

PHILIP LEE FALK JOHNSON

Biology-Psychology Bldg #144, Room 1210
College Park, MD 20742

(301)405-6176
plfj@umd.edu

EDUCATION

- University of California**, Berkeley, CA 2004–2009
Ph.D., Biophysics with a designed emphasis in Computational and Genomic Biology
Advisor: Montgomery Slatkin
Dissertation: Unbiased population genetic inference from high-throughput sequencing data.
- Harvard University**, Cambridge, MA 1997–2001
A.B., Computer Science and Biology, with Honors
Advisor: George Church
Thesis: Higher order hidden Markov models for DNA-binding site identification.

POSITIONS

- University of Maryland**, College Park, MD Jan. 2015–
Assistant Professor, Department of Biology
- Emory University**, Atlanta, GA 2009–2014
Postdoctoral fellow
Advisor: Rustom Antia
- National Center for Biotechnology Information**, Bethesda, MD 2001–2004
Senior systems analyst

FELLOWSHIPS & AWARDS

- NIH Pathway to Independence K99GM104158 2013–2014
- NSF Postdoctoral Fellowship in Biological Informatics 2010–2011
- Alan J. Bearden Memorial Award for outstanding dissertation research 2009
- Chang-Lin Tien Fellowship (Berkeley graduate fellowship) 2007–2009

PUBLICATIONS

1. Weissman JL, Stoltzfus A, Westra ER, and **Johnson PLF**. (2020). Avoidance of self during CRISPR immunization. *Trends in Microbiology*, 28:543–53.
2. Weissman JL and **Johnson PLF**. (2020). Network-based prediction of novel CRISPR-associated genes in metagenomes. *mSystems*, 5.
3. Weissman JL, Fagan WF, and **Johnson PLF**. (2019). Linking high GC content to the repair of double strand breaks in prokaryotic genomes. *PLoS Genetics*, 15:e1008493.
4. Weissman JL, Laljani RMR, Fagan WF, and **Johnson PLF**. (2019). Visualization and prediction of CRISPR incidence in microbial trait-space to identify drivers of antiviral immune strategy. *The ISME Journal*, 13:2589–602.
5. Weissman JL, Yiu HH, and **Johnson PLF**. (2019). What bacteria do when they get sick. *Frontiers Young Minds*, 7.
6. Weissman JL, Fagan WF, and **Johnson PLF**. (2018). Selective maintenance of multiple CRISPR arrays across prokaryotes. *The CRISPR Journal*, 1:405–13.

7. Loreille O, Ratnayake S, Bazinet AL, Stockwell TB, Sommer DD, Rohland N, Mallick S, **Johnson PLF**, Skoglund P, Onorato AJ, Bergman NH, Reich D, and Irwin JA. (2018). Biological sexing of a 4000-year-old Egyptian mummy head to assess the potential of nuclear DNA recovery from the most damaged and limited forensic specimens. *Genes*, 9.
8. Weissman JL, Holmes R, Barrangou R, Moineau S, Fagan WF, Levin B, and **Johnson PLF**. (2018). Immune loss as a driver of coexistence during host-phage coevolution. *The ISME Journal*, 12:585–97.
9. Akondy RS*, **Johnson PLF***, Nakaya HI, Edupuganti S, Mulligan MJ, Lawson B, Miller JD, Pulendran B, Antia R, and Ahmed R. (2015). Initial viral load determines the magnitude of the human CD8 T cell response to yellow fever vaccination. *Proc Natl Acad Sci U S A*, 112:3050–5.
10. Schroeder H, Ávila Arcos MC, Malaspinas AS, Poznik GD, Sandoval-Velasco M, Carpenter ML, Moreno-Mayar JV, Sikora M, **Johnson PLF**, Allentoft ME, Samaniego JA, Haviser JB, Dee MW, Stafford TW, Salas A, Orlando L, Willerslev E, Bustamante CD, and Gilbert MTP. (2015). Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. *Proc Natl Acad Sci U S A*, 112:3669–73.
11. Malaspinas AS, Lao O, Schroeder H, Rasmussen M, Raghavan M, Moltke I, Campos PF, Sagredo FS, Rasmussen S, Gonçalves VF, Albrechtsen A, Allentoft ME, **Johnson PLF**, Li M, Reis S, Bernardo DV, DeGiorgio M, Duggan AT, Bastos M, Wang Y, Stenderup J, Moreno-Mayar JV, Brunak S, Sicheritz-Ponten T, Hodges E, Hannon GJ, Orlando L, Price TD, Jensen JD, Nielsen R, Heinemeier J, Olsen J, Rodrigues-Carvalho C, Lahr MM, Neves WA, Kayser M, Higham T, Stoneking M, Pena SDJ, and Willerslev E. (2014). Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. *Curr Biol*, 24:R1035–7.
12. Fu Q, Li H, Moorjani P, Jay F, Slepchenko SM, Bondarev AA, **Johnson PLF**, Aximu-Petri A, Prüfer K, de Filippo C, Meyer M, Zwyns N, Salazar-García DC, Kuzmin YV, Keates SG, Kosintsev PA, Razhev DI, Richards MP, Peristov NV, Lachmann M, Douka K, Higham TFG, Slatkin M, Hublin JJ, Reich D, Kelso J, Viola TB, and Pääbo S. (2014). Genome sequence of a 45,000-year-old modern human from western Siberia. *Nature*, 514:445–9.
13. **Johnson PLF**, Goronzy JJ, and Antia R. (2014). A population biological approach to understanding the maintenance and loss of the T-cell repertoire during aging. *Immunology*, 142:167–75.
14. Prüfer K, Racimo F, Patterson N, Jay F, Sankararaman S, Sawyer S, Heinze A, Renaud G, Sudmant PH, de Filippo C, Li H, Mallick S, Dannemann M, Fu Q, Kircher M, Kuhlwilm M, Lachmann M, Meyer M, Ongyerth M, Siebauer M, Theunert C, Tandon A, Moorjani P, Pickrell J, Mullikin JC, Vohr SH, Green RE, Hellmann I, **Johnson PLF**, Blanche H, Cann H, Kitzman JO, Shendure J, Eichler EE, Lein ES, Bakken TE, Golovanova LV, Doronichev VB, Shunkov MV, Derevianko AP, Viola B, Slatkin M, Reich D, Kelso J, and Pääbo S. (2014). The complete genome sequence of a Neanderthal from the Altai Mountains. *Nature*, 505:43–9.
15. Jónsson H, Ginolhac A, Schubert M, **Johnson PLF**, and Orlando L. (2013). mapDamage2.0: fast approximate Bayesian estimates of ancient DNA damage parameters. *Bioinformatics*, 29:1682–4.
16. Orlando L, Ginolhac A, Zhang G, Froese D, Albrechtsen A, Stiller M, Schubert M, Cappellini E, Petersen B, Moltke I, **Johnson PLF**, Fumagalli M, Vilstrup JT, Raghavan M, Korneliussen T, Malaspinas AS, Vogt J, Szklarczyk D, Kelstrup CD, Vinther J, Dolocan A, Stenderup J, Velazquez AMV, Cahill J, Rasmussen M, Wang X, Min J, Zazula GD, Seguin-Orlando A, Mortensen C, Magnussen K, Thompson JF, Weinstock J, Gregersen K, Røed KH, Eisenmann

