

Trevor Bedford

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Employment

- 2008– Howard Hughes Medical Institute Associate, *University of Michigan*
ADVISOR: M. Pascual.
Research on the intersection of ecological dynamics and genetic processes.
- 2008 Intern, *Wolfram Research Inc.*
SUPERVISOR: S. Wolfram.
Solutions for data presentation and analysis in Wolfram|Alpha.

Education

- 2003–2008 PhD in Biology, *Harvard University*
ADVISOR: D. L. Hartl.
- 1999–2002 BA in Biological Sciences (with honors), *University of Chicago*
ADVISOR: M. Feder.

Grants, honors & awards

- 2005–2008 NFS Graduate Research Fellowship
- 2003–2005 NIH Genetics and Genomics Training Grant
- 2001 Howard Hughes Undergraduate Fellow
- 1999–2002 University of Chicago – University Scholar

Teaching

2006 Teaching fellow: Bio 152, Population Genetics, Harvard University.
Professor: J. Wakeley.

2005 Teaching fellow: BS 50, Genetics and Genomics, Harvard University.
Professors: D. L. Hartl and M. Ruvolo.

Academic mentoring: Michelle White (undergraduate, Harvard University), Jehee Choi (undergraduate, Harvard University), Rebekah Rogers (PhD candidate, Harvard University).

Professional service

Referee: Bioinformatics, Complex Systems, Genome Research, Journal of Biology, Molecular Biology and Evolution, PLoS One, Virulence.

Technical skills

Quantitative techniques: dynamical systems, Markov processes, population genetics, coalescent theory, phylogenetic analysis.

Statistical analysis: model testing through maximum-likelihood and Bayesian inference, Markov chain Monte Carlo, dimensionality reduction techniques.

Programming: C++, Java, Mathematica, Processing, R, Perl, Ruby.

Graphic design and typesetting: HTML, Photoshop, Illustrator, L^AT_EX.

Molecular biology: *Drosophila* and bacterial culture, molecular cloning, PCR, sequencing and other standard techniques.

Publications & talks

JOURNAL ARTICLES

Bedford T, Pascual M. Genealogical trees reveal tempo of adaptation in human influenza A. In prep.

Bedford T. PACT: posterior analysis of coalescent trees. In prep. [\[CODE\]](#)

Rogers RL, **Bedford T**, Lyons AM, Hartl DL. 2010. Adaptive impact of the chimeric gene *Quetzalcoatl* in *Drosophila melanogaster*. Proc. Natl. Acad. Sci. USA 107: 10943–10948. [\[PDF\]](#)

Bedford T, Cobey S, Beerli P, Pascual M. 2010. Global migration dynamics underlie evolution and persistence of human influenza A (H₃N₂). *PLoS Pathog.* 6: e1000918. [PDF]
[Rated 6.0 by Faculty of 1000]

Bedford T, Hartl DL. 2009. Optimization of gene expression by natural selection. *Proc. Natl. Acad. Sci. USA.* 106: 1133–1138. [PDF]

Rogers RL, **Bedford T**, Hartl DL. 2009. Formation and longevity of chimeric and duplicate genes in *Drosophila melanogaster*. *Genetics* 181: 313–322. [PDF]

Bedford T, Hartl DL. 2008. Overdispersion of the molecular clock: temporal variation of gene-specific substitution rates in *Drosophila*. *Mol. Biol. Evol.* 25: 1631–1638. [PDF]

Bedford T, Wapinski I, Hartl DL. 2008. Overdispersion of the molecular clock varies between yeast, *Drosophila* and mammals. *Genetics* 179: 977–984. [PDF]

Volkman SK, Lozovsky E, Barry AE, **Bedford T**, Bethke L, Myrick A, Day KP, Hartl DL, Wirth DF, Sawyer SA. 2007. Genomic heterogeneity in the density of noncoding single-nucleotide and microsatellite polymorphisms in *Plasmodium falciparum*. *Gene* 387: 1–6. [PDF]

Castillo-Davis CI, **Bedford TB**, Hartl DL. 2004. Accelerated rates of intron gain/loss and protein evolution in duplicate genes in human and mouse malaria parasites. *Mol. Biol. Evol.* 21: 1422–1427. [PDF]

Nielsen KM, Kasper J, Choi M, **Bedford T**, Kristiansen K, Wirth DF, Volkman SK, Lozovsky ER, Hartl DL. 2003. Gene conversion as a source of nucleotide diversity in *Plasmodium falciparum*. *Mol. Biol. Evol.* 20: 726–734. [PDF]

Feder ME, **Bedford T**, Albright DR, Michalak P. 2002. Evolvability of Hsp70 expression under artificial selection for inducible thermotolerance in independent populations of *Drosophila melanogaster*. *Phys. Biochem. Zool.* 75: 325–334. [PDF]

TALKS

Ecology and Evolution of Infectious Diseases, Cornell University, June 2010. “Global migration patterns of the human influenza virus.”

Phyloseminar.org, April 2010. “Adaptation and migration in the human influenza virus.”

Departmental Seminar, Department of Ecology and Evolutionary Biology, University of Michigan, February 2010. “Adaptation and migration in the human influenza virus.”

Departmental Seminar, School of Computational Science, Florida State University, October 2009. “Global migrational dynamics of human influenza A (H₃N₂).”

Thesis Defense, Harvard University, May 2008. “Evolutionary molecular clocks: Patterns of sequence change and expression divergence.”

G4 Symposium, Harvard University, May 2007. “Amino acid substitution patterns in yeast

genomes suggest adaptive evolution.”

NKS Wolfram Science Conference, Washington DC, June 2006. Invited talk. “Using cellular automata to uncover evolutionary landscapes.”

Medical and Population Genetics Program Meeting, Broad Institute, April 2004. “Gene duplication and intron evolution in *Plasmodium*.”

Honors thesis presentation, University of Chicago, May 2002. “Selection for enhanced inducible thermotolerance and Hsp70 expression in *Drosophila melanogaster*.”

POSTER PRESENTATIONS

Society for Molecular Biology and Evolution Annual Meeting, Barcelona, June 2008. “Population size mediates overdispersion and robustness in protein evolution.”

Society for Molecular Biology and Evolution Annual Meeting, Halifax, June 2007. “Clustered ‘ticks’ in the molecular evolutionary clocks of yeast proteins.” [Selected for a graduate student poster award]

Outreach

My work on influenza has been widely reported on by many sources, including Yahoo! News, ABC News, US News and World Report, MSNBC and Fox News.