

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

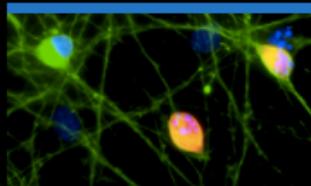
Helping scientists accelerate discovery by
operating a platform for research communication
that encourages and recognises the most
responsible behaviours in science

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

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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

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](#)[Comput](#)[Develo](#)[Ecolog](#)

A selection of recent highlights

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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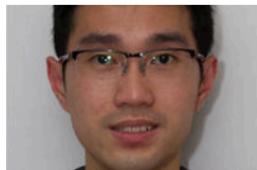
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States)



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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

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300+ Reviewing Editors

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

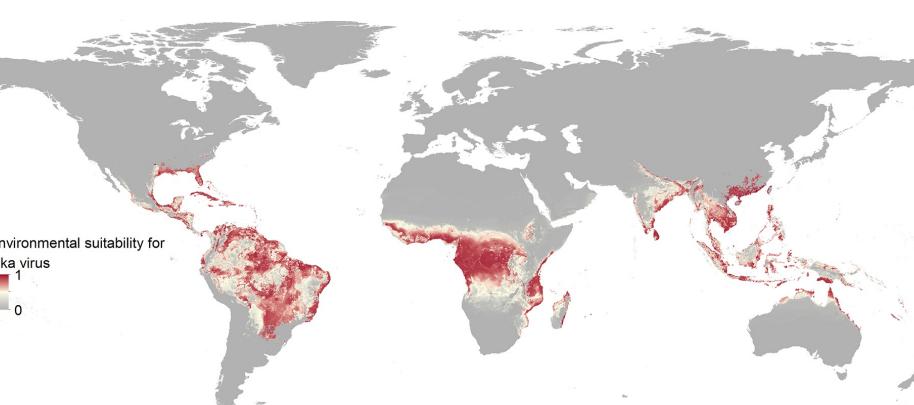
THE eLIFE EDITORIAL PROCESS

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



Intraneurial 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>

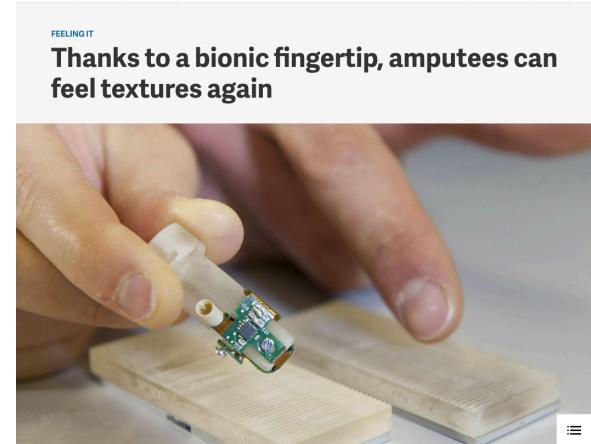
Published April 19, 2016

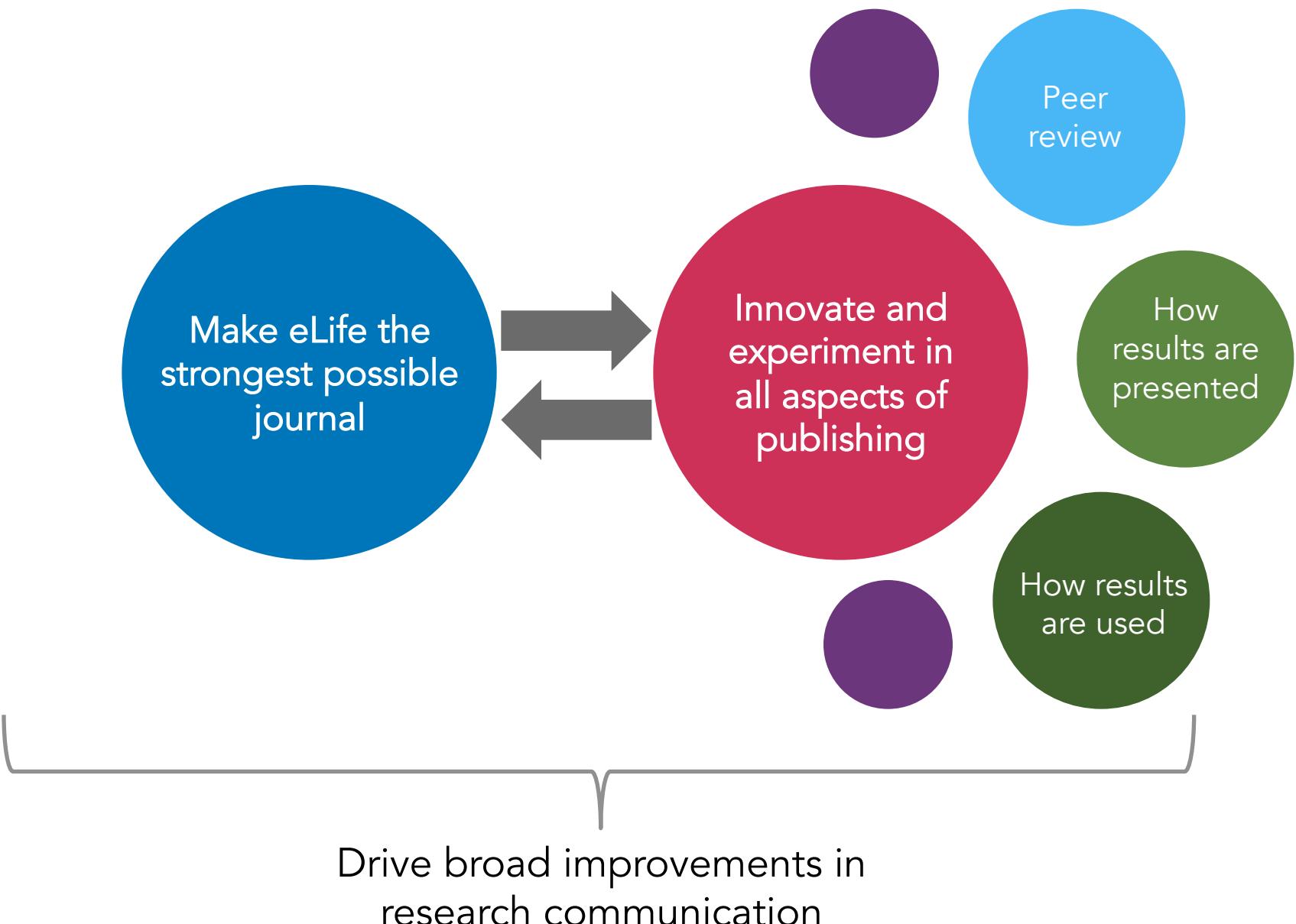
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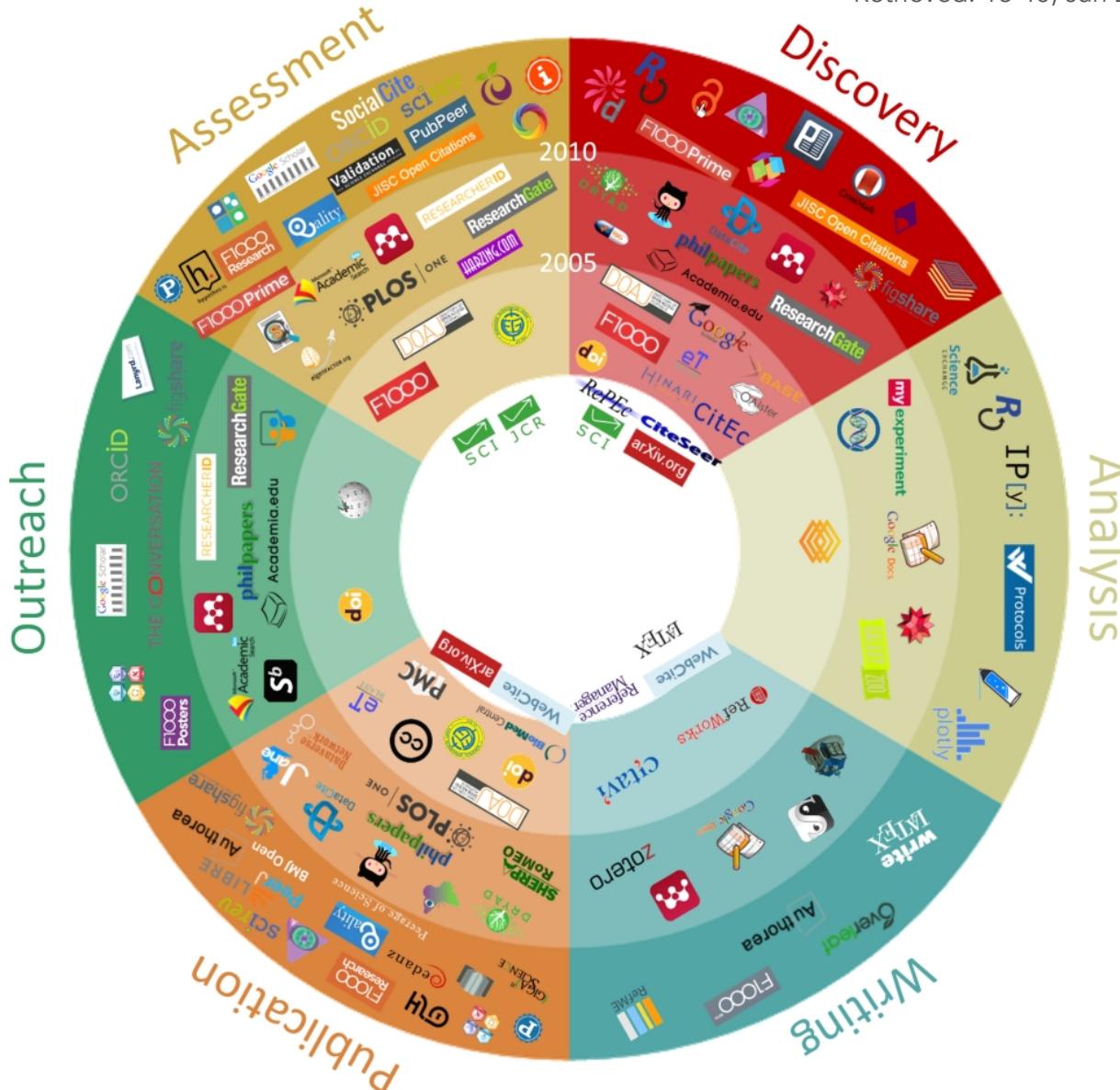


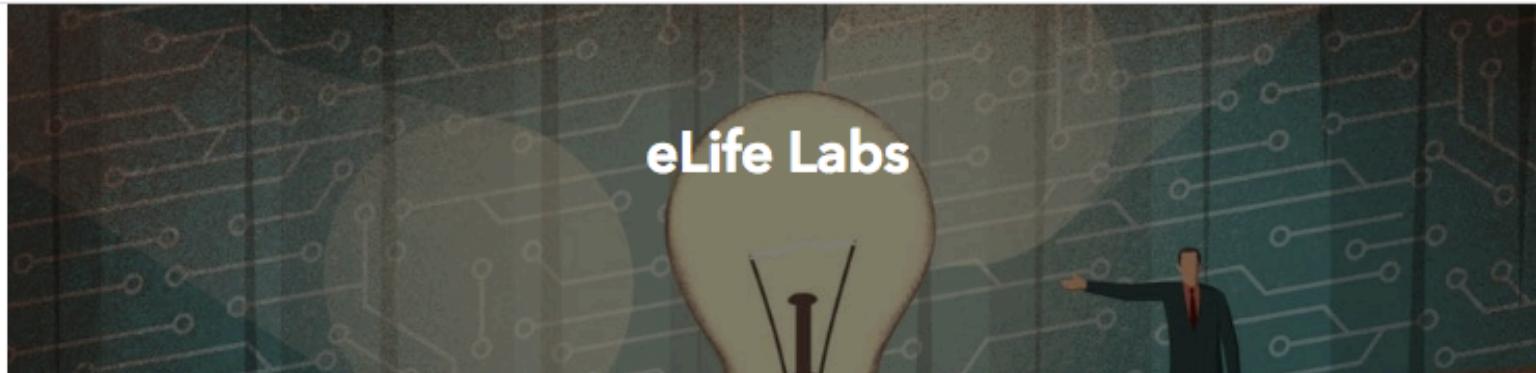


Innovation at eLife

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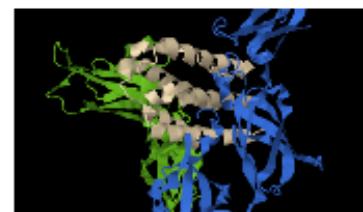
Latest



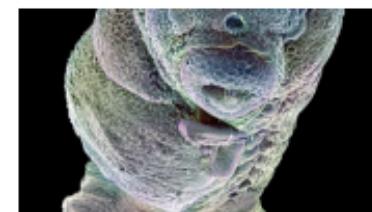
Composing reproducible manuscripts using R Markdown



Hack Cambridge Recurse entries: eXplore, Knowledge Direct, SciChat



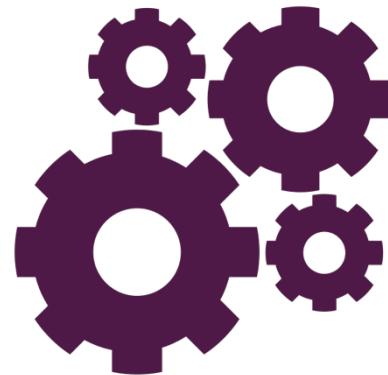
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INNOVATION & EXPERIMENTATION



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Accelerating discovery

Simplifying submission



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bit.ly/elife-author-guide

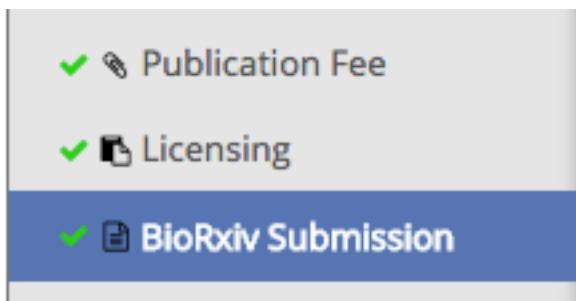


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Preprints

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

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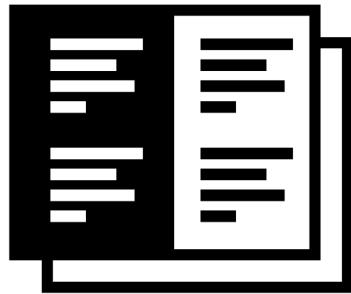


The screenshot shows a vertical list of submission steps. The first two steps, 'Publication Fee' and 'Licensing', have green checkmarks next to them. The third step, 'BioRxiv Submission', is highlighted with a blue background and also has a green checkmark. To the right of this list is a question: 'Would 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?

