



PLOS

From Open Access to
Open Science : a
publisher's perspective

Véronique Kiermer
Executive Editor, PLOS
Public Library of Science

Brussels | November 2017



@verokiermer

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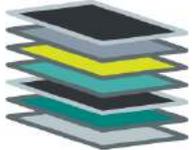
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Why PLoS Became a Publisher

Patrick O Brown, Michael B Eisen, Harold E Varmus

Published: October 13, 2003 • <https://doi.org/10.1371/journal.pbio.0000036>

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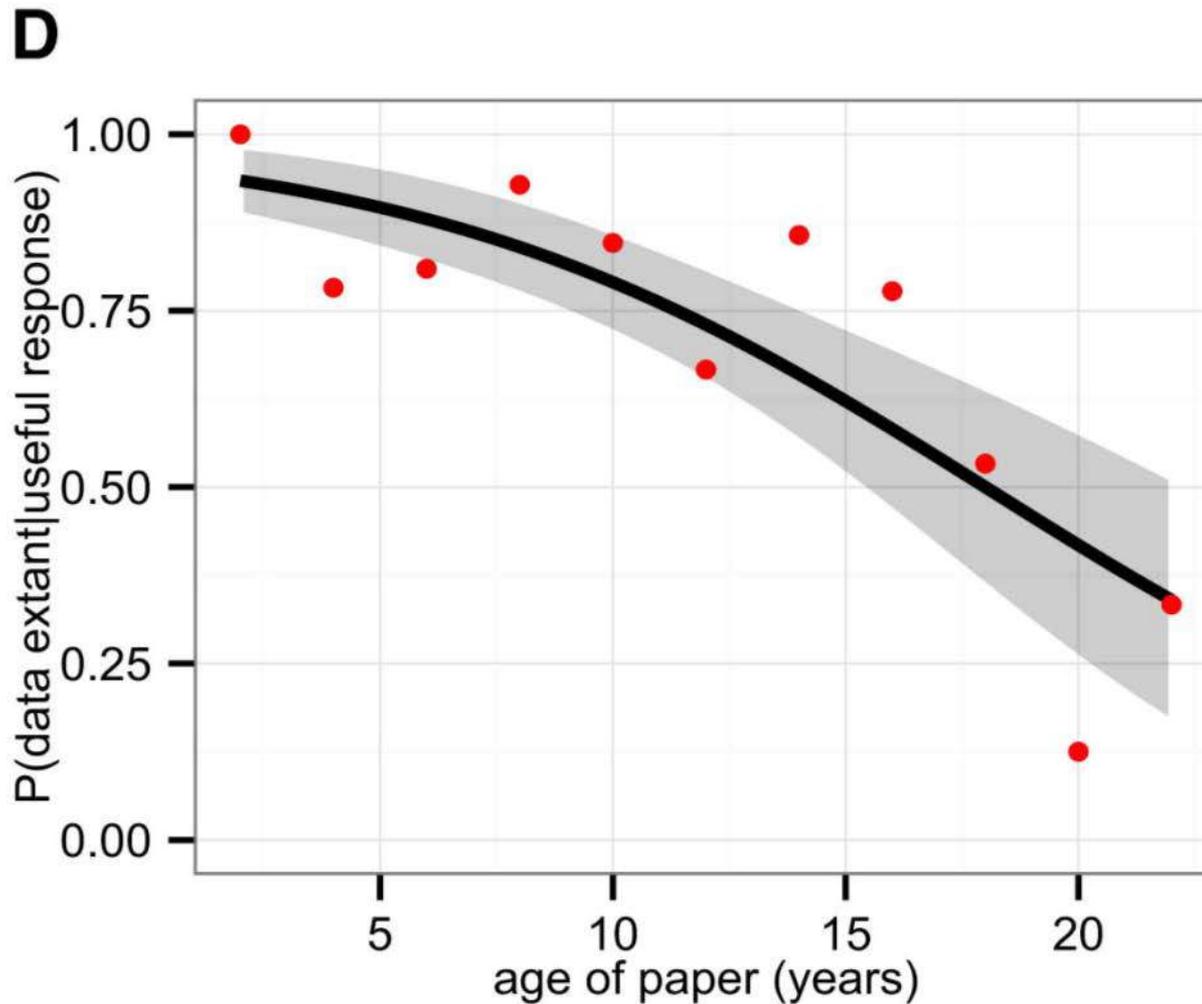
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From Open Access to Open Science

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Vines, Timothy et al. "The Availability of Research Data Declines Rapidly with Article Age." *Current Biology* 24, no. 1 (June 1, 2014): 94–97. doi:10.1016/j.cub.2013.11.014.

