Evolutionary Genetics

LV 25600-01 | Lecture with exercises | 4KP

Reproducible Research

Jean-Claude Walser
jean-claude.walser [at] env.ethz.ch

HS2024

14°

Blick

Erfundene Tierversuche in Labor des Unispitals

Falsche Mäusegehirne bringen Starforscher in Bedrängnis

Adriano Aguzzi ist einer der bedeutendsten Wissenschaftler der Schweiz. Doch nun wackelt das Denkmal des Neuropathologen: An seinem Institut wurden Forschungsergebnisse gefälscht – und weder er noch die Universität Zürich haben transparent über die Vorfälle informiert.

False mouse brains put star researchers in trouble

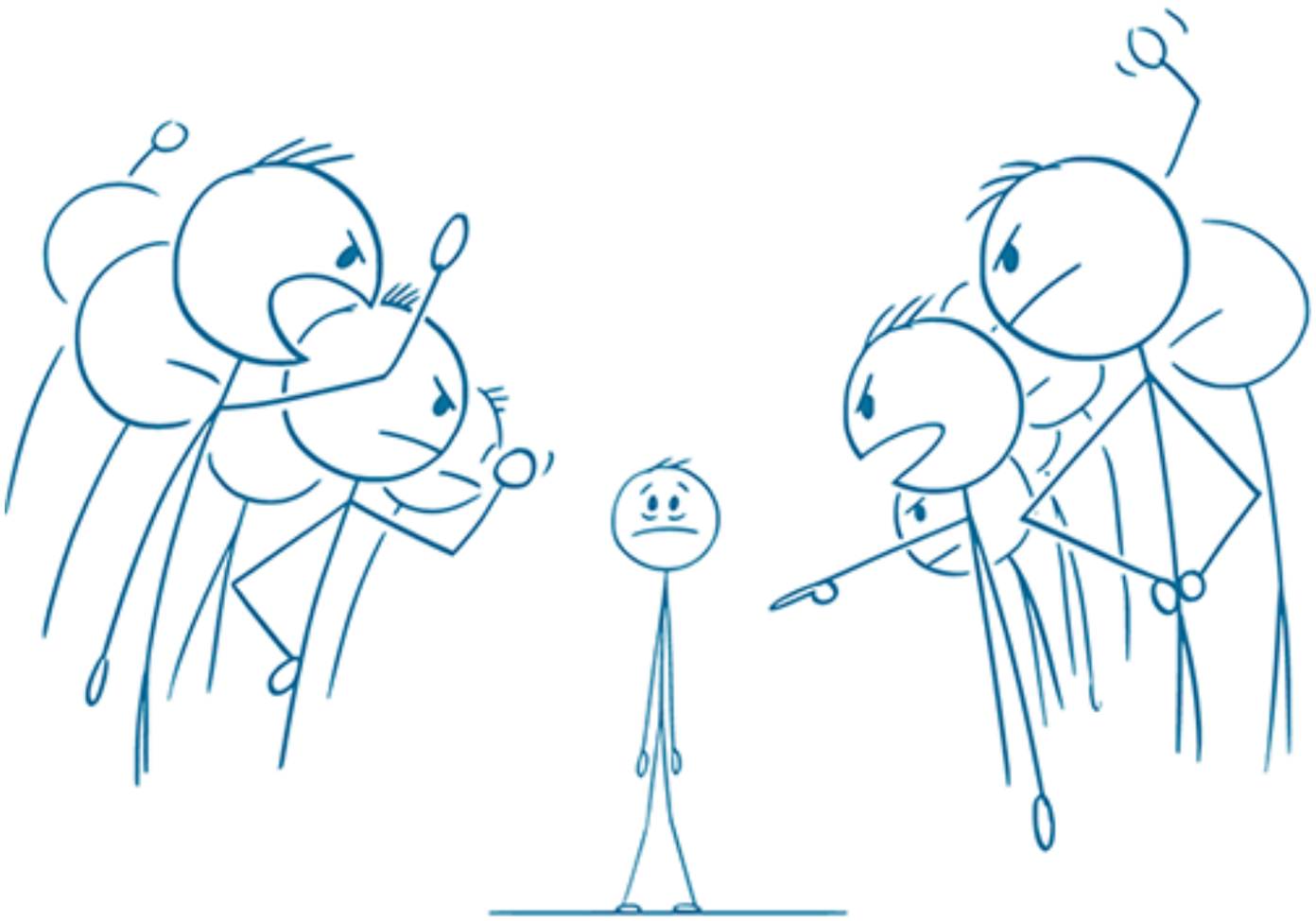
20 minuten

Front Wetter US-Wahlen Nahostkonflikt Schweiz #WIRSINDZUKUNFT Sport Zürich Bern

Gefälschte Tierversuche setzen Star-Forscher unter Druck

Ein ehemaliger Mitarbeiter von Adriano Aguzzi am Institut für Neuropathologie am Unispital Zürich manipulierte Daten von Tierversuchen.

How can we be sure that it is not a scapegoat?



scapegoat - a person who is blamed for the wrongdoings, mistakes, or faults of others, especially for reasons of expediency.

Search publications for: **Aguzzi**

53 results

3 days ago

Antiprion prophylaxis by gene transfer of a soluble prion antagonist

Author response

Nicolas Genoud, David Ott, Nathalie Braun, Marco Prinz, Petra Schwarz, Ueli Suter, Didier Trono, Adriano Aguzzi

The American Journal of Pathology (2008)

12 comments

6 days ago

Chronic Lymphocytic Inflammation Specifies the Organ Tropism of Prions

Mathias Heikenwalder, Nicolas Zeller, Harald Seeger, Marco Prinz, Peter-Christian Klöhn, Petra Schwarz, Nancy H. Ruddle, Charles Weissmann, Adriano Aguzzi

Science (2005)

2 comments

1 week ago

Triggering receptor expressed on myeloid cells-2 is involved in prion-induced microglial activation but does not contribute to prion pathogenesis in mouse brains

Caihong Zhu, Uli S Herrmann, Bei Li, Irina Abakumova, Rita Moos, Petra Schwarz, Elisabeth J Rushing, Marco Colonna, Adriano Aguzzi

Neurobiology of Aging (2015)

2 comments

NZZ

KOMMENTAR
von Anna Weber

Fälschungsskandal an der Uni Zürich: Der Fall Adriano Aguzzi steht für längst bekannte Probleme in der Forschung

"Science is not about making predictions or performing experiments. Science is about explaining."

— Bill Gaede

*Guillermo "Bill" Gaede is an Argentine engineer and programmer who is best known for Cold War industrial spying conducted while he worked at AMD and Intel.

Title
Abstract
Introduction
Materials and Methods
Results
Discussion
Conclusion
Data Availability
Author Contributions
Funding
Acknowledgments
Supplementary Material
References

Research

The mutational spectrum of non-CpG DNA varies with CpG content

Jean-Claude Walser[1] and Anthony V. Furano[2]

Section on Genomic Structure and Function, Laboratory of Molecular and Cellular Biology, National Institute of Diabetes and Digestive and Kidney diseases, National Institutes of Health, Bethesda, Maryland 20892-0830, USA

The accumulation of base substitutions (mutations) not subject to natural selection is the neutral mutation rate. Because this rate reflects the in vivo processes involved in maintaining the integrity of genetic information, the factors that affect the neutral mutation rate are of considerable interest. Mammals exhibit two dramatically different neutral mutation rates: the CpG mutation rate, wherein the C of most CpGs (i.e., methyl-CpG) mutate at 10–50 times that of C in any other context or of any other base. The latter mutations constitute the non-CpG rate. The high CpG rate results from the spontaneous deamination of methyl-C to T and incomplete restoration of the ensuing T:G mismatches to C:Gs. Here, we determined the neutral non-CpG mutation rate as a function of CpG content by comparing sequence divergence of thousands of pairs of neutrally evolving chimpanzee and human orthologs that differ primarily in CpG content. Both the mutation rate and the mutational spectrum (transition/transversion ratio) of non-CpG residues change in parallel as sigmoidal (logistic) functions of CpG content. As different mechanisms generate transitions and transversions, these results indicate that both mutation rate and mutational processes are contingent on the local CpG content. We consider several possible mechanisms that might explain how CpG exerts these effects.

[Supplemental material is available online at http://www.genome.org.]

DNA base substitutions (mutations) are the most frequent class of genetic variants. Thus, determining the factors that affect the base mutation rate (i.e., the number of base substitutions over time) remains a major concern of geneticists and molecular evolutionists (e.g., Nachman and Crowell 2000; Hwang and Green 2004; Duret 2009). Mutations not subject to natural selection are considered neutral and the neutral mutation rate is considered to closely reflect or equal the actual mutation rate (Ochman 2003). Thus, the neutral mutation rate is a basic biological parameter, which can be estimated from the number of interspecies base differences (sequence divergence) between neutrally evolving orthologous sequences (i.e., those sharing a common ancestral sequence, e.g., Nachman and Crowell 2000).

The neutral mutation rate varies considerably between and within chromosomes. Although numerous factors have been correlated with the neutral mutation rate (e.g., Krawczak et al. 1998; Hardison et al. 2003; Hwang and Green 2004; Chimpanzee Sequencing Analysis Consortium 2005; Gaffney and Keightley 2005; Hellmann et al. 2005; Taylor et al. 2006), the mechanism(s) accounting for these correlations remain elusive (e.g., Hodgkinson et al. 2009; for review, see Duret 2009).

One of the more intriguing covariates of the neutral mutation rate is its positive correlation with CpG content. In part, this correlation is not surprising because most CpGs in mammals are uniquely hypermutable (e.g., Hwang and Green 2004). The Cs of most CpGs are methylated (Ehrlich and Wang 1981), which enhances the deamination of C, in this case producing a TG mismatch. The net result is that methyl-CpGs mutate at 10–50 times the rate of C in any other context (Coulondre et al. 1978; Duncan and Miller 1980; Bulmer 1986; Sved and Bird 1990), or of any other base (Hwang and Green 2004). Consequently, CpGs not under selection are replaced over time by TpG/CpAs.

Inexplicably, however, the positive correlation between CpG content and the neutral mutation rate persists even if mutations at CpG sites are not counted, i.e., if only non-CpG mutations are measured (Chimpanzee Sequencing Analysis Consortium 2005; Gaffney and Keightley 2005; Hellmann et al. 2005; Tyekucheva et al. 2008). A prevailing reasonable explanation for this odd result was that the non-CpG mutation rate and CpG content were joint manifestations of the chromosomal environment (Hellmann et al. 2005; Tyekucheva et al. 2008).

We recently considered an alternative, that CpGs (i.e., methyl-CpGs), or mutations thereof, somehow directly affect the mutation of flanking non-CpG DNA. This explanation would have far-reaching implications given the epigenetic role of CpG methylation in gene regulation, chromatin structure, imprinting, and the silencing of transposable elements and other genomic insertions (Lees-Murdock and Walsh 2008; Cedar and Bergman 2009). We addressed this issue by examining the sequence divergence of thousands of neutrally evolving orthologous sequences in the chimpanzee and human genomes that differed primarily in CpG content (Walser et al. 2008).