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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

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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

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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

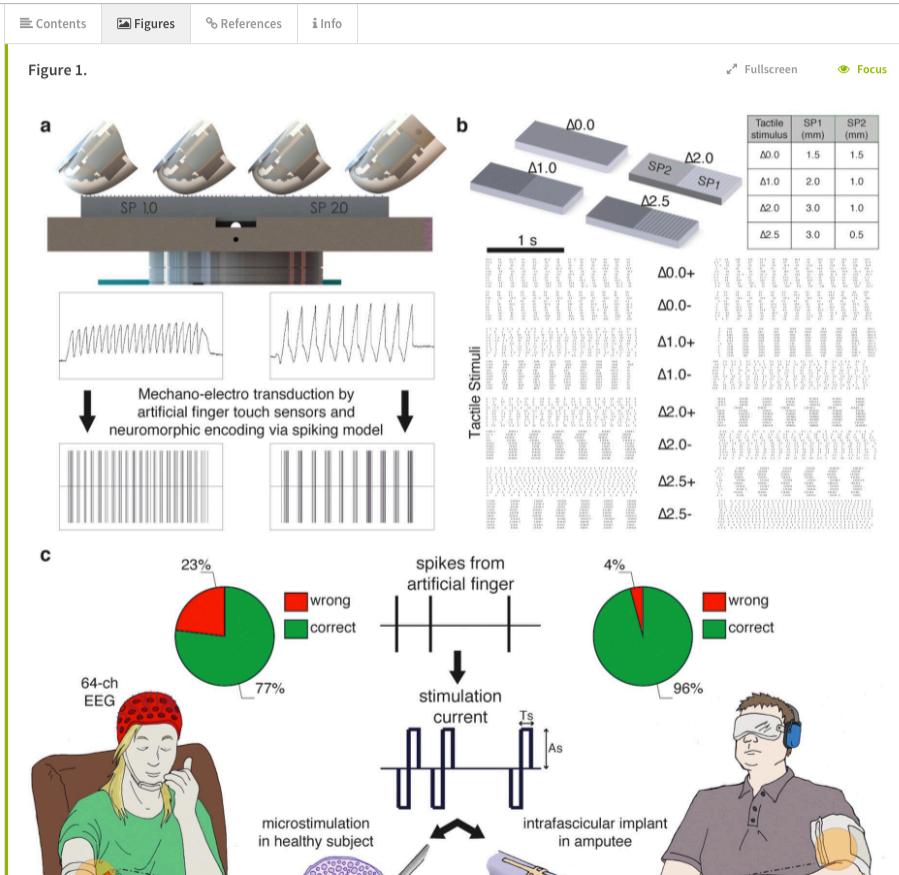
Results

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



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

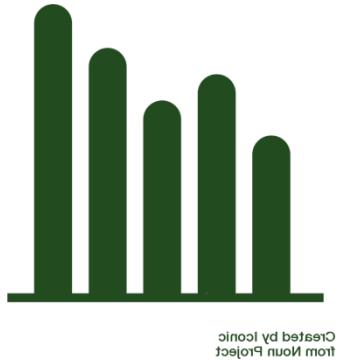
Discussion

Conclusions

Authors' contributions

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

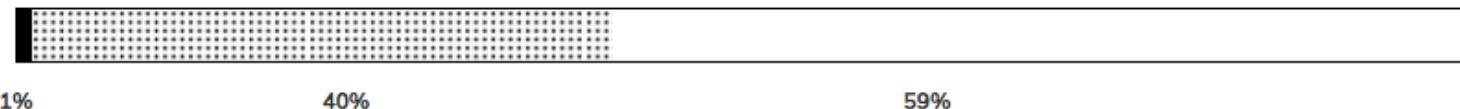
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Exposing the data behind the impact factor to highlight its limitations

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

How many citations are open today?



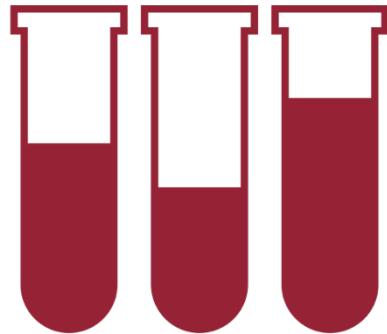
As of March 2017, the fraction of publications with open references has grown from 1% to more than 40% out of the nearly 35 million articles with references deposited with Crossref (to date).