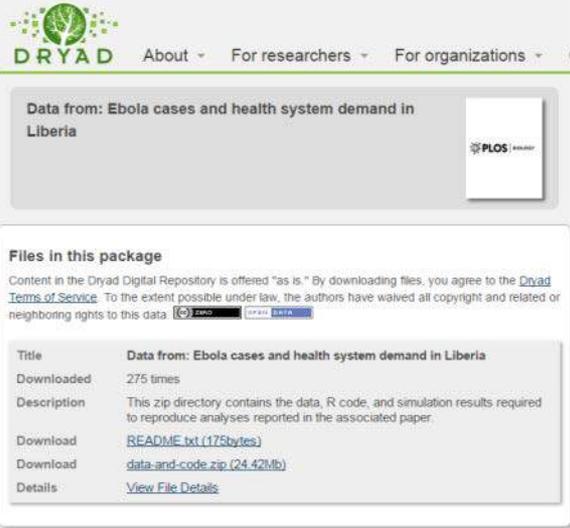
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- PLOS journals require authors to make **all data underlying the findings** described in their manuscript fully available without restriction, with rare exceptions.
- When submitting a manuscript online, authors must provide a ***Data Availability Statement*** describing compliance with PLOS's policy.

Since March 2014



PLOS data availability policy



The screenshot shows the Dryad Digital Repository interface. At the top, there is a navigation bar with the Dryad logo and links for 'About', 'For researchers', and 'For organizations'. Below this, a header section displays the title 'Data from: Ebola cases and health system demand in Liberia' and a PLOS logo. A section titled 'Files in this package' contains a disclaimer about the 'as is' nature of the data and a link to the 'Dryad Terms of Service'. Below the disclaimer, a table lists the files in the package:

Title	Data from: Ebola cases and health system demand in Liberia
Downloaded	275 times
Description	This zip directory contains the data, R code, and simulation results required to reproduce analyses reported in the associated paper.
Download	README.txt (175bytes)
Download	data-and-code.zip (24.42Mb)
Details	View File Details

Citation: Lemmon ZH, Bukowski R, Sun Q, Doebley JF (2014) The Role of *cis* Regulatory Evolution in Maize Domestication. PLoS Genet 10(11): e1004745. doi:10.1371/journal.pgen.1004745

Editor: Hunter Fraser, Stanford University, United States of America

Received: June 5, 2014; **Accepted:** September 9, 2014; **Published:** November 6, 2014

Copyright: © 2014 Lemmon et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Data Availability: The authors confirm that all data underlying the findings are fully available without restriction. The raw sequence data has been deposited in NCBI Sequence Read Archive with accessions SRX710894-711341 and the Gene Expression Omnibus (GEO) Series with accession number GSE61810 (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE61810>). Supplemental datasets have been made available from the Dryad Digital Repository: <http://dx.doi.org/10.5061/dryad.4kh67>.

Data Availability Statements openly available, and machine-readable as part of the PLOS search API

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

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Open methods: partnerships between journals and protocols platforms

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The Evolution of Mammalian Gene Families

Jeffrey P. Demuth¹, Tjiu De Baat², Avron E. Slijkhuis³, Nello Cristianini⁴, Matthew W. Hahn⁵

1 Department of Biology and School of Informatics, Indiana University, Bloomington, Indiana, United States of America, **2** School of Electronics and Computer Science, SO Group, University of Southampton, Southampton, United Kingdom, **3** Department of Molecular Genetics and Microbiology, Duke University, Durham, North Carolina, United States of America, **4** Department of Statistics, University of California Davis, Davis, 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 may provide clues to the evolutionary forces that have shaped mammalian genomes. Here we analyze the gene families contained within the whole genomes of human, chimpanzee, mouse, rat, and dog. In total we find that more than half of the 3,999 families present in the mammalian common ancestor have either expanded or contracted along at least one lineage. Additionally, we find that a large number of families are completely lost from one or more mammalian genomes, and a similar number of gene families have arisen subsequent to the mammalian common ancestor. Along the lineage leading to modern humans we infer the gain of 609 genes and the loss of 66 genes since the split from chimpanzees, including changes likely driven by adaptive natural selection. Our results imply that humans and chimpanzees differ by at least 4% (1,418 of 22,000 genes) in their complement of genes, which stands in stark contrast to the predicted 1.5% difference between orthologous nucleotide sequences. This genomic “revolving door” of gene gain and loss represents a large number of genetic differences separating humans from our closest relatives.

Citation: Demuth JP, De Baat T, Slijkhuis AE, Cristianini N, Hahn MW (2006) The Evolution of Mammalian Gene Families. *PLoS ONE* 1(1): e88. doi:10.1371/journal.pone.0005091

INTRODUCTION

Exploring the obvious morphological, physiological, and behavioral traits that separate rodents from their closest relatives, the chimpanzees, is challenging given the low level of nucleotide divergence between the two species [1]. More than 30 years have passed since King and Wilson first pointed out this apparent paradox, noting that “the genetic distance between humans and the chimpanzee is probably too small to account for their substantial organismal differences” [2]. To explain the paradox, King and Wilson proposed that regulatory changes rather than protein-coding mutations were responsible for the vast majority of observed biological differences [2]. Evidence gathered since that time demonstrates that amino acid (Aa), ribonucleic acid (RNA), and regulatory sequence (RS) changes have been involved in the evolution of uniquely human phenotypes.

