

# Trevor Bedford

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## Employment

- 2012– Newton International Fellow, University of Edinburgh.
- 2011 EMBO Fellow, University of Edinburgh.
- 2008–2011 HHMI Associate, University of Michigan.  
Advisor: Mercedes Pascual.
- 2008 Intern, Wolfram Research Inc.  
Supervisor: Stephen Wolfram.

## Education

- 2003–2008 PhD in Biology, Harvard University.  
Advisor: Daniel Hartl.
- 1999–2002 BA in Biological Sciences (*with honors*), University of Chicago.  
Advisor: Martin Feder.

## Grants, honors & awards

- 2012–2013 Newton International Fellowship, The Royal Society, £159,000.
- 2011–2013 EMBO Long Term Fellowship, European Molecular Biology Organization, €55,310.
- 2005–2008 NSF Graduate Research Fellowship, National Science Foundation.
- 2003–2005 NIH Genetics and Genomics Training Program, National Institutes of Health.
- 2003 HHMI Predoctoral Fellowship (*alternate*), Howard Hughes Medical Institute.
- 2001 HHMI Undergraduate Fellowship, Howard Hughes Medical Institute.
- 1999–2002 University Scholarship, University of Chicago.

## Teaching

- 2010 Completed an intensive 7-week “Postdoctoral Short-Course on College Teaching in Science and Engineering” at the University of Michigan.

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

2005 Teaching fellow: BS 50, Genetics and Genomics, Harvard University.  
Professors: Daniel Hartl and Maryellen Ruvolo.

Academic mentoring: Michelle White (undergraduate, Harvard University), Jehhee Choi (undergraduate, Harvard University), Rebekah Rogers (PhD candidate, Harvard University), Ed Baskerville (PhD candidate, University of Michigan), Daniel Zinder (PhD candidate, University of Michigan).

## Professional service

Referee: American Naturalist, Bioinformatics, Complex Systems, Emerging Infectious Diseases, Genome Research, Journal of Biology, Journal of the Royal Society Interface, Molecular Biology and Evolution, Molecular Ecology, National Science Foundation, PLoS One, Proc Natl Acad USA, 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, Python.

Graphic design and typesetting: HTML, Photoshop, Illustrator, L<sup>A</sup>T<sub>E</sub>X.

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

## Publications & talks

### JOURNAL ARTICLES

2011 Baskerville EB, Dobson AP, **Bedford T**, Allesina S, Anderson TM, Pascual M. Spatial guilds in the Serengeti food web revealed by a Bayesian group model. PLoS Comput Biol 7: e1002321. (PDF)

2011 **Bedford T**, Cobey S, Pascual M. Strength and tempo of selection revealed in viral gene genealogies. BMC Evol Biol 11: 220. (PDF)

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

- 2010 **Bedford T**, Cobey S, Beerli P, Pascual M. Global migration dynamics underlie evolution and persistence of human influenza A (H<sub>3</sub>N<sub>2</sub>). *PLoS Pathog* 6: e1000918. (PDF) (*Faculty of 1000 "Must Read"*)
- 2009 **Bedford T**, Hartl DL. Optimization of gene expression by natural selection. *Proc Natl Acad Sci USA* 106: 1133–1138. (PDF)
- 2009 Rogers RL, **Bedford T**, Hartl DL. Formation and longevity of chimeric and duplicate genes in *Drosophila melanogaster*. *Genetics* 181: 313–322. (PDF)
- 2008 **Bedford T**, Hartl DL. Overdispersion of the molecular clock: temporal variation of gene-specific substitution rates in *Drosophila*. *Mol Biol Evol* 25: 1631–1638. (PDF)
- 2008 **Bedford T**, Wapinski I, Hartl DL. Overdispersion of the molecular clock varies between yeast, *Drosophila* and mammals. *Genetics* 179: 977–984. (PDF)
- 2007 Volkman SK, Lozovsky E, Barry AE, **Bedford T**, Bethke L, Myrick A, Day KP, Hartl DL, Wirth DF, Sawyer SA. Genomic heterogeneity in the density of noncoding single-nucleotide and microsatellite polymorphisms in *Plasmodium falciparum*. *Gene* 387: 1–6. (PDF)
- 2004 Castillo-Davis CI, **Bedford TB**, Hartl DL. 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)
- 2003 Nielsen KM, Kasper J, Choi M, **Bedford T**, Kristiansen K, Wirth DF, Volkman SK, Lozovsky ER, Hartl DL. Gene conversion as a source of nucleotide diversity in *Plasmodium falciparum*. *Mol Biol Evol* 20: 726–734. (PDF)
- 2002 Feder ME, **Bedford T**, Albright DR, Michalak P. Evolvability of Hsp70 expression under artificial selection for inducible thermotolerance in independent populations of *Drosophila melanogaster*. *Phys Biochem Zool* 75: 325–334. (PDF)

