# Trevor Bedford

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## Faculty positions

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| 2018– | **Associate Professor**, Fred Hutchinson Cancer Research Center<br>Vaccine and Infectious Disease Division |
| 2018– | **Associate Professor**, Fred Hutchinson Cancer Research Center<br>Computational Biology Program |
| 2019– | **Associate Professor**, Fred Hutchinson Cancer Research Center<br>Human Biology Division |
| 2019– | **Affiliate Associate Professor**, University of Washington<br>Department of Genome Sciences |
| 2020– | **Affiliate Associate Professor**, University of Washington<br>Department of Epidemiology |
| 2016–2020 | **Affiliate Assistant Professor**, University of Washington<br>Department of Epidemiology |
| 2013–2017 | **Assistant Professor**, Fred Hutchinson Cancer Research Center<br>Vaccine and Infectious Disease Division, Computational Biology Program |

## Postgraduate training

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| 2012–2013 | **Newton International Fellow**, University of Edinburgh<br>Institute of Evolutionary Biology |
| 2011 | **EMBO Fellow**, University of Edinburgh<br>Institute of Evolutionary Biology |
| 2008–2011 | **HHMI Associate**, University of Michigan<br>Department of Ecology and Evolutionary Biology |

## Education

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

## Honors & awards

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| 2020 | 40 Under 40, Fortune Magazine. |
| 2020 | Webby Award, Special Achievement, International Academy of Digital Arts and Sciences. |
| 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

### Ongoing research support

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| 2020–2023 | INV-018979. Bill and Melinda Gates Foundation.<br>Nextstrain funding for Africa PGI.<br>Principal investigator. |
| 2018–2020 | Seattle Flu Study. Gates Ventures.<br>Principal investigator. |
| 2017–2022 | Wellcome Trust Collaborative Award 206298/Z/17/Z. Wellcome Trust.<br>Putting genomic surveillance at the heart of viral epidemic response.<br>Co-investigator with PI Andrew Rambaut. |
| 2017–2022 | R01 AI125392-01. National Institutes of Health.<br>Mechanisms of influenza transmission bottlenecks: impact on viral evolution.<br>Co-investigator with PI Thomas Friedrich. |
| 2016–2021 | R01 AI127893-01. National Institutes of Health.<br>High-throughput experiments to guide influenza vaccine strain selection.<br>Co-investigator with PI Jesse Bloom. |
| 2016–2021 | R35 GM119774-01. National Institutes of Health.<br>Real-time tracking of virus evolution for vaccine strain selection and epidemiological investigation.<br>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   R01 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

2020–       Instructor, Introduction to Computational Molecular Biology, UW Genome Sciences.

2018–       Instructor, Tools for Computational Biology, UW MCB.

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 Engineering" at the University of Michigan.

2006        Teaching fellow, Population Genetics, Harvard University.

2005        Teaching fellow, Genetics and Genomics, Harvard University.

## Student and postdoctoral mentoring

2020–       Marlin Figgins, PhD student, Department of Applied Mathematics, University of Washington.

2020–       Cassia Wagner, MSTP student, University of Washington.

2019–       Nicola Müller, postdoc, FHCRC.

2019–       Maya Lewinsohn, MSTP student, Department of Genome Sciences, University of Washington.

2018–       Katie Kistler, PhD student, Molecular and Cellular Biology Program, University of Washington.

2017–    John Huddleston, PhD student, Molecular and Cellular Biology Program, University of Washington.

2017–    Louise Moncla, postdoc, FHCRC.

2017–    James Hadfield, postdoc, FHCRC.

2016–2018    Gytis Dudas, postdoc, FHCRC.

2016-2017    Stephanie Stacy, Undergraduate, Summer Undergraduate Research Program, FHCRC.

2015–2020    Allison Black, PhD student, Department of Epidemiology, University of Washington.

2015–2019    Sidney Bell, PhD student, Molecular and Cellular Biology Program, University of Washington.

2015-2016    Charlton Callender, Undergraduate, Summer Undergraduate Research Program, FHCRC.

2014–2016    Alvason Li, postdoc, FHCRC.

2014–2015    Charles Cheung, postdoc, FHCRC.


## Professional service

2020–    Member: Standing Committee on Emerging Infectious Diseases and 21st Century Health Threats, National Academies of Sciences, Engineering, and Medicine.

2018–    Advisor: WHO Global Influenza Surveillance and Response System.

2016–2017    Organizing committee: Epidemics$^6$ conference.

2016–2017    Technical working group member: WHO Public Health Research Agenda for Influenza.

2015    Organizing committee: Epidemics$^5$ 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 Ecology, National Science Foundation, Nature, Nature Communications, Nature Genetics, Phil Trans R Soc B, PLoS Biology, PLoS One, PLoS Pathogens, Proc Natl Acad USA, Science, Virology, Virulence, Wellcome Trust.


## Publications & talks

Journal articles (87 papers, 8270 citations, h-index of 40)

2021    **Müller NF**, **Wagner C**, Frazar CD, Roychoudhury P, **Lee J**, ..., Jerome KR, Lindquist S, Greninger AL, Nickerson DA, **Bedford T** (43 authors). Viral genomes reveal patterns of the SARS-CoV-2 outbreak in Washington State. Sci Transl Med. *In press*.

2021    Barrat-Charlaix P, **Huddleston J**, **Bedford T**, Neher RA. Limited predictability of amino acid substi-

tutions in seasonal influenza viruses. Mol Biol Evol. *In press*.

2021    Kinganda-Lusamaki E, **Black A**, Mukadi DB, **Hadfield H**, Mbala-Kingebeni P, ..., Peeters M, Wiley MR, Ahuka-Mundeke S, **Bedford T**, Muyembe Tamfum J-J (29 authors). Integration of genomic sequencing into the response to the Ebola virus outbreak in Nord Kivu, Democratic Republic of the Congo. Nat Med. *In press*.

2021    Mbala-Kingebeni P, Pratt P, Mutafali Ruffin M, Pauthner MG, Bile F, ..., **Bedford T**, Andersen KG, Wiley MR, Ahuka-Mundeke S, Muyembe Tamfum J-J (50 authors). Ebola virus transmission initiated by systemic Ebola virus disease relapse. N Engl J Med. *In press*.

2021    Kim AE, Brandstetter E, Wilcox N, Heimonen J, Graham C, ..., Rieder MJ, **Bedford T**, Boeckh M, Englund JA, Chu HY on behalf of the Seattle Flu Study Investigators (25 authors). Evaluating specimen quality and results from a community-wide, home-based respiratory surveillance study. J Clin Microbiol. JCM.02934-20.

2021    **Kistler KE**, **Bedford T**. Evidence for adaptive evolution in the receptor-binding domain of seasonal coronaviruses OC43 and 229E. eLife 10: e64509.

2021    **Huddleston J**, **Hadfield J**, **Sibley TR**, **Lee J**, **Fay K**, **Ilcisin M**, **Harkins E**, **Bedford T**, Neher RA, Hodcroft EB. Augur: a bioinformatics toolkit for phylogenetic analyses of human pathogens. JOSS 6: 2906.

2020    Jackson LK, **Potter B**, Schneider SE, Fitzgibbon M, Blair K, Farah H, Krishna U, **Bedford T**, Peek R, Salama NR. *Helicobacter pylori* diversification during chronic infection within a single host generates sub-populations with distinct phenotypes. PLoS Pathog 16: e1008686.

2020    Müller NF, Wüthrich D, Goldman N, Sailer N, Saalfrank C, ..., **Hadfield J**, **Bedford T**, Battegay M, Schneider-Sliwa R, Egli A (24 authors). Characterising the epidemic spread of influenza A/H3N2 within a city through phylogenetics. PLoS Pathog 16: e1008984.

2020    Emanuels A, Heimonen J, O'Hanlon J, Kim AE, Wilcox N, ..., Starita LM, Nickerson DA, **Bedford T**, Englund JA, Chu HY, on behalf of Seattle Flu Study investigators (21 authors). Remote household observation for non-influenza respiratory viral illness. Clin Infect Dis: ciaa1719.