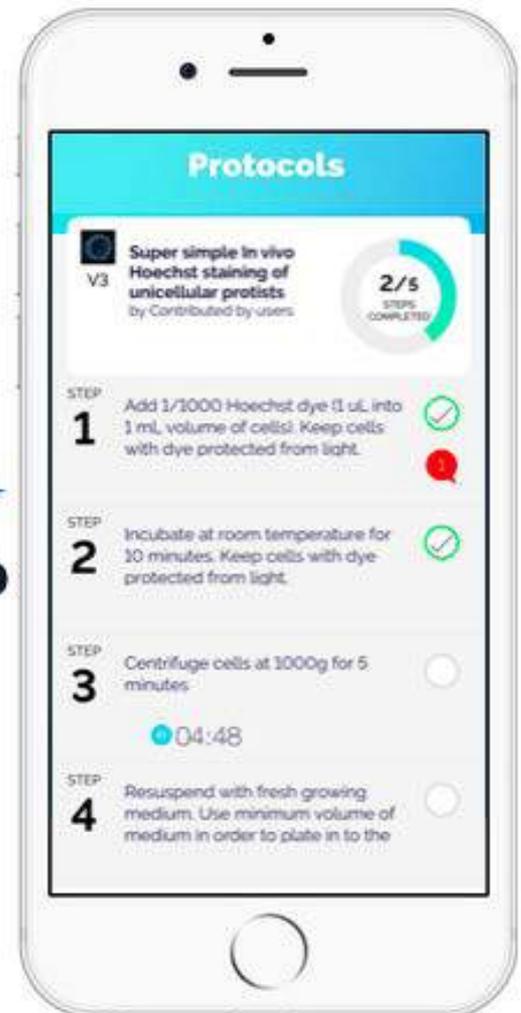
A third source of differentiation, recently mentioned in conjunction with orthologous sequences, is the differential duplication and deletion of chromosomal regions [3]. Among human segmental duplications larger than 20 kilobases, 31% are not present in chimpanzee [3]. In total, it is estimated that at least 2.7% of the total genome has been uniquely duplicated subsequent to the human-chimpanzee split [3]. This number does not take

repeat data to have been 1,188 new gene duplications in the human genome since our split with chimpanzee (3,909 duplications/gene/100 * 22,000 genes * 6.1%). Assuming equal numbers of gene gains and losses and similar rates of turnover in changes, the total number of genes in humans not present in chimps would be 2.7% (or ~11% of all genes). This estimate of total gene divergence implied by rates of gene duplication has been widely overlooked due to the previous emphasis on nucleotide divergence between orthologous genes. Although this hypothesis creates identical rates of gene gain and loss, our course calculations have not considered that new gene duplications are also the most likely genes to be lost, the consistency of gene number among fully sequenced mammals suggests that this is not an extreme assumption across short evolutionary time periods.

Academic Editor: Justin Benowitz, University of Chicago, United States of America

Received: October 25, 2005 **Accepted:** November 14, 2005 **Published:** December 20, 2005

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Materials and methods

Methods and protocols for *Drosophila* rearing, media preparations, and microbial manipulations are available as a collection in protocols.io dx.doi.org/10.17504/protocols.io.hdtb26n.

PLOS

CodeOcean

Validation of functional calibration and strap-down joint drift correction for computing 3D joint angles of knee, hip, and trunk in alpine skiing

Benedikt Fasel¹, Jörg Spill^{2*}, Pascal Schütz³, Silvio Lorenzetti⁴, Kamler Antonia^{5*}

Abstract

To obtain valid 3D joint angles with inertial sensors careful sensor-to-segment calibration (i.e. functional or anatomical calibration) is required and measured angular velocity at each sensor needs to be integrated to obtain segment and joint orientation (i.e. joint angles). Existing functional and anatomical calibration procedures were optimized for gait analysis and calibration movements were impractical to perform in outdoor settings. Thus, the aims of this study were 1) to propose and validate a set of calibration movements that were optimized for alpine skiing and could be performed outdoors and 2) to validate the 3D joint angles of the knee, hip, and trunk during alpine skiing. The proposed functional calibration movements consisted of squats, trunk rotations, hip abductions, and upright standing. The joint drift correction previously proposed for alpine ski racing was improved by adding a second step to reduce necessary azimuth drift. The system was validated by adding a second step at the maximum bat speed of 21 km/h and for measurement durations of 120 seconds. Calibration repeatability was on average $\pm 2.7^\circ$ (i.e. 3D joint angles changed on average $\pm 2.7^\circ$ for two repeated sets of calibration movements) and all movements could be executed wearing ski boots. Joint angle precision was $\pm 1.9^\circ$ for all angles and accuracy ranged from -0.7° to 4.2° where the presence of an athlete-specific bias was observed especially for the flexion angle. The improved joint drift correction reduced azimuth drift from over 25° to less than 5° . In conclusion, the system was valid for measuring 3D joint angles during alpine skiing and could be used outdoors. Errors were similar to the values reported in other studies for gait. The system may be well suited for within-athlete analysis but care should be taken for between-athlete analysis because of a possible athlete-specific joint angle bias.