These orthologs were the repaired DNA fossils that had been interspersed throughout the genome at different times in the primate lineage of humans and chimpanzees by six now extinct families of L1 non-LTR retrotransposons. As L1 fossils are not under selection, the CpG content of these otherwise very similar sequences should differ. Thus, the CpG content of the younger L1 fossils should be higher than that of the older ones and, if our supposition was correct, so should their mutation rate, regardless of chromosomal location. And this is the result we obtained (Walser et al. 2008).

Our current examination of non-CpG mutations over a considerably wider range of CpG content than previously (Walser et al. 2008) revealed two unexpected findings: First, the correlation between the two is best fit by a sigmoid (logistic) function. Thus, both a certain threshold CpG content is required to have a substantial effect on the overall non-CpG mutation rate, and "saturation"

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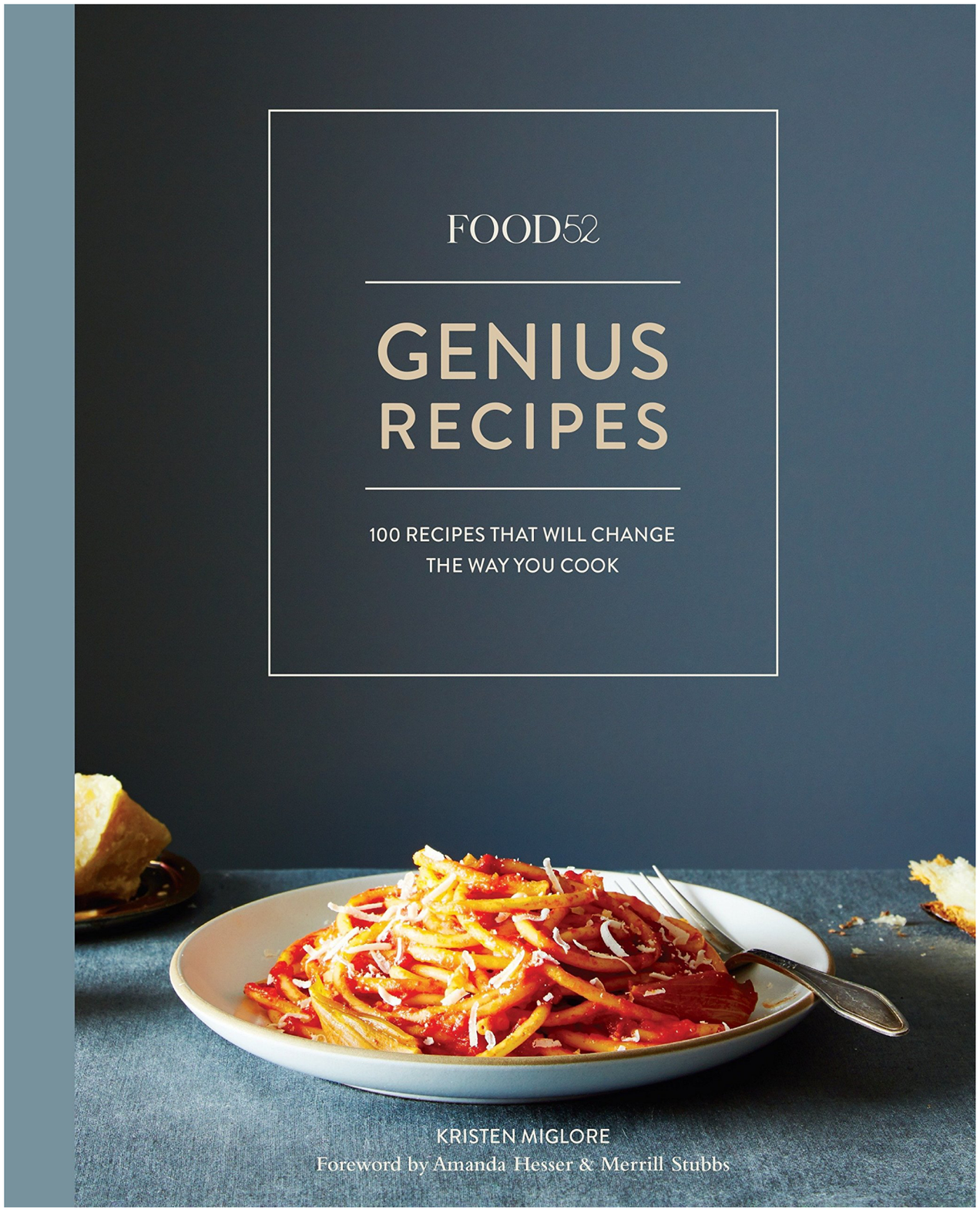


Roasted Applesauce

FROM JUDY RODGERS

No cinnamon, no cloves—this sauce is straight apple.

It comes from Judy Rodgers's *Zuni Café Cookbook* and—as with everything served at her San Francisco restaurant—it's smart and simple, balancing the apples only as needed with small amounts of salt, sugar, and apple cider vinegar. Not only does this quick oven method free you from stewing and stewing applesauce on the stovetop, but it does the magic that roasting always does. All the sugars concentrate, allowing apples to become the best version of themselves. There's just a little bit of butter too, sliced into wafers that melt into bronzed apple tops and a rich sauce.

Makes about 3 cups (710ml)

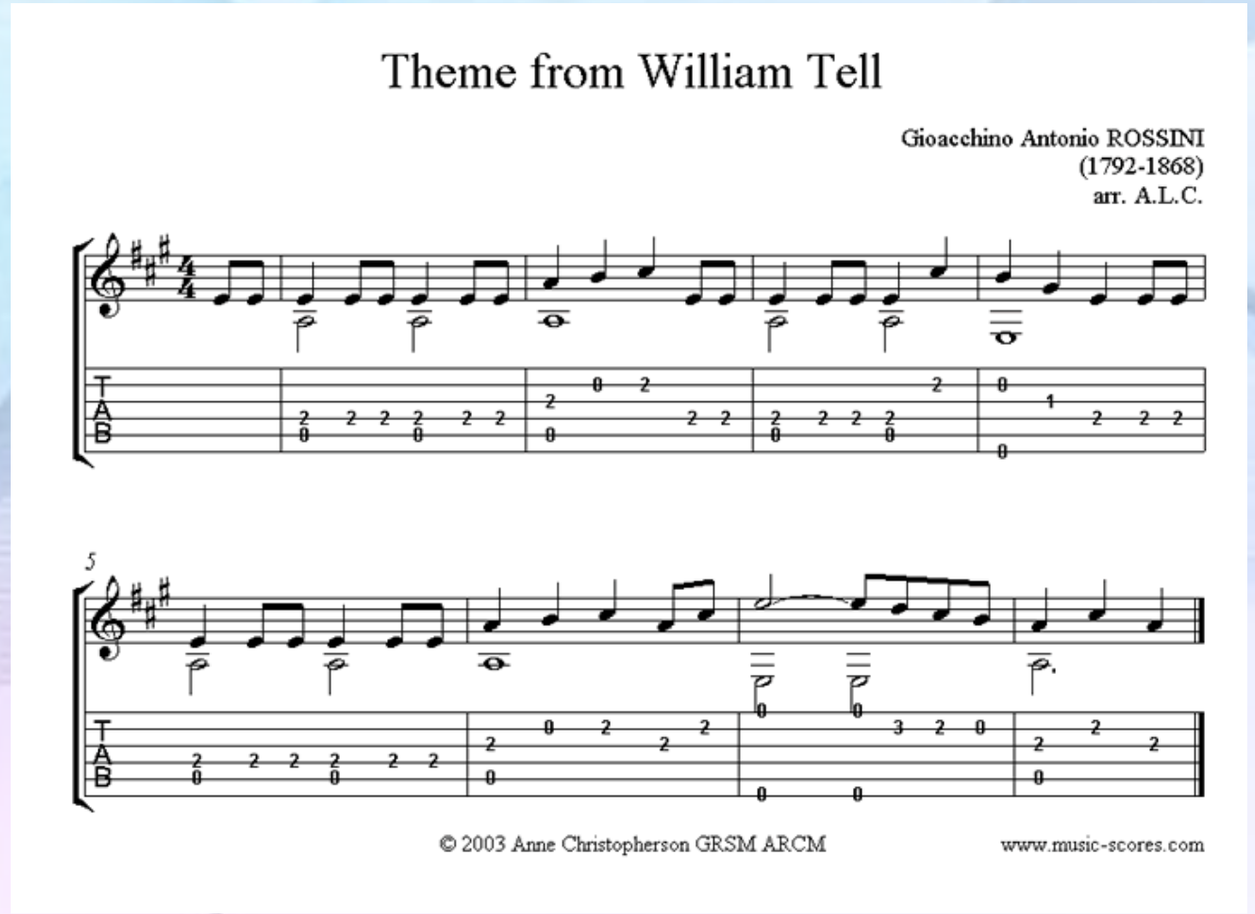
3½ to 4 pounds (1.6 to 1.8kg) apples (Rodgers recommends crisp eating apples, like Sierra Beauties, Braeburns, Pippins, Golden Delicious, or Galas)
Pinch of salt
Up to 2 teaspoons sugar, as needed
About 2 tablespoons unsalted butter
A splash of apple cider vinegar, as needed

1 Preheat oven to 375°F (190°C).

2 Peel, core, and quarter the apples. Toss with a little salt and, unless they are very sweet, a bit of sugar to taste. If they are tart enough to make you squint, add the full measure of sugar. Spread in a shallow baking dish that crowds the apples in a single layer. Drape with slivers of the butter, cover tightly with a lid or aluminum foil, and bake until the apples start to soften, 15 to 30 minutes, depending on your apples.

3 Uncover, raise the heat to 500°F (260°C), and return the pan to the oven. Leave the apples to dry out and color slightly, about 10 minutes.