#### TALKS

- 2012 Population Genetics Group, Nottingham, UK. “The population genetics of the human influenza virus.”
- 2011 Epidemics<sup>3</sup>, Boston, MA. “Canalization of the evolutionary trajectory of the human influenza virus.” (*Award for Best Oral Presentation by a Young Investigator.*)
- 2011 Thematic Seminar, Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow. Invited talk. “Canalization of the evolutionary trajectory of the human influenza virus.”
- 2011 RAPIDD Phylodynamics Workshop, NESCent, Durham, NC. Invited talk. “Modeling the global dynamics of the human influenza virus.”
- 2011 Infectious Disease Epidemiology Seminar, Harvard School of Public Health. Invited talk. “Modeling the antigenic and spatial dynamics of the influenza virus.”
- 2010 Departmental Seminar, Department of Ecology and Evolutionary Biology, University of Michigan. “Beyond phylogenies: Uncovering the evolutionary dynamics of the influenza virus.”

- 2010 Ecology and Evolution of Infectious Diseases, Cornell University. “Global migration patterns of the human influenza virus.”
- 2010 Phyloseminar.org. “Adaptation and migration in the human influenza virus.”
- 2010 Departmental Seminar, Department of Ecology and Evolutionary Biology, University of Michigan. “Adaptation and migration in the human influenza virus.”
- 2009 Departmental Seminar, School of Computational Science, Florida State University. “Global migration dynamics of human influenza A (H<sub>3</sub>N<sub>2</sub>).”
- 2008 Thesis Defense, Harvard University. “Evolutionary molecular clocks: Patterns of sequence change and expression divergence.”
- 2007 G<sub>4</sub> Symposium, Harvard University. “Amino acid substitution patterns in yeast genomes suggest adaptive evolution.”
- 2006 NKS Wolfram Science Conference, Washington DC. Invited talk. “Using cellular automata to uncover evolutionary landscapes.”
- 2004 Medical and Population Genetics Program Meeting, Broad Institute. “Gene duplication and intron evolution in *Plasmodium*.”
- 2002 Honors thesis presentation, University of Chicago. “Selection for enhanced inducible thermo-tolerance and Hsp70 expression in *Drosophila melanogaster*.”

#### POSTER PRESENTATIONS

- 2011 Early Career Scientists Symposium, Department of Ecology and Evolutionary Biology, University of Michigan. “Antigenic and spatial dynamics of influenza H<sub>3</sub>N<sub>2</sub>.”
- 2008 Society for Molecular Biology and Evolution Annual Meeting, Barcelona. “Population size mediates overdispersion and robustness in protein evolution.”
- 2007 Society for Molecular Biology and Evolution Annual Meeting, Halifax. “Clustered ‘ticks’ in the molecular evolutionary clocks of yeast proteins.” (*Graduate student poster award*)

## Software

PACT: Posterior Analysis of Coalescent Trees. Developer. [\(CODE\)](#)

## 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.