STORY

PLOS ONE | <https://doi.org/10.1371/journal.pone.0181446> July 28, 2017

CODE OCEAN

Functional calibration for trunk and lower limb inertial sensors

Inertial Sensor Functional Calibration

Here you can find the code to functionally align inertial sensors to their respective segments. The set of calibration movements to perform along with illustrative videos can be found under the DOI: 10.1371/journal.pone.0181446. The functional calibration has been further described and validated in the article Fasel B, Spill J, Schütz P, Lorenzetti S, Antonia K (2017) Validation of functional calibration and strap-down joint drift correction for computing 3D joint angles of knee, hip, and trunk in alpine skiing. PLOS ONE, DOI:10.1371/journal.pone.0181446.

Note that the calibration movements have been initially proposed for in-field motion capture of alpine ski racing. However, the functional calibration can also be applied to any other domain as long as the person is able to well perform the required calibration movements.

Structure

Data

The inertial data of all sensors is stored in `data\swissdata.mat`. The data is

Executable Code

protocols.io

Home > researchers > Benedikt Fasel > Functional calibration for trunk and lower limb inertial sensors

VIEWING PROTOCOL

Steps

- 1 Squats with rolling spine
Roll squats with rolling spine. Roll back feet. Before you can roll to the right, perform the flexion movements until the pelvis reaches the ankles. Perform this movement three times.
- 2 Trunk rotations

Video Protocol

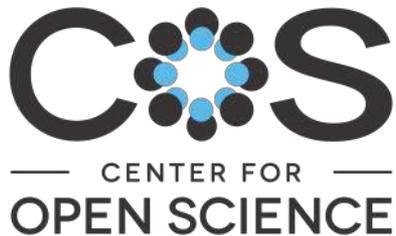
Protocols.io



Credit: Lenny Teytelman, protocols.io

Benedikt Fasel et al., 2017, PLOS ONE DOI: [10.1371/journal.pone.0181446](https://doi.org/10.1371/journal.pone.0181446)