2020    Chu HY, Boeckh M, Englund JA, Famulare M, Lutz BR, ..., Newman KL, **Sibley TR**, Zigman Suchsland ML, Wolf C, Shendure J, **Bedford T**, on behalf of the Seattle Flu Study Research Group (30 authors). The Seattle Flu Study: a multi-arm community-based prospective study protocol for assessing influenza prevalence, transmission, and genomic epidemiology. BMJ Open 10: e037295.

2020    Rogers JH, Link AC, McCulloch D, Brandstetter E, Newman KL, ..., Richardson M, Nickerson DA, Starita LM, **Bedford T**, Chu HY, on behalf of Seattle Flu Study Investigators (21 authors). Characteristics of COVID-19 in homeless shelters: A community-based surveillance study. Ann Intern Med: 10.7326/M20-3799.

2020    **Bedford T**, Greninger AL, Roychoudhury P, Lea M Starita, Famulare M, ..., Armstrong GL, Baird GS, Chu HY, Shendure J, Jerome KR (56 authors). Cryptic transmission of SARS-CoV-2 in Washington State. Science 370: 571–575.

2020    Weil AA, Newman KL, Ong TD, Davidson GH, Logue J, ..., Zhong W, Starita LM, **Bedford T**, Roxby AC, Chu HY (17 authors). Cross-sectional prevalence of SARS-CoV-2 among skilled nursing facility employees and residents across facilities in Seattle. J Gen Intern Med 35: 3302–3307.

2020    **Huddleston J**, Barnes JR, Rowe T, Kondor R, Wentworth DE, ..., Barr I, Subbarao K, Barrat-Charlaix P, Neher RA, **Bedford T** (19 authors). Integrating genotypes and phenotypes improves long-term forecasts of seasonal influenza A/H3N2 evolution. eLife 9: e60067.

2020    Hilton SK, **Huddleston JL**, **Black A**, North K, Dingens AS, **Bedford T**, Bloom JD. dms-view: Interactive visualization tool for deep mutational scanning data. J Open Source Softw 5: 2353.

2020    **Black A**, MacCannell DR, **Sibley TR**, **Bedford T**. Ten recommendations for supporting open pathogen genomic analysis in public health. Nat Med 26: 832–841.

2020    Deng X, Gu W, Federman S, Du Plessis L, Pybus O, ..., **Bedford T**, ..., Chai S, Villarino E, Bonin B, Wadford D, Chiu CY (47 authors). A genomic survey of SARS-CoV-2 reveals multiple introductions into Northern California without a predominant lineage. Science 369: 582–587.

2020    CDC COVID-19 Response Team, Jorden MA, Rudman SL, Villarino E, Hoferka S, ..., **Bedford T**, ..., Famulare M, Nickerson DA, Rieder MJ, Shendure J, Starita LM (27 authors). Evidence for limited early spread of COVID-19 within the United States, January–February 2020. Morb Mortal Wkly Rep 69: 680–684.

2020    Chu HY, Englund JA, Starita LM, Famulare M, Brandstetter E, ..., Jackson M, Hughes JP, Boeckh M, Shendure J, **Bedford T** (30 authors). Early detection of Covid-19 through a citywide pandemic surveillance platform. N Engl J Med 383: 185–187.

2020    Caudill VR, Qin S, Winstead R, Kaur J, Tisthammer K, ..., **Bedford T**, ..., Tran K, Tran L, Winters EJ, Wong A, Pennings PS (56 authors). CpG-creating mutations are costly in many human viruses. Evol Ecol 34: 339–359.

2020    Castro LA, **Bedford T**, Meyers LA. Early prediction of antigenic transitions for influenza A/H3N2. PLoS Comput Biol 16: e1007683.

2020    **Moncla LH**, **Bedford T**, Dussart P, Horm SV, Rith S, Buchy P, Karlsson EA, Li L, Liu Y, Zhu H, Guan Y, Friedrich TC, Horwood PF. Quantifying within-host evolution of H5N1 influenza in humans and poultry in Cambodia. PLoS Pathog 16: e1008191.

2019    **Dudas G**, **Bedford T**. The ability of single genes vs full genomes to resolve time and space in outbreak analysis. BMC Evol Biol 19: 232.

