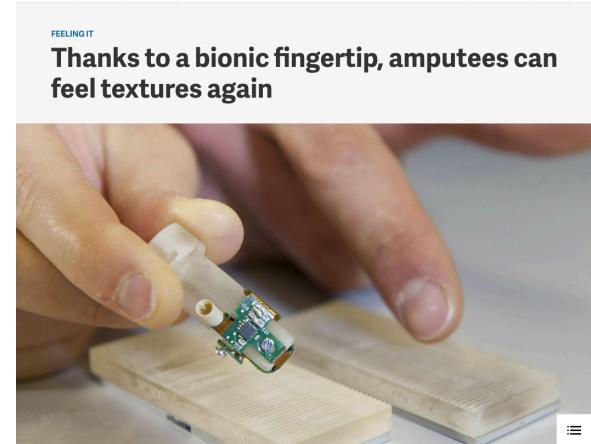
Published April 19, 2016

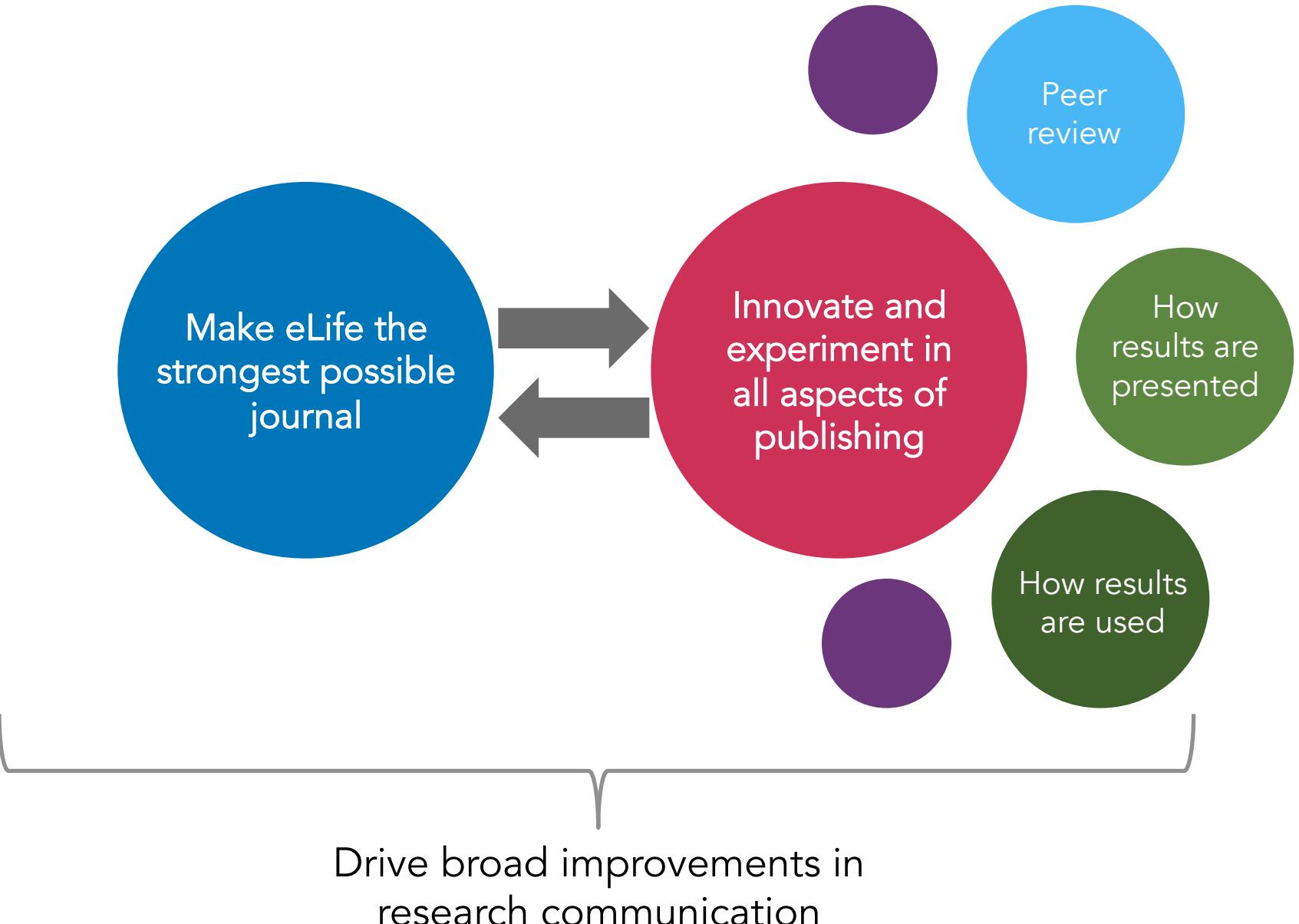
Cite as eLife 2016;5:e15272

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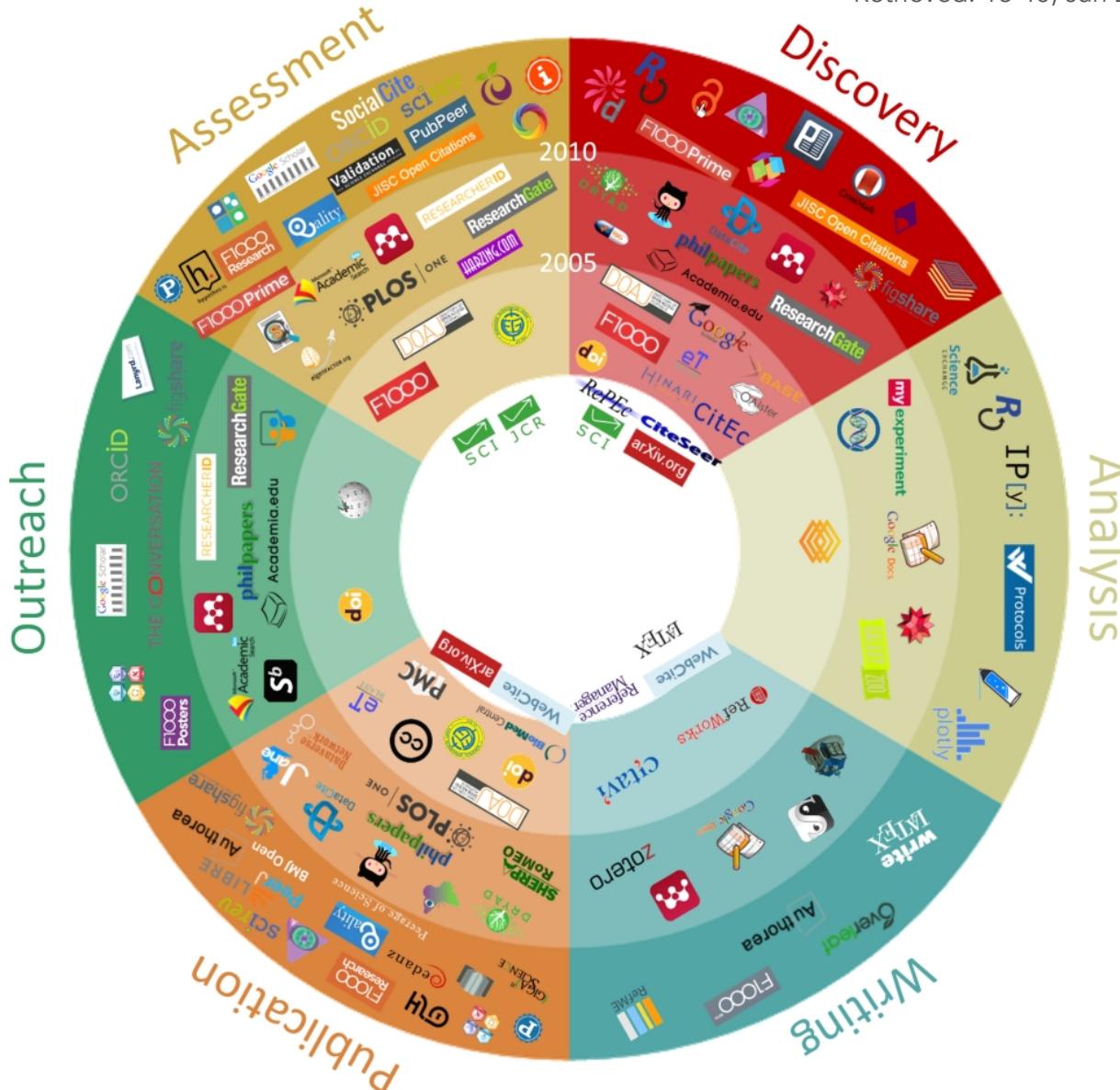


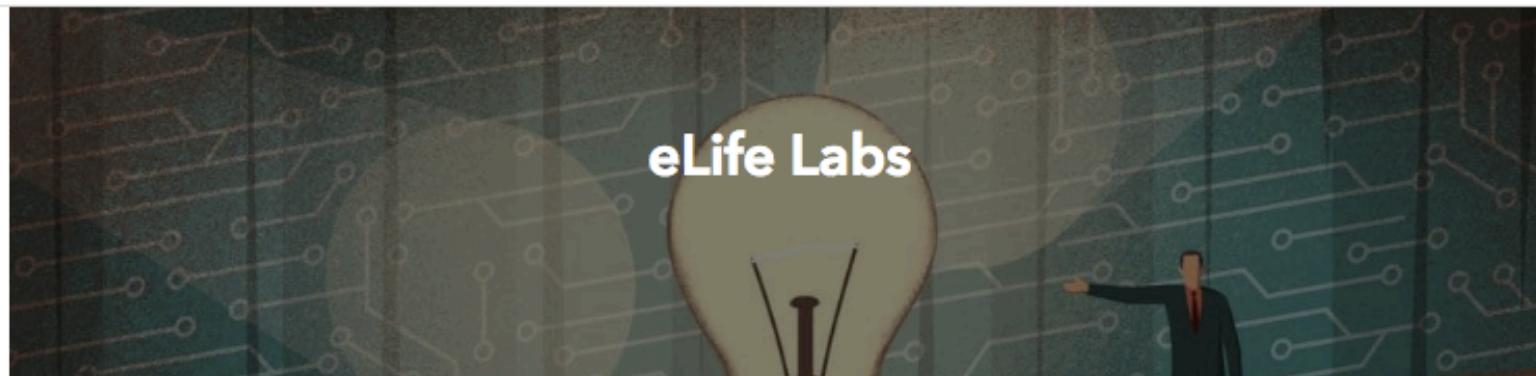


# Innovation at eLife

## 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



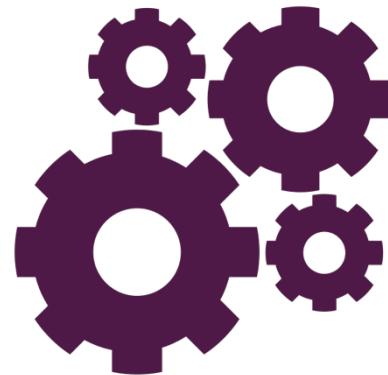
Proteopedia for sharing macromolecule concepts online



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)

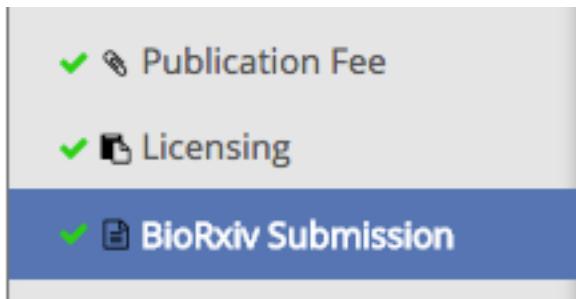


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## Preprints

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:

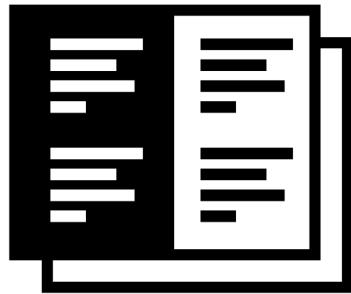


The screenshot shows a vertical list of submission steps. The first two steps, 'Publication Fee' and 'Licensing', have green checkmarks next to them. The third step, 'BioRxiv Submission', is highlighted with a blue bar at the bottom and has a green checkmark next to it. To the right of this list is a 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



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# Lens

eLife's open-source, online reading tool



Tue, 08 Mar 2016

## 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

[PDF](#) [Source XML](#) [Lens JSON](#)

DOI: 10.7554/eLife.09148

### Abstract

Restoration of touch after hand amputation is a desirable feature of ideal prostheses. Here, we show that texture discrimination can be artificially provided in human subjects by implementing a neuromorphic real-time mechano-neuro-transduction (MNT), which emulates to some extent the firing dynamics of SA1 cutaneous afferents. The MNT process was used to modulate the temporal pattern of electrical spikes delivered to the human median nerve via percutaneous microstimulation in four intact subjects and via implanted intrafascicular stimulation in one transradial amputee. Both approaches allowed the subjects to reliably discriminate spatial coarseness of surfaces as confirmed also by a hybrid neural model of the median nerve. Moreover, MNT-evoked EEG activity showed physiologically

[Contents](#) [Figures](#) [References](#) [Info](#)

### Abstract

[eLife digest](#)

#### Main Text

##### Introduction

##### Results

Experiments with intact subjects using needle microstimulation of the median nerve

Translatability from needle microstimulation to TIME-based stimulation

Experiments with a transradial amputee

Analysis of neural coding strategies

##### Discussion

#### Materials and methods

Sensored finger

Mechano-neuro-transduction (MNT) process

Percutaneous electrical microstimulation of the median nerve with intact subjects

Intraneuronal stimulation of the median nerve with implanted interface in transradial amputee

Three-alternative forced-choice (3AFC) psychophysical protocol

EEG signals recording

EEG signal processing

EEG functional connectivity analysis and EEG graph analysis

Hybrid electrical-biophysical model of the median nerve for the comparison between microstimulation needle and implanted TIME

#### Acknowledgements

#### Article Commentary

##### Decision letter

##### Author response

eLife 2016;5:e09148

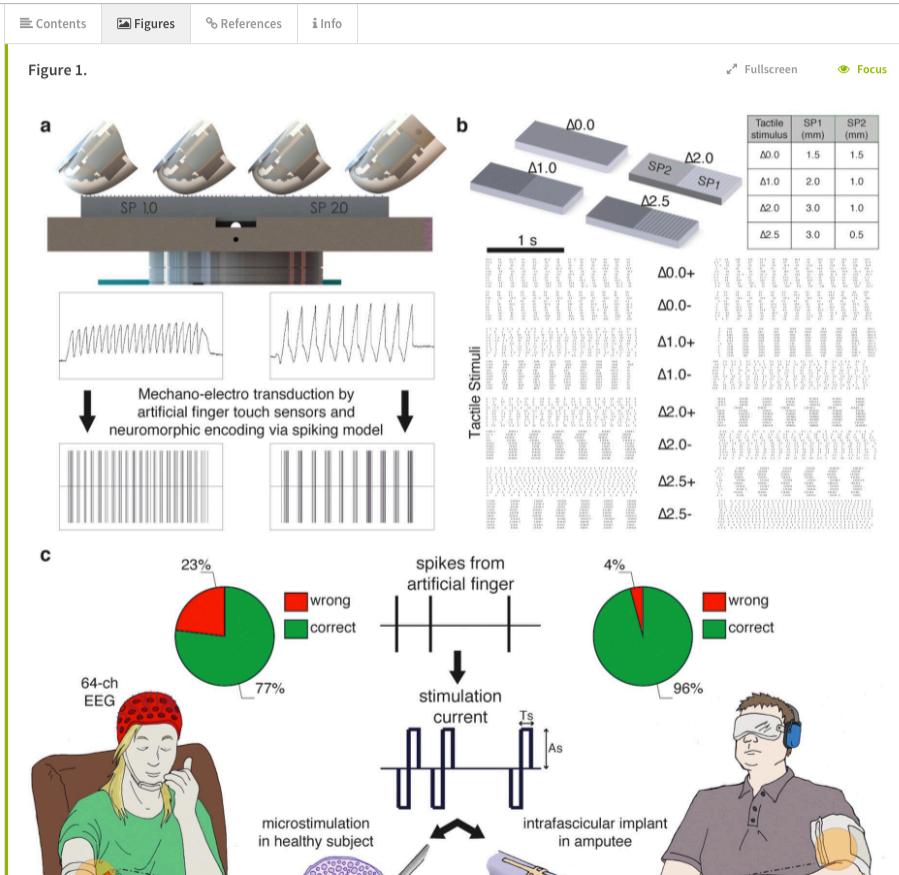
## Results

### Experiments with intact subjects using needle microstimulation of the median nerve

The MNT process translates surface coarseness into the injection of current pulses into the nerve. It qualitatively mimics the neuronal activity recorded during human microneurographic experiments (Oddo et al., 2011b). The MNT approach was initially tested in four intact volunteers using percutaneous electrical microstimulation of the median nerve (Vallbo et al., 1984b; Torebjörk and Ochoa, 1980) (Figure 1a, Figure 2). The participants - without visual or acoustic cues about the stimuli - were asked to discriminate surface pairs (Figure 1b) that differed in the Spatial Period (SP) of alternating ridges and grooves (gratings), i.e., in the distance between consecutive ridges separated by grooves (defined in Figure 2a), which was a constant quantity in each half grating (as shown in Figure 1b).

Via percutaneous electrical neural microstimulation, they reported mechanical sensation pertaining to the palmar side of the first four fingers of the hand. Microstimulation allowed users to reach discrimination ability above 77% (107/138, Figure 1c, Figure 3a) during a three-alternative forced-choice (3AFC) psychophysical procedure (Perez et al., 2010; Gibson and Craig, 2005) mediated by the artificial touch system, which is based on the use of a MEMS sensor embedded into a human-sized robotic fingertip (Video 1). Confidence analyses indicated that percutaneous electrical microstimulation successfully induced percepts that were used to assess the coarseness of textured surfaces (Figure 3b). The capability to discriminate between the two sides of the surface pairs was correlated with the difference between their spatial periods (Figure 3c).

As described hereafter, the comparison between the EEG activity that was evoked by the natural mechanical tactile stimulation of the real fingertip in the right hand and the one evoked by the substitutive electrical stimulation showed no significant differences in source topography, response timing, and clustering of cortical connections between the two stimulation modalities. Event-related potentials (Figure 4a) after substitutive electrical ( $n = 4$ , estimated power 0.75, Figure 4—figure supplement 2) and natural mechanical stimulation ( $n = 4$ , estimated power 0.79, Figure 4—figure supplement 3) conditions did not reveal any statistical difference (Montecarlo statistics with cluster correction for multiple comparisons). Furthermore, a network graph analysis approach (Vecchio et al., 2015a) revealed a lateralized EEG frequency modulation that was evoked both by electrical and mechanical stimuli (Figure 4b). Indeed, the primary sensorimotor areas in the hemisphere contralateral to the stimulus presented a significant reduction (3-way ANOVA [https://lens.elife sciences.org/09148/index.html?\\_ga=1.251679115.303271206.1463581989](https://lens.elife sciences.org/09148/index.html?_ga=1.251679115.303271206.1463581989)



eLife 2016;5:e09148



The screenshot shows a web-based document editor with a dark-themed interface. At the top right is a navigation bar with three dots, the text "sciencefair", and a close button (an "X"). Below the navigation bar is a header section with tabs: "Contents" (selected), "Figures", and "Info". The main content area is divided into two columns. The left column contains the "Main Text" and "Background" sections. The "Background" section contains a detailed paragraph about arthropod disease vectors and super-infection. The right column contains a hierarchical tree view of the document structure, with "Background", "Methods", "Results", and "Conclusions" collapsed, and "Main Text" expanded. Under "Main Text", "Background", "Methods", and "Results" are further expanded, showing sub-sections like "Mosquito feeds" and "Feeding behaviour following infection".

Main Text

Background

Many arthropod disease vectors have multiple opportunities to become infected with the same pathogen species during their lifetime (super-infection). The impact of super-infection within vectors to parasite transmission is largely unknown, and may have substantial impacts on epidemiology. For example, in the laboratory, pathogen transmission can be enhanced when different parasite species co-occur in the same individual vector, a phenomenon that has been observed in some [1 - 4] but not all mosquito species that have been tested [1, 4].

The aim of this study was to investigate the potential epidemiological consequences of super-infection of mosquitoes by malaria parasites. Super-infection of vectors by successive parasite infections has been examined in a variety of infectious diseases [5 - 7], but to knowledge, the

Background

Background

Methods

Results

Conclusions

Main Text

Background

Methods

Mosquito feeds

Statistical analysis

Results

Feeding behaviour following infection

Re-exposure to parasites and infection

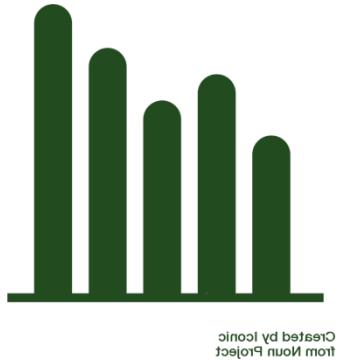
Discussion

Conclusions

Authors' contributions

<https://github.com/codeforscience/sciencefair>

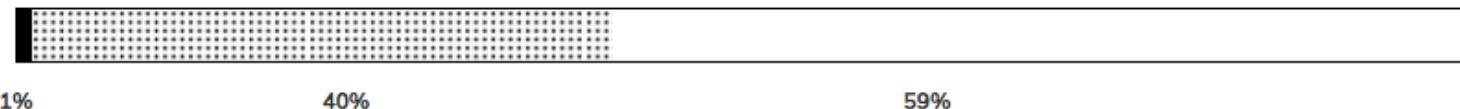
# Improving research evaluation



# 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?



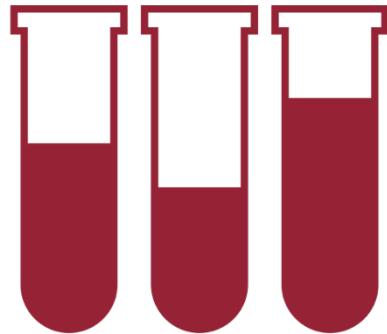
As of March 2017, the fraction of publications with open references has grown from 1% to more than 40% out of the nearly 35 million articles with references deposited with Crossref (to date).