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

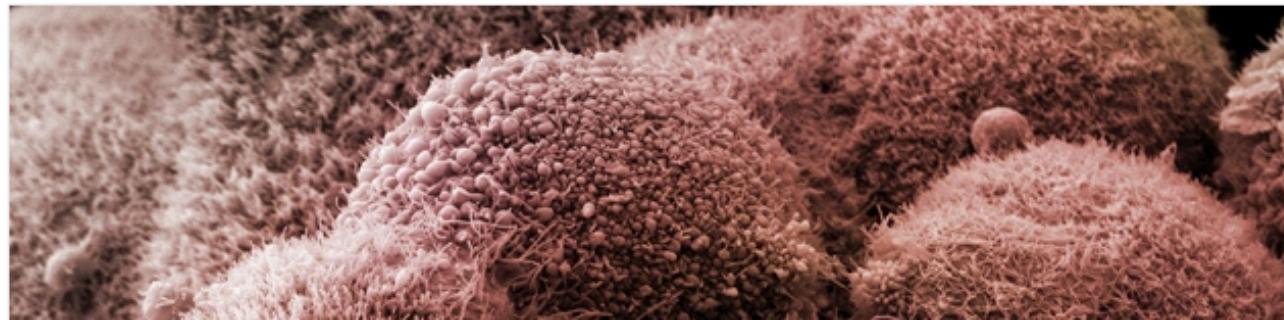
18 January 2017

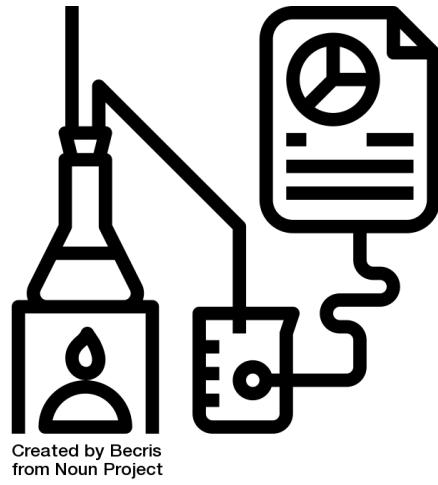


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Research reproducibility

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 ₆ -3x FLAG Tagged Proteins for Mass Spectrometry from <i>Arabidopsis</i> | Feb 2016 |
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| 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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The Evolution of Mammalian Gene Families

Jeffrey P. Dangl¹, Ido Amit^{2,3}, Juan C. Zapata^{1,4}, Natacha M. Balaton¹, Michael J. Flicek¹, and Christopher W. Ponting^{1,5}, ¹ Department of Biology and School of Biochemistry, Indiana University, Bloomington, Indiana, United States of America, ² Wellcome Trust Sanger Institute, Hinxton, United Kingdom, ³ Department of Molecular Genetics and Microbiology, Duke University, Durham, North Carolina, United States of America, ⁴ Department of Biochemistry, University of California, San Diego, California, United States of America

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 provide clues to the evolutionary forces that have shaped mammalian genomes. Here we analyze the gene families found within the entire genomes of humans, chimpanzees, mouse, rat, and dog. Our analysis shows that the rate of gene loss has been higher than the rate of gene duplication in all lineages, although some families have expanded or contracted along at least one lineage. Additionally, we find that a large number of families are completely lost along the lineage leading to modern humans. This contrasts with the retention of ~600 genes after the loss of 60 genes since the split from chimpanzee, including changes likely driven by adaptive natural selection. Our results imply that humans and chimpanzees have lost ~10% of their original gene families. The rate of gene loss has been higher in primates than in other mammals, off-setting a 1.5% difference between orthologous nucleotide sequences. This pattern "reversing" over 100 million years of evolution represents a large number of genetic differences separating humans from our closest relatives.

DOI: <https://doi.org/10.1371/journal.pbio.0040001>

Academic Editor: John Novembre, University of Chicago, United States of America

Received: October 20, 2005; Accepted: November 14, 2006; Published: December 2006

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Competing interests: The authors have declared that no competing interests exist.

* To whom reprint requests should be addressed. E-mail: jpd@indiana.edu

Published online December 2006 | DOI: <https://doi.org/10.1371/journal.pbio.0040001> | This article is available online open access at <http://www.plos.org/plosbio/0040001>

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Protocols

Super simple live flow cytometry of unicellular protists

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STEP 1 Add 1/1000 Hoechst dye (1 mL into 1 mL volume of cells). Keep cells with dye protected from light.

STEP 2 Incubate at room temperature for 10 minutes. Keep cells with dye protected from light.

STEP 3 Centrifuge cells at 1000g for 5 minutes.