Registered Reports: an open process

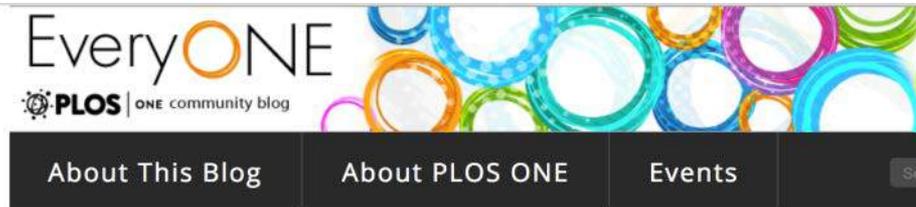


79 journals have adopted Registered Reports

<https://cos.io/rr/>

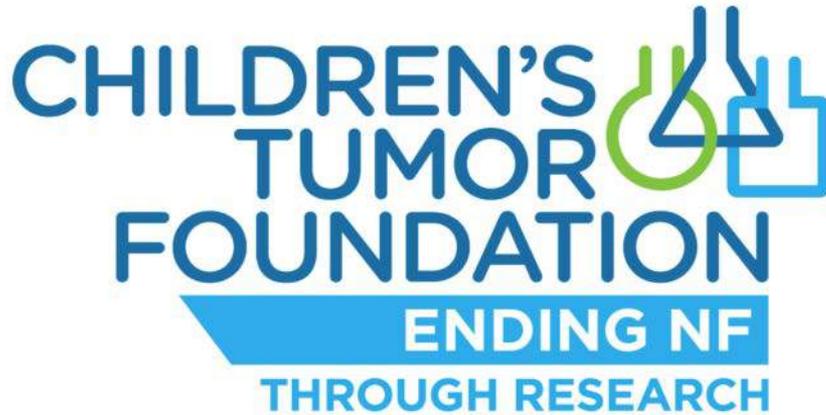


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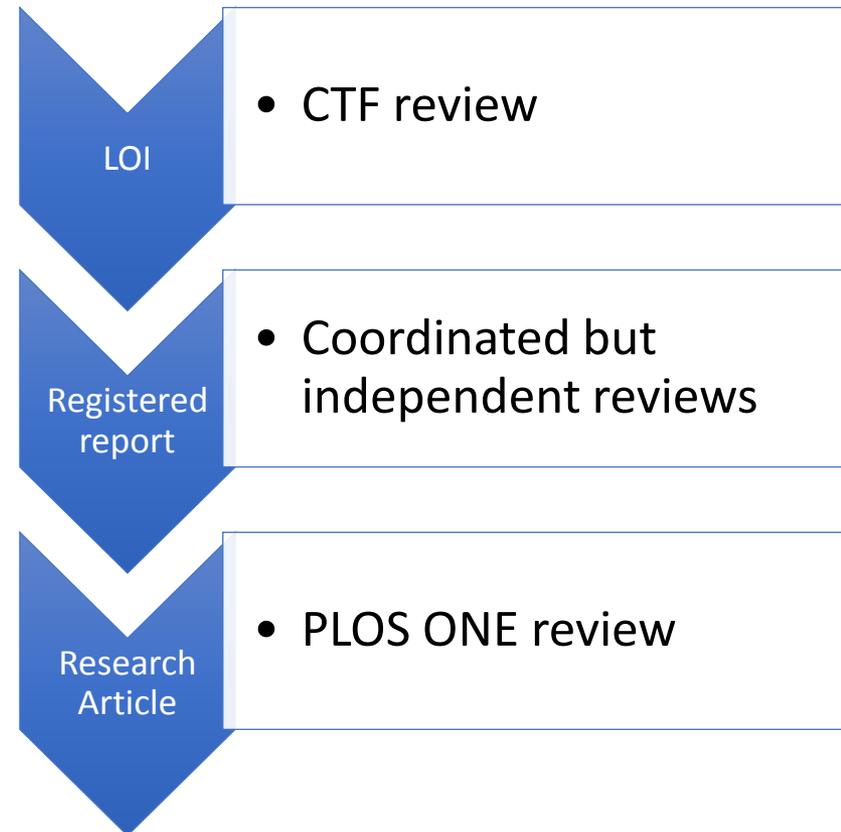
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PLOS ONE partners with the Children's Tumor Foundation to trial Registered Reports

Posted September 26, 2017 by PLOS ONE Editors in Editorial and Publishing Policy & News



Publication bias



The literature is not an accurate record of the universe of results obtained in laboratories worldwide but a skewed version of reality

For Open Science to succeed it must be rewarded

Rewarding research data sharing is essential. Researchers who make research data open and FAIR for reuse and/or reuse and reproduce data should be rewarded, both in their career assessment and in the evaluation of projects (...). This should go hand in hand with other career policies and research institutions.

European Open Science Cloud Declaration, Oct 2017

The Metric Tide

Report of the Independent Review
of the Role of Metrics in Research
Assessment and Management

July 2015



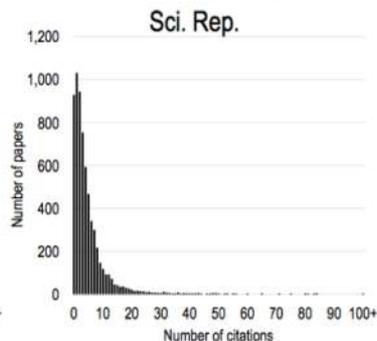
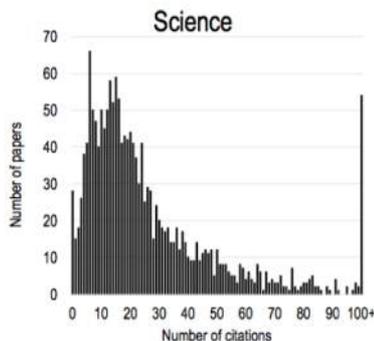
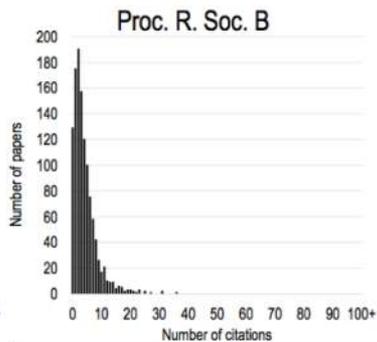
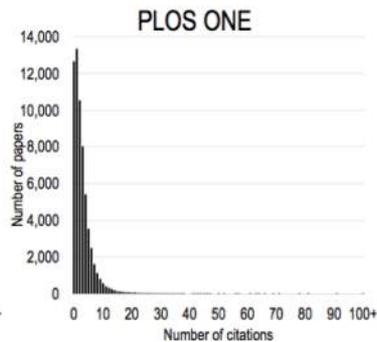
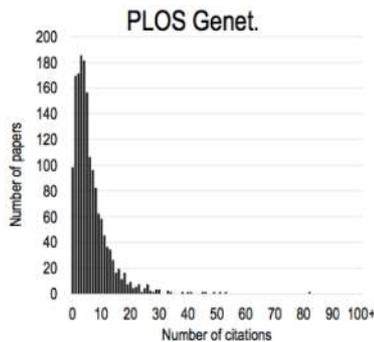
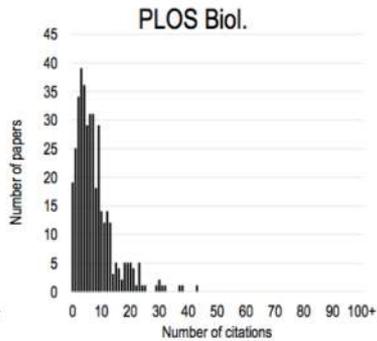
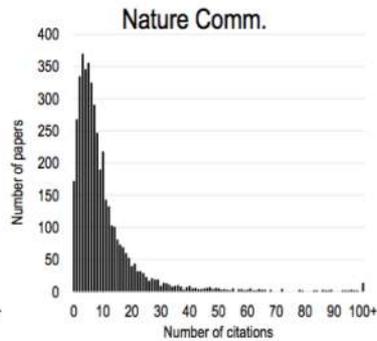
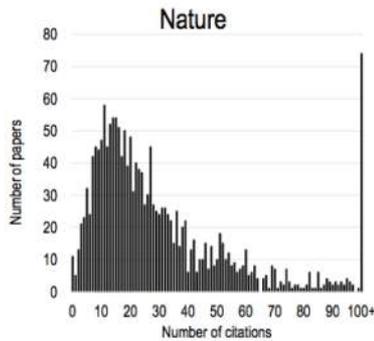
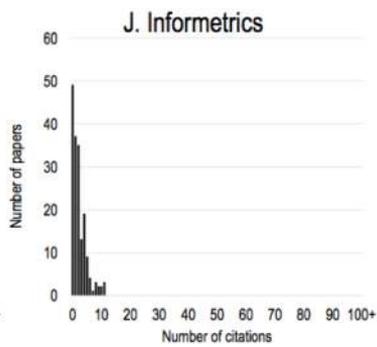
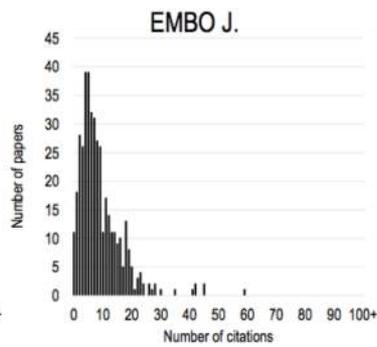
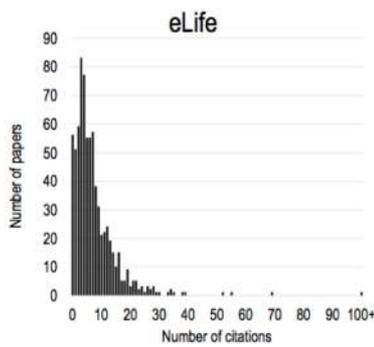
DOI: 10.13140/RG.2.1.4929.13