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**

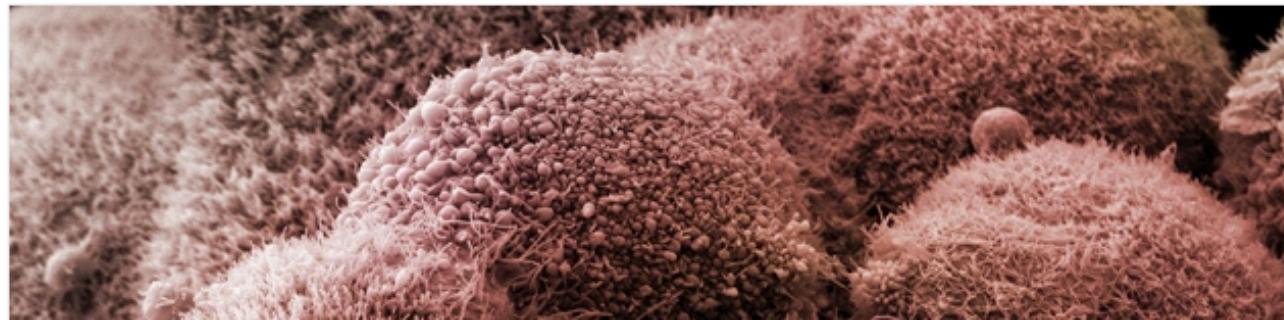
18 January 2017

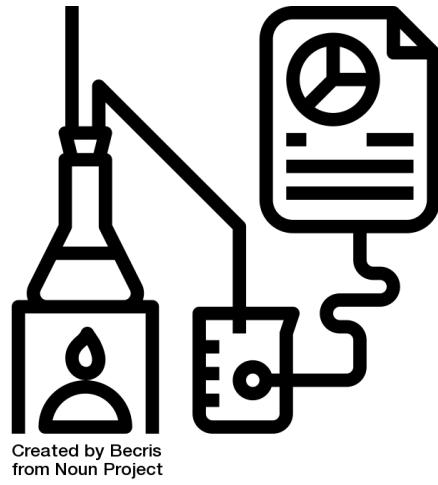


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## Research reproducibility

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
Protein Expression Protocol for an Adenylate Cyclase Anchored by a <i>Vibrio</i> Quorum Sensing Receptor	Mar 2016
Heterologous Expression and Purification of the Magnesium Transporter A (MgtA) in <i>Escherichia coli</i>	Feb 2016
Tandem Purification of His <sub>6</sub> -3x FLAG Tagged Proteins for Mass Spectrometry from <i>Arabidopsis</i>	Feb 2016
Purification and Identification of Novel Host-derived Factors for Influenza Virus Replication from Human Nuclear Extracts	Nov 2015
Reporter Assay for Semen-mediated Enhancement of HIV-1 Infection	Sep 2015
PRODIGY: A Contact-based Predictor of Binding Affinity in Protein-protein Complexes	Aug 2015
<i>Aspergillus terreus</i> Infection of Fruits and Terrein Quantification by HPLC Analysis	Jul 2015
Chromosome Dosage Analysis in Plants Using Whole Genome Sequencing	May 2015
Cryo-focused Ion Beam Sample Preparation for Imaging Vitreous Cells by Cryo-electron Tomography	Jan 2015
Whole Genome Bisulfite Sequencing and DNA Methylation Analysis from Plant Tissue	Jul 2014
<i>Dictyostelium</i> Cultivation, Transfection, Microscopy and Fractionation	May 2014
FLP/FRT Induction of Mitotic Recombination in <i>Drosophila</i> Germline	Apr 2014
Protein Extraction from <i>Drosophila</i> Females and Ovaries	Apr 2014



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## Following

Partnership of [@PLOS](#) and [@ProtocolsIO](#) - a step towards more reproducible methods sections [protocols.io/groups/protocolsio](https://protocols.io/groups/protocolsio) ...

**PLOS**

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# The Evolution of Mammalian Gene Families

Jeffrey C. Dangl<sup>1</sup>, Yiqi Du<sup>1</sup>, Juan E. Sastre<sup>1,2</sup>, Nataša Utrino<sup>3</sup>, Matthew J. Hahn<sup>1\*</sup>

<sup>1</sup> Department of Biology and Kresge Institute of Biosciences, Indiana University, Bloomington, Indiana, United States of America, <sup>2</sup> Division of Genetics, University of Rochester, 550 Elmwood, University of Rochester, Rochester, United Kingdom, <sup>3</sup> Department of Molecular Genetics and Microbiology, University of Southern California, Los Angeles, California, United States of America

**✉ matthew.hahn@indiana.edu**

**Abstract** Gene families are groups of homologous genes that are likely to have highly similar functions. Differences in family size due to lineage-specific gene duplication and gene loss may provide clues to the evolutionary forces that have shaped mammalian genomes. Here we analyze the gene families contained within the whole genomes of humans, chimpanzees, mouse, rat, and dog. Our results show that the number of gene families in each genome is approximately constant, and that most families are expanded or contracted along at least one lineage. Additionally, we find that a large number of families are conspiracy loci—ones that are more abundant in some genomes, and a smaller number of gene families affect adaptation at the level of genes rather than the split transcriptome, including changes likely driven by adaptive natural selection. Our results imply that humans and chimpanzees share ~10% of their gene families, and that the number of shared gene families between humans and dogs is off-set by a 1.6% difference between orthologous translatable sequences. This genomic “revealing date” of gene gain and loss represents a large number of genetic differences separating humans from our closest relatives.

**Keywords:** PLOS ONE | DOI: <https://doi.org/10.1101/1870> The author(s) have declared that no competing interests exist.

## INTRODUCTION

Explaining the often-mysterious, physiological, and behavioral consequences of gene duplications and subsequent expansions, a challenging given the low rate of nucleotide substitutions in the genome [1]. More than fifteen years ago, King and Wilson [2] proposed that the number of genes in a genome is conserved, noting that “the number of genes in a genome is not reduced by natural selection.” In other words, they proposed that “most genes are dispensable.” To explore the prediction, King and Wilson [2] analyzed changes rather than gains and losses in gene families, and found that the number of shared conserved differences [3]. More recently, changes rather than gains and losses in gene families have been used to explore the “conservation of gene families” hypothesis [4–6]. Evidence gathered over the last two decades suggests that gene families are not conserved, and that regulatory sequence [7,8] changes have both been involved in the most recent rounds of evolution [9].

Gene families are often considered in comparison to orthologous regions, or in the differential duplication and loss of genes. For example, the number of gene families with differential rates of gain and loss (i.e., exponential duplicates) range from 20 (bacteria), 55% on average to 1,000 (humans) [2]. So, is it a conservation of gene families that is the hallmark of evolution? Or, is it the number of gene families that is conserved? Interestingly, gene families do not follow a simple pattern of gain and loss, and instead represent a non-linear relation. The best approximation is that there is a positive relationship between the number of gene families and the number of genes in a genome [2]. Within accounting for differences in the number of genes in different species, the “conservation of gene families” hypothesis is supported by the observation that the number of gene families is correlated with a property of the genome, namely the degree of recombination.

The most common, ubiquitous feature of gene families is evolutionary expansion or those that include intact genes. Gene duplications can occur via a variety of mechanisms, including gene conversion, unequal crossing over, and gene conversion change its genome [10–12], and gene loss has been found to occur as a common alternative mechanism [13]. Gene conversion is a process by which one allele replaces another, and is often used to refer to changes in the human proteome [14–16]. Using this nomenclature, we would

explore those in base pairs (1–100) are gene duplicates in the human genome, our split with chimpanzee (~100 duplications per genome), and the number of genes in each genome. The number of genes and similar rates of net changes in the total number of genes in each genome are conserved, while the number of gene families is not ( $\sim 17\%$  of all genes). The number of total gene duplicates (as a ratio of gene duplicates) has been widely reported, but the number of gene families is also an important measure of genome evolution. Although this hypothesis violates classical concepts of evolution, it is consistent with the idea that new gene families are also the most likely to be lost, and the number of gene families among fully sequenced genomes is not significantly different from the number of gene families in the human genome [2].

**Competing interests:** The author(s) have declared that no competing interests exist.

\* **to whom correspondence should be addressed:** [matthew.hahn@indiana.edu](mailto:matthew.hahn@indiana.edu)

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## Protocols

**Super simple *In vivo* Hoechst staining of unicellular protists**  
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**Z/S ratio controls**

**STEP 1** Add 1/2000 Hoechst dye (1 μl. into 1 ml. volume of cell). Keep cells with dye protected from light.

**STEP 2** Incubate at room temperature for 30 minutes. Keep cells with dye protected from light.

**STEP 3** Centrifuge cells at 3000g for 5 minutes

**04:45**

**STEP 4** Resuspend with fresh growing medium. Use minimum volume of medium in order to plate in to the

**Academic Editor:** Jason Weis, Indiana University at Bloomington, United States of America  
**Received:** March 20, 2017; **Accepted:** December 1, 2016; **Published:** April 6, 2017

**Citation:** Dangl JC, Du Y, Sastre JE, Utrino N, Hahn MJ (2017) The Evolution of Mammalian Gene Families. *PLOS ONE* 12(4): e0174070. <https://doi.org/10.1371/journal.pone.0174070>

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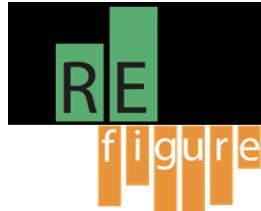
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## Longest post onset detection of Zika RNA in semen in multiple case studies

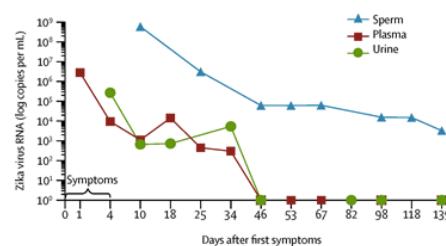
Christa Osuna

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: 36.1)	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	1:320	1:320	NT

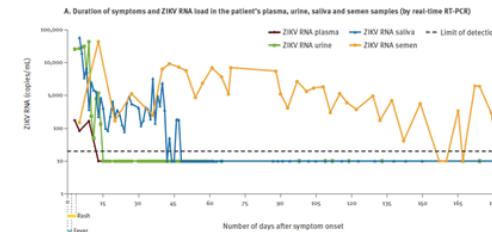
\*Number of days after symptom onset.

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  
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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, 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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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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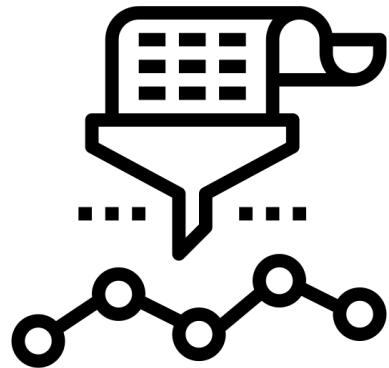
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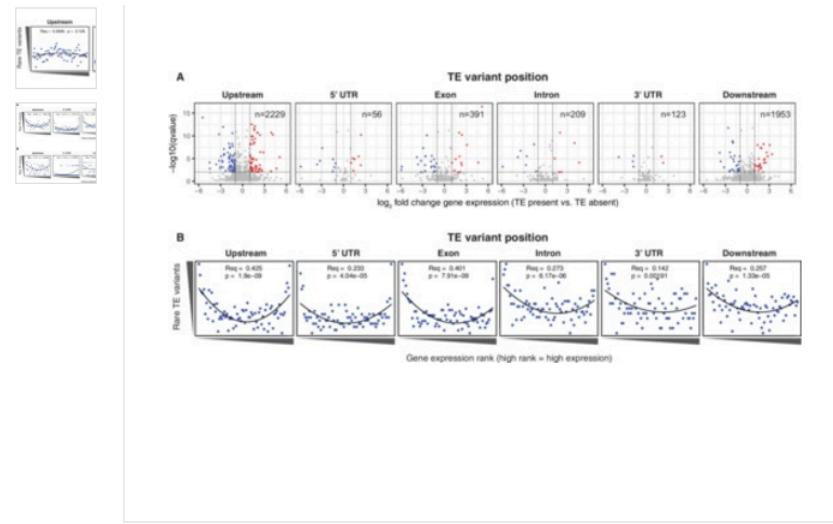
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**Figure 4.**

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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.

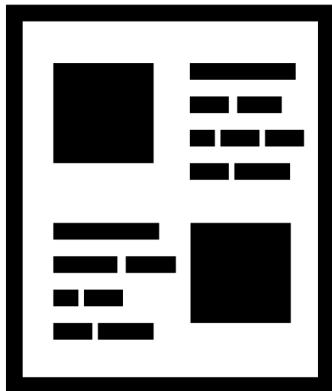
List of genes differentially expressed dependent on the presence/absence of nearby TE variants.