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

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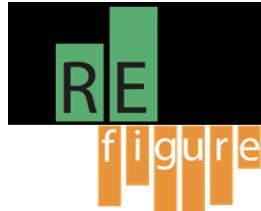


44



44

ReFigure



Figures hyperlinked to original paper

<basic navigation menu>

Report/Flag

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

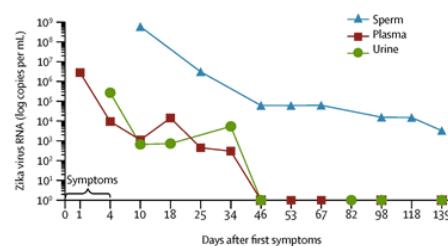
Christa Osuna

| 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;

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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^{ON} 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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Abstract

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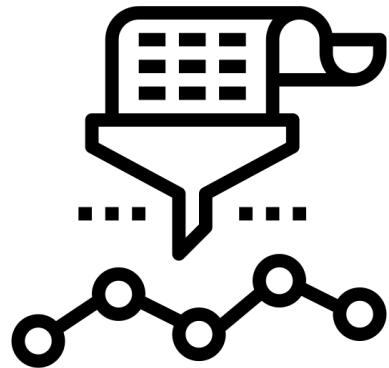
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Data-sharing

Data Availability policy, eLife author guide:

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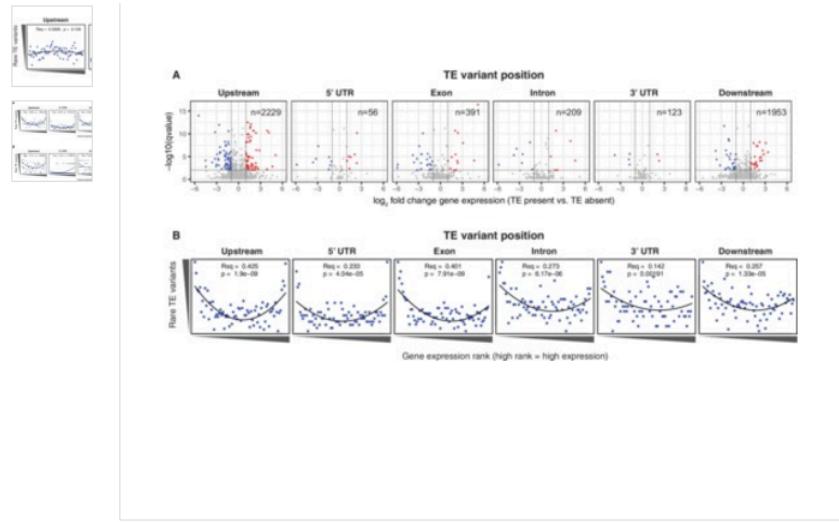


Figure 4.

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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 ± 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.

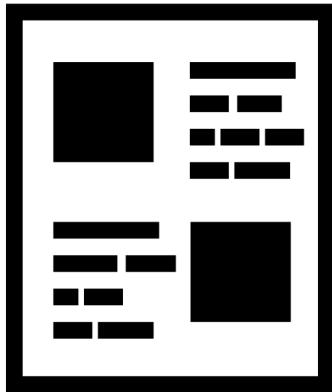
List of genes differentially expressed dependent on the presence/absence of nearby TE variants.

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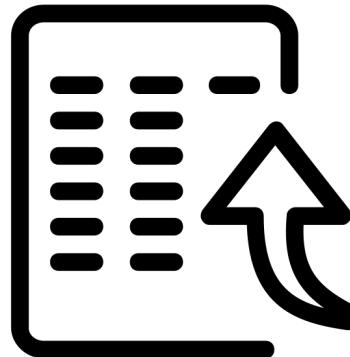
eLife 2016;5:e20777

Can we bring the data closer to the narrative?



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+



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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.

