

Trevor Bedford

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Faculty positions

- 2013– **Assistant Member**, Fred Hutchinson Cancer Research Center
Vaccine and Infectious Disease Division, Computational Biology Program
- 2016– **Affiliate Assistant Professor**, University of Washington
Department of Epidemiology

Postgraduate training

- 2012–2013 **Newton International Fellow**, University of Edinburgh
Institute of Evolutionary Biology
- 2011 **EMBO Fellow**, University of Edinburgh
Institute of Evolutionary Biology
- 2008–2011 **HHMI Associate**, University of Michigan
Department of Ecology and Evolutionary Biology
- 2008 **Intern**, Wolfram Research Inc.

Education

- 2003–2008 **PhD in Biology**, Harvard University
- 1999–2002 **BA in Biological Sciences** (*with honors*), University of Chicago

Honors & awards

- 2017 Open Science Prize Winner, NIH, Wellcome Trust and HHMI.
- 2016–2020 Pew Scholar in the Biomedical Sciences, Pew Charitable Trusts.
- 2016 Open Science Prize Finalist, NIH, Wellcome Trust and HHMI.
- 2012–2014 Marie Curie International Incoming Fellow, European Commission (*Declined*).
- 2012–2013 Newton International Fellow, The Royal Society.
- 2011–2013 Long Term Fellow, European Molecular Biology Organization.

- 2005–2008 NSF Graduate Research Fellowship, National Science Foundation.
- 2003–2005 NIH Genetics and Genomics Training Program, National Institutes of Health.
- 2001 HHMI Undergraduate Fellowship, Howard Hughes Medical Institute.
- 1999–2002 University Scholarship, University of Chicago.

Research support

- 2017–2022 RO1 AI125392-01. National Institutes of Health.
Mechanisms of influenza transmission bottlenecks: impact on viral evolution.
Co-investigator with PI Thomas Friedrich.
- 2016–2021 RO1 AI127893-01. National Institutes of Health.
High-throughput experiments to guide influenza vaccine strain selection.
Co-investigator with PI Jesse Bloom.
- 2016–2021 R35 GM119774-01. National Institutes of Health.
Real-time tracking of virus evolution for vaccine strain selection and epidemiological investigation.
Principal investigator.
- 2015–2020 U19 AI117891-01. National Institutes of Health.
Dynamics and evolution of immune responses to influenza viruses.
Co-investigator with PIs Rafi Ahmed and Rustom Antia.
- 2014–2019 RO1 GM113246-01. National Science Foundation and National Institutes of Health.
Leveraging deep sequencing data to understand antibody maturation.
Co-investigator with PI Erick Matsen.
- 2014–2019 U54 GM111274. National Institutes of Health.
Center for Statistics and Quantitative Infectious Diseases.
Co-investigator with PI Betz Halloran, co-lead of project on “Understanding transmission with integrated genetic and epidemiologic inference”.

Teaching & mentoring

COURSES AND WORKSHOPS

- 2015– Instructor, Pathogen Evolution, Selection and Immunity, Summer Institute in Statistics and Modeling in Infectious Diseases.
- 2014–2016 Lectures on data science and visualization for interns at the FHCRC.
- 2013 Presented phylodynamic inference practical at GenEpi workshop, London School of Hygiene and Tropical Medicine.
- 2012 Lecturer, Structured Population Models in Epidemiology, École Normale Supérieure.
- 2010 Completed an intensive 7-week “Postdoctoral Short-Course on College Teaching in Science and En-

gineering” at the University of Michigan.

2006 Teaching fellow, Population Genetics, Harvard University.

2005 Teaching fellow, Genetics and Genomics, Harvard University.

STUDENT AND POSTDOCTORAL MENTORING

2017– John Huddleston, PhD student, University of Washington.

2017– Louise Moncla, postdoc, FHCRC.

2017– James Hadfield, postdoc, FHCRC.

2016– Gytis Dudas, postdoc, FHCRC.

2015– Sidney Bell, PhD student, University of Washington.

2015– Allison Black, PhD student, University of Washington.

2014–2016 Alvason Li, postdoc, FHCRC.

2014–2015 Charles Cheung, postdoc, FHCRC.

SUPERVISED TRAINEES

2012–2013 Gytis Dudas, PhD candidate, University of Edinburgh.

