Amanda C. Perofsky, Ph.D.

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Bio

Dr. Amanda Perofsky is an Assistant Research Professor in Bouvé College of Health Sciences at Northeastern University, with joint appointments in the Network Science Institute, Roux Institute, and Institute for Experiential AI. Dr. Perofsky is a computational biologist whose research focuses on the ecological, evolutionary, and behavioral drivers of infectious disease dynamics, with aims to improve disease surveillance and better understand and predict future outbreaks. Specifically, she combines statistical, mathematical, and computational approaches to investigate respiratory virus transmission patterns and epidemiology, with a focus on influenza, SARS-CoV-2, and RSV. She also produces operational forecasts and scenario projections of respiratory virus outbreaks.

Education

2018	PhD in Ecology, Evolution, and Behavior, The University of Texas at Austin, Austin, Texas Advisor: Lauren Ancel Meyers
2009	B.Sc. in Ecology, B.Sc. in Biology, University of Georgia, Athens, Georgia *Summa cum laude* with Highest Honors

Academic Positions

2025 –	Assistant Research Professor, Bouvé College of Health Sciences, Northeastern University With joint appointments in the Network Science Institute, Roux Institute, and Institute for Experiential AI.
2021 – 2025	Guest Researcher, Fogarty International Center, National Institutes of Health
2021 – 2025	Epidemiological Data Scientist, Brotman Baty Institute for Precision Medicine, University of Washington
2018 – 2021	Postdoctoral Research Fellow, Fogarty International Center, National Institutes of Health Advisor: Cécile Viboud

Awards & Fellowships

2023	NIH/Fogarty Director's Individual Merit Award, *For excellence in scientific research in epidemiological modeling with a focus on influenza antigenic evolution and the role of human mobility in COVID-19 disease dynamics*
2020, 2021	NIH/Fogarty Director's Group Merit Award, *For outstanding modeling work to support the COVID-19 pandemic response domestically and internationally*
2020	Young Scientist Award, European Scientific Working group on Influenza (ESWI) Conference
2019	NIH/Fogarty Director's Individual Merit Award, *For outstanding efforts to forecast weekly influenza-like illness activity in 27 US military facilities in collaboration with DoD*
2017, 2018	Graduate School Summer Semester Continuing Fellowship, UT-Austin
2017	College of Natural Sciences Graduate Student Professional Development Award, UT-Austin
2013 – 2015	NSF Graduate Research Fellowship (awarded 2012)
2011 – 2012	UT-Austin Integrative Biology Graduate Recruitment Fellowship
2010 – 2011	NIH Post-baccalaureate IRTA Fellowship
2008	Elected, Phi Beta Kappa Honors Society
2008	NSF Research Experiences for Undergraduates (REU) Internship
2005 – 2009	National Merit Scholarship, University of Georgia
2005 – 2009	Georgia HOPE Scholarship (full tuition)

Research support

Pending

	NIH, *Phylogenomic Epidemiology and Responses in Mitochondrial Etiology of RSV* Role: Co-I; PI: Nídia S. Trovão (University of Illinois – Urbana Champaign) Expected submission: Feb 2026; Proposed funding period: Aug 2026 – July 2031

Completed

2022 – 2024	CDC (BAA 75D30122C14368), *Collaborative technology development and analyses to support genetic epidemiology in Washington State*, $2M Role: Epidemiology Lead; PIs: Lea Starita and Trevor Bedford
2021 – 2023	Gates Ventures award to Seattle Flu Study, $11.6M Role: Key Personnel; PIs: Trevor Bedford, Michael Boeckh, Helen Chu, Janet Englund, Michael Famulare, Tina Lockwood, Barry Lutz, Jay Shendure, Lea Starita, and Cécile Viboud
2018	NSF Research Exchange Grant, Infectious Disease Evolution Across Scales (IDEAS) Research Coordination Network, *How does influenza evolution impact the epidemiology of annual epidemics?* $2800
2015 – 2017	NSF BEACON (DBI-0939454), *Factors that influence gut microbiota diversity and intestinal bacteria transmission dynamics in wild lemurs*, $16000 Role: PI, with co-PIs Lauren Ancel Meyers and Rebecca Lewis
2015	Ecology, Evolution, & Behavior Dissertation Improvement Grant, UT-Austin, $8000
2012	Small Research Grant, American Society of Primatologists, $2000
2012	Small Research Grant, International Primatological Society, $1500
2011	Ecology, Evolution, & Behavior Startup Grant, UT-Austin, $2000

Publications

1. Bents SJ, Martin ET, Stevens-Ayers T, Andrews C, Adler A, **Perofsky AC**, et al. Multiplex serology reveals age-specific immunodynamics of respiratory pathogens in the wake of the COVID-19 pandemic. Nat Commun. 2025;16(1):11015.
2. Elias-Warren A, Bennett JC, Iwu CD, Starita LM, Stone J, Capodanno B, … **Perofsky AC**, … et al. Epidemiology of Human Metapneumovirus Infection in a Community Setting, Seattle, Washington, USA. J Infect Dis. 2025;232(Supplement_1):S78-S92.
3. Hansen CL, Lee L, Bents SJ, **Perofsky AC**, Sun K, Starita LM, et al. Scenario Projections of Respiratory Syncytial Virus Hospitalizations Averted Due to New Immunizations. JAMA Netw Open. 2025;8(6):e2514622.
4. Kostandova N, Corgel R, Bansal S, Berube S, Cleary E, Hansen C, … **Perofsky AC**, … et al. Improving mobility data for infectious disease research. Nat Hum Behav. 2025;9(7):1309-12.
5. Tran-Kiem C, Paredes MI, **Perofsky AC,** Frisbie LA, Xie H, Kong K, et al. Fine-scale patterns of SARS-CoV-2 spread from identical pathogen sequences. Nature. 2025;640(8057):176-85.
6. **Perofsky AC**, Huddleston J, Hansen CL, Barnes JR, Rowe T, Xu X, et al. Antigenic drift and subtype interference shape A(H3N2) epidemic dynamics in the United States. eLife. 2024;13:RP91849. **Featured on *eLife’s* podcast**
7. Mathis SM, Webber AE, Leon TM, Murray EL, Sun M, White LA, …, **Perofsky AC**, …, et al. Evaluation of FluSight influenza forecasting in the 2021-22 and 2022-23 seasons with a new target laboratory-confirmed influenza hospitalizations. Nat Commun. 2024;15(1):6289.
8. **Perofsky AC**, Hansen CL, Burstein R, Boyle S, Prentice R, Marshall C, et al. Impacts of human mobility on the citywide transmission dynamics of 18 respiratory viruses in pre- and post-COVID-19 pandemic years. Nat Commun. 2024;15(1):4164. **Featured in *Nature Communications* Editors’ Highlights for “Public Health”**
9. Paredes MI, **Perofsky AC**, Frisbie L, Moncla LH, Roychoudhury P, Xie H, et al. Local-scale phylodynamics reveal differential community impact of SARS-CoV-2 in a metropolitan US county. PLoS Pathog. 2024;20(3):e1012117.
10. Hansen C, **Perofsky AC**, Burstein R, Famulare M, Boyle S, Prentice R, et al. Trends in Risk Factors and Symptoms Associated with SARS-CoV-2 and Rhinovirus Test Positivity in King County, Washington, June 2020 to July 2022. JAMA Netw Open. 2022;5(12):e2245861.

11. **Perofsky AC**, Tