

Joseph David Parker Scientist / Bioinformatician

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DOB: 11th December 1981

Evolutionary biologist developing novel models and methods for real-time phylogenomics

April 2015 – Present

Royal Botanic Gardens, Kew

Independent research in biodiversity informatics and evolutionary biology, in particular real-time phylogenomics, field-based DNA sequencing, and associated biodiversity informatics to support Kew's strategic aims. Develop new projects for my research and seek funding through RCUK, industry, Kew Foundation and other funding sources. Advice and oversight (and workpackage leadership: Plant And Fungal Trees of Life WP1) of central 2020 Kew outputs. Supervision of project students. Co-ordinate journal clubs, training, and other departmental activities related to scholarship.

Early Career Research Fellow

April 2011 – February 2015

School of Biological & Chemical Sciences, Queen Mary, University of London PDRA

Phylogenomic analyses of eukaryote genomic coding sequence (CDS) data to detect signatures of molecular convergence. Developed and implemented novel methods for adaptive molecular convergence detection and designed, developed and tested a robust and flexible high-throughput pipeline and Java API, including web-based (CGI, PHP/MySQL) interface. Deployed on multiple computing clusters, resulting in publications in *Nature*, *Current Biology* (and in prep.)

January 2012 – Present

London Cycling Campaign / Southwark Cyclists

Data analysis, policy engagement with local government, planning engineers and community stakeholders in support of successful 'Space For Cycling' campaign. Results included local council's formal adoption of 'presumption for sustainable transport' and 'segregated space for cycling' policies.

Volunteer

March 2010 – November 2011

Imperial College BSc Biology

Postdoctoral demonstrator (bioinformatics and phylogenetics) and tutor (evolutionary biology). Set, marked & discussed students' essays (in small groups). Demonstrated bioinformatics techniques (in large groups).

Tutor/demonstrator

March 2009 – March 2011

MRC Human Immunology Unit, WIMM

Phylogenetic and bioinformatics analyses (including machine-learning) of experimental and sequence data relating to SIV and HIV infection with particular focus on drivers of broadly-neutralizing antibody development. Designed HIV antigens for the NGIN consortium, incorporated into successful trimeric HIV vaccines under trial in animal models.

PDRA

January 2009 – Present

Kitson Consulting Limited, Bristol

Co-founded informatics and scientific computing consultancy, specialising in bespoke solutions for SME clients using open-source software.

Director, Co-founder

September 2008

Bayesian Analysis of Tip-Significance (BATS)

Delivered a public implementation of Java software developed during my PhD: user-friendly GUI, manuals and teaching materials for Dept. Zoology, Oxford University

Developer

January 2005 – June 2008

Oxford University (various)

Tutor and senior practical teaching assistant in statistics, population biology, genetics and phylogenetics for Magdalene College, St. John's College & Dept. Zoology, Univ. Oxford.

Tutor/demonstrator

May 2007 – May 2008 (part-time)

Sotones Music Co-op

Developed dynamic, media-rich web presence for a record label using PHP/MySQL, Javascript, XHTML and CSS technologies. Developed CMS from scratch following consultation with musicians and label managers.

Director, Web Developer

Education

Oct 2004 - Sept 2008

Oxford University

PhD (DPhil) The within- and among-host evolution of chronically-infecting human RNA viruses.

NERC-funded studentship focused on the computational analysis of viral sequence data to investigate pathogen evolution. My thesis advanced our understanding of substitution rate heterogeneity among and between viral metapopulations; phylogeographic structure over varying spatial scales, including compartmentalisation; and archiving of viral sub-populations. Outputs included publications in highly-ranked international journals, conference posters and oral presentations.

Developed a variety of novel analyses for phylodiversity, selection and phylogeographic inference. Implemented novel and existing analyses in Java, Perl, Python, PHP/MySQL and XHTML. Applications deployed on Apple XGrid and various UNIX systems, as well as executable binaries for personal computers. Developed plugins and enhancements for existing popular bioinformatics projects including **award-winning** Shannon Entropy plugin for Geneious. Worked on Macintosh, Windows and UNIX platforms in local and cluster computing environments.

Other duties included teaching (see above) maintenance and administration of key software and personnel pages on research group website. Ran junior researchers' association including provision of statistics, communications, and media training culminating in residential training with a five-figure budget.

Sept 2001 - July 2004

Imperial College London

BSc Biology (Honours) 1st class

Modules taken included: Population genetics; macroevolution; bioinformatics; introduction to programming; computational modelling for biologists; resource management; marine microbiology.

Sept 1993 - June 2000

King Edward VI School, Southampton

A-Level **Chemistry (A)**, **Physics (A)**, **Biology (A)**. 10 GCSEs grades A*/A.

Additional information

- Conversational French and full driving licence.
- I am a fluent Java, Perl, LAMP (Linux/Apache/MySQL/PHP), R and Bourne Shell developer.
- I have C, Python, Ruby/RoR and Javascript development experience. Currently learning Angular.js
- I am keen on cycling, outdoor activities and team sports. Since 2006 I have been a qualified watchleader for OYT (award-winning sail training charity working with young people) and I am a qualified scuba diving instructor, rescue boat cox, radio operator, first-aider (including O₂ admin) and incident manager.
- During my time at Imperial College I organised and led a two-month expedition to survey biodiversity in a previously unstudied area of Paraguay.
- I enjoy performing music and have had extensive experience of broadcast and print media, having held key posts including Live Reviews Editor, Science Correspondent, Station Manager, Technical Manager and Production Manager at award-winning student outlets. I am experienced in a range of media production software in addition to my academic programming and web development interests.

References available on request

Dr. Joe Parker, Queen Mary University of London
List of publications / awards

Journal Publications

* Indicates equal contribution. (total citations: 377; h-index: 8)

Parker J, & Rossiter, S.J. (in prep.) Application Note: CONTEXT – A Phylogenomic Dataset Browser. Preview: <http://bit.ly/1JsSiWl>

Parker, J. & Pybus, O.G. (in prep) Error rate and statistical power of distance-based measures of phylogeny-trait association. Preview: <http://bit.ly/1eR60H0>

Parker J, & Rossiter, S.J. (in prep.) Application Note: Genome Convergence Pipeline (GCP) – an application for the efficient and user-friendly detection of adaptive molecular convergence in phylogenomic datasets. Preview: <http://bit.ly/1BLTf5J>

Thézé, J., Lowes, S., Parker, J. & Pybus, O.G. (2015) Evolutionary and phylogenetic analysis of the hepaciviruses and pegiviruses. Submitted: *Genome Biol. Evol.*

Kuo, H.-C., Chen, S.-F., Fang, Y.-P., Cotton, J.A., Parker, J., Csorba, G., Lim, B., Chen, C.-H., Chou C.-H., & Rossiter, S.J. (2015) A test of non-allopatric divergence in putative island endemic sister bat species. In press: *Mol. Ecol.*

Parker, J.*, Tsagkogeorga, G.*, Cotton, J.A., Liu, Y., Provero, P., Stupka, E. & Rossiter, S.J. (2013) Genome-wide signatures of convergent evolution in echolocating mammals. *Nature* 502(7470):2280231. doi:10.1038/nature12511. *These authors contributed equally to this article. Cited 51 times.

Tsagkogeorga, G.*, Parker, J.*, Stupka, E., Cotton, J.A., & Rossiter, S.J. (2013) Phylogenomic analyses elucidate evolutionary relationships of the bats (Chiroptera) *Curr. Biol.* 23(22):2262-2267. *These authors contributed equally to this article.

Heyndrickx, L., et al., NGIN Consortium (2013) Selected HIV-1 Env trimeric formulations act as potent immunogens in a rabbit vaccination model. *PLoS ONE* 8(9):e74552.

Gray RR*, Parker J*, Lemey P, Salemi M, Katzourakis A, Pybus OG. (2011) The mode and tempo of hepatitis C virus evolution within and among hosts. *BMC Evol Biol.* 11(1):131. *These authors contributed equally to this article. Cited 41 times.

Bowles, E.J.*, Parker, J.*, Heyndrickx, L., Grevstad, B., Jansson, M., Vanham, G., Stewart-Jones, G. (2011) Elicitation of neutralising antibodies using patient-derived gp140 immunogens from a long-term non-progressor. *AIDS Rev. Hum. Retrovir.* 27(10):A48.

Clegg SR, Coyne KP, Parker J, Dawson S, Godsall SA, Pinchbeck G, Cripps PJ, Gaskell RM, Radford AD. (2011) Molecular epidemiology and phylogeny reveals complex spatial dynamics of endemic canine parvovirus. *J. Virol.* 85:7892-99. Cited 19 times.

Şahin G, Bowles E., Parker J, Uchtenhagen H., Sheik-Khalil E., Taylor S., Pybus O., Mäkitalo B., Sallow L., Spångberg M, Thorstenson R, Achour R., Fenyö E-M, Stewart-Jones G., & Spetz A-L. (2010) Generation of neutralizing antibodies and divergence of SIVmac239 in Cynomolgus Macaques following short-term early antiretroviral therapy. *PLoS Path.* 6(9):e1001084.

Rosario M, Fulkerson J, Soneji S, Parker J, Im EJ, Borthwick N, Bridgeman A, Bourne C, Joseph J, Sadoff JC, Hanke T (2010) Safety and immunogenicity of novel recombinant BCG and modified vaccinia virus Ankara vaccines in neonate rhesus macaques. *J Virol.* 84(15):7815-21. Cited 21 times.

Humphreys, I., Fabris, P., Parker, J., Huang, G., Flemming, V., Klenerman, P. & Barnes, E. (2009) Detailed characterisation of the of the HCV genotype-3a envelope 2 protein in hepatitis C virus reveals two novel hypervariable regions under selection pressure early in acute infection. *J Virol.* 83(22):11456-66.

Tee, K. K., Pybus, O. G., Parker, J. Ng, K. P., Kamarulzaman, A. & Takebe, Y. (2009) Estimating the date of origin of an HIV-1 circulating recombinant form. *Virology.* 387(1):229-34. Cited 16 times.

Parker J, Rambaut A & Pybus OG (2008) Correlating viral phenotypes with phylogeny: Accounting for phylogenetic uncertainty. *Infect Genet Evol* 8:239-246. Cited 158 times.

Published software

CONTEXT – A Phylogenomic Dataset Browser – an application for the efficient and user-friendly calculation and display of genomic sequence alignment and phylogeny statistics. Native Java API implementing analysis, I/O parsing and rendering of multiple sequence alignments and phylogenies, optimised for large genomic datasets. Version 0.8.1 Prerelease; public Git repository at: <https://github.com/lonelyjoeparker/qmul-genome-convergence-pipeline/blob/master/CONTEXT.md> executable build snapshot at: <http://bit.ly/1JGQZ5m>

Genome Convergence Pipeline – Adaptive Biological Convergence Detection API. Java API and mixed C++, Perl, PHP and MySQL dependencies for the detection of molecular convergence in CDS alignments of eukaryote genomic in HTC cluster deployments. Alpha release, public Git repository at: <https://github.com/lonelyjoeparker/qmul-genome-convergence-pipeline/blob/master/README.md>; executable build snapshot at: <http://bit.ly/1OgKyXJ>

BaTS – Bayesian associations of Tip Significance. Java. Bayesian methods to measure phylogeny-trait, or phylogeny-location associations from sequence data, correcting for phylogenetic uncertainty. Freeware Beta versions Mac OSX, Windows, Linux. <http://evolve.zoo.ox.ac.uk/Evolve/BaTS.html>

BEFI-BaTS – Alpha release (development) of BaTS incorporating additional measures of phylodiversity and phylogeny-trait association that integrate branch-length information. Freeware, Public alpha: www.lonelyjoeparker.com/?page_id=274 Git repository: <https://github.com/lonelyjoeparker/befi-bats-gui>

HADPACK – HIV Antigen Determination PACKAGE. Mixed Java and Perl. Library of methods and workflows for the generation of phylogenetic parameters from HIV/SIV sequence data, and their correlation with database annotations and clinical indicators. Partial dependencies for proprietary data; public release featuring only open-sourced annotation reference data in development.

SHIAT – Shannon Heterogeneity in Alignments Tool. Java. A suite of methods for near-instantaneous estimates of pairwise, sitewise and average diversity and heterogeneity in sequence alignments. Freeware Beta versions for Mac OSX, Windows, Linux with plugins ported to Geneious and CLCBio. <http://evolve.zoo.ox.ac.uk/Evolve/SHIAT.html>

Conference Presentations and Posters

Presenting author is underlined.

Parker, J. Why Aren't We Benchmarking Bioinformatics? Presented at the *KCL Benchmarking 2016 Symposium*. 20th April 2016, London, UK. Slides: <http://bit.ly/1WG7B4L>.

Parker, J. Convergence for everyone? Detecting disparate signals of genomic adaptive convergence in several different datasets: initial results, lessons, and perspectives. Invited presentation at the *19th Evolutionary Biology Meeting at Marseilles*. 15th-18th September 2014, Marseille, France. Slides: <http://bit.ly/1IOkv5v>

Davies, K.J.T., Bennett, N.C., Tsagkogeorga, G., Parker, J., Rossiter, S.J. & Faulkes, C.G. Genetic insights into the behavioural and morphological diversity of African mole-rats (family: Bathyergidae). Presented at the *14th congress of the European Society for Evolutionary Biology*. 19-24th August 2013, Lisbon, Portugal.

Mao, X., Bailey, S., Parker, J., Tsagkogeorga, G. & Rossiter, S.J. Comparative Genomic and Phylogeographic Analysis of Horseshoe Bats. Presented at the *International Bat Research Conference*, 11-15th August 2013, San Jose, Costa Rica

Parker, J., Tsagkogeorga, G*, Cotton JA, Stupka, E & Rossiter, SJ. Signatures of genome-wide convergent molecular evolution: initial results. Poster presented at *SMBE 2012*, June 23-26 2012, Dublin, Republic of Ireland.

Parker, J., Bowles, E.J.*, Heyndrickx, L., Grevstad, B., Jansson, M., Vanham, G., Stewart-Jones, G. Temporal Analysis of SIVmac239 Infection and Evolution in 12 Cynomolgous Macaques. Poster presented at *Keystone Symposium on HIV Vaccines and Viral Immunity*, March 21st-26th, 2010, Banff, Canada.

Competitive awards

*Indicates Principal Investigator

- £3,603** **Parker, J.* (2015-2016)** Communications and computation platforms for real-time, field-based DNA collection, sequencing and analysis. *Kew Foundation Pilot Study Fund (UK)*
- £3,000** **Parker, J.* (2015-2016)** Fellowship Programme. *Software Sustainability Institute (UK)*.
- £10,000** **Pybus, O.G.*, Takebe, Y.*, Parker, J & Tee, K.K. (2010)**. The evolutionary and spatial dynamics of human viral pathogens. *The Daiwa-Adrian Awards 2010, Daiwa Foundation (Japan)*.

Invited External Talks and Lectures

Parker, J. Interpreting tree space in the context of very large empirical datasets. Invited seminar presented to Department of Mathematics lunchtime seminar series, *University of Portsmouth*. November 19th, 2014. Slides: <http://bit.ly/1Xpqt7S>

Parker, J. Highly Parallel Phylogenetics of genomic coding sequence (CDS) data using high-throughput computing resources. Invited seminar presented to MSc (Evolutionary Biology) students, *University College, Dublin*. October 17th, 2013. Slides: <http://bit.ly/1Qdu0kH>

Parker, J., Tsagkogeorga, G., Cotton JA, Stupka, E & Rossiter, SJ. Developing a flexible platform for high-throughput phylogenomics: case study, conclusions and lessons for the future. Presented at the *Tropical biodiversity in the 21st century symposium / Genomic Observatories 3 Workshop*, Natural History Museum, London, UK, June 3rd-4th, 2013.

Parker, J., Bowles, E.J., Stewart-Jones, G. Bioinformatic approaches to immunogen design: Understanding Env sequence features associated with broad neutralization. Presented at the *2nd Annual NGIN Meeting*, May 25th-26th, 2010, CEA, Fontenay-aux-Roses, France.

Other Recent Talks

Parker, J. Using DNA sequences to explore peculiar similarities in bat and whale hearing genes. Lecture to Year 10 & 11 students at *St. Paul's Way Trust School* (foundation trust), 25th January, 2012, London, UK.

Parker, J. Lend me your ears: Exploring peculiar similarities in bat and whale hearing genes. Presented at *Café Scientifique* (public science-engagement event), 9th November, 2011, London, UK.

Book Chapters

Parker, J. Convergence for everyone? Detecting disparate signals of genomic adaptive convergence in several different datasets: initial results, lessons, and perspectives. *In prep: Evolutionary Biology: 18th Meeting 2014*. Pontarotti, P (Ed). Springer, New York. Preview: <http://bit.ly/1SY08eX>