Trevor Bedford

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Faculty positions

2018– **Associate Member**, Fred Hutchinson Cancer Research Center
Vaccine and Infectious Disease Division, Computational Biology Program

2016– **Affiliate Assistant Professor**, University of Washington
Department of Epidemiology

2013–2017 **Assistant Member**, Fred Hutchinson Cancer Research Center
Vaccine and Infectious Disease Division, Computational Biology Program

Postgraduate training

2012–2013 **Newton International Fellow**, University of Edinburgh
Institute of Evolutionary Biology

2011 **EMBO Fellow**, University of Edinburgh
Institute of Evolutionary Biology

2008–2011 **HHMI Associate**, University of Michigan
Department of Ecology and Evolutionary Biology

2008 **Intern**, Wolfram Research Inc.

Education

2003–2008 **PhD in Biology**, Harvard University

1999–2002 **BA in Biological Sciences** *(with honors)*, University of Chicago

Honors & awards

2017 Open Science Prize Winner, NIH, Wellcome Trust and HHMI.

2016–2020 Pew Scholar in the Biomedical Sciences, Pew Charitable Trusts.

2016 Open Science Prize Finalist, NIH, Wellcome Trust and HHMI.

2012–2014 Marie Curie International Incoming Fellow, European Commission *(Declined)*.

2012–2013	Newton International Fellow, The Royal Society.
2011–2013	Long Term Fellow, European Molecular Biology Organization.
2005–2008	NSF Graduate Research Fellowship, National Science Foundation.
2003–2005	NIH Genetics and Genomics Training Program, National Institutes of Health.
2001	HHMI Undergraduate Fellowship, Howard Hughes Medical Institute.
1999–2002	University Scholarship, University of Chicago.

Research support

2018–2019	Seattle Flu Study. Anonymous donor. 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	R01 AI125392-01. National Institutes of Health. Mechanisms of influenza transmission bottlenecks: impact on viral evolution. Co-investigator with PI Thomas Friedrich.
2016–2021	R01 AI127893-01. National Institutes of Health. High-throughput experiments to guide influenza vaccine strain selection. Co-investigator with PI Jesse Bloom.
2016–2021	R35 GM119774-01. National Institutes of Health. Real-time tracking of virus evolution for vaccine strain selection and epidemiological investigation. Principal investigator.
2015–2020	U19 AI117891-01. National Institutes of Health. Dynamics and evolution of immune responses to influenza viruses. Co-investigator with PIs Rafi Ahmed and Rustom Antia.
2014–2019	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

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

2018–   Katie Kistler, PhD student, University of Washington.

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

2017–   Louise Moncla, postdoc, FHCRC.

2017–   James Hadfield, postdoc, FHCRC.

2016–2018   Gytis Dudas, postdoc, FHCRC.

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

2015–2019   Sidney Bell, PhD student, University of Washington.

2014–2016   Alvason Li, postdoc, FHCRC.

2014–2015   Charles Cheung, postdoc, FHCRC.

Supervised trainees

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

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

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

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

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

2004–2005   Jehee Choi, undergraduate, Harvard University.

2004–2005   Michelle White, undergraduate, Harvard University.

Professional service

2018–   Informal 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 (56 PAPERS, 3844 CITATIONS, H-INDEX OF 27)

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: bty407.

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 inter-

face. 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 constraints on B cell affinity maturation. Phil Trans R Soc B 370: 20140244.

2015   **Bedford T**, Riley S, Barr IG, Broor S, Chadha M, ..., Tashiro M, Wang D, Xu X, Lemey P, Russell CA (26 authors). Global circulation patterns of seasonal influenza viruses vary with antigenic drift. Nature 523: 217–220.

2015   Park DJ, Dudas G, Wohl S, Goba A, Whitmer SLM, ..., **Bedford T**, Gnirke A, Ströher U, Rambaut A, Garry RF, Sabeti PC (86 authors). Ebola virus epidemiology, transmission, and evolution during seven months in Sierra Leone. Cell 161: 1–11.

2015   Frost SDW, Pybus OG, Gog JR, Viboud C, Bonhoeffer S, **Bedford T**. Eight challenges in phylodynamic inference. Epidemics 10: 88–92.

2015   Vrancken B, Lemey P, Rambaut A, **Bedford T**, Longdon B, Gunthard H, Suchard MA. Simultaneously estimating evolutionary history and repeated traits phylogenetic signal: applications to viral and host phenotypic evolution. Methods Ecol Evol 6: 67–82.

2015   Dudas G, **Bedford T**, Lycett S, Rambaut A. Reassortment between influenza B lineages and the emergence of a co-adapted PB1-PB2-HA gene complex. Mol Biol Evol 32: 162–172.

2014   Zinder D, **Bedford T**, Baskerville EB, Woods RJ, Roy M, Pascual M. Seasonality in the migration and establishment of H3N2 influenza lineages with epidemic growth and decline. BMC Evol Biol 14: 272.

2014   Faria NR, Rambaut A, Suchard MA, Baele G, **Bedford T**, Ward MJ, Tatem AJ, Sousa JD, Arinaminpathy N, 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

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

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

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

Last updated: February 15, 2019