2019    **Potter BI**, Kondor R, **Hadfield J**, **Huddleston J**, Barnes J, Rowe T, Guo L, Xu X, Neher RA, **Bedford T**, Wentworth DE. Evolution and rapid spread of a reassortant A(H3N2) virus that predominated the 2017-2018 influenza season. Virus Evol 5: vez046.

2019    **Black A**, **Moncla LH**, Laiton-Donato K, **Potter B**, Pardo L, Tovar C, Rojas DP, Longini IM, Halloran ME, Peláez-Carvajal D, Ramírez JD, Mercado-Reyes M, **Bedford T**. Genomic epidemiology supports multiple introductions and cryptic transmission of Zika virus in Colombia. BMC Infect Dis 19: 963.

2019    **Hadfield J**, Brito AF, Swetnam DM, Vogels CBF, Tokarz RE, Andersen KG, Smith RC, **Bedford T**, Grubaugh ND. Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. PLoS Pathog 15: e1008042.

2019    **Bell SM**, Katzelnick L, **Bedford T**. Dengue genetic divergence generates within-serotype antigenic variation, but serotypes dominate evolutionary dynamic. eLife 8: e42496.

2019    Lee JM, Eguia R, Zost SJ, Choudhary S, Wilson PC, **Bedford T**, Stevens-Ayers T, Boeckh M, Hurt

A, Lakdawala SS, Hensley SE, Bloom JD. Mapping person-to-person variation in viral mutations that escape polyclonal serum targeting influenza hemagglutinin. eLife 8: e49324.

2019    Dale GA, Wilkins DJ, Bohannon CD, Dilernia D, Hunter E, **Bedford T**, Antia R, Sanz I, Jacob J. Clustered mutations at the murine and human IgH locus exhibit significant linkage consistent with templated mutagenesis. J Immunol: ji1801615.

2019    Soh YQS, **Moncla LH**, Eguia R, **Bedford T**, Bloom JD. Comprehensive mapping of avian influenza PB2 protein as a function of virus adaptation to humans. eLife 8: e45079.

2018    Neher R, **Bedford T**. Real-time analysis and visualization of pathogen sequence data. J Clin Microbiol 56: e00480-18.

2018    Wen FT, **Bell SM**, **Bedford T**, Cobey S. Estimating vaccine-driven selection in seasonal influenza. Viruses 10: 509.

2018    Lee JM, **Huddleston J**, Doud MB, Hooper KA, Wu NC, **Bedford T**, Bloom JD. Deep mutational scanning of hemagglutinin helps predict evolutionary fates of human H3N2 influenza variants. Proc Natl Acad Sci USA 115: E8276–E8285.

2018    **Hadfield J**, Megill C, **Bell SM**, **Huddleston J**, **Potter B**, **Callender C**, Sagulenko P, **Bedford T**, Neher RA. Nextstrain: real-time tracking of pathogen evolution. Bioinformatics: 34: 4121–4123.

2018    Xue KS, **Moncla LH**, **Bedford T**, Bloom JD. Within-host evolution of human influenza virus. Trends Microbiol 26: 781–793.

2018    Rouet F, Nouhin J, Zheng D, Roche B, **Black A**, ..., Barin F, Plantier JC, **Bedford T**, Ramos A, Saphonn V (26 authors). Massive iatrogenic outbreak of human immunodeficiency virus type 1 in rural Cambodia, 2014-2015. Clin Infect Dis 66: 1733–1741.

2018    Morris DH, Gostic KM, Pompei S, **Bedford T**, Łuksza M, Neher RA, Grenfell BT, Lässig M, McCauley JW. Predictive modeling of influenza shows the promise of applied evolutionary biology. Trends Microbiol 26: 102–118.

2018    **Dudas G**, Max Carvalho L, Rambaut A, **Bedford T**. MERS-CoV spillover at the camel-human interface. eLife 7: e31257.

2018    Cybis GB, Sinsheimer JS, **Bedford T**, Rambaut A, Lemey P, Suchard MA. Bayesian nonparametric clustering in phylogenetics: modeling antigenic evolution in influenza. Stat Med 37: 195–206.