2012 Michael Landis, Google Summer of Code student, NESCent.

2010–2011 Daniel Zinder, PhD candidate, University of Michigan.

2009–2011 Ed Baskerville, PhD candidate, University of Michigan.

2007–2008 Rebekah Rogers, PhD candidate, Harvard University.

2004–2005 Jehee Choi, undergraduate, Harvard University.

2004–2005 Michelle White, undergraduate, Harvard University.

Professional service

2016–2017 Organizing committee: Epidemics⁶ conference.

2016–2017 Technical Working Group member: WHO Public Health Research Agenda for Influenza.

2015 Organizing committee: Epidemics⁵ conference.

2014– Associate editor: Virus Evolution.

Ad-hoc referee: American Naturalist, Bioinformatics, BMC Evolutionary Biology, Cell, Complex Systems, eLife, Emerging Infectious Diseases, Genome Biology and Evolution, Genome Research, Journal of Biology, Journal of the Royal Society Interface, Molecular Biology and Evolution, Molecular Ecol-

ogy, National Science Foundation, Nature, Nature Communications, Nature Genetics, Phil Trans R Soc B, PLoS One, PLoS Pathogens, Proc Natl Acad USA, Science, Virology, Virulence.

Publications & talks

JOURNAL ARTICLES (47 PAPERS, 1987 CITATIONS, H-INDEX OF 22)

- 2017 **Bell SM, Bedford T.** Modern-day SIV viral diversity generated by extensive recombination and cross-species transmission. *PLoS Pathog.* *In press.*
- 2017 Grubaugh ND, Ladner JT, Kraemer MUG, **Dudas G**, Tan AL, ..., **Bedford T**, Pybus OG, Isern S, Palacios G, Andersen KG (67 authors). Genomic epidemiology reveals multiple introductions of Zika virus into the United States. *Nature* 546: 401–405.
- 2017 Faria NR, Quick J, Morales I, Thézé J, Jesus JG, ..., **Bedford T**, Teixeira MNR, Sabino EC, Alcantara LCJ, Loman N, Pybus OG (71 authors). Establishment and cryptic transmission of Zika virus in Brazil and the Americas. *Nature* 546: 406–410.
- 2017 Quick J, Grubaugh ND, Pullan ST, Claro IM, Smith AD, ..., **Bedford T**, ..., Simpson JT, Pybus OG, Andersen KG, Loman NJ (28 authors). Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. *Nat Protoc.* *In press.*
- 2017 Cybis GB, Sinsheimer JS, **Bedford T**, Rambaut A, Lemey P, Suchard MA. Bayesian nonparametric clustering in phylogenetics: modeling antigenic evolution in influenza. *Stat Med* 10.1002/sim.7196.
- 2017 **Dudas G**, Max Carvalho L, **Bedford T**, Tatem AJ, Baele G, ..., Ströher U, Wury I, Suchard MA, Lemey P, Rambaut A (93 authors). Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic. *Nature* 544: 309–315.
- 2016 **Black A**, Breyta R, **Bedford T**, Kurath G. Geography and host species shape the evolutionary dynamics of U genogroup infectious hematopoietic necrosis virus. *Virus Evol* 2: vew034.
- 2016 Lipsitch M, Barclay W, Raman R, Russell CJ, Belser JA, ..., **Bedford T**, ..., Herfst S, Murcia PR, Roche B, Wilke CO, Russell CA (19 authors). Viral factors in influenza pandemic risk assessment. *eLife* 5: e18491.
- 2016 **Bedford T**, Malik HS. Did a single amino acid change make Ebola virus more virulent? *Cell* 167: 892–894.
- 2016 Wen F, **Bedford T**, Cobey S. Explaining the geographic origins of seasonal influenza A (H₃N₂). *Proc R Soc B* 283: 20161312.
- 2016 Harvey WT, Benton DJ, Gregory V, Hall JPJ, Daniels RS, **Bedford T**, Haydon DT, Hay AJ, McCauley JW, Reeve R. Identification of low- and high-impact hemagglutinin amino acid substitutions that drive antigenic drift of influenza A(H1N1) viruses. *PLoS Pathog* 12: e1005526.
- 2016 Neher RA, **Bedford T**, Daniels RS, Russell CA, Shraiman BI. Prediction, dynamics, and visualization of antigenic phenotypes of seasonal influenza viruses. *Proc Natl Acad Sci USA* 113: E1701–E1709.
- 2016 Karcher MD, Palacios JA, **Bedford T**, Suchard MA, Minin VN. Quantifying and mitigating the effect

of preferential sampling on phylodynamic inference. *PLoS Comp Biol* 12: e1004789.