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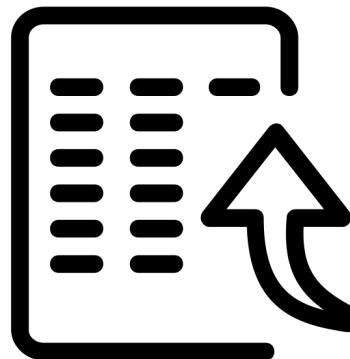
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# Data-driven, interactive science, with d3.js plots and IPython Notebooks

---

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.

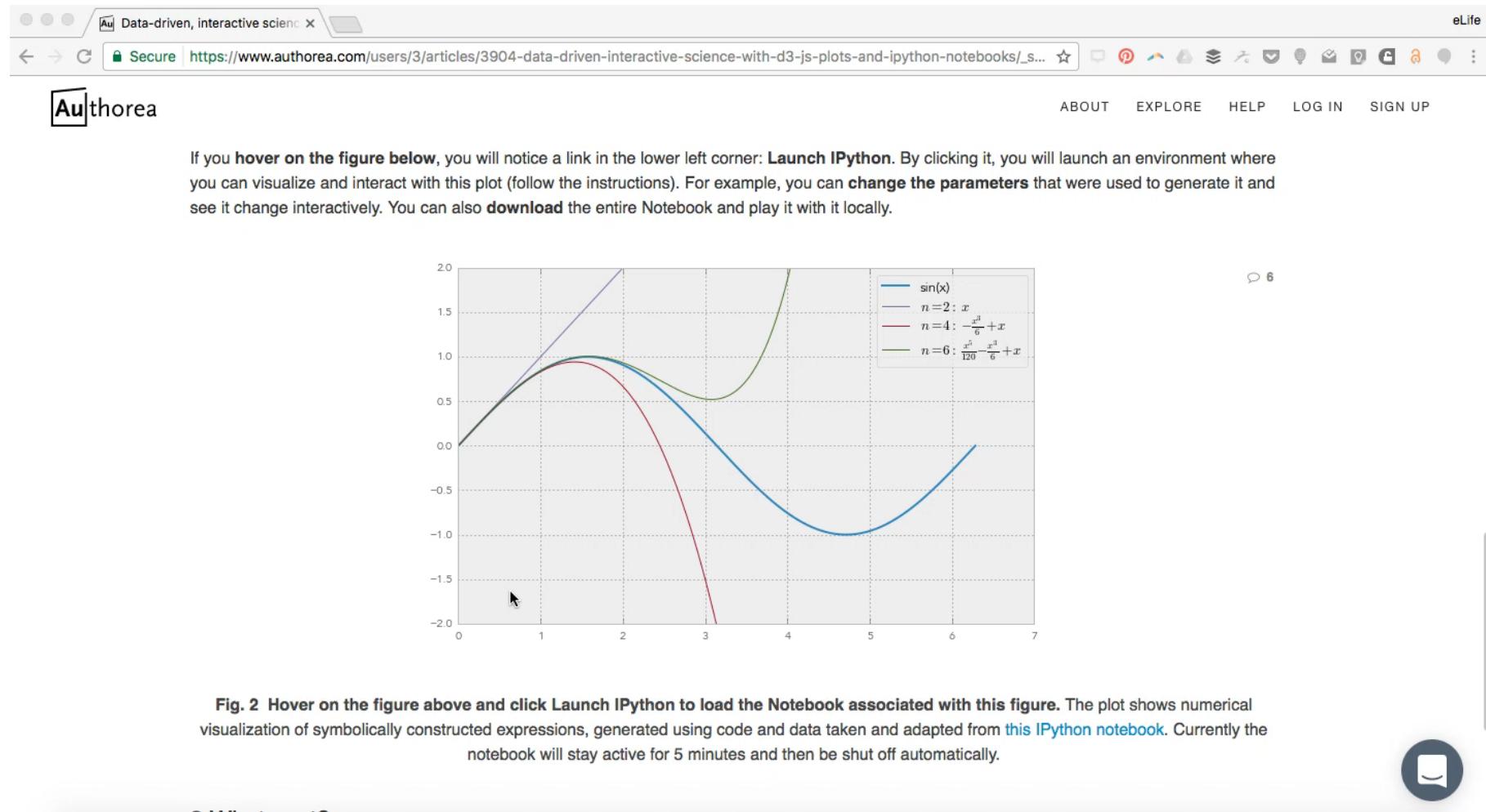
You should know that this entire visualization is running within Authorea. The Javascript, HTML, CSS and all the data associated with this image are all part of this blog post. They are individual files which can be found by clicking on the folder icon on the top left corner of this page.

1

# The executable figure

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**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 users can add a badge to their GitHub repository to make their code reproducible. A call-to-action button says "Tell us your GitHub repo" with a placeholder "user/project OR github url". To the right, a note specifies that the URL should point to a Jupyter notebook named "index.ipynb".

