

Trevor Bedford

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Faculty positions

- 2023– **Affiliate Professor**, University of Washington
Department of Epidemiology and Department of Genome Sciences
- 2022– **Professor**, Fred Hutchinson Cancer Center
Vaccine and Infectious Disease, Human Biology and Public Health Sciences Divisions
- 2021– **Investigator**, Howard Hughes Medical Institute
- 2020–2023 **Affiliate Associate Professor**, University of Washington
Department of Epidemiology
- 2019–2021 **Associate Professor**, Fred Hutchinson Cancer Research Center
Human Biology Division
- 2019–2023 **Affiliate Associate Professor**, University of Washington
Department of Genome Sciences
- 2018–2021 **Associate Professor**, Fred Hutchinson Cancer Research Center
Vaccine and Infectious Disease and Public Health Sciences Divisions
- 2016–2020 **Affiliate Assistant Professor**, University of Washington
Department of Epidemiology
- 2013–2017 **Assistant Professor**, Fred Hutchinson Cancer Research Center
Vaccine and Infectious Disease and Public Health Sciences Divisions

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

2023	Finalist, Luminary Leader Global Health Impact Award, Washington Global Health Alliance.
2022	Finalist, Falling Walls Science Breakthrough of the Year, Falling Walls Foundation.
2022	STATUS List, Stat News.
2021–2026	MacArthur Fellow, John D. and Catherine T. MacArthur Foundation.
2021–	HHMI Investigator, Howard Hughes Medical Institute.
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	Finalist, Open Science Prize, 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

2022–2027	Centers for Disease Control and Prevention. Northwest Pathogen Genomics Center of Excellence. Co-investigator with PI Allison Black.
2022–2027	Ro1 AI165821, National Institutes of Health. Forecasting influenza evolution on a heterogeneous immune landscape. Co-PI with PI Jesse Bloom.
2021–2028	HHMI Investigator Award, Howard Hughes Medical Institute. Principal Investigator.
2021–2026	Nextstrain Support, John Templeton Foundation. Principal Investigator.
2021–2024	Howard Hughes Medical Institute. Transformation to endemicity: the next stage of COVID-19.

Co-PI with PIs David Baker, Jesse Bloom, Harmit Malik, Erick Matsen, Joseph Mougous, Jay Shendure and David Veesler.

- 2021–2028 75N93021C00015. National Institutes of Health.
Center of Excellence for Influenza Research and Response (CEIRR).
Co-investigator with PI Scott Hensley.
- 2020–2024 INV-018979. Bill and Melinda Gates Foundation.
Nextstrain funding for Africa PGI.
Principal investigator.
- 2018–2024 RO1 AI140891. National Institutes of Health.
Complete Mapping of Immune Selection from Antibodies to HIV.
Co-investigator with PIs Jesse Bloom and Julie Overbaugh.
- 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

- 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.
- 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

- 2020–2021 Instructor, Introduction to Computational Molecular Biology, UW Genome Sciences.
- 2018–2021 Instructor, Tools for Computational Biology, UW MCB.
- 2015–2023 Instructor, Pathogen Evolution, Selection and Immunity, Summer Institute in Statistics and Modeling in Infectious Diseases, University of Washington.
- 2014– 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

- 2023– Nashwa Ahmed, PhD student, Molecular and Cellular Biology Program, University of Washington.
- 2022– Cécile Tran Kiem, postdoc, FHCC.
- 2022– Eslam Abousamra, MPH student, Department of Epidemiology, University of Washington.
- 2021– Katie Kistler, postdoc, FHCC.
- 2022 Allison Li, Undergraduate, Summer Undergraduate Research Program, FHCC.
- 2021 Eslam Abousamra, Undergraduate, Summer Undergraduate Research Program, FHCRC.
- 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.
- 2019–2023 Maya Lewinsohn, MSTP student, Department of Genome Sciences, University of Washington.
- 2018–2021 Katie Kistler, PhD student, Molecular and Cellular Biology Program, University of Washington.
- 2017–2020 John Huddleston, PhD student, Molecular and Cellular Biology Program, University of Washington.
- 2017–2022 Louise Moncla, postdoc, FHCRC.
- 2017–2019 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