- V, Rubin CJ, Miller DC, Antczak DF, Bertelsen MF, Brunak S, Al-Rasheid KAS, Ryder O, Andersson L, Mundy J, Krogh A, Gilbert MTP, Kjær K, Sicheritz-Ponten T, Jensen LJ, Olsen JV, Hofreiter M, Nielsen R, Shapiro B, Wang J, and Willerslev E. (2013). Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. *Nature*, 499:74–8.
17. Fu Q, Mittnik A, **Johnson PLF**, Bos K, Lari M, Bollongino R, Sun C, Giemsch L, Schmitz R, Burger J, Ronchitelli AM, Martini F, Cremonesi RG, Svoboda J, Bauer P, Caramelli D, Castellano S, Reich D, Pääbo S, and Krause J. (2013). A revised timescale for human evolution based on ancient mitochondrial genomes. *Curr Biol*, 23:553–9.
 18. **Johnson PLF**, Yates AJ, Goronzy JJ, and Antia R. (2012). Peripheral selection rather than thymic involution explains sudden contraction in naive CD4 T-cell diversity with age. *Proc Natl Acad Sci U S A*, 109:21432–7.
 19. Gargis AS, Kalman L, Berry MW, Bick DP, Dimmock DP, Hambuch T, Lu F, Lyon E, Voelkerding KV, Zehnbauser BA, Agarwala R, Bennett SF, Chen B, Chin ELH, Compton JG, Das S, Farkas DH, Ferber MJ, Funke BH, Furtado MR, Ganova-Raeva LM, Geigenmüller U, Gunselman SJ, Hegde MR, **Johnson PLF**, Kasarskis A, Kulkarni S, Lenk T, Liu CSJ, Manion M, Manolio TA, Mardis ER, Merker JD, Rajeevan MS, Reese MG, Rehm HL, Simen BB, Yeakley JM, Zook JM, and Lubin IM. (2012). Assuring the quality of next-generation sequencing in clinical laboratory practice. *Nat Biotechnol*, 30:1033–6.
 20. **Johnson PLF**, Kochin BF, Ahmed R, and Antia R. (2012). How do antigenically varying pathogens avoid cross-reactive responses to invariant antigens? *Proc Biol Sci*, 279:2777–85.
 21. **Johnson PLF** and Hellmann I. (2011). Mutation rate distribution inferred from coincident SNPs and coincident substitutions. *Genome Biol Evol*, 3:842–50.
 22. **Johnson PLF**, Kochin BF, McAfee MS, Stromnes IM, Regoes RR, Ahmed R, Blattman JN, and Antia R. (2011). Vaccination alters the balance between protective immunity, exhaustion, escape, and death in chronic infections. *J Virol*, 85:5565–70.
 23. Burbano HA, Hodges E, Green RE, Briggs AW, Krause J, Meyer M, Good JM, Maricic T, **Johnson PLF**, Xuan Z, Rooks M, Bhattacharjee A, Brizuela L, Albert FW, de la Rasilla M, Fortea J, Rosas A, Lachmann M, Hannon GJ, and Pääbo S. (2010). Targeted investigation of the Neandertal genome by array-based sequence capture. *Science*, 328:723–5.
 24. Green RE, Krause J, Briggs AW, Maricic T, Stenzel U, Kircher M, Patterson N, Li H, Zhai W, Fritz MH, Hansen NF, Durand EY, Malaspina AS, Jensen JD, Marques-Bonet T, Alkan C, Prüfer K, Meyer M, Burbano HA, Good JM, Schultz R, Aximu-Petri A, Butthof A, Höber B, Höffner B, Siegemund M, Weihmann A, Nusbaum C, Lander ES, Russ C, Novod N, Affourtit J, Egholm M, Verna C, Rudan P, Brajkovic D, Kućan Ž, Gušić I, Doronichev VB, Golovanova LV, Lalueza-Fox C, de la Rasilla M, Fortea J, Rosas A, Schmitz RW, **Johnson PLF**, Eichler EE, Falush D, Birney E, Mullikin JC, Slatkin M, Nielsen R, Kelso J, Lachmann M, Reich D, and Pääbo S. (2010). A draft sequence of the Neandertal genome. *Science*, 328:710–22.
 25. Reich D, Green RE, Kircher M, Krause J, Patterson N, Durand EY, Viola B, Briggs AW, Stenzel U, **Johnson PLF**, Maricic T, Good JM, Marques-Bonet T, Alkan C, Fu Q, Mallick S, Li H, Meyer M, Eichler EE, Stoneking M, Richards M, Talamo S, Shunkov MV, Derevianko AP, Hublin JJ, Kelso J, Slatkin M, and Pääbo S. (2010). Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature*, 468:1053–60.
 26. **Johnson PLF** and Slatkin M. (2009). Inference of microbial recombination rates from metagenomic data. *PLoS Genet*, 5:e1000674.

27. Green RE, Malaspina AS, Krause J, Briggs AW, **Johnson PLF**, Uhler C, Meyer M, Good JM, Maricic T, Stenzel U, Prüfer K, Siebauer M, Burbano HA, Ronan M, Rothberg JM, Egholm M, Rudan P, Brajković D, Kučan Ž, Gušić I, Wikström M, Laakkonen L, Kelso J, Slatkin M, and Pääbo S. (2008). A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. *Cell*, 134:416–26.
28. **Johnson PLF** and Slatkin M. (2008). Accounting for bias from sequencing error in population genetic estimates. *Mol Biol Evol*, 25:199–206.
29. Briggs AW, Stenzel U, **Johnson PLF**, Green RE, Kelso J, Prüfer K, Meyer M, Krause J, Ronan MT, Lachmann M, and Pääbo S. (2007). Patterns of damage in genomic DNA sequences from a Neandertal. *Proc Natl Acad Sci U S A*, 104:14616–21.
30. Cross PC, **Johnson PLF**, Lloyd-Smith JO, and Getz WM. (2007). Utility of R_0 as a predictor of disease invasion in structured populations. *J R Soc Interface*, 4:315–24.
31. Getz WM, Lloyd-Smith JO, Cross PC, Bar-David S, **Johnson PLF**, Porco TC, and Sánchez MS. (2006). Modeling the invasion and spread of contagious disease in heterogeneous populations. In Z Feng, U Dieckmann, and SA Levin, editors, *Disease Evolution: Models, Concepts and Data Analyses*, AMS-DIMACS Series, pages 113–44. American Mathematical Society, Providence, RI.
32. **Johnson PLF** and Slatkin M. (2006). Inference of population genetic parameters in metagenomics: a clean look at messy data. *Genome Res*, 16:1320–7.
33. Cross PC, Lloyd-Smith JO, **Johnson PLF**, and Getz WM. (2005). Duelling timescales of host movement and disease recovery determine invasion of disease in structured populations. *Ecol Lett*, 8:587–95.
34. International Human Genome Sequencing Consortium. (2004). Finishing the euchromatic sequence of the human genome. *Nature*, 431:931–45.
35. Bulyk ML, **Johnson PLF**, and Church GM. (2002). Nucleotides of transcription factor binding sites exert interdependent effects on the binding affinities of transcription factors. *Nucleic Acids Research*, 30:1255–61.