- 2016 Lorenzo-Redondo R, Fryer HR, **Bedford T**, Kim EY, Archer J, ..., Malim MH, Rambaut A, Haase AT, McLean AR, Wolinsky SM (16 authors). Persistent HIV-1 replication maintains the tissue reservoir during therapy. *Nature* 530: 51–56.
- 2015 Neafsey DE, Juraska M, **Bedford T**, Benkeser D, Valim C, ..., Yu Q, Lapierre D, Birren BW, Gilbert PB, Wirth DF (63 authors). Genetic diversity and protective efficacy of the RTS,S/ASo1 malaria vaccine. *New Engl J Med* 373: 2025–2037.
- 2015 Machkovech HM, **Bedford T**, Suchard MA, Bloom JD. Positive selection in CD8+ T-cell epitopes of influenza nucleoprotein revealed by a comparative analysis of human and swine viral lineages. *J Virol* 89: 11275–11283.
- 2015 Neher RA, **Bedford T**. nextflu: real-time tracking of seasonal influenza virus evolution in humans. *Bioinformatics* 31: 3546–3548.
- 2015 Meyer AG, Spielman SJ, **Bedford T**, Wilke CO. Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak. *Virus Evol* 1: vev006.
- 2015 Cybis G, Sinsheimer J, **Bedford T**, Mather AE, Lemey P, Suchard MA. Assessing phenotypic correlation through the multivariate phylogenetic latent liability model. *Ann Appl Stat* 9: 969–991.
- 2015 McCoy CO, **Bedford T**, Minin VN, Bradley P, Robins H, Matsen FA. Quantifying evolutionary constraints on B cell affinity maturation. *Phil Trans R Soc B* 370: 20140244.
- 2015 **Bedford T**, Riley S, Barr IG, Broor S, Chadha M, ..., Tashiro M, Wang D, Xu X, Lemey P, Russell CA (26 authors). Global circulation patterns of seasonal influenza viruses vary with antigenic drift. *Nature* 523: 217–220.
- 2015 Park DJ, Dudas G, Wohl S, Goba A, Whitmer SLM, ..., **Bedford T**, Gnirke A, Ströher U, Rambaut A, Garry RF, Sabeti PC (86 authors). Ebola virus epidemiology, transmission, and evolution during seven months in Sierra Leone. *Cell* 161: 1–11.
- 2015 Frost SDW, Pybus OG, Gog JR, Viboud C, Bonhoeffer S, **Bedford T**. Eight challenges in phylodynamic inference. *Epidemics* 10: 88–92.
- 2015 Vrancken B, Lemey P, Rambaut A, **Bedford T**, Longdon B, Gunthard H, Suchard MA. Simultaneously estimating evolutionary history and repeated traits phylogenetic signal: applications to viral and host phenotypic evolution. *Methods Ecol Evol* 6: 67–82.
- 2015 Dudas G, **Bedford T**, Lycett S, Rambaut A. Reassortment between influenza B lineages and the emergence of a co-adapted PB1-PB2-HA gene complex. *Mol Biol Evol* 32: 162–172.
- 2014 Zinder D, **Bedford T**, Baskerville EB, Woods RJ, Roy M, Pascual M. Seasonality in the migration and establishment of H3N2 influenza lineages with epidemic growth and decline. *BMC Evol Biol* 14: 272.
- 2014 Faria NR, Rambaut A, Suchard MA, Baele G, **Bedford T**, Ward MJ, Tatem AJ, Sousa JD, Arinaminpathy N, Pèpin J, Posada D, Peeters M, Pybus OG, Lemey P. The early spread and epidemic ignition of HIV-1 in human populations. *Science* 346: 56–61.
- 2014 Roche B, Drake JM, Brown J, Stallknecht DE, **Bedford T**, Rohani P. Adaptive evolution and environmental durability jointly structure phylodynamic patterns in avian influenza viruses. *PLoS Biol* 12:

e1001931.