- 2023– Coordinating Group Member: Pathogen Genomics Centers of Excellence, Centers for Disease Control and Prevention.
- 2022 Taskforce member: Coronavirus Vaccines R&D Roadmap.
- 2022 Policy report co-author: Getting to and Sustaining the Next Normal A Roadmap for Living with COVID.
- 2020–2021 Member: Standing Committee on Emerging Infectious Diseases and 21st Century Health Threats, National Academies of Sciences, Engineering, and Medicine.
- 2020–2021 Member: Advisory Board, The COVID Tracking Project.
- 2018– Advisor: Global Influenza Surveillance and Response System, World Health Organization.
- 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 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 (115 PAPERS, 17,188 CITATIONS, H-INDEX OF 56)

Perofsky AC, **Huddleston J**, Hansen C, Barnes JR, Rowe T, ..., Barr IG, Subbarao K, Krammer F, **Bedford T**, Viboud C (26 authors). Antigenic drift and subtype interference shape A(H3N2) epidemic dynamics in the United States. eLife. Accepted.

Paredes MI, **Ahmed N**, **Figgins M**, Colizza V, Lemey P, McCrone JT, **Müller NF**, **Tran Kiem C**, **Bedford T**. Underdetected dispersal and extensive local transmission drove the 2022 mpox epidemic. Cell. In press.

- 2024 Oltean HN, Black A, Lunn SM, Smith N, Templeton A, ..., Bickel JB, Hughes JP, Lindquist S, Baseman JG, **Bedford T** (13 authors). Changing genomic epidemiology of COVID-19 in long-term care facilities during the 2020-2022 pandemic, Washington State. *BMC Public Health* 24: 182.
- 2023 **Kistler KE, Bedford T**. An atlas of continuous adaptive evolution in endemic human viruses. *Cell Host Microbe* 31: 1-12.
- 2023 **Lee J, Hadfield J, Black A, Sibley TR, Neher RA, Bedford T, Huddleston J**. Joint visualization of seasonal influenza serology and phylogeny to inform vaccine composition. *Front Bioinform* 3: 1-22.
- 2023 Oltean HN, Allen KJ, Frisbie L, Lunn SM, Torres LM, ..., Wolgamot G, Hughes JP, Baseman JG, **Bedford T**, Lindquist S (43 authors). Implementation and evaluation of a sentinel surveillance system for SARS-CoV-2 genomic data: Washington State, 2020-2021. *Emerg Infect Dis* 29: 242-251.
- 2023 **Lewinsohn MA, Bedford T, Müller NF, Feder AF**. State-dependent evolutionary models reveal modes of solid tumor growth. *Nat Ecol Evol* 7: 581-596.
- 2023 Tang M, **Dudas G, Bedford T**, Minin VN. Fitting stochastic epidemic models to gene genealogies using linear noise approximation. *Ann Appl Stat* 17: 1-22.
- 2022 Hansen CL, Perofsky A, Burstein R, Famulare M, Boyle S, ..., Shendure J, **Bedford T**, Chu HY, Starita LM, Viboud C (30 authors). Trends in risk factors and symptoms associated with SARS-CoV-2 and rhinovirus test positivity in King County, Washington: A test-negative design study of the greater Seattle Coronavirus Assessment Network. *JAMA Netw* 5: e2245861.
- 2022 Tegally H, San JE, Cotten M, Tegomoh B, Mboowa G, ..., **Bedford T**, ..., de Oliveira T, Happi C, Lessells R, Nkengasong J, Wilkinson E (395 authors). The evolving SARS-CoV-2 epidemic in Africa: Insights from rapidly expanding genomic surveillance. *Science* 378: eabq5358.
- 2022 Weil AA, Luitken KG, Casto AM, Bennett JC, Hanlon JO, ..., Shendure J, **Bedford T**, Hughes JP, Starita LM, Chu HY (29 authors). Genomic surveillance of SARS-CoV-2 Omicron variants on a university campus. *Nat Commun* 13: 5240.
- 2022 Happi C, Adetifa I, Mbala P, Njouom R, Nakoune E, ..., **Bedford T**, ..., Lessells R, Ogwell AE, Kebede Y, Tessema SK, de Oliveira T (33 authors). Urgent need for a non-discriminatory and non-stigmatizing nomenclature for monkeypox virus. *PLoS Biol* 20: e3001769
- 2022 **Müller NF, Kistler K, Bedford T**. A Bayesian approach to infer recombination patterns in coronaviruses. *Nat Commun* 13: 4186.
- 2022 **Paredes MI**, Lunn SM, Famulare M, Frisbie LA, Painter I, ..., Torres ML, Lindquist S, **Bedford T**, Allen KJ, Oltean HN (45 authors). Associations between SARS-CoV-2 variants and risk of COVID-19 hospitalization among confirmed cases in Washington State: a retrospective cohort study. *Clin Infect Dis* 75: e536-e544.
- 2022 **Kistler KE, Huddleston J, Bedford T**. Rapid and parallel adaptive mutations in spike S1 drive clade success in SARS-CoV-2. *Cell Host Microbe* 30: 545-555.
- 2022 Geyer RE, Kotnik JH, Lyon V, Brandstetter E, Zigman Suchsland M, ..., Nickerson DA, Starita LM, **Bedford T**, Lutz B, Thompson MJ (15 authors). Diagnostic accuracy of an at-home, rapid self-test for influenza: prospective comparative accuracy study. *JMIR Public Health Surveill* 8: e28268.
- 2022 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* 68: 143–152.
- 2021 Santiago GA, Kalinich CC, Cruz-López F, González GL, Flores B, ..., **Bedford T**, ..., Ellis B, Waterman SH, Paz-Bailey G, Grubaugh ND, Muñoz-Jordán JL (18 authors). Tracing the origin, spread, and molecular evolution of Zika virus, Puerto Rico, 2016–2017. *Emerg Infect Dis* 27: 2971–2973.
- 2021 Weil AA, Sohlberg SL, O’Hanlon JA, Casto AM, Emanuels AW, ..., Lockwood CM, Starita LM, **Bedford T**, Shendure JA, Chu HY (36 authors). SARS-CoV-2 epidemiology on a public university campus in Washington State. *Open Forum Infect Dis* 8: ofab464.
- 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* 597: 703–708.
- 2021 Braun K, Moreno G, **Wagner C**, Accola MA, Rehauer WM, Baker D, Koelle K, O’Connor DH, **Bedford T**, Friedrich TC, **Moncla LH**. Acute SARS-CoV-2 infections harbor limited within-host diversity and transmit via tight transmission bottlenecks. *PLoS Pathog* 17: e1009849.
- 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* 93: 5931–5941.
- 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* 175: e212025.
- 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* 13: eabfo202.
- 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-Mundeké 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* 27: 710–716.
- 2021 Mbala-Kingebeni P, Pratt P, Mutafali Ruffin M, Pauthner MG, Bile F, ..., **Bedford T**, Andersen KG, Wiley MR, Ahuka-Mundeké 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. *J Open Source Softw* 6: 2906.
- 2021 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* 73: e4411–e4418.
- 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 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: vezo46.
- 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, 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.
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- 2015 Neher RA, **Bedford T**. nextflu: real-time tracking of seasonal influenza virus evolution in humans. *Bioinformatics* 31: 3546–3548.
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- 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*