TEACHING

Statistics and Modeling for Biologists (BIOL705/BIOL709F/BIOL609-1195) Spring 2018-2020
Graduate course

Seminar on Statistical Learning in Ecology and Evolution (BIOL608J) Fall 2018, Spring 2019
Graduate seminar

Population & evolutionary genetics (BSCI405/BSCI339J/BIOL709C) Spring 2016-7; Fall 2018-9
Advanced undergraduate / graduate course

Introduction to BEES (BEES608A) Fall 2016, 2018
Mutation & neutrality lecture

SERVICE

Member, Dept of Biology Faculty Advisory Committee 2016-2018

Member, University of Maryland Hockmeyer fellowship review committee 2016, 2017

Reviewer , National Institute of Justice Graduate Research Fellowship	2016-2018
Reviewer , National Institute of Justice Forensic Biology/DNA panel	2016-2019
Member , graduate admissions committee for BISI-CBBG track at UMD	2016, 2017, 2019
Member , graduate admissions committee for BISI-BEES track at UMD	2016
Coordinator of weekly Behavior, Ecology, Evolution, and Systematics (BEES) seminar series	Fall 2015-2018
Member , CDC Nex-StoCT Working Group to develop guidelines for next-generation sequencing technology applied to clinical testing.	2011
Reviewer for the following journals: <i>Bioinformatics</i> , <i>Genetics</i> , <i>Genome Research</i> , <i>Journal of the Royal Society Interface</i> , <i>Molecular Biology and Evolution</i> , <i>Molecular Ecology</i> , <i>Molecular Ecology Resources</i> , <i>PLoS Computational Biology</i> , <i>PLoS Genetics</i> , <i>PLoS One</i> , <i>Proceedings of the National Academy of Sciences</i> , <i>Proceedings of the Royal Society B</i> , <i>eLife</i>	2009-

MENTORING

Hao Yiu, BISI-BEES graduate student	2016-
Shauna Rasband, BISI-BEES graduate student (on-campus adviser)	2018-
Wei Xiao, BISI-CBBG graduate student	Winter 2018-
Can Liu, BISI-MOCB graduate student (on-campus adviser)	Fall 2017-
Jake Weissman, BEES graduate student	2015-2019
Rui Yin, MOCB rotation student	Fall 2019
Alex DeYonke, CBBG rotation student	Fall 2019
Neha Nanajkar, CBBG rotation student	Fall 2019
Theresa Alexander, CBBG rotation student	Fall 2018
Rong Guo, CBBG rotation student	Spring 2017
Seth Commichaux, CBBG rotation student	Fall 2016
Rohan Laljani, undergraduate	Fall 2017-
Vinay Veluvolu, undergraduate	Summer 2018-
Aidan Bissel-Siders, undergraduate	Fall 2017-
Brian Liu, undergraduate	Summer 2016-Spring 2017

INVITED PRESENTATIONS

UMD Bioscience Day, Nov 2019
 Immunity Across Scales workshop prior to EEID meeting, May 2018
 MOCB Concentration Area, University of Maryland, College Park, Apr 2018
 Phylopizza, National Museum of Natural History, Smithsonian Institution, May 2017
 Laboratory for Physical Sciences, University of Maryland, College Park, Mar 2017
 Institute for Genome Sciences Seminar, University of Maryland, Baltimore, Jan 2017
 U Penn Math-Biology Seminar, Oct 2016
 Penn State Theoretical Biology Seminar, Dec 2015
 Modeling the spread and control of Ebola in W. Africa, January 2015
 Centre for Geogenetics, University of Copenhagen, February 2014
 Dept of Biology, University of Maryland, College Park, February 2013
 Dept of Biology, University of Rochester, January 2013

Southeastern Branch, American Society of Microbiology annual meeting, October 2012

Neanderthal Consortium Planning Meeting, Opatija, September 2011

Dept of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, August 2009

Evolutionary Genetics: the impact of next gen sequencing technologies, Wittenberg, March 2009

Workshop on Bacterial Genomics, Oxford, September 2007