- 2014 Lemey P, Rambaut A, **Bedford T**, Faria N, Bielejec F, Baele G, Russell CA, Smith DJ, Pybus OG, Brockmann D, Suchard MA. Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H₃N₂. *PLoS Pathog* 10: e1003932.
- 2014 **Bedford T**, Suchard MA, Lemey P, Dudas G, Gregory V, Hay AJ, McCauley JW, Russell CA, Smith DJ, Rambaut A. Integrating influenza antigenic dynamics with molecular evolution. *eLife* 3: e01914.
- 2014 Landis MJ, **Bedford T**. PhyloWood: interactive web-based animations of biogeographic and phylogeographic histories. *Bioinformatics* 30: 123–124.
- 2013 Volz EM, Koelle K, **Bedford T**. Viral phylodynamics. *PLoS Comput Biol* 9: e1002947.
- 2013 Zinder D, **Bedford T**, Gupta S, Pascual M. The roles of competition and mutation in shaping antigenic and genetic diversity in influenza. *PLoS Pathog* 9: e1003104.
- 2012 **Bedford T**, Rambaut A, Pascual M. Canalization of the evolutionary trajectory of the human influenza virus. *BMC Biol* 10: 38.
- 2012 Baele G, Lemey P, **Bedford T**, Rambaut A, Suchard MA, Alekseyenko AV. Improving the accuracy of demographic and molecular clock model comparison while accommodating phylogenetic uncertainty. *Mol Biol Evol* 29: 2157–2167.
- 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.
- 2011 **Bedford T**, Cobey S, Pascual M. Strength and tempo of selection revealed in viral gene genealogies. *BMC Evol Biol* 11: 220.
- 2010 Rogers RL, **Bedford T**, Lyons AM, Hartl DL. Adaptive impact of the chimeric gene *Quetzalcoat1* in *Drosophila melanogaster*. *Proc Natl Acad Sci USA* 107: 10943–10948.
- 2010 **Bedford T**, Cobey S, Beerli P, Pascual M. Global migration dynamics underlie evolution and persistence of human influenza A (H₃N₂). *PLoS Pathog* 6: e1000918. (*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.
- 2009 Rogers RL, **Bedford T**, Hartl DL. Formation and longevity of chimeric and duplicate genes in *Drosophila melanogaster*. *Genetics* 181: 313–322.
- 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.
- 2008 **Bedford T**, Wapinski I, Hartl DL. Overdispersion of the molecular clock varies between yeast, *Drosophila* and mammals. *Genetics* 179: 977–984.
- 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.
- 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.

- 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.
- 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.

INVITED PRESENTATIONS

- 2017 Global Infectious Disease Seminar, Center for Infectious Disease Reseach, Seattle, WA.
- 2017 Immunology and Evolution of Influenza Symposium, Emory University, Atlanta, GA.
- 2017 Applied Bioinformatics and Public Health Microbiology, Wellcome Genome Campus, Hinxton, UK.
- 2017 Biosystems Science and Engineering Seminar, ETH Zurich, Basel, Switzerland.
- 2017 Gordon Research Conference on Chemical and Biological Terrorism Defense, Ventura, CA.
- 2017 Pew Annual Meeting, Santa Barbara, CA.
- 2016 BD2K Open Data Science Symposium, Bethesda, MD.
- 2016 Plenary talk, Options IX for the Control of Influenza, Chicago, IL.
- 2016 WHO Workshop on Predictive Models for Improving Influenza Vaccine Virus Selection, Princeton University, Princeton, NJ.
- 2016 Microbiology Seminar, Korea University College of Medicine, Seoul, Republic of Korea.
- 2016 Federation Meeting of Korean Basic Medical Scientists, Incheon, Republic of Korea.
- 2016 MIDAS Network Meeting, Washington, DC.
- 2016 4th Annual IDM Symposium, Institute for Disease Modeling, Bellevue, WA.
- 2016 Ecology and Evolution Seminar, University of Chicago, Chicago, IL.
- 2016 Structure and Computation Affinity Group Seminar, Scripps Research Institute, San Diego, CA.
- 2016 Infectious Disease Epidemiology Seminar, Harvard School of Public Health, Boston, MA.
- 2016 VIDDD Seminar, Fred Hutchinson Cancer Research Center, Seattle, WA.
- 2016 Influenza Division, VSDB Meeting, Centers for Disease Control and Prevention, Atlanta, GA.
- 2015 4th Informal Consultation on Influenza Vaccine Virus Selection, World Health Organization, Hong Kong, SAR China.
- 2015 Global Infectious Disease Seminar, AIDS Vaccine Research Laboratory, University of Wisconsin, Madison, WI.
- 2015 Evolution Seminar, JF Crow Institute, University of Wisconsin, Madison, WI.
- 2015 Keynote talk, BCCDC Research Week Symposium, Vancouver, Canada.

