

# Trevor Bedford

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## Faculty positions

- 2020– **Affiliate Associate Professor**, University of Washington  
Department of Epidemiology
- 2019– **Associate Professor**, Fred Hutchinson Cancer Research Center  
Human Biology Division
- 2019– **Affiliate Associate Professor**, University of Washington  
Department of Genome Sciences
- 2018– **Associate Professor**, Fred Hutchinson Cancer Research Center  
Vaccine and Infectious Disease Division and Public Health Sciences Division
- 2016–2020 **Affiliate Assistant Professor**, University of Washington  
Department of Epidemiology
- 2013–2017 **Assistant Professor**, Fred Hutchinson Cancer Research Center  
Vaccine and Infectious Disease Division and Public Health Sciences Division

## 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

## Education

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

## Honors & awards

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 ( <i>Declined</i> ).
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

2021–2028	75N93021C00015. National Institutes of Health. Center of Excellence for Influenza Research and Response (CEIRR). Co-investigator with PI Scott Hensley.
2020–2023	INV-018979. Bill and Melinda Gates Foundation. Nextstrain funding for Africa PGI. Principal investigator.
2018–2021	Seattle Flu Study. Gates Ventures. Principal investigator.
2017–2022	Wellcome Trust Collaborative Award 206298/Z/17/Z. Wellcome Trust. Putting genomic surveillance at the heart of viral epidemic response. Co-investigator with PI Andrew Rambaut.
2017–2022	RO1 AI125392. National Institutes of Health. Mechanisms of influenza transmission bottlenecks: impact on viral evolution. Co-investigator with PI Thomas Friedrich.
2016–2021	RO1 AI127893. National Institutes of Health. High-throughput experiments to guide influenza vaccine strain selection. Co-investigator with PI Jesse Bloom.

2016–2026 R35 GM119774. National Institutes of Health.  
Real-time tracking of virus evolution for vaccine strain selection and epidemiological investigation.  
Principal investigator.

#### COMPLETED RESEARCH SUPPORT

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 M. Elizabeth 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, University of Washington.

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

2021– Miguel Paredes, MSTP student, Department of Epidemiology, University of Washington.

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

2020– Cassia Wagner, MSTP student, Department of Genome Sciences, 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<sup>6</sup> conference.

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

2015 Organizing committee: Epidemics<sup>5</sup> 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 (97 PAPERS, 9853 CITATIONS, H-INDEX OF 42)

- 2021 Annavajhala MK, Mohri H, Wang P, Nair M, Zucker JE, ..., Tagliavia M, Huang Y, **Bedford T**, Ho DD, Uhlemann A-C (13 authors). Emergence and expansion of SARS-CoV-2 B.1.526 after identification in New York. *Nature*: s41586-021-03908-2.
- 2021 Braun K, Moreno G, **Wagner C**, Accola MA, Rehrauer WM, Baker D, Koelle K, O'Connor DH, **Bedford T**, Friedrich TC, **Moncla LH**. Limited within-host diversity and tight transmission bottlenecks limit SARS-CoV-2 evolution in acutely infected individuals. *PLoS Pathog.* *In press*.
- 2021 Srivatsan S, Heidl S, Pfau B, Martin BK, Han PD, ..., **Bedford T**, ..., Konnick EQ, Debley JS, Shendure J, Lockwood CM, Starita LM (36 authors). SwabExpress: An end-to-end protocol for extraction-free COVID-19 testing. *Clin Chem: hvab* 132.
- 2021 Corey L, Beyrer C, Cohen MS, Michael NL, **Bedford T**, Rolland M. SARS-CoV-2 variants in patients with immunosuppression. *N Engl J Med* 385: 562–566.
- 2021 Perchetti GA, Zhu H, Mills MG, Shrestha L, **Wagner C**, ..., Mathias P, **Bedford T**, Jerome KR, Greninger AL, Roychoudhury P (14 authors). Specific allelic discrimination of N501Y and other SARS-CoV-2 mutations by ddPCR detects B.1.1.7 lineage in Washington State. *J Med Virol: jmv*.27155.
- 2021 Konings F, Perkins MD, Kuhn JH, Pallen MJ, Alm EJ, ..., **Bedford T**, ..., Tong S, van der Werf S, von Gottberg A, Ziebuhr J, Van Kerkhove MD (47 authors). SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. *Nat Microbiol* 6: 821–823.
- 2021 Chung E, Chow EJ, Wilcox NC, Burstein R, Brandstetter E, ..., Hughes JP, Starita LM, **Bedford T**, Englund JA, Chu HY (23 authors). Symptoms and RNA levels in pediatric vs adult SARS-CoV-2 infections in the community setting. *JAMA Pediatr.* *In press*.
- 2021 Heimonen JT, McCulloch DJ, O'Hanlon J, Ashley Erin Kim, Emanuels A, ..., Boeckh M, Starita LM, **Bedford T**, Englund JA, Chu HY (19 authors). A remote household-based approach to influenza self-testing and antiviral treatment. *Influenza Other Respir Viruses* 15: 469–477.
- 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: eabf*0202.
- 2021 **Moncla LH**, **Black A**, DeBolt C, Lang M, Graff NR, Pérez-Osorio AC, **Müller NF**, Haselow D, Lindquist S, **Bedford T**. Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State. *eLife* 10: e66448.
- 2021 Jackson ML, Hart GR, McCulloch DJ, Adler A, Brandstetter E, ..., Starita L, Englund JA, **Bedford T**, Chu H, Famulare M (17 authors). Effects of weather-related social distancing on city-scale transmission of respiratory viruses. *BMC Infect Dis* 21: 335.
- 2021 Barrat-Charlaix P, **Huddleston J**, **Bedford T**, Neher RA. Limited predictability of amino acid substitutions in seasonal influenza viruses. *Mol Biol Evol* 38: 2767–2777.
- 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 se-

quencing into the response to the Ebola virus outbreak in Nord Kivu, Democratic Republic of the Congo. *Nat Med* 27: 710–716.

- 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* 384: 1240–1247.
- 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* 59: e02934-20.
- 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, ..., **Bedford T**, Battegay M, Schneider-Sliwa R, Egli A, Stadler T (25 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: ciaa* 1719.
- 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/H<sub>3</sub>N<sub>2</sub>. *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 H<sub>5</sub>N<sub>1</sub> 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(H<sub>3</sub>N<sub>2</sub>) virus that predominated the 2017–2018 influenza season. *Virus Evol* 5: ve046.
- 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*: j11801615.
- 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, Raghwanji 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, Théze 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 (H<sub>3</sub>N<sub>2</sub>). *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: vevo06.
- 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*

- 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, P  pin 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 (H<sub>3</sub>N<sub>2</sub>). 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 Plenary talk, 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.
- 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 Research, 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<sup>7</sup>, Charleston, SC.
- 2017 Epidemics<sup>6</sup>, Sitges, Spain.
- 2017 Ecological Society of America Annual Meeting, Portland, OR.
- 2015 Epidemics<sup>5</sup>, 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<sup>3</sup>, 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 >300k followers.

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