4 When the tips of the apples have become golden and the fruit is tender, scrape them into a bowl and stir into a chunky "mash." Season with salt and sugar to taste, then consider a splash of apple cider vinegar to brighten the flavor. (Try a drop on a spoonful to see if you like it.) Serve hot or warm.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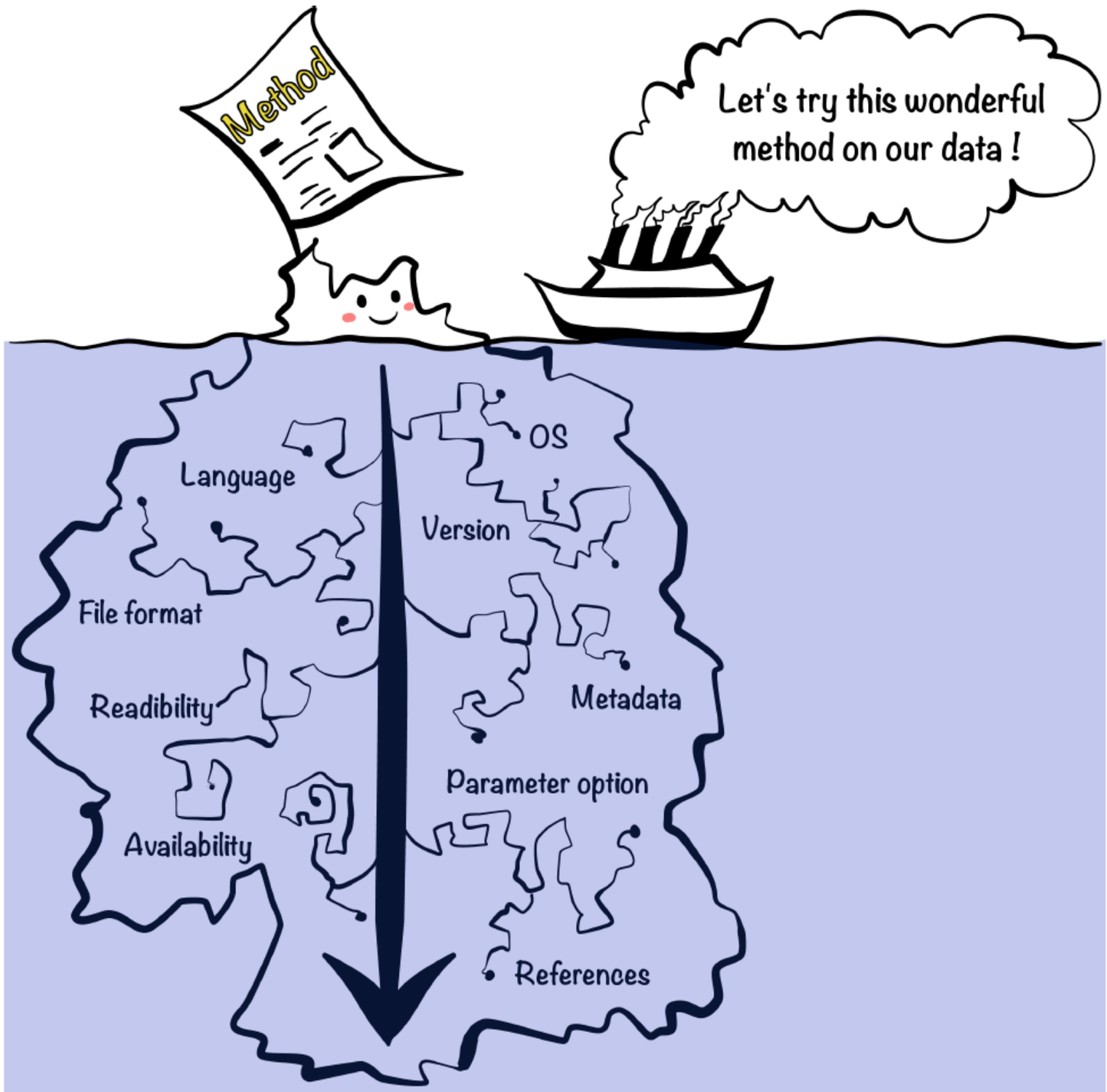
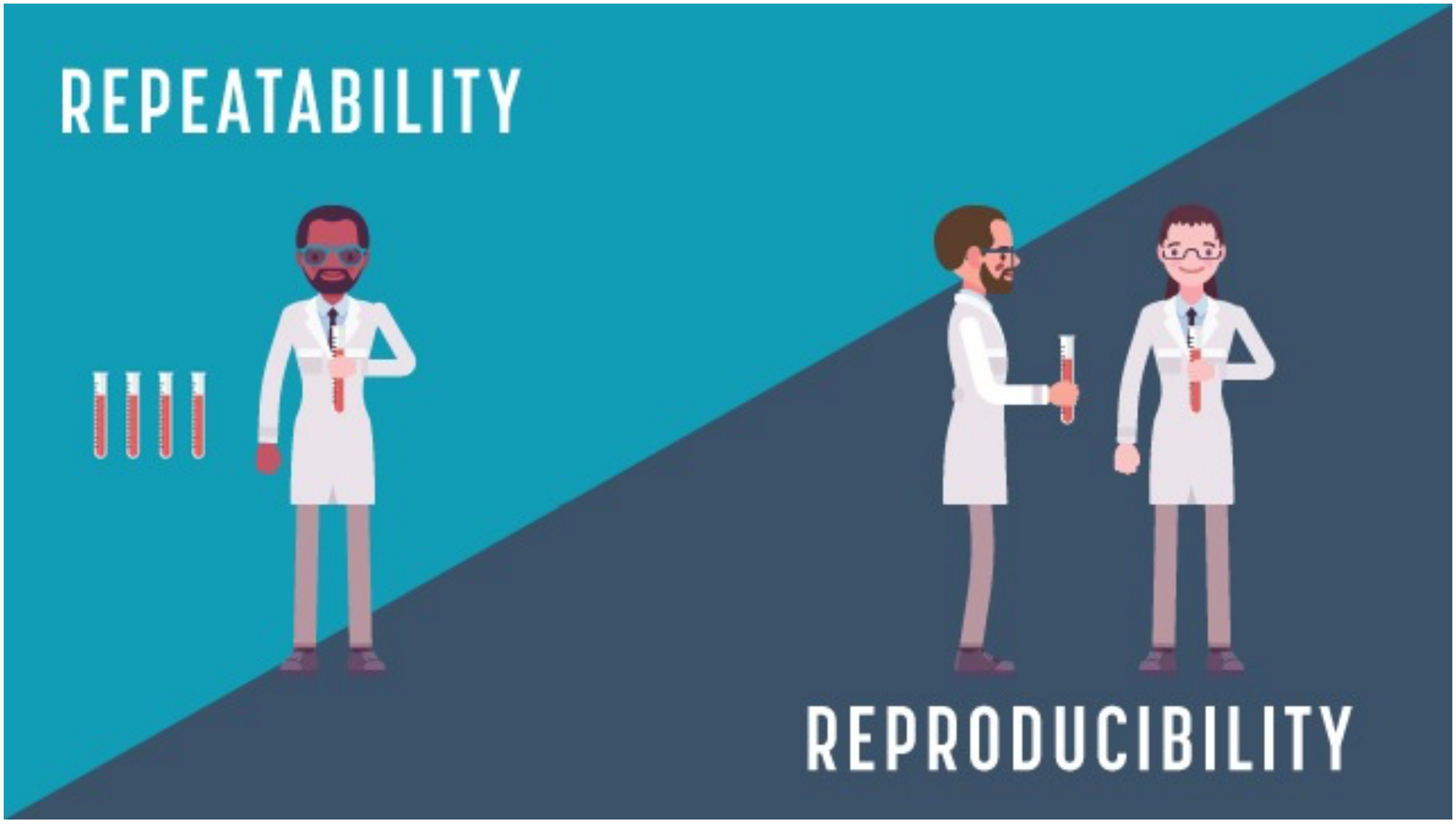

Method
Let's try this wonderful method on our data !
Language
OS
Version
File format
Readibility
Metadata
Parameter option
Availability
References

Reality check on reproducibility

A survey of Nature *readers revealed a high level of concern about the problem of irreproducible results. Researchers, funders and journals need to work together to make research more reliable.*



Source: https://www.technologynetworks.com/informatics/articles/repeatability-vs-reproducibility

Repeatability is a measure of the likelihood that, having produced one result from an experiment, you can try the same experiment, with the same setup, and produce that same result. It is a way for researchers to verify that their own results are true and are not just **chance artefacts**.

The **reproducibility** of data is a measure of whether a different research team can attain results published in a paper using the same methods. This shows that the results are **not artefacts of the unique setup in one research lab**. It is easy to see why reproducibility is desirable, as it reinforces findings and protects against rare cases of fraud, or less rare cases of human error, in the production of significant results.

Replicability - Different team, different experimental setup. If an observation is replicable it should be able to be made by a different team, using a different measuring system and dataset, in a different location, on multiple trials. This would therefore involve collecting data anew.

Source: https://www.technologynetworks.com/informatics/articles/repeatability-vs-reproducibility

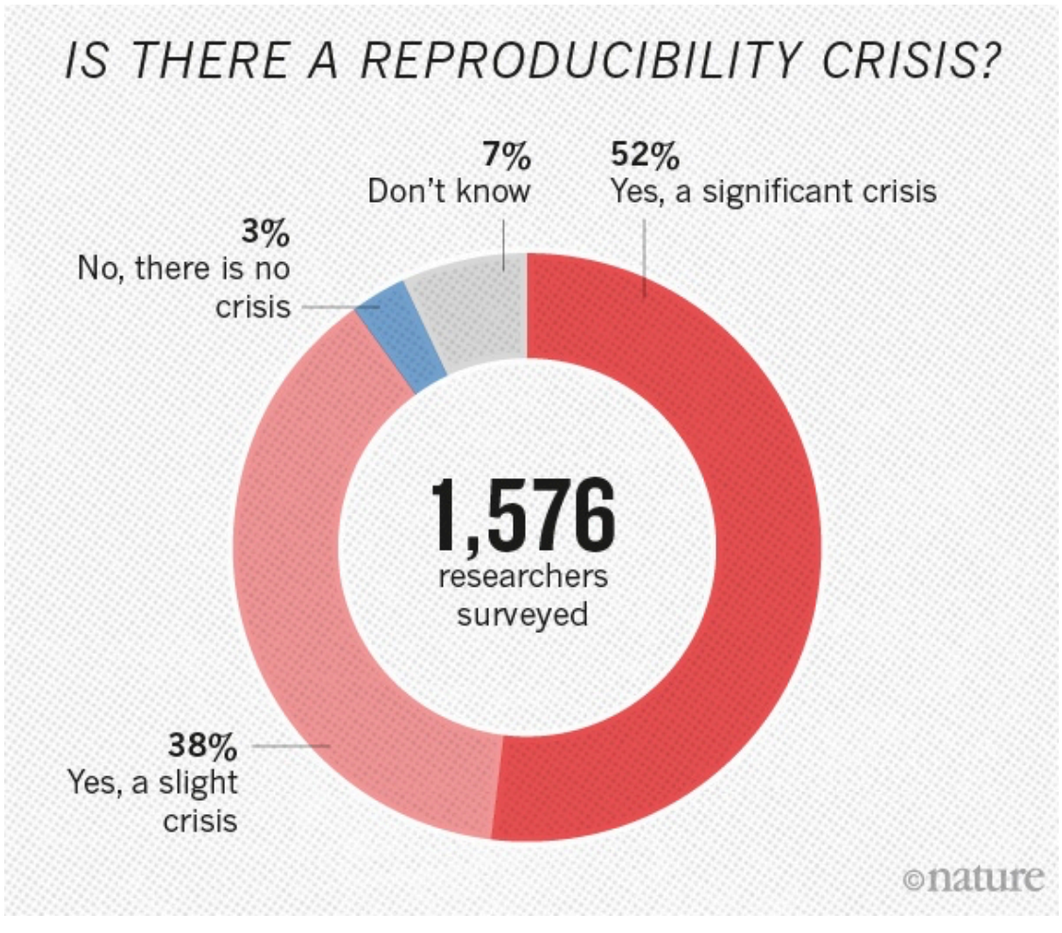
Q1 How can we improve **repeatability**?