- 2015 Forecasting Evolution, Calouste Gulbenkian Foundation, Lisbon, Portugal.
- 2015 Keynote talk, Ecology and Evolution of Infectious Diseases, Athens, GA.
- 2015 RAPIDD Workshop on Modeling and Predicting Influenza Phenotypes, Cambridge University, Cambridge, UK.
- 2014 Laboratory Medicine Grand Rounds, University of Washington School of Medicine, Seattle, WA.
- 2014 Evolution of Drug Resistance Workshop, Kavli Institute for Theoretical Physics, University of California, Santa Barbara, CA.
- 2014 VIDDD Seminar, Fred Hutchinson Cancer Research Center, Seattle, WA.
- 2013 Infectious Disease Dynamics Workshop, Isaac Newton Institute for Mathematical Sciences, Cambridge University, Cambridge, UK.
- 2013 Spring Symposium, Centre for Immunity, Infection and Evolution, University of Edinburgh, Edinburgh, UK.
- 2012 Institute of Biologie Seminar, École Normale Supérieure, Paris, France.
- 2012 Infectious Disease Epidemiology Seminar, School of Public Health, Imperial College, London, UK.
- 2012 Ecology and Evolution Seminar, Centre d'Ecologie Fonctionnelle et Evolutive, Université Montpellier, Montpellier, France.
- 2012 Institute Seminar, Institute of Medical Virology and Epidemiology of Viral Diseases, Universitäts Klinikum Tübingen, Tübingen, Germany.
- 2012 Virology Seminar, MRC National Institute for Medical Research, London, UK.
- 2012 Next-Generation Molecular and Evolutionary Epidemiology of Infectious Disease, The Royal Society, Kavli International Centre, Buckinghamshire, UK.
- 2012 VIDDD Seminar, Fred Hutchinson Cancer Research Center, Seattle, WA.
- 2012 Scottish Phylogeny Discussion Group, University of Glasgow, Glasgow, UK.
- 2012 Viral Evolution: Linking Genetics to Epidemics, University of Cologne, Cologne, Germany.
- 2011 Thematic Seminar, Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Glasgow, UK.
- 2011 RAPIDD Phylodynamics Workshop, NESCent, Durham, NC.
- 2011 Infectious Disease Epidemiology Seminar, Harvard School of Public Health, Boston, MA.
- 2010 Departmental Seminar, Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI.
- 2010 Phyloseminar.org, webcast.
- 2010 Departmental Seminar, Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI.
- 2009 Departmental Seminar, School of Computational Science, Florida State University, Tallahassee, FL.

2006 NKS Wolfram Science Conference, Washington, DC.

CONFERENCE ABSTRACTS

2015 Epidemics⁵, Clearwater Beach, FL.

2013 Mathematical and Computational Evolutionary Biology, Montpellier, France.

2013 HIV Dynamics and Evolution, Utrecht, Netherlands.

2012 Society for Molecular Biology and Evolution Annual Meeting, Dublin, Ireland.

2012 Population Genetics Group, Nottingham, UK.

2011 Epidemics³, Boston, MA. (*Award for Best Oral Presentation by a Young Investigator.*)

2010 Ecology and Evolution of Infectious Diseases, Cornell University, Ithaca, NY.

2008 Society for Molecular Biology and Evolution Annual Meeting, Barcelona, Spain. Poster presentation.

2007 Society for Molecular Biology and Evolution Annual Meeting, Halifax, Canada. Poster presentation. (*Graduate student poster award*)

Outreach

2015 Science outreach video “Tracking down the sneeze that started seasonal flu” published on Vox.com.