San Francisco Declaration on Research Assessment

Identifies needs:

- To **eliminate the use of journal-based metrics**, such as Journal Impact Factors, in funding, appointment and promotion considerations;
- To assess research on **its own merit** rather than on the basis of the journal in which the research is published;
- To capitalize on the **opportunities of online publication**.



“The co-option of **Journal Impact Factors** as a tool for assessing individual articles and their authors, a task for which they were never intended, is a deeply embedded problem within academia and one that has no easy solutions.”

Lariviere et al., 2016
 bioRxiv DOI: 10.1101/062109



“As competition for jobs and promotions increases, the inflated value given to publishing in a small number of so-called “high impact” journals has put pressure on authors to rush into print, cut corners, exaggerate their findings, and overstate the significance of their work.

Such publication practices, abetted by the hypercompetitive grant system and job market, are changing the atmosphere in many laboratories in disturbing ways.”

Rescuing US biomedical research from its systemic flaws

Bruce Alberts , Marc W. Kirschner , Shirley Tilghman, and Harold Varmus

PNAS | April 22, 2014 | vol. 111 | no. 16 | 5773–5777

doi: 10.1073/pnas.1404402111



PERSPECTIVE

Current Incentives for Scientists Lead to Underpowered Studies with Erroneous Conclusions

Andrew D. Higginson^{1*}, Marcus R. Munafò^{2,3*}

1 Centre for Research in Animal Behaviour, College of Life and Environmental Sciences, University of Exeter, Exeter, United Kingdom, **2** MRC Integrative Epidemiology Unit (IEU) at the University of Bristol, Bristol, United Kingdom, **3** UK Centre for Tobacco and Alcohol Studies, School of Experimental Psychology, University of Bristol, Bristol, United Kingdom

“Given finite resources, the importance placed on novel findings, and the emphasis on a relatively small number of publications, scientists wishing to accelerate their career progression should conduct a large number of exploratory studies, each of which will have low statistical power.”

Multiple stakeholders



Each major stakeholder can:

- Facilitate
- Encourage
- Develop incentives

Publishers must facilitate precise credit



Role of journals PLOS Article-Level Metric

- Views
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- Discussions
- Recommendations



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RESEARCH ARTICLE

An Economic Geography of the United States: From Commutes to Megaregions

Garrett Dash Nelson , Alasdair Rae

Published: November 30, 2016 • <http://dx.doi.org/10.1371/journal.pone.0166083>

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RESEARCH ARTICLE

Smek promotes corticogenesis through regulating Mbd3's stability and Mbd3/NuRD complex recruitment to genes associated with neurogenesis

Byoung-San Moon, Hyung-Mun Yun, Wen-Hsuan Chang, Bradford H. Steele, Mingyang Cai, Si Ho Choi, **Wange Lu**

Published: May 3, 2017 • <https://doi.org/10.1371/journal.pbio.1005381>

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Roles: Conceptualization, Funding acquisition, Project administration, Supervision, Writing – review & editing

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Affiliation: Broad Center for Regenerative Medicine and Stem Cell Research, Department of Stem Cell Biology and Regenerative Medicine, Keck School of Medicine, University of Southern California, Los Angeles, California, United States of America