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- 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.
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- 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.
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- 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

- 2023 Division of Viral Products Seminar Series, Food and Drug Administration, Silver Spring, MD.
- 2023 Symposium on Adaptation and Immune escape of RNA viruses, Biozentrum, University of Basel, Basel, Switzerland.
- 2023 John J. Holland Lecture, American Society for Virology Annual Meeting, Athens, GA.
- 2022 Virus Evolution and Molecular Epidemiology (VEME) Bioinformatics Workshop, Panama City, Panama.
- 2022 Science for Resilience – Learnings from the Pandemic, Institute for Advanced Studies, Vienna, Austria.
- 2022 Africa PGI Webinar Series, Africa CDC, Addis Ababa, Ethiopia.
- 2022 Vaccines and Related Biological Products Advisory Committee Meeting, Food and Drug Administration, Silver Spring, MD.
- 2022 Viruses and Vaccines Seminar, Brotman Baty Institute, Seattle, WA.

2021 Plenary talk, Epidemics⁸ Conference.

2021 Stetten Lecture, National Institute of General Medical Sciences, Bethesda, MD.

2021 Plenary talk, HVTN/CoVPN Conference.

2021 VIDD Seminar, Fred Hutchinson Cancer Research Center, Seattle, WA.

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 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.
- 2009 Departmental Seminar, School of Computational Science, Florida State University, Tallahassee, FL.
- 2006 NKS Wolfram Science Conference, Washington, DC.

CONFERENCE ABSTRACTS

- 2019 Epidemics⁷ Conference, Charleston, SC.

- 2017 Epidemics⁶ Conference, Sitges, Spain.
- 2017 Ecological Society of America Annual Meeting, Portland, OR.
- 2015 Epidemics⁵ Conference, 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 Conference, 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

- 2020–2023 COVID-19 pandemic scientific communication and outreach through Twitter to >450k followers.
- 2015 Science outreach video “Tracking down the sneeze that started seasonal flu” published on Vox.com.