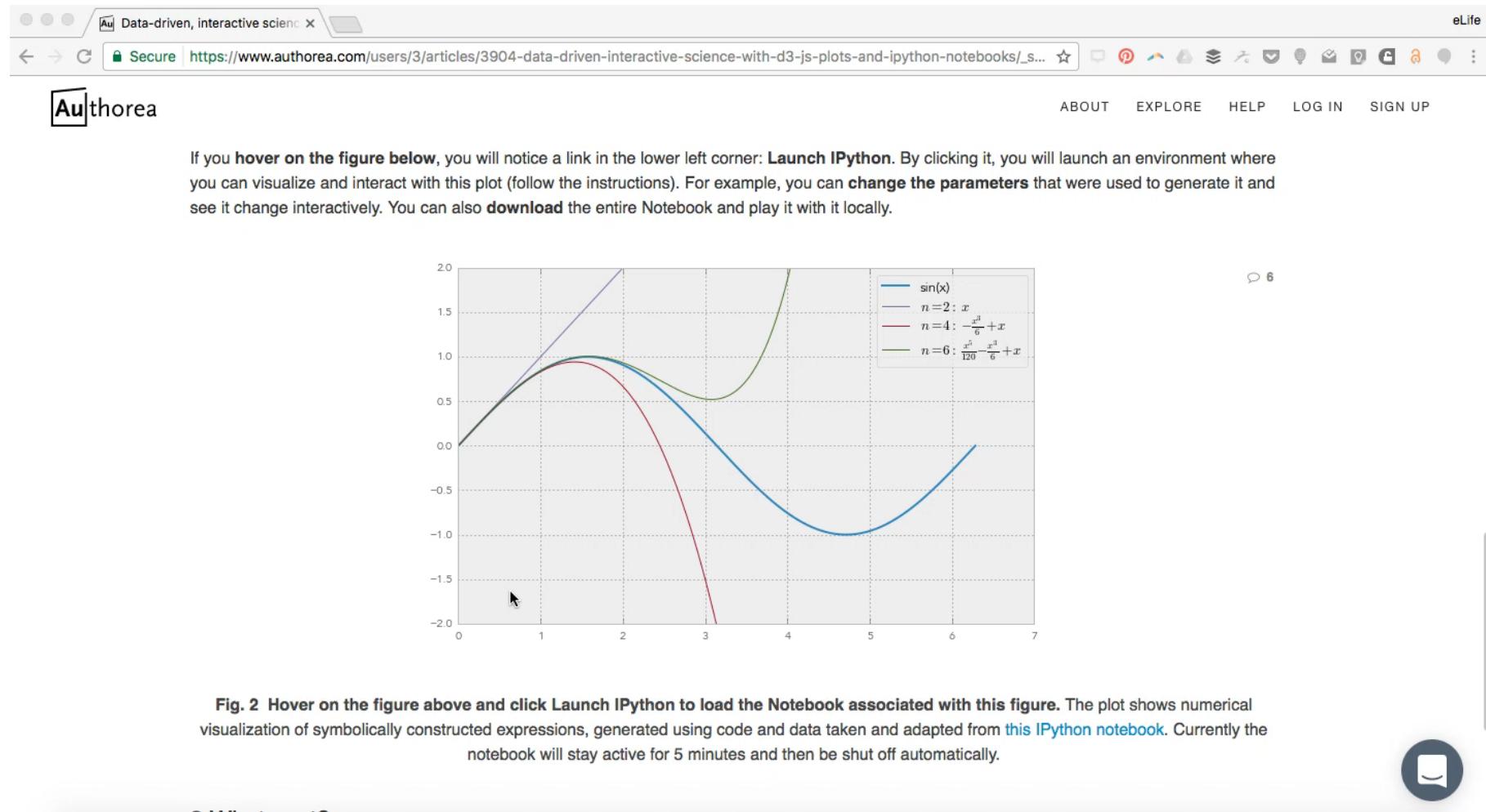
You should know that this entire visualization is running within Authorea. The Javascript, HTML, CSS and all the data associated with this image are all part of this blog post. They are individual files which can be found by clicking on the folder icon on the top left corner of this page.

(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 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

binder

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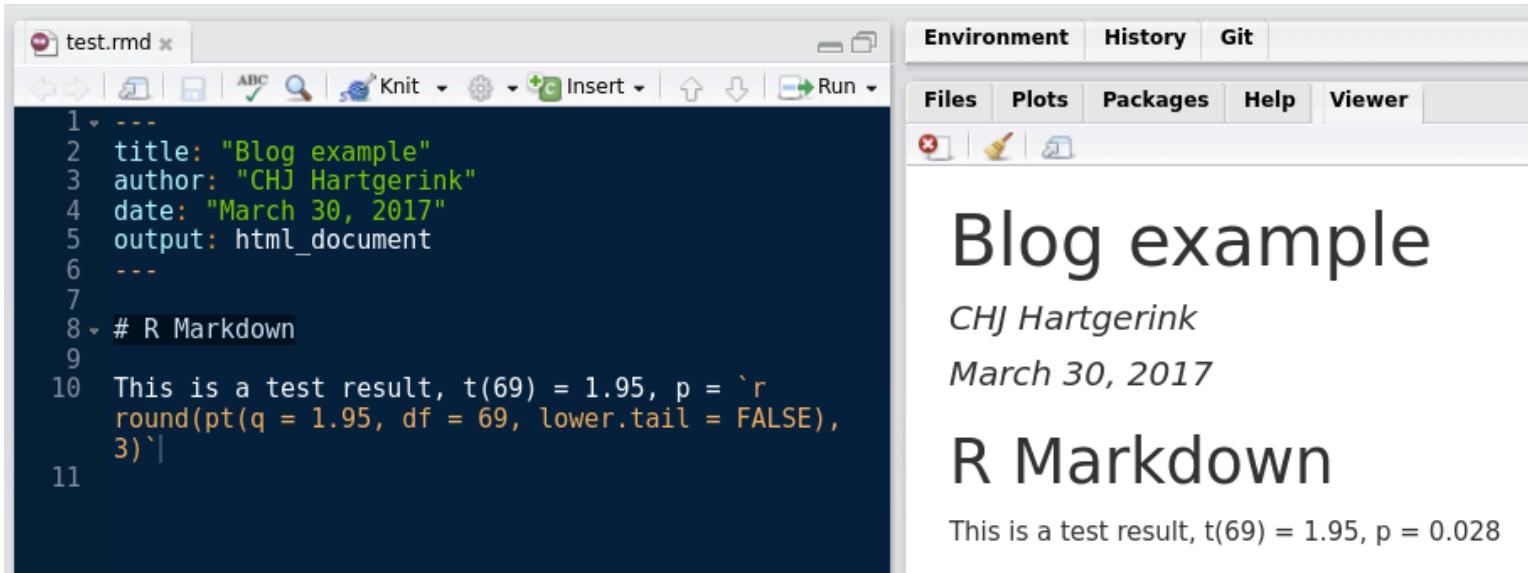
1

