

PHILIP LEE FALK JOHNSON

1510 Clifton Rd
Atlanta, GA 30322

(510)318-2792
plfjohnson@emory.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.

RESEARCH EXPERIENCE

Emory University, Atlanta, GA 2009–present

NSF postdoctoral fellow in biological informatics

Advisor: Rustom Antia

Continued independent research developing population genetic models of metagenomic data and ancient DNA. Started new line of research working with Dr. Antia to model adaptive immune system dynamics, including genetic diversity.

National Center for Biotechnology Information, Bethesda, MD 2001–2004

Senior systems analyst

Developed computational tools to validate human genome assembly, detect centromeric sequence, identify CpG islands and automate RefSeq creation.

FELLOWSHIPS & AWARDS

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. **Johnson PLF** and Hellmann I. (2011). Mutation rate distribution inferred from coincident SNPs and coincident substitutions. *Genome Biol Evol*, 3:842–50.
2. **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.
3. 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.
4. 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.
5. 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.
 6. **Johnson PLF** and Slatkin M. (2009). Inference of microbial recombination rates from metagenomic data. *PLoS Genet*, 5:e1000674.
 7. Green RE, Malaspinas 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, Kućan 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.
 8. **Johnson PLF** and Slatkin M. (2008). Accounting for bias from sequencing error in population genetic estimates. *Mol Biol Evol*, 25:199–206.
 9. 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.
 10. 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.
 11. 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 113–144. American Mathematical Society, Providence, RI.
 12. **Johnson PLF** and Slatkin M. (2006). Inference of population genetic parameters in metagenomics: a clean look at messy data. *Genome Res*, 16:1320–7.
 13. 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*, 8:587–595.
 14. International Human Genome Sequencing Consortium. (2004). Finishing the euchromatic sequence of the human genome. *Nature*, 431:931–45.
 15. 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 Res*, 30:1255–61.

TEACHING

Survey of Genetics (student instructor with M. Slatkin, G. Barnes, D. Rohksar) Fall 2007
Undergraduate course, University of California, Berkeley

Introduction to Systems in Biology and Medicine (student instructor with H. Lim) Spring 2007
Undergraduate course, University of California, Berkeley

Evolution (student instructor with N. Patel, C. Bergman) February 2007
Graduate short course, Cold Spring Harbor Laboratory

SERVICE

Member, CDC Nex-StoCT Working Group to develop guidelines for next-generation sequencing technology applied to clinical testing. 2011

Reviewer for *Bioinformatics*, *Genetics*, *Genome Research*, *Molecular Biology and Evolution*, *Molecular Ecology*, *Molecular Ecology Resources*, *PLoS Genetics*, *PLoS One*, *Proceedings of the National Academy of Sciences* 2009-

INVITED PRESENTATIONS

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