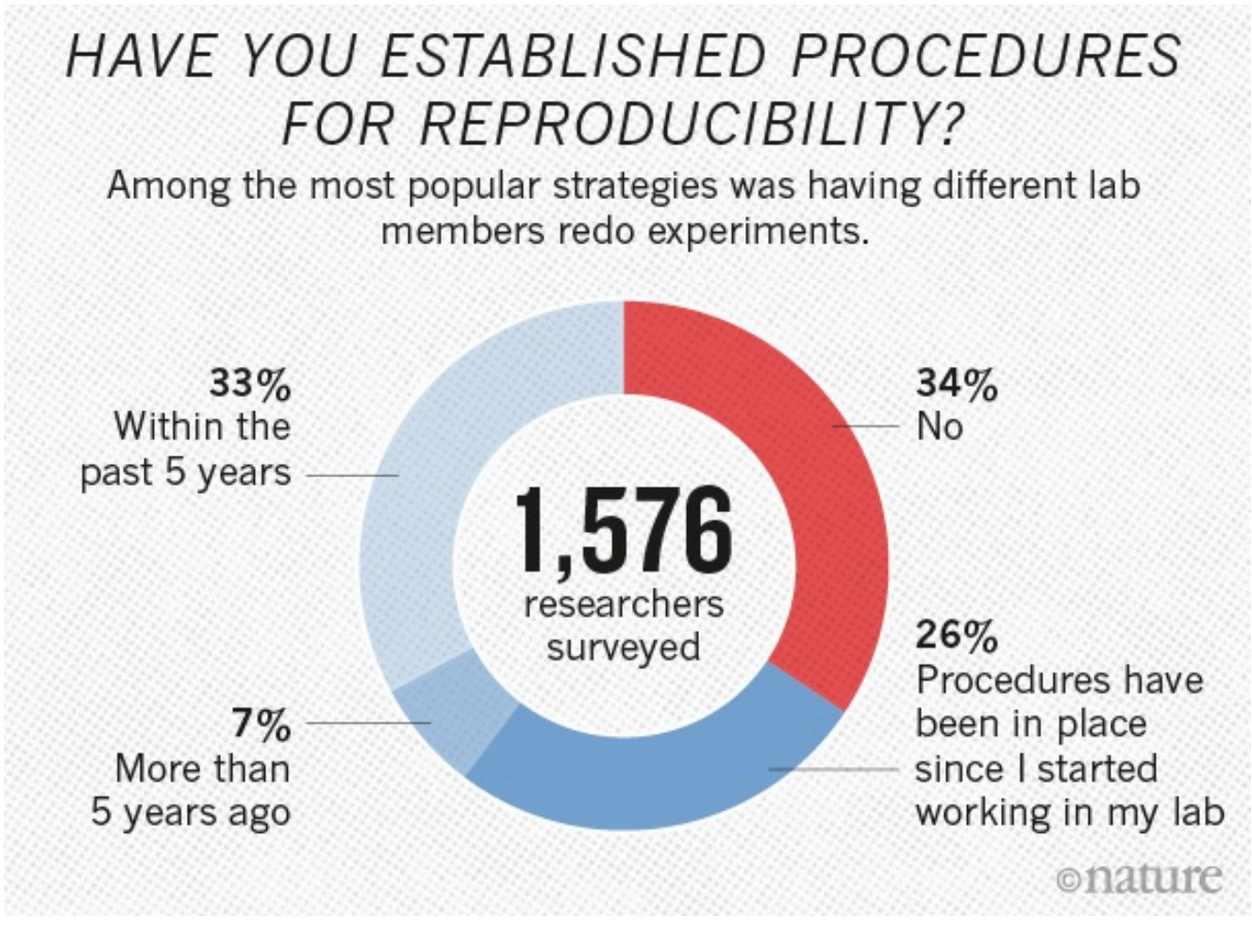
Q2 How can we improve **reproducibility**?

Q3 How can we improve **replicability**?

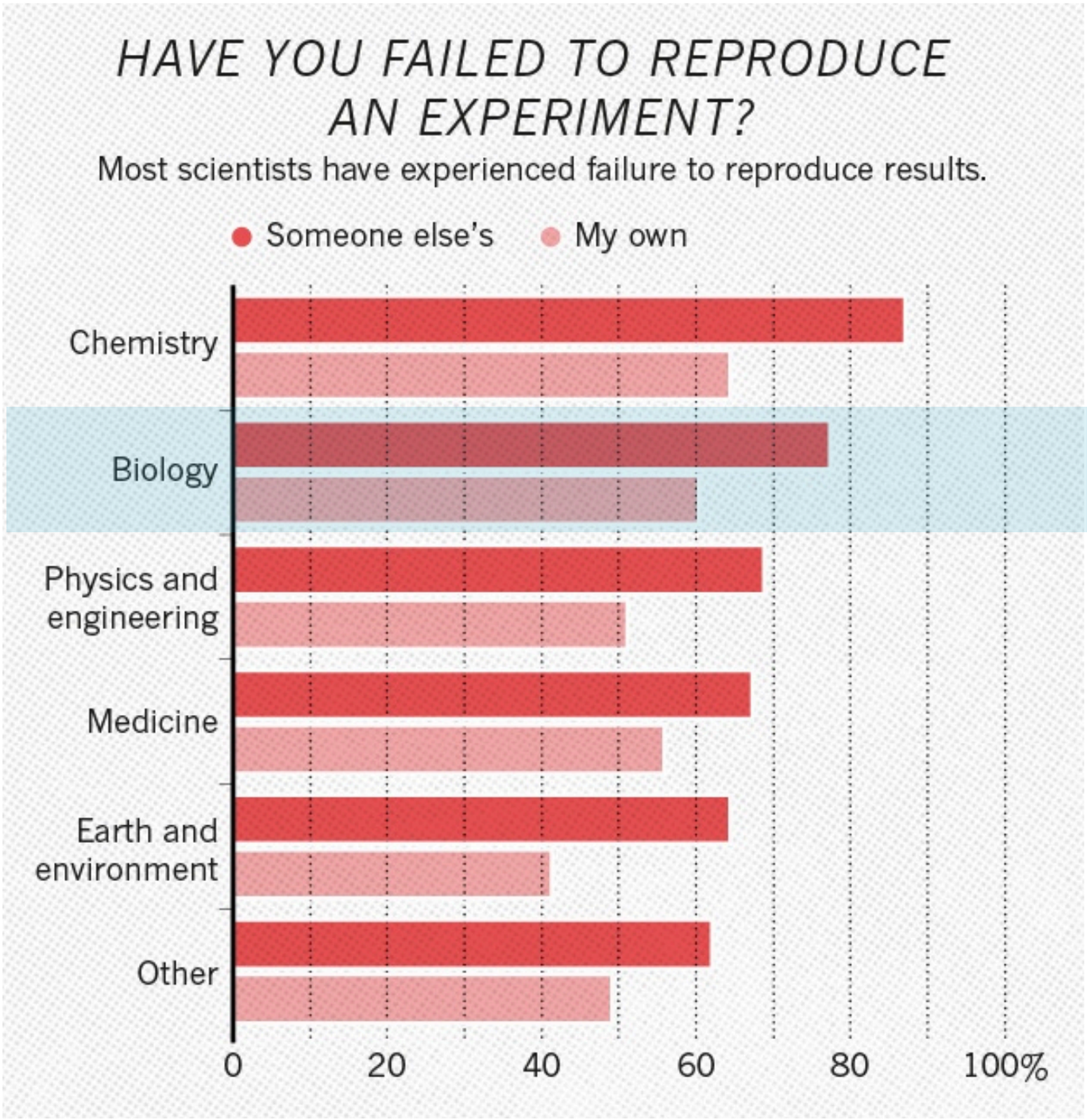
YouTube: Is there a reproducibility crisis in science? - Matt Anticole

The collective effort of science depends on researchers being able to reproduce the work of others. In a recent survey of 1,576 researchers, 70% of them admitted having difficulty in reproducing experiments proposed by other scientists. For 50%, this reproducibility issue even concerns their own experiments.

