

PUBLISHING LIVING SYSTEMATIC REVIEWS

Rebecca Lawrence
Managing Director, F1000

13 SEPTEMBER 2017
Cape Town, South Africa

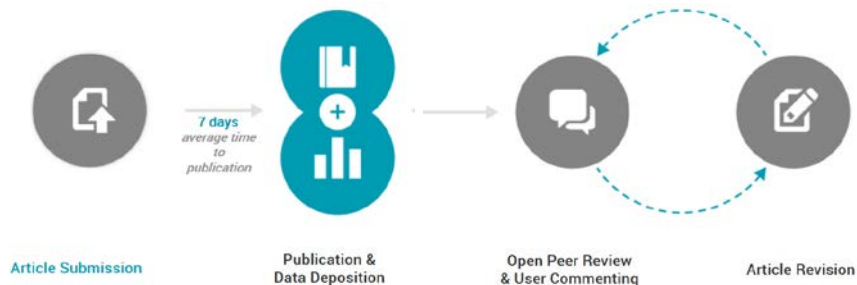
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CONFLICT OF INTEREST DECLARATION

I am employed as Managing Director of F1000 that could be perceived as a direct conflict of interest in the content of this presentation.

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Indexed in PubMed, Scopus etc

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For all
researchers

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For Wellcome-funded
researchers

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For Gates Foundation-funded
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RESEARCH ARTICLE

Geographic-genetic analysis of *Plasmodium falciparum* parasite populations from surveys of primary school children in Western Kenya [version 1; referees: awaiting peer review]

Irene Omedo , Polycarp Mogeni , Kirk Rockett², Alice Kamau , Christina Hubbart², Anna Jeffreys², Lynette Isabella Ochola-Oyler¹, Etienne P. de Villiers ,^{1,3,4} Caroline W. Gitonga⁵, Abdulsalan M. Noor^{3,5}, Robert W. Snow ,^{3,5} Dominic Kwiatkowski^{2,6}, Philip Bejon^{1,7}

[Author affiliations](#)
[Grant information](#)

Abstract

Background. Malaria control, and finally malaria elimination, requires the identification and targeting of residual foci or hotspots of transmission. However, the level of parasite mixing within and between geographical locations is likely to impact the effectiveness and durability of control interventions and thus should be taken into consideration when developing control programs.

Methods. In order to determine the geographic-genetic patterns of *Plasmodium falciparum* parasite populations at a sub-national level in Kenya, we used the Sequenom platform to genotype 111 genome-wide distributed single nucleotide polymorphic (SNP) positions in 2486 isolates collected from children in 95 primary schools in western Kenya. We analysed these parasite genotypes for genetic structure using principal component analysis and assessed local and global clustering using statistical measures of spatial autocorrelation. We further examined the region for spatial barriers to parasite movement as well as directionality in the patterns of parasite movement.

Results. We found no evidence of population structure and little evidence of spatial autocorrelation of parasite genotypes (correlation coefficients <0.03 among parasite pairs in distance classes of 1 km, 2 km and 5 km; p value=0.01). An analysis of the geographical distribution of allele frequencies showed weak evidence of variation in distribution of alleles, with clusters representing a higher than expected number of samples with the major allele being identified for 5 SNPs. Furthermore, we found no evidence of the existence of spatial barriers to parasite movement within the region, but

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VIEWS

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ARTICLE AFTER PEER REVIEW

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RESEARCH ARTICLE

REVISED Free serum haemoglobin is associated with brain atrophy in secondary progressive multiple sclerosis [version 2; referees: 3 approved]

 Alex Lewin^{1,5*},  Shea Hamilton ^{2*}, Aviva Witkov², Paul Langford ², Richard Nicholas³, Jeremy Chataway⁴,  Charles R.M. Bangham ²

* Equal contributors


 Author details

 Grant information


Abstract

Background: A major cause of disability in secondary progressive multiple sclerosis (SPMS) is progressive brain atrophy, whose pathogenesis is not fully understood. The objective of this study was to identify protein biomarkers of brain atrophy in SPMS.


Methods: We used surface-enhanced laser desorption-ionization time-of-flight mass spectrometry to carry out an unbiased search for serum proteins whose concentration correlated with the rate of brain atrophy, measured by serial MRI scans over a 2-year period in a well-characterized cohort of 140 patients with SPMS. Protein species were identified by liquid chromatography-electrospray ionization


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
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Referee Status:   

Invited Referees

Version(s)	1	2	3
REVISED Version 2 published 23 Dec 2016		 read report	 read report
Version 1 published 15 Nov 2016	 read report	 read report	 read report

1 Hans Lassmann, Medical University of Vienna, Austria
Simon Hametner, Medical University of Vienna, Austria

2 George Harauz, University of Guelph, Canada
Vladimir V. Bamm, University of Guelph, Canada

3 Franz Fazekas, Medical University of Graz, Austria
Michael Khalil, Medical University of Graz, Austria

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LSR – HOW COULD 'TRADITIONAL' JOURNALS KEEP UP-TO-DATE

The image displays three overlapping screenshots of the eLIFE journal website, illustrating various features and navigation options. The top screenshot shows the article "Increasing suppression of saccade-related transients along the human visual hierarchy" by Tal Golan et al., with a red circle highlighting the "RESEARCH ADVANCE" label. The middle screenshot shows the article "Human intracranial recordings link suppressed transients rather than 'filling-in' to perceptual continuity across blinks" by Tal Golan et al., with a red circle highlighting the "RESEARCH ARTICLE" label. The bottom screenshot shows the abstract of the same article, with a red box highlighting the "BUILT UPON BY" section, which lists the article "Increasing suppression of saccade-related transients along the human visual hierarchy" by Tal Golan et al. as a "RESEARCH ADVANCE Aug 29, 2017".

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NEUROSCIENCE

Increasing suppression of saccade-related transients along the human visual hierarchy

Tal Golan, Ido Davidesco, Meir Meshulam, David M Groppe, Pierre Mégevand

The Hebrew University of Jerusalem, Israel; New York University, United States; Weizmann Institute for Medical Research, United States; The Kremlil Neuroscience Center, College of Physicians and Surgeons, United States

RESEARCH ADVANCE

CITED 0 VIEWS 234 COMMENTS 0

Article

Figures and data

Side by side

Jump to

Abstract

A key hallmark of visual perceptual awareness is robustly noticeable eye and eyelid movements. In previous work (Golan et al., 2016) we found that excitatory broadband transients, driven by eye blinks, are suppressed in high. Here, we utilized the broad anatomical coverage of iEEG neurosurgical patients to test whether a similar stability in small saccades. We compared saccades (1.5°-3.5°) in

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NEUROSCIENCE

Human intracranial recordings link suppressed transients rather than 'filling-in' to perceptual continuity across blinks

Tal Golan, Ido Davidesco, Meir Meshulam, David M Groppe, Pierre Mégevand, Erin M Yeagle, Matthew S Goldfinger, Michal Harel, Lucia Melloni [see all](#)

The Hebrew University of Jerusalem, Israel; New York University, United States; Weizmann Institute of Science, Israel; Hofstra Northwell School of Medicine, United States; The Feinstein Institute for Medical Research, United States; Max Planck Institute for Brain Research, Germany; School of Medicine, New York University, United States; Columbia University College of Physicians and Surgeons, United States; Nathan Kline Institute, United States [see all](#)

RESEARCH ARTICLE Sep 29, 2017

CITED 1 VIEWS 95 COMMENTS 0

CITE AS: eLife 2016;5:e17243. DOI: 10.7554/eLife.17243

Article

Figures and data

Side by side

Jump to

Abstract

We hardly notice our eye blinks, yet an externally generated retinal interruption of a similar duration is perceptually salient. We examined the neural correlates of this perceptual distinction using intracranially measured ECoG signals from the human visual cortex in 14 patients. In early visual areas (V1 and V2), the disappearance of the stimulus due to either invisible blinks or salient blank video frames ('gaps') led to a similar drop in activity level, followed by a positive overshoot beyond baseline, triggered by stimulus reappearance. Ascending the visual hierarchy, the reappearance-related overshoot gradually subsided for blinks but not for gaps. To contrast, the disappearance-related

BUILT UPON BY

Increasing suppression of saccade-related transients along the human visual hierarchy

Tal Golan et al.

RESEARCH ADVANCE Aug 29, 2017

THREADED PUBLICATIONS

EDITORIAL OPEN ACCESS

Linked publications from a single trial: a thread of evidence

Douglas G Altman, Curt D Furberg, Jeremy M Grimshaw and Daniel R Shanahan

Trials 2014, 15:369 | <https://doi.org/10.1186/1745-6215-15-369> | © Altman et al.; licensee BioMed Central Ltd. 2014

situation is further complicated by the ever-growing body of literature. A single clinical trial can result in multiple publications: the study protocol and traditional results paper or papers, as well as commentaries, secondary analyses and, eventually, systematic reviews, among others [8].

PLOS ONE
TENTH ANNIVERSARY

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RESEARCH ARTICLE

Gameplay as a Source of Intrinsic Motivation in a Randomized Controlled Trial of Auditory Training for Tinnitus

Derek J. Hoare, Nicolas Van Labbe, Abby McCormack, Magdalena Sareda, Sandra Smith, Victoria L. Kowalkowski, Mike Sharples, Deborah A. Hall

Published: September 12, 2014 • <https://doi.org/10.1371/journal.pone.0107430>

Article	Authors	Metrics	Comments
Abstract			
Introduction			
Methods			
Results			
Discussion			
Conclusion			
Supporting Information			
Author Contributions			

Abstract

Background

Previous studies of frequency discrimination training (FDT) for tinnitus based training programmes relying on extrinsic factors to motivate improvement in tinnitus symptoms.

Purpose

CrossMark

Document is current

Any future updates will be listed below

Gameplay as a Source of Intrinsic Motivation in a Randomized Controlled Trial of Auditory Training for Tinnitus
Crossref DOI Link: <http://dx.doi.org/10.1371/journal.pone.0107430>
Published: 2014-09-12

Funding

Clinical Trials (BETA)

Clinical trials referenced in this document

Clinical trial number nct02095262 at ClinicalTrials.gov

Other documents that mention this clinical trial

Relationship between tinnitus pitch and edge of hearing loss in individuals with a narrow tinnitus bandwidth (Pre-Results)
International Journal of Audiology
<http://dx.doi.org/10.3109/14992027.2014.979373>

Agreement and Reliability of Tinnitus Loudness Matching and Pitch Likeness Rating (Results)
PLOS One
<http://dx.doi.org/10.1371/journal.pone.0114553>

REPURPOSING ERRATA/RETRACTION SYSTEM

The image displays three overlapping screenshots from the PubMed and Trials journals websites, illustrating the relationship between a study protocol and its erratum.

Top Screenshot (PubMed): Shows the original study protocol article. The title is "Chinese medicine combined with calcipotriol betamethasone and calcipotriol ointment for Psoriasis vulgaris (CMBCOP): study protocol for a randomized controlled trial." The authors listed are Wen ZH, Xuan ML, Yan YH, Li XY, Yao DN, Li G, Guo XF, Qu AH, Lu CJ¹. The article is dated 2014 Jul 22;15:294. A red box highlights the "Erratum in" section, which states: "Erratum to: 'Chinese medicine combined with calcipotriol betamethasone and calcipotriol ointment for Psoriasis vulgaris (CMBCOP): study protocol for a randomized controlled trial'. [Trials. 2016]"


Middle Screenshot (PubMed): Shows the erratum article. The title is "Erratum to: 'Chinese medicine combined with calcipotriol betamethasone and calcipotriol ointment for Psoriasis vulgaris (CMBCOP): study protocol for a randomized controlled trial'." The authors listed are Wen ZH^{1,2}, Xuan ML¹, Yan YH³, Li XY¹, Yao DN³, Li G¹, Guo XF¹, Qu AH¹, Lu CJ⁴. The article is dated 2016 Jul 26;17(1):357. A red box highlights the "Erratum for" section, which states: "Chinese medicine combined with calcipotriol betamethasone and calcipotriol ointment for Psoriasis vulgaris (CMBCOP): study protocol for a randomized controlled trial. [Trials. 2014]"


Bottom Screenshot (Trials): Shows the original study protocol article. The title is "Chinese medicine combined with calcipotriol betamethasone and calcipotriol ointment for Psoriasis vulgaris (CMBCOP): study protocol for a randomized controlled trial." The authors listed are Ze-Huai Wen, Mei-Ling Xuan, Yu-Hong Yan, Xiao-Yan Li, Dan-Ni Yao. The article is dated 2014 15:2172. A red box highlights the note: "The original article was published in Trials 2014 15:2172"

F1000 APPROACH TO LIVING PUBLICATIONS

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METHOD ARTICLE



UPDATE A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast [version 3; referees: 2 approved]

 METRICS


1722


 VIEWS


Open Peer Review

Referee Status:  

	Invited Referees
Version(s)	1 2

 Maria Natalia Bo Wang¹, M

 Author

 Grant

Abst

In the fission yeast *Schizosaccharomyces pombe*, CRISPR/Cas9 systems have been used to generate targeted deletions and insertions. However, the traditional method of cloning the sgRNA without restriction enzymes (restriction-free cloning) is laborious and expensive. To increase the efficiency of this method, we have developed a new method to clone the sgRNA without restriction enzymes (restriction-free cloning) using a CRISPR/Cas9 system. This improved method thus avoids errors occurring during the ligation step that is required for the first method, and is faster and less expensive. CRISPR4P designs primers for both the traditional and ligation-free cloning method.

We have indicated in the previous version of the paper that we are developing alternative methods. Now we have replaced this text with a brief description of the optimized method as above, and added the alternative steps to the step-by-step procedure and an updated the protocol and Supplemental File 1. We also provide an updated Supplemental Table 1 containing the oligos used with the new method.

TRACKING VERSIONING

The image is a collage of overlapping screenshots from various academic platforms, primarily focusing on the Wellcome Open Research article "A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast".

- Top Left:** A screenshot of the Wellcome Open Research article page. It shows the title, authors (María Rodríguez-López, Cristina Cotoal, Oscar Fernández-Sánchez, Natalia Borbarán Bravo, Heike Abendroth, Jin Weng, Mikel Zarategui, and Jörg Bähler), and a notification box stating: "There is a newer version of this article available. SUPPRESS THIS MESSAGE FOR ONE DAY".
- Top Right:** A screenshot of the CrossMark interface. It displays the article title and a prominent yellow box with a warning icon and the text: "Updates are available. New version dated 2017-05-05".
- Middle Left:** A screenshot of the PubMed Central (PMC) interface. It shows the article title and a list of versions: "PMC5445975.1; 2016 Nov 23", "PMC5445975.2; 2017 Jan 3", and "PMC5445975.3; 2017 May 5".
- Bottom Left:** A screenshot of the Wellcome Open Research article page, showing the title, authors, and a list of versions: "Version 3. Wellcome Open Res. 2016; 1: 19. Published online 2017 May 5. doi: 10.12688/wellcomeopenres.10038.3".
- Bottom Right:** A screenshot of the Wellcome Open Research article page, showing the title, authors, and a list of versions: "Version 3. Wellcome Open Res. 2016; 1: 19. Published online 2017 May 5. doi: 10.12688/wellcomeopenres.10038.3".

The screenshots illustrate the process of tracking and updating research articles across different platforms, highlighting the importance of versioning in academic publishing.