2017    Langat P, Raghwani J, **Dudas G**, Bowden T, Edwards S, ..., **Bedford T**, ..., Russell C, Pybus O, Kellam P, McCauley J, Watson SJ (14 authors). Genome-wide evolutionary dynamics of influenza B viruses on a global scale. PLoS Pathog 13: e1006749.

2017    **Bell SM**, **Bedford T**. Modern-day SIV viral diversity generated by extensive recombination and cross-species transmission. PLoS Pathog 13: e1006466.

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 12: 1261–1276.

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/AS01 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 con-

straints 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, Pépin 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 *Quetzalcoatl* 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

2021   AGBT General Meeting.

2020   Mathematics and Statistics of Genomic Epidemiology Workshop, Casa Matemática Oaxaca and Banff International Research Station for Mathematical Innovation and Discovery.

2020   VIDD Seminar, Fred Hutchinson Cancer Research Center, Seattle, WA.

2020   AMD Virtual, Centers for Disease Control and Prevention, Atlanta, GA.

2020   COVID-19 Medical Grand Rounds, UCSF Department of Medicine, San Francisco, CA.

2020   COVID-19 Dynamics and Evolution.

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| 2020 | Keynote talk, AACR Virtual Meeting: COVID-19 and Cancer. |
| 2020 | Biology of Genomes, Cold Spring Harbor, NY. |
| 2020 | AAAS Annual Meeting, Seattle, WA. |
| 2020 | MCMB Seminar Series, SF State University, San Francisco, CA. |
| 2020 | CCB Seminar Series, UC Berkeley, Berkeley, CA. |
| 2019 | BioHub Seminar Series, BioHub, San Francisco, CA. |
| 2019 | EPPIcenter Seminar Series, UCSF, San Francisco, CA. |
| 2019 | Options X for the Control of Influenza, Singapore. |
| 2019 | Distinguished Scientist Seminar Series, Rocky Mountain Laboratories, Hamilton, MT. |
| 2019 | Northwest Data Science Summit, University of Washington, Seattle, WA. |
| 2019 | Population Biology, Ecology and Evolution Seminar, Emory University, Atlanta, GA. |
| 2018 | SMBE Satellite Workshop on Genome Evolution in Pathogen Transmission and Disease, Kyoto, Japan. |
| 2018 | Grand Challenges Annual Meeting, Berlin, Germany. |
| 2018 | Plenary talk, International Conference on Emerging Infectious Diseases, Atlanta, GA. |
| 2018 | Emerging Infections and Pandemic Risk, Institut Pasteur, Paris, France. |
| 2018 | AMD Seminar, Centers for Disease Control and Prevention, Atlanta, GA. |
| 2018 | Plenary talk, HIV Dynamics and Evolution, Leavenworth, WA. |
| 2018 | 6th Annual IDM Symposium, Institute for Disease Modeling, Bellevue, WA. |
| 2018 | Bioinformatics and Genomics Seminar, University of North Carolina, Charlotte, NC. |
| 2018 | Annual International Symposium, Institute for Systems Biology, Seattle, WA. |
| 2018 | NIHE/OUCRU Workshop on Influenza Epidemiology and Evolution in Vietnam, Hanoi, Vietnam. |
| 2018 | Department of Hygiene Seminar, Hokkaido University, Sapporo, Japan. |
| 2018 | CREST International Symposium on Big Data Applications, Tokyo, Japan. |
| 2017 | BioHub Seminar, Chan Zuckerberg BioHub, San Francisco, CA. |
| 2017 | VIDD Seminar, Fred Hutchinson Cancer Research Center, Seattle, WA. |
| 2017 | Viral Pathogenesis Symposium, Fred Hutchinson Cancer Research Center, Seattle, WA. |
| 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    VIDD 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    VIDD 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    VIDD 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

2019    Epidemics[7], Charleston, SC.

2017    Epidemics[6], Sitges, Spain.

2017    Ecological Society of America Annual Meeting, Portland, OR.

2015    Epidemics[5], 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    Epidemics[3], 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

2020     COVID-19 pandemic scientific communication and outreach through Twitter to >275k followers.

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