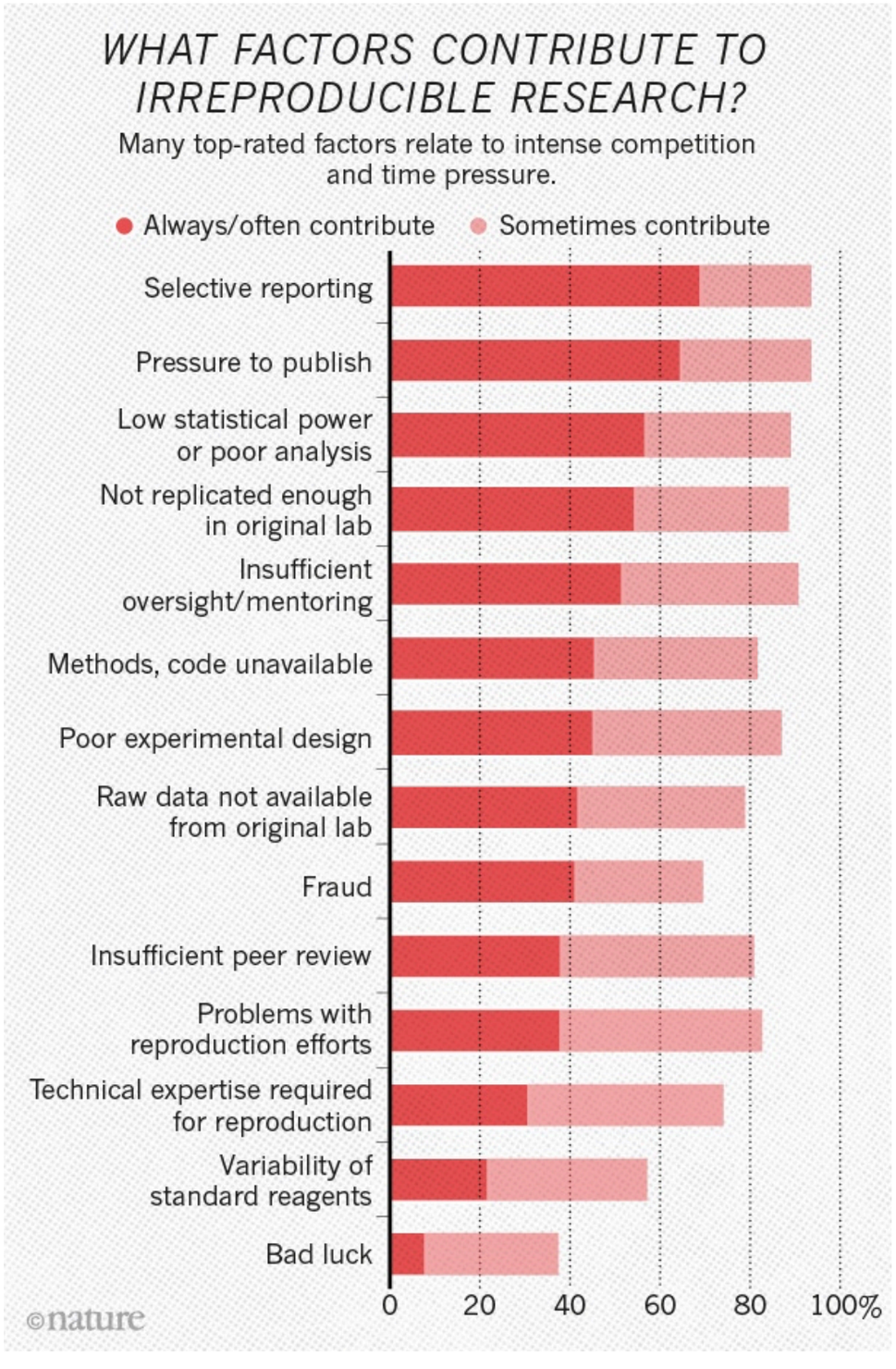


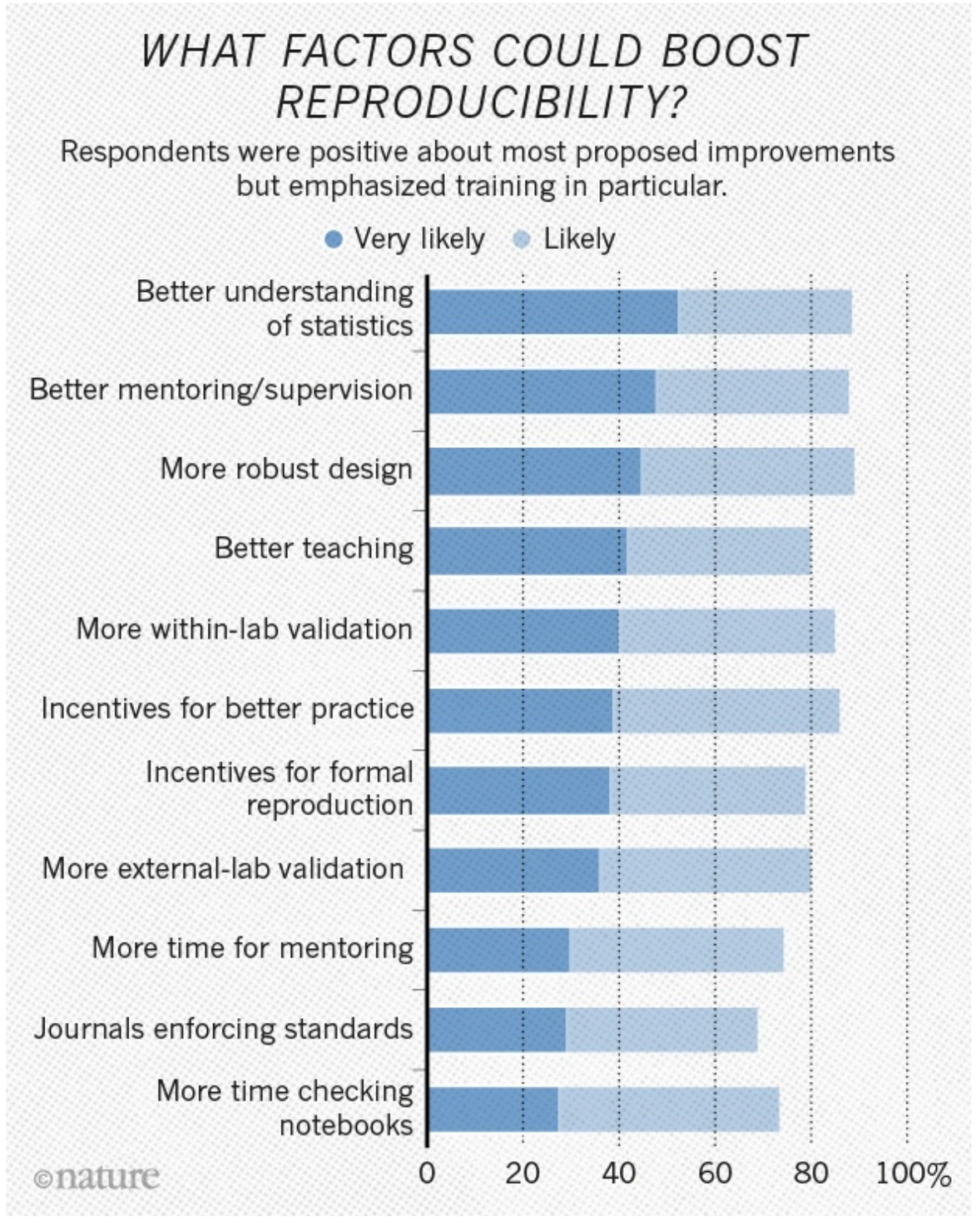


Source: Baker (2016) 1,500 scientists lift the lid on reproducibility. Nat News . 533:452.



Source: Baker (2016) 1,500 scientists lift the lid on reproducibility. Nat News . 533:452.





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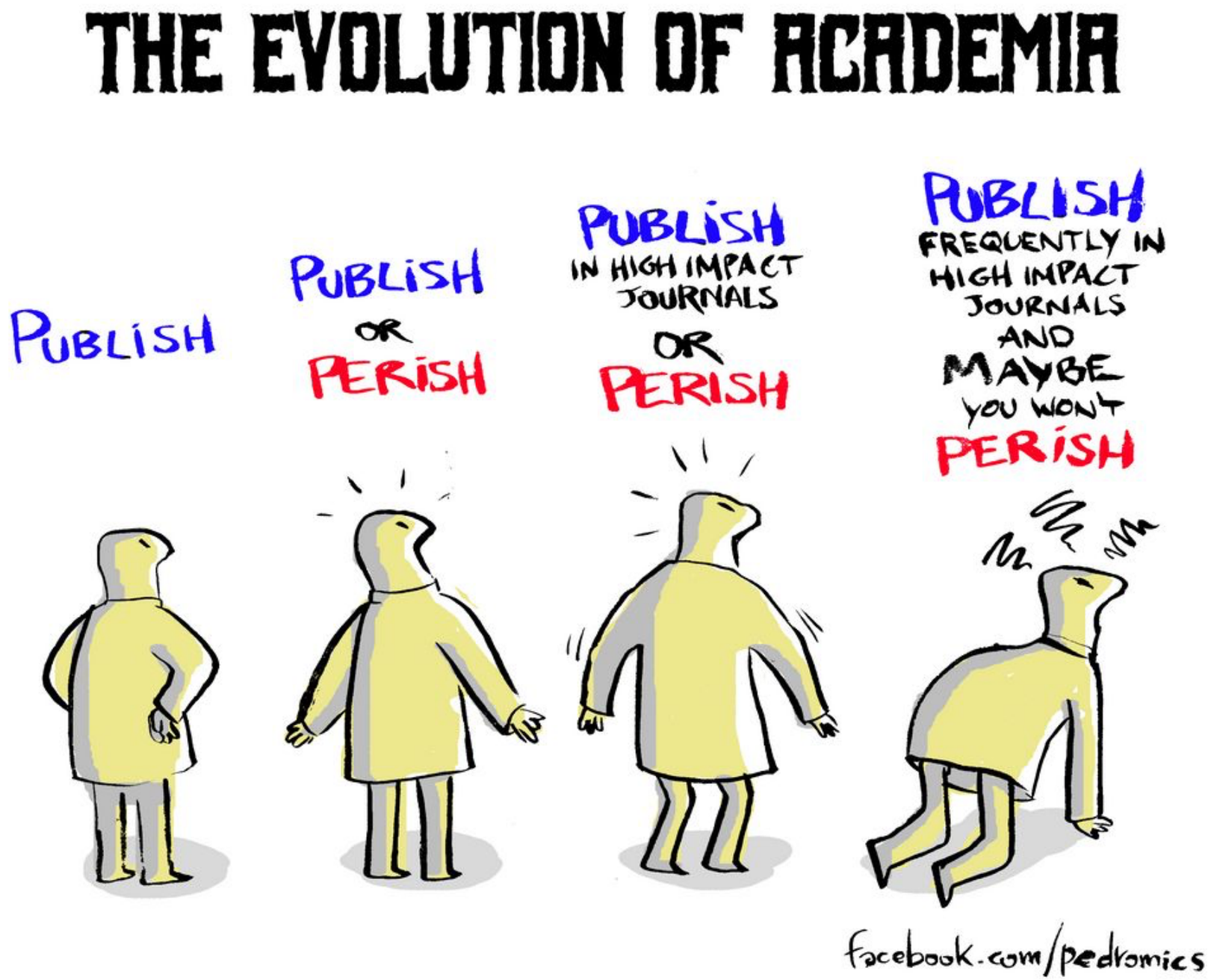
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- Honest Mistakes
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Molecular Breeding
January 2015, 35:54

Date: 25 Jan 2015

Development of a leafy *Brassica rapa* fixed line collection for genetic diversity and population structure analysis

Wenxing Pang, Xiaonan Li, Su Ryun Choi, Vignesh Dhandapani, Subin Im, Min Young Park, Chang Soon Jang, Man-Sung Yang, In Ki Ham, Eun Mo Lee, Wankyu Kim, Soo-Seong Lee, Guusje Bonnema, Suhyoung Park, Zhongyun Piao, Yong Pyo Lim

Article Metrics

(Illumina). Paired-end short read sequences for Kenshin were generated by the Illumina Genome Analyzer-IIx system. Low quality Illumina reads were identified and trimmed using fastqc (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). The Bowtie2 aligner was used to align the high-quality short read sequences of Kenshin to the reference genome sequence and a BAM alignment file was generated along with the consensus sequence. SAMtools and BCFtools were employed to call SNPs and

FastQC is for qualitiy control but not for data manipulations.

An Apple a Day: Which Bacteria Do We Eat With Organic and Conventional Apples?