REGULARLY UPDATED FIGURES

From Dinas et al, 2017: <https://f1000research.com/articles/6-286/v2>

	First author	Random sequence generation	Allocation concealment	Blinding of participants and researchers	Blinding of outcome assessment	Incomplete outcome data	Selective reporting	Other bias
	RCTs							
Bang, 2014	+	-	-	-	-	+	+	+
Greulich, 2014	+	+	-	+	+	+	+	+
Greulich, 2014a	+	+	-	?	+	+	+	+
Hecksteden, 2013	+	+	-	+	+	+	+	+

Table 2. Risk of bias assessment using the Cochrane Collaboration's tool.

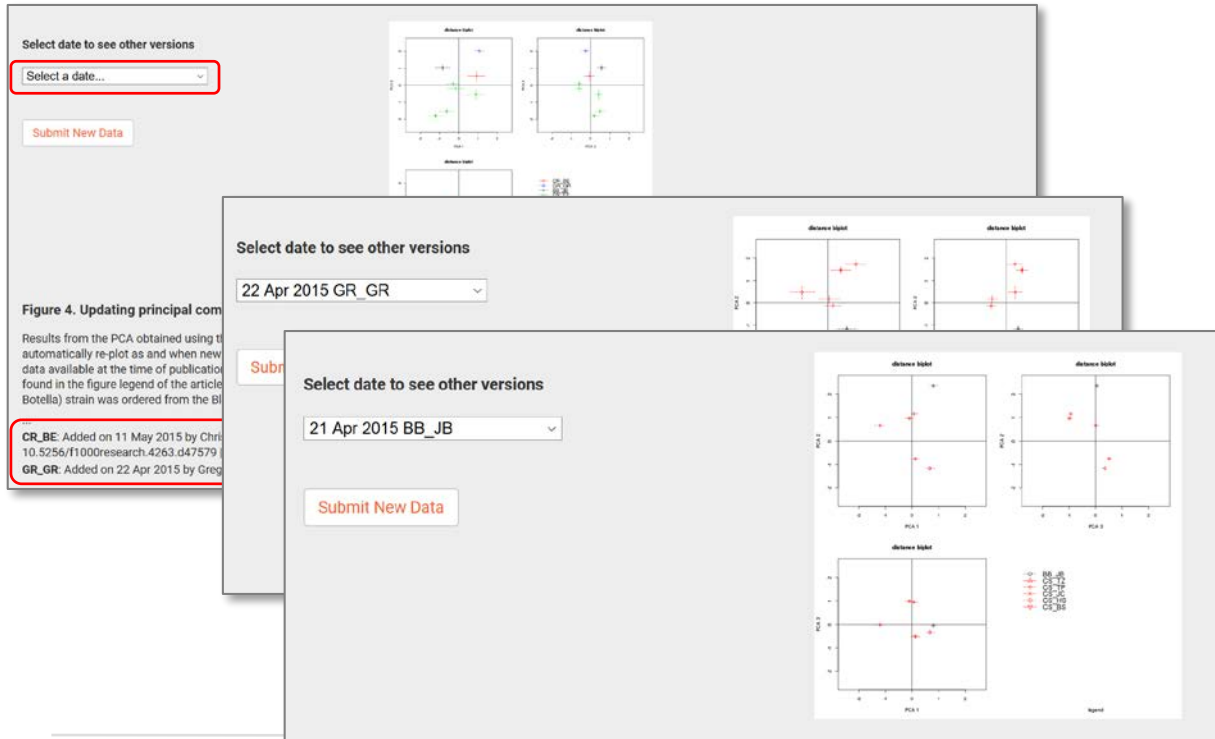
+ Low risk of bias; - High risk of bias; ? Unclear risk of bias; RCT: Randomised controlled trials; CT: Controlled trials; SGS: Single group design studies; CSS: Cross sectional studies.

Up-to-date, as of 26 May 2017

Can update date if rerun the search & no new data to add

LIVING FIGURES

<https://f1000research.com/articles/3-176/v2>



CONCLUSION

- There are existing mechanisms that can be repurposed by traditional journals to link updates & cross-publisher
- The technology is now available to update through versioning and living elements within articles that
 - minimise time/effort for authors & reviewers
 - enable timely updates
 - retain archival record
 - ensure transparency of changes across all major sites

QUESTIONS



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