binder

mybinder.org

Jeremy

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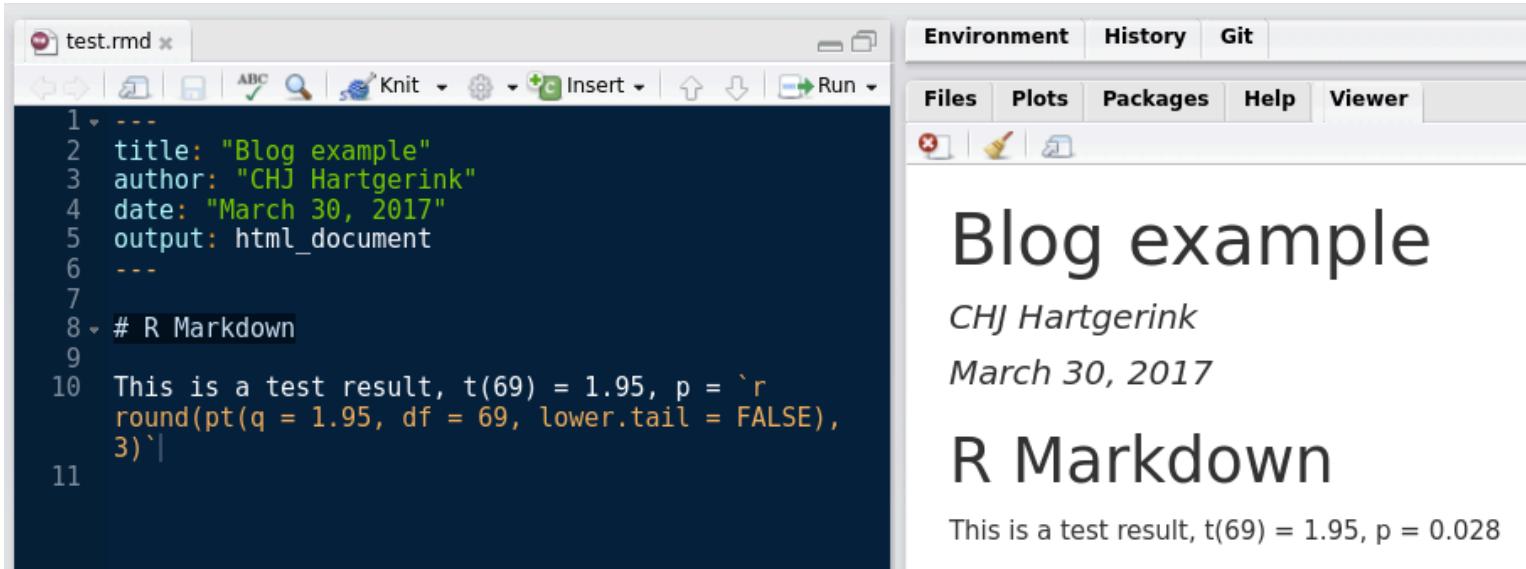
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This should contain Jupyter notebooks. If one of them is called index.ipynb it will be where your Binder starts. Any extra folders or files (e.g. data) will be included. See an [example](#) repo that uses Binder.

# 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:

```
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
```

On the right, the "Viewer" panel shows the rendered output:

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**  
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Christophe Pouzat, reviewer  
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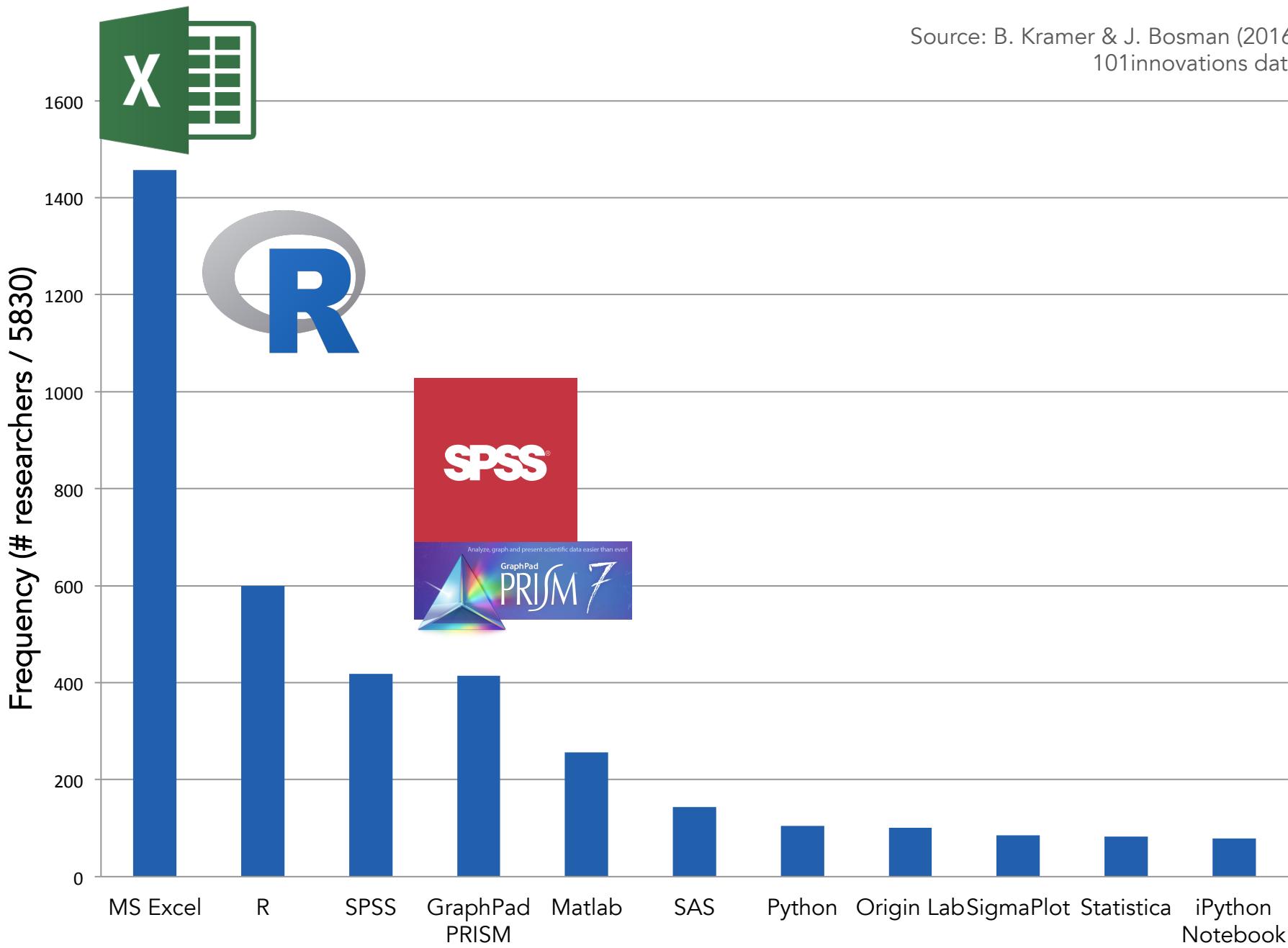


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- Static version of peer-reviewed article
- Persistence and accuracy
- Who stores? Who hosts? Who computes?
- Computational analyses and methods are not widespread



# 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