*Birgit Wassermann, Henry Müller and Gabriele Berg**

Institute of Environmental Biotechnology, Graz University of Technology, Graz, Austria

frontiers in Microbiology

ORIGINAL RESEARCH
published: 24 July 2019
doi: 10.3389/fmicb.2019.01629

Apples are among the most consumed fruits world-wide. They represent a source of direct human exposure to bacterial communities, which is less studied. We analyzed the apple microbiome to detect differences between tissues and the impact of organic and conventional management by a combined approach of 16S rRNA gene amplicon analysis and qPCR, and visualization using fluorescence *in situ* hybridization and confocal laser scanning microscopy (FISH-CLSM). Each apple fruit harbors different tissues (stem, peel, fruit pulp, seeds, and calyx), which were colonized by distinct bacterial communities. Interestingly, fruit pulp and seeds were bacterial hot spots, while the peel was less colonized. In all, approximately 10^8 16S rRNA bacterial gene copy numbers were determined in each g apple. Abundances were not influenced by the management practice but we found a strong reduction in bacterial diversity and evenness in conventionally managed apples. In addition, despite the similar structure in general dominated by *Proteobacteria* (80%), *Bacteroidetes* (9%), *Actinobacteria* (5%), and *Firmicutes* (3%), significant shifts of almost 40% of bacterial genera and orders were monitored. Among them, especially bacterial signatures known for health-affecting potential were found to be enhanced in conventionally managed apples. Our results suggest that we consume about 100 million bacterial cells with one apple. Although this amount was the same, the bacterial composition was significantly different in conventionally and organically produced apples.

What is the health-relevant information from the abstract and can you spot a problem?

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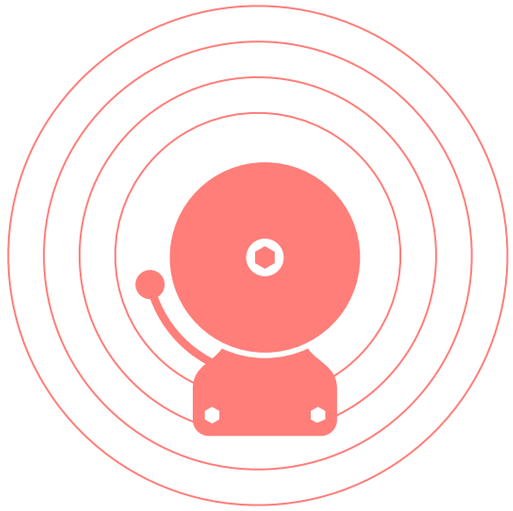

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Apple are a "source" of bacteria. What a big suprise!

Fruit pulp and seeds are bacterial hot spots. Think again!

What? Good, bad or what? Outside or inside an apple?

"Read not to contradict and confute; nor to believe and take for granted; nor to find talk and discourse; but to weigh and consider."

—Francis Bacon

Cell Reports

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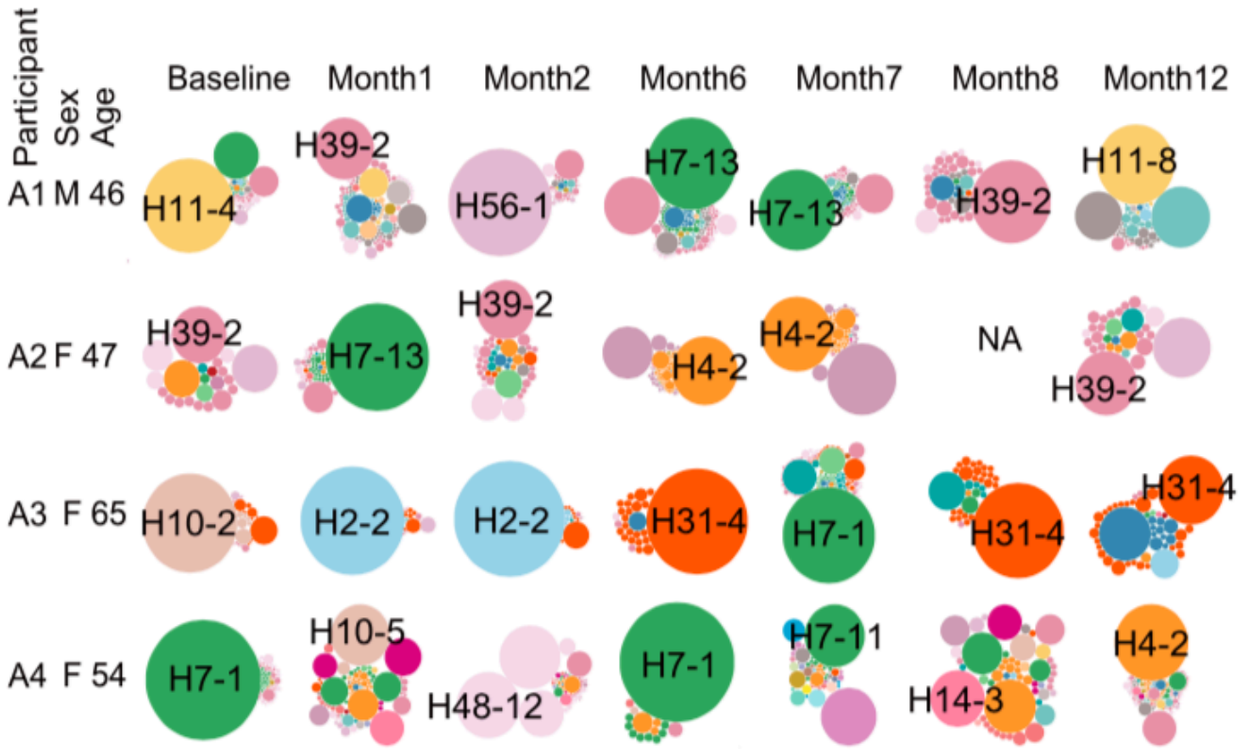
Resource

Single-gene long-read sequencing illuminates *Escherichia coli* strain dynamics in the human intestinal microbiome

Dalong Hu,[1] Nicholas R. Fuller,[2,3] Ian D. Caterson,[1,2,3] Andrew J. Holmes,[1] and Peter R. Reeves[1,4,*]



Flagellin diversity was discovered as strain differences in im- mune responses, which were codified and used for serotyping. The variable flagellin domains are known in serology as the H an- tigen, and 53 H antigens were distinguished in E. coli, of which 52 have the high-level divergence, with essentially no significant sequence alignment

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This is a typical study of a very limited and questionable design, were the authors made many mistakes, did not include any controls, group whatever they liked, interpreted the reults according to their personal belives, and did not care about reproducibility (for good reasons I guess?).

Science Integrity Digest

A blog about science integrity, by Elisabeth Bik, for Harbers-Bik LLC. Support my work at Patreon.com/elisabethbik

eliesbik

February 15, 2024

The rat with the big balls and the enormous penis – how Frontiers published a paper with botched AI-generated images

A review article with some obviously fake and non-scientific illustrations created by Artificial Intelligence (AI) was the talk on X (Twitter) today.

The figures in the paper were generated by the AI tool Midjourney, which generated some pretty, but nonsensical, illustrations with unreadable text.

It appears that neither the editor nor the two peer reviewers looked at the figures at all. The paper was peer-reviewed within a couple of weeks and published two days ago.

Dear readers, today I present you: the rat with the enormous family jewels and the dıəlocttal stem ells.

Retraction Watch

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Retracted coronavirus (COVID-19) papers

Retracted

1. "5G Technology and induction of coronavirus in skin cells," published in *Biological Regulators & Homeostatic Agents* on July 16, 2020, withdrawn on July 24, 2020. Our coverage here.
2. "A data-mining based analysis of traditional Chinese medicine in diagnosing and treating COVID-19," published on June 24, 2021 in *The Anatomical Record*; unknown when retracted.
3. "A deep learning model and machine learning methods for the classification of potential coronavirus treatments on a single human cell," published on October 17, 2020 in the *Journal of Nanoparticle Research*; retracted on August 16, 2021.
4. "A Retrospective Analysis and Comparison of Prisoners and Community-Based Patients with COVID-19 Requiring Intensive Care During the First Phase of the Pandemic in West Texas," published on August 29, 2021 in the *Journal of Primary Care & Community Health*; retracted on July 16, 2021
5. "A review of convalescent plasma transfusion in COVID-19: Old wine reserved for special occasions," published in Lung India on September 16, 2020; retracted December 31, 2020.
6. "A Study of Potential SARS-CoV-2 Antiviral Drugs and Preliminary Research of Their Molecular Mechanism, Based on Anti-SARS-CoV Drug Screening and Molecular Dynamics Simulation," published on December 1, 2020 in the *Journal of Computational Biology*; retracted on June 25, 2021.
7. "Acute kidney injury and collapsing glomerulopathy associated with COVID-19 and APOL1 high risk genotype," Abstract 111 and Abstract 621, both published in the *Journal of Investigative Medicine*; both retracted on April 1, 2021.

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The Retraction Watch Database
Please see this user guide before you get started

Author(s): Type to search
Country(s):
Title: Type to search
Reason(s) for Retraction:
Subject(s):
Article Type(s):
Journal:
Publisher:
Affiliation(s): ETH
Notes:
URL:

Original Paper
From Date: To: mm/dd/yyyy
PubMedID:
DOI:

Retraction or Other Notices
From Date: To: mm/dd/yyyy
PubMedID:
DOI:
Nature of Notice: Paywalled:

Clear Search
Search

28 Item(s) Found

Retraction or Other Notices Title/Subject(s)/Journal --- Publisher/Affiliation(s)/Retraction Watch Post URL(s)	Reason(s)	Author(s)	Original Paper Date/PubMedID/DOI	Retraction or Other Notices Date/PubMedID/DOI	Article Type(s) Nature of Notice	Countries Paywalled? Notes
The Manganese(I)–Catalyzed Asymmetric Transfer Hydrogenation of Ketones: Disclosing the Macrocylic Privilege (BLS) Biochemistry; *Angewandte Chemie --- Wiley* Departement Chemie und Angewandte Biowissenschaften, Eidgenössische Technische Hochschule (ETH) Zürich, 8093 Zürich, Switzerland http://retractionwatch.com/2020/08/18/top-chemistry-journal-retracts-paper-for-faked-data/	+Falsification/Fabrication of Data +Investigation by Journal/Publisher	Alessandro Passera Antonio Mezzetti	11/29/2019 31725945 10.1002/anie.201912605	08/17/2020 33645005 10.1002/anie.202009851	Research Article Retraction	Switzerland No
Extruded meat analogues based on yellow, heterotrophically cultivated Auxenochlorella protothecoides microalgae (BLS) Microbiology; (BLS) Nutrition; *Innovative Food Science & Emerging Technologies --- Elsevier* ETH Zurich, Department of Health Science and Technology, Institute of Food, Nutrition and Health, Sustainable Food Processing Laboratory, Schmelzbergstrasse 9, 8092 Zurich, Switzerland Planted Foods AG, Schmelzbergstrasse 7, 8092 Zurich, Switzerland ETH Zurich, Department of Health Science and Technology, Institute of Food, Nutrition and Health, Food Process Engineering Laboratory, Schmelzbergstrasse 9, 8092 Zurich, Switzerland ETH Zurich, Department of Health Science and Technology, Institute of Food, Nutrition and Health, Food and Soft Materials Laboratory, Schmelzbergstrasse 9, 8092 Zurich, Switzerland ETH Zurich, Scientific Center for Optical and Electron Microscopy (ScopeM), 8093 Zurich, Switzerland	+Error in Text +Lack of Approval from Author	Martin P Caporgno Lukas Bocker Christina Mussner Eric Stirnemann Iris Haberkorn Horst Adelmann Stephan Handschin Erich J Windhab Alexander Mathys	03/05/2020 00000000 10.1016/j.ifset.2020.102319	03/05/2020 00000000 10.1016/j.ifset.2020.102319	Correction/Erratum/Corrigendum Research Article Retraction	Switzerland No
Social Bayes: Using Bayesian Modeling to Study Autistic Trait–Related Differences in Social Cognition (SOC) Psychology; *Biological Psychiatry --- Elsevier* Max Planck Institute for Metabolism Research, Cologne, Germany Translational Neuromodeling Unit, ETH Zürich, Zurich, Switzerland Max Planck Institute of Psychiatry, Munich, Germany Department of Psychiatry, University Hospital Cologne, Cologne, Germany http://retractionwatch.com/2019/10/01/doing-the-right-thing-authors-retract-paper-on-autism-and-social-clues-after-realizing-an-error/	+Doing the Right Thing +Error in Data +Error in Methods +Error in Results and/or Conclusions	Meltem Sevgi Andreea O Diaconescu Marc Tittgemeyer Leonhard Schilbach	12/09/2015 26831352 10.1016/j.biopsych.2015.11.025	09/23/2019 31558222 10.1016/j.biopsych.2019.08.017	Research Article Retraction	Germany Switzerland No
IMF shape constraints from stellar populations and dynamics from CALIFA (PHY) Astronomy; (PHY) Astrophysics; *Monthly Notices of the Royal Astronomical Society: Letters --- Oxford Academic* Kapteyn Astronomical Institute, University of Groningen, Postbus 800, NL-9700 AV Groningen, the Netherlands Instituto de Astrofisica de Canarias, Via Lactea s/n, La Laguna, Tenerife, Spain Departamento de Astrofisica, Universidad de La Laguna, E-38205 La Laguna, Tenerife, Spain University of California Observatories, 1156 High Street, Santa Cruz, CA 95064, USA Max Planck Institute for Astronomy, Konigstuhl 17, D-69117 Heidelberg, Germany	+Duplicate Publication through Error by Journal/Publisher	M Lyubenova I Martin-Navarro G van de Ven J Falcon-Barroso L Galbany A Gallazzi R Garcia-Benito R Gonzalez Delgado B Husemann F la Barbera	09/05/2016 00000000 10.1093/mnras/stw2434	06/01/2019 00000000 10.1093/mnrasl/slw173	Research Article Retraction	Argentina Australia Austria Chile Germany Italy Mexico Netherlands Spain Switzerland

23397

Run script "__doPostBack('grdRetraction','Select$23397')"

http://retractiondatabase.org/RetractionSearch.aspx?

Predatory journals are easy to please. They seem to accept papers with little regard for quality, at a fraction of the cost charged by mainstream open-access journals. These supposedly scholarly publishing entities are murky operations, making money by collecting fees while failing to deliver on their claims of being open access and failing to provide services such as peer review and archiving.

Source: Moher *et al.* (2017) Stop this waste of people, animals and money. *Nature* 549, 23–25.

2 – Gold Open Access – same publishing process as above. The difference is that when an article is accepted for publication, the author/s or funder/s pay an Article Processing Charge (APC). The final version of the published article is then free to read for everyone. The APC to publish Gold Open Access in *Nature* is £8890.00/$12290.00/€10290.00.

nature

[Beall's List - Potential, possible, or probable predatory scholarly open-access publishers]

Frontiers' peer review process is flawed. It is stacked in favor of accepting as many papers as possible in order to generate more revenue for the company. Frontiers is included on my list, and I recommend against publishing in its journals, which are rather expensive to publish in anyway.

Is frontiers in microbiology a predatory Journal?

The **Frontiers journals** use **open peer review**, where the names of reviewers of accepted articles are made public. As of 2017, 24 of their journals had impact factors. ... Some journals, such as Frontiers in Human Neuroscience or **Frontiers in Microbiology** are considered megajournals on their own.


frontiers
in Microbiology


frontiers
in Buyologie

For Better Science

BY LEONID SCHNEIDER, ON RESEARCH INTEGRITY, BIOMEDICAL ETHICS AND ACADEMIC PUBLISHING

Beall-listed Frontiers empire strikes back

BY LEONID SCHNEIDER
SEPTEMBER 14, 2016

COMMENTS 65

Willy
December 1, 2018

I think that both views have their own right to co-exist. I published articles in Frotniers and agree that their review process is sloppy. I also published articles with Wiley and Elsevier and experienced their review process as biased, unfair, and not constructive.

I reviewed for Frontiers and admit that my criticism of trash manuscripts was dismissed. However, it was possible to withdraw from the reviewing process so not to be stained by junk papers. I reviewed for Elsevier, Wiley, AAAS, NPG and others. Elsevier surely has the highest trash fraction among the manuscripts. However, they are happy to reject such manuscripts. Still, Elsevier is steering towards junk status as well as their reviewing process is flawed by nepotism. Plus, I consider Elsevier predatory as they bully university into a loan-shark style subscription model (https://www.the-scientist.com/news-opinion/universities-in-germany-and-sweden-lose-access-to-elsevier-journals-64522).

I agree with CVAK in that Frontiers gives room to unconventional authors and ideas – and I applaud them for this. They also waive fees if one can't afford them as they have done for me.

The bottom line is that publishers are just the executive branch of science. They scientific system with its focus on quantity enables all sorts of spam, regardless of the publishers. Just remember the Mozart effect (https://www.nature.com/articles/365611a0) or the memory of water (https://www.nature.com/articles/333816a0). Still, this is part of scientific discovery.

"[P]ublisher are just the executive branch of science."

Scientists publish their results to share them with the scientific community. It is common for peer-reviewed scientific journals to charge a fee for publishing a paper (**A**rticle **P**rocessing **C**harges). Depending on the journal, the cost of publication can be high. Recently, these fees have been questioned.

Interesting to read: Budzinski et al. (2020) Drivers of article processing charges in open access. Scientometrics 124, 2185–2206.

Example: From 2021, the publisher will charge €9,500 to make a paper open access (OA) in Nature.

bioRxiv

THE PREPRINT SERVER FOR BIOLOGY

bioRxiv is an open access preprint repository for the biological sciences co-founded by John Inglis and Richard Sever in November 2013. It is hosted by the Cold Spring Harbor Laboratory. As preprints, papers hosted on bioRxiv are not peer-reviewed, but undergo basic screening and checked against plagiarism.

--Wikipedia

PUBPEER

The online journal club

PubPeer is a website that allows users to discuss and review scientific research after publication, i.e. post-publication peer review.

--Wikipedia

Home / Search

The PubPeer database contains all articles. Search results return articles with comments.

Birgit Wassermann

advanced search

To leave the first comment on a specific article, paste a unique identifier such as a **DOI**, **PubMed ID**, or **arXiv ID** into the search bar.

Login to save this search and receive email alerts

Search publications for: **Birgit Wassermann**

1 result

1 year ago

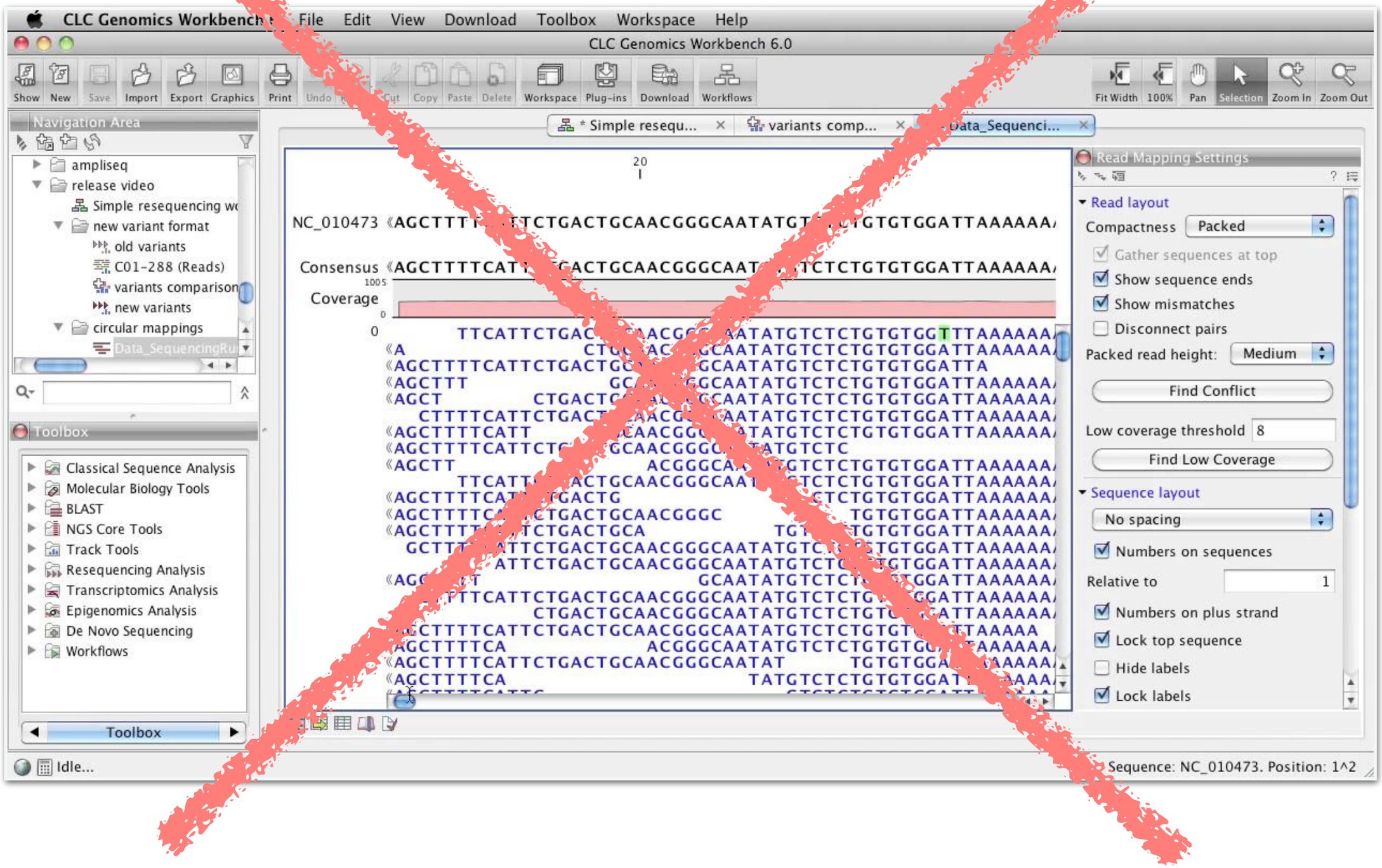
An Apple a Day: Which Bacteria Do We Eat With Organic and Conventional Apples?

Birgit Wassermann, Henry Müller, Gabriele Berg

Frontiers in Microbiology (2019)

2 comments

What can you do to make your research (better) reproducible?