<http://orcid.org/0000-0001-5848-3189>

- Abstract**
- Author summary
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- Results
- Discussion
- Materials and methods

Abstract

The fact that the Mbd3/NuRD complex completely methylates CpG islands and neuronal differentiation of NPCs, we found that Smek promotes Mbd3 polyubiquitination and

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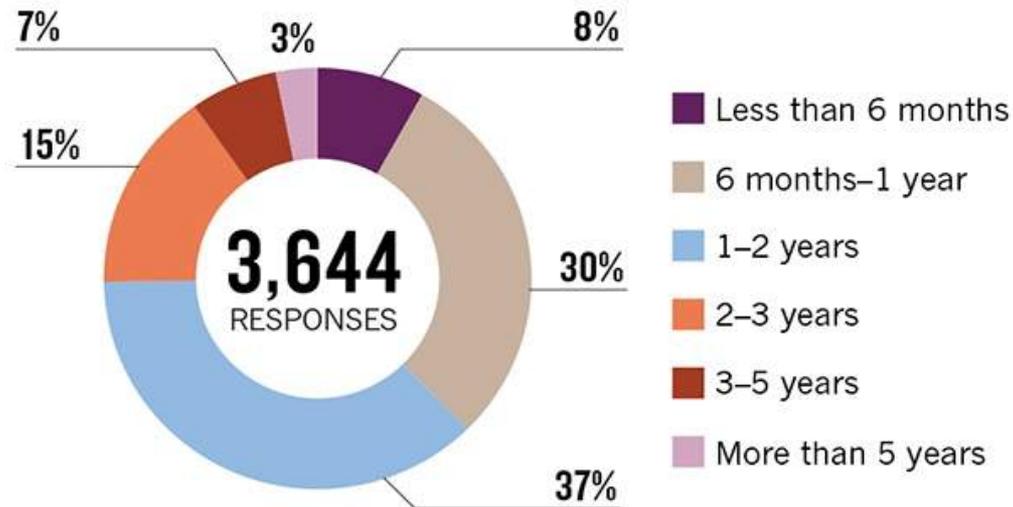
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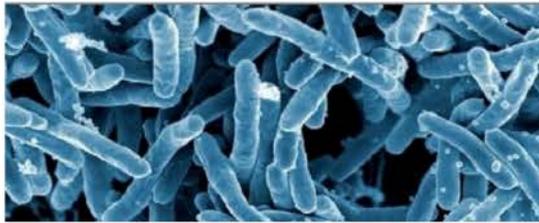
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Open in action

In public health emergencies:

- Release of data before publication
- Encourage deposition of manuscripts on preprint server

Accelerate dissemination of critical knowledge.

The screenshot shows the PLOS Collections website interface. At the top, there are links for 'plos.org', 'create account', and 'sign in'. Below this is a navigation bar with 'About', 'Browse', and a search box. The main content area features a large image of a mosquito on human skin, with a text box on the left titled 'Zika'. The text in the box reads: 'Zika is an arbovirus infection transmitted by several different species of Aedes mosquitoes, including Aedes aegypti in the New World. Towards the end of 2015, the Pan American Health Organization announced a possible link between zika and congenital birth defects, in particularly a neurodevastating birth defect known as microcephaly. The causal link between zika and ...'. Below the text is a 'More >' link. At the bottom of the screenshot, the bioRxiv logo is displayed, with the text 'bioRxiv beta THE PREPRINT SERVER FOR BIOLOGY'. Below the logo is a search bar with the text 'Search' and a magnifying glass icon, and a link to 'Advanced Search'.



Insect Armageddon

By THE EDITORIAL BOARD OCT. 29, 2017



Roman Muradov

There is alarming new [evidence](#) that insect populations worldwide are in rapid decline. As Prof. [Dave Goulson](#) of the University of Sussex, a co-author of a new insect study, [put it](#), we are “on course for ecological Armageddon” because “if we lose the insects, then everything is going to collapse.”



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OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

More than 75 percent decline over 27 years in total flying insect biomass in protected areas

Caspar A. Hallmann , Martin Sorg, Eelke Jongejans, Henk Siepel, Nick Hofland, Heinz Schwan, Werner Stenmans, Andreas Müller, Hubert Sumser, Thomas Hörrn, Dave Goulson, Hans de Kroon

Published: October 18, 2017 • <https://doi.org/10.1371/journal.pone.0185809>

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Abstract

Global declines in insects have sparked wide interest among scientists, politicians, and the general public. Loss of insect diversity and abundance is expected to provoke cascading effects on food webs and to jeopardize ecosystem services. Our understanding of the extent and underlying causes of this decline is based on the abundance of single species or taxonomic groups only, rather than changes in insect biomass which is more relevant for ecological

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Abstract

Introduction

Materials and methods

Results

Discussion

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Acknowledgments

References

Reader Comments (4)

Media Coverage (10)

Figures

S1 Appendix. Malaise trap permissions.

<https://doi.org/10.1371/journal.pone.0185809.s001>
(PDF)



permits

S2 Appendix. Malaise traps.