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:

```
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**
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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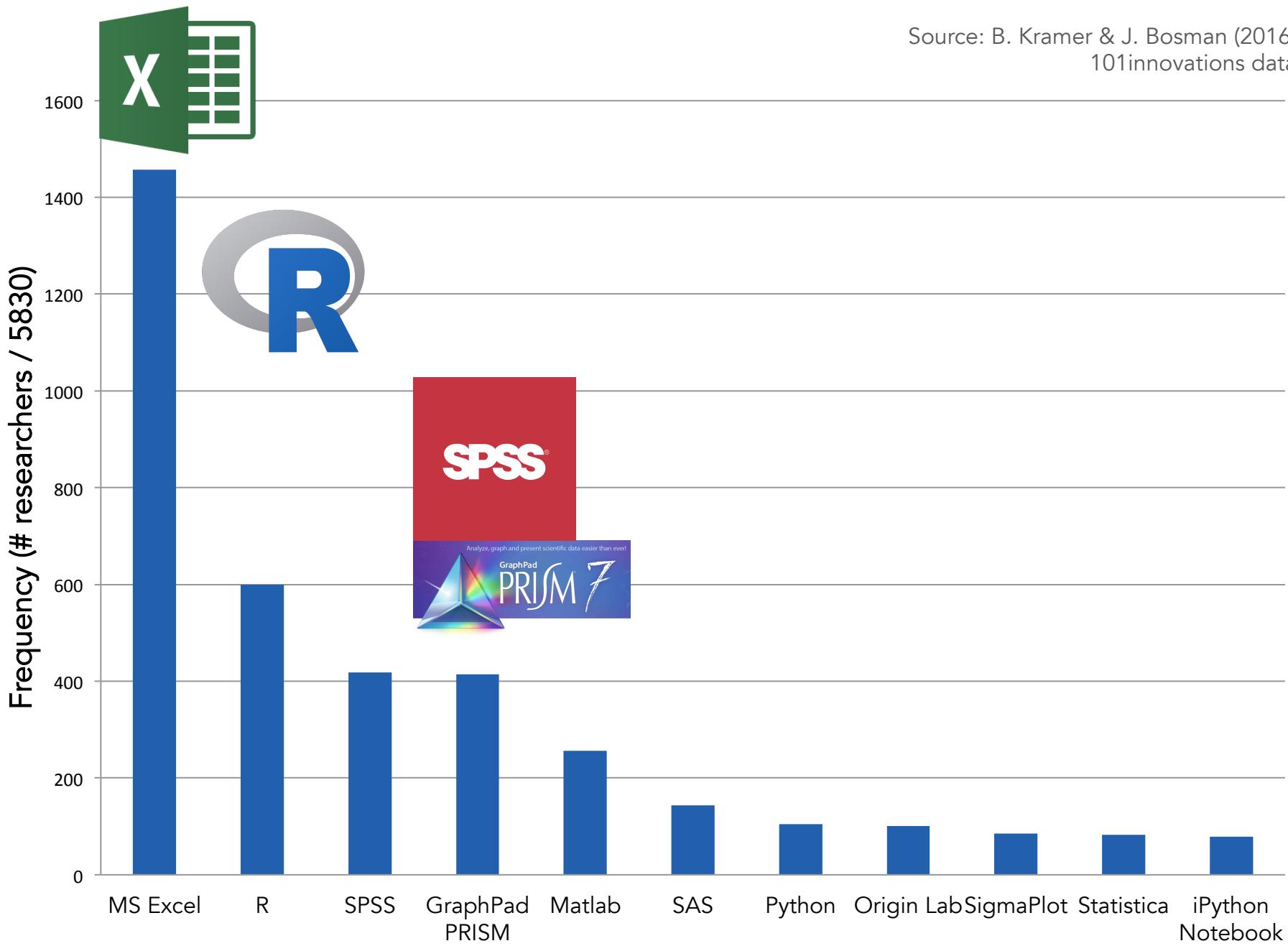


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Challenges

- 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)
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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