CLC Genomics Workbench File Edit View Download Toolbox Workspace Help
CLC Genomics Workbench 6.0
Show New Save Import Export Graphics Print Undo Cut Copy Paste Delete Workspace Plug-ins Download Workflows
Fit Width 100% Pan Selection Zoom In Zoom Out
Navigation Area
ampliseq
release video
Simple resequencing w
new variant format
old variants
C01-288 (Reads)
variants comparison
new variants
circular mappings
Data_SequencingRu
Toolbox
Classical Sequence Analysis
Molecular Biology Tools
BLAST
NGS Core Tools
Track Tools
Resequencing Analysis
Transcriptomics Analysis
Epigenomics Analysis
De Novo Sequencing
Workflows
Toolbox
* Simple resequ...
variants comp...
Data_Sequenci...
20
NC_010473
Consensus
Coverage
1005
0
0
Read Mapping Settings
Read layout
Compactness Packed
Gather sequences at top
Show sequence ends
Show mismatches
Disconnect pairs
Packed read height: Medium
Find Conflict
Low coverage threshold 8
Find Low Coverage
Sequence layout
No spacing
Numbers on sequences
Relative to 1
Numbers on plus strand
Lock top sequence
Hide labels
Lock labels
Idle...
Sequence: NC_010473. Position: 1^2

Material and Methods (Manuscript)

In a first step, all paired-end raw reads were merged using FLASh (version 1.2.9, Magoc and Salzberg 2011) with minimum overlap of 5nt and maximal mismatch ration of 0.8.

Supplementary Data (Script or MD-Report)

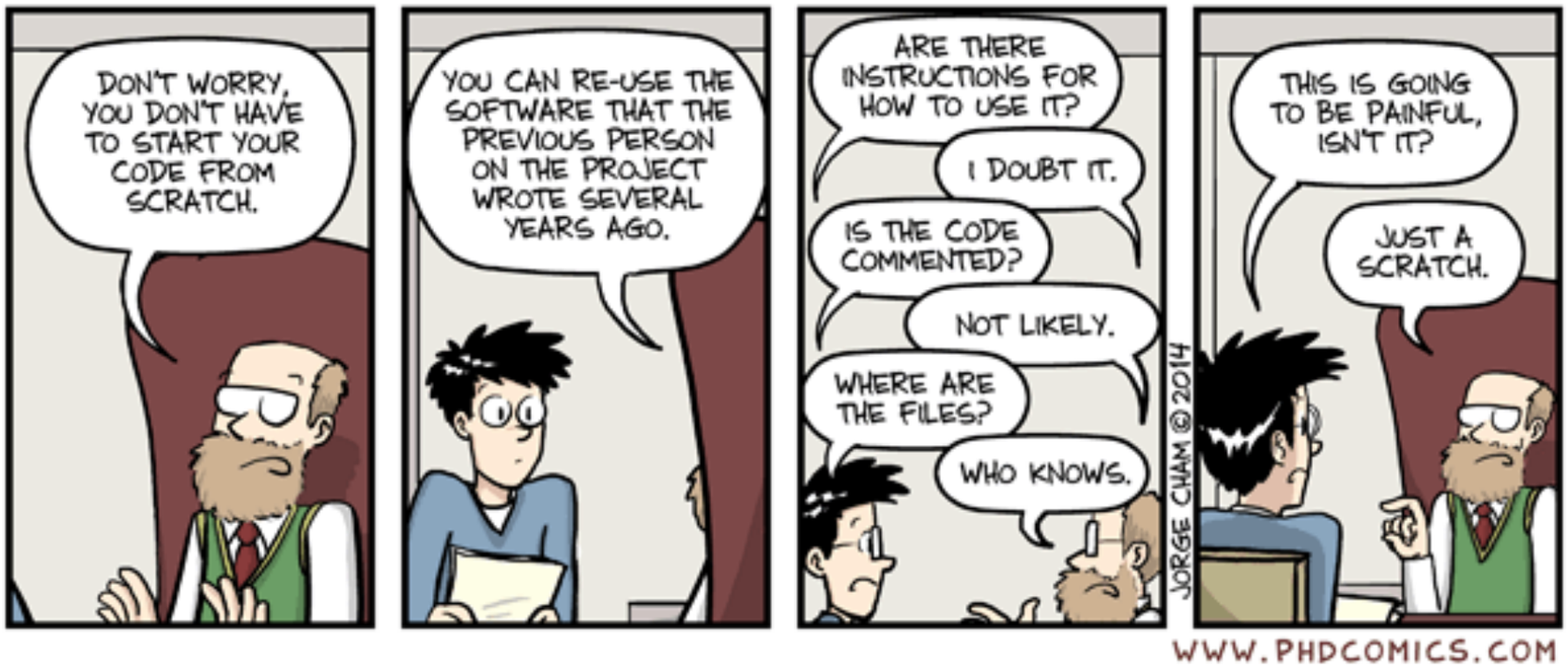
```
## (a) Merging overlapping paired-end reads
# -v Version (1.2.9)
# -m minimum overlap (default 10bp)
# -x max mismatch ration (default 0.25)

flash -m 5 -x 0.8 random_1000_R1.fq random_1000_R2.fq -o
merged | tee flash.log
```

DRYAD

The Dryad Digital Repository is a curated resource that makes research data discoverable, freely reusable, and citable. Dryad provides a general-purpose home for a wide diversity of data types.

https://datadryad.org


DON'T WORRY, YOU DON'T HAVE TO START YOUR CODE FROM SCRATCH.
YOU CAN RE-USE THE SOFTWARE THAT THE PREVIOUS PERSON ON THE PROJECT WROTE SEVERAL YEARS AGO.
ARE THERE INSTRUCTIONS FOR HOW TO USE IT?
I DOUBT IT.
IS THE CODE COMMENTED?
NOT LIKELY.
WHERE ARE THE FILES?
WHO KNOWS.
THIS IS GOING TO BE PAINFUL, ISN'T IT?
JUST A SCRATCH.
JORGE CHAM © 2014
WWW.PHDCOMICS.COM

```
error_correction.ph
error_correction_PE.ph
error_correction_PE_1.ph
error_correction_PE_new.ph
error_correction_SR_newer.ph
error_corection_SR_v190423.ph
error_correction_SR_newest.ph
```

Get Organised!

Bioinformatics is not a messy buisness but requires organizational skills. There are many little (and for some people obvious) ways to get organized.

- File names
- Sufixes
- Special characters
- Temporary files
- Style

```
ReadME.txt
error_correction_SR_v190116.ph.archive
error_correction_SR_v190423.ph.archive
error_correction_SR_v190502.ph
error_correction_PE_v200317.ph.archive
error_correction_PE_v200421.ph
```

Question - Aim

Input file(s) - original and parsed

Program & Version (& Link)
Parameters (& References)

Output file(s) / Log-file(s)

Interpretation / Disscusion

Date: XX.YY.ZZ

Aim
Find differences between two nucleotide sequences.

Input
my file: Pram_sequence_A0021.fasta
NCBI file: AY762091 (AY762091.fasta)

Pairwise alignment: LALIGN (Online Version 3.2.1)

http://www.ebi.ac.uk/Tools

Option: default

MATRIX	GAP OPEN	GAP EXTEND	E() THRESHOLD	OUTPUT FORMAT	GRAPHICS
+5/-4	-12	-4	10.0	MARKX 0	yes

Results

```
Waterman-Eggert score: 682;  170.3 bits; E(1) <  1e-47
98.6% identity (98.6% similar) in 140 nt overlap (1-140:1-140)

               10        20        30        40        50        60
A0021    ACACGTGCTACAATGGCCGTTACAGAGGGAAGCGAAACCGCGAGGTGGAGCCAATCTCAG...
         ::::::::::::::::::::::::::::::  ::::::::::::::::::::::::::...
AY76091  ACACGTGCTACAATGGCCGTTACAGAGGGATTCGAAACCGCGAGGTGGAGCCAATCTCAG...
               10        20        30        40        50        60
```

Discussion

My sequence (Pram sequence) aligns nicely with AY762091 from the NCBI database. There are, however, two nucleotide changes (red box).

Markdown Editor

```
### Merge Reads

In a first step, all paired-end raw reads were successfully merged
using **FLASh** (version 1.2.11, Magoc and Salzberg 2011) with minimum
overlap of 5nt and maximal mismatch ration of 0.8.

```bash
## (a) Merging overlapping paired-end reads
# Version
flash -v | head -n 1
# Merge R1 and R2 reads
flash -m 5 -x 0.8 random_1000_R1.fq random_1000_R2.fq -o merged | tee
flash.log
# Parameters:
# -m minimum overlap (default 10bp)
# -x max mismatch ration (default 0.25)
```

The merging rate was 87%.

```bash
grep "^@M" -c random_1000_R[12].fq
grep "^@M" -c random_1000_merged.fq
```
```

HTML / PDF Report

Merge Reads

In a first step, all paired-end raw reads were successfully merged using **FLASh** (version 1.2.11, Magoc and Salzberg 2011) with minimum overlap of 5nt and maximal mismatch ration of 0.8.

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# Version
flash -v | head -n 1
# Merge R1 and R2 reads
flash -m 5 -x 0.8 random_1000_R1.fq random_1000_R2.fq -o merged | tee flash.log
# Parameters:
# -m minimum overlap (default 10bp)
# -x max mismatch ration (default 0.25)
```

The merging rate was 87%.

```bash
grep "^@M" -c random_1000_R[12].fq
grep "^@M" -c random_1000_merged.fq
```

Headers

Headers are set using a hash before the title. The number of hashes before the title text will determine the depth of the header. Header depths are from 1-6

- H1 : `# Header 1`
- H2 : `## Header 2`
- H3 : `### Header 3`
- H4 : `#### Header 4`
- H5 : `##### Header 5`
- H6 : `###### Header 6`

Text Styling

- Links : `[Title](URL)`
- Bold : `**Bold**`
- Italicize : `*Italics*`
- Strike-through : `~~text~~`
- Highlight : `==text==`
- Paragraphs : Line space between paragraphs
- Line break : Add two spaces to the end of the line
- Lists : `* an asterisk for every new list item.`
- Quotes : `> Quote`
- Inline Code : `alert('Hello World');`
- Horizontal Rule (HR) : `\--------`


ATOM


StackEdit
In-browser Markdown editor

Project Jupyter exists to develop open-source software, open-standards, and services for interactive computing across dozens of programming languages.

A Quick Recap

Ask questions!

Not hesitate to ask for help if you have problems understanding or using a published method.

Reproducibility

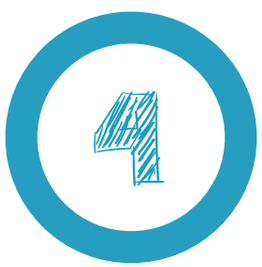
Avoid applications with GUIs and use terminal command instead.

Provide Script / Write Reports

Precise description of the workflow including versions and parameters.

Share your findings!

Think carfully about where to publish your work and do it for the right reasons.



Zen

Be organized.