<https://doi.org/10.1371/journal.pone.0185809.s002>
(PDF)

S1 Code.

<https://doi.org/10.1371/journal.pone.0185809.s003>
(PDF)



code

S1 Dataset.

<https://doi.org/10.1371/journal.pone.0185809.s004>
(CSV)



data

S2 Dataset.

<https://doi.org/10.1371/journal.pone.0185809.s005>
(CSV)



S1 Fig. Map of study area.

Insect trap locations (yellow points) in Nordrhein-Westfalen (n = 57), Rheinland-Pfalz (n = 1) and Brandenburg (n = 5), as well as weather stations (crosses) used in the present analysis.

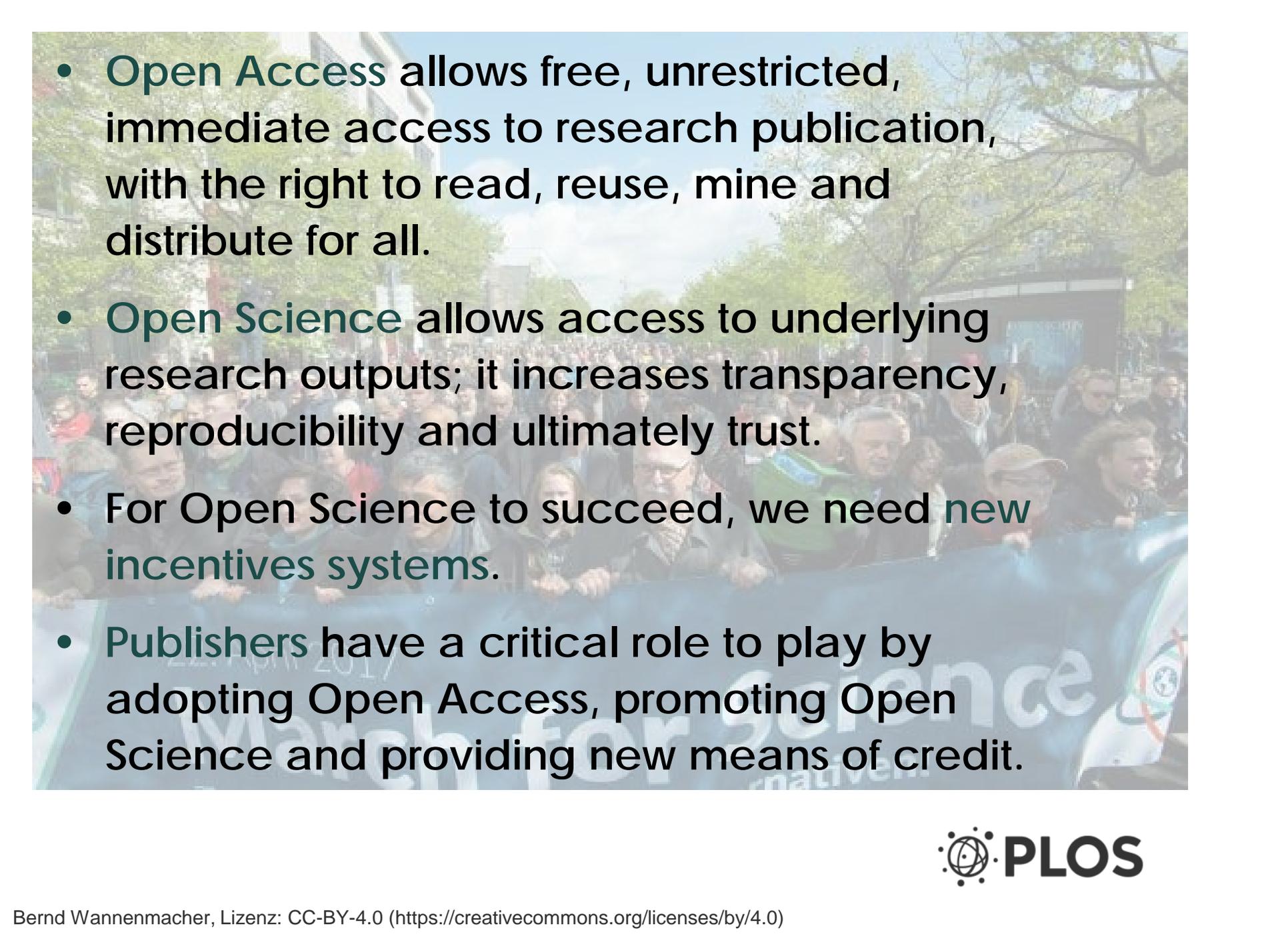
<https://doi.org/10.1371/journal.pone.0185809.s006>
(TIFF)

S2 Fig. Temporal variation in weather variables.

Annual means (A-C), daily means (D-F), and mean daily residual values (G-I) of temperature, precipitation and wind speed respectively. In all panels, black lines depict data while blue and red lines represent long term and seasonal fitted means of the variables, respectively.

<https://doi.org/10.1371/journal.pone.0185809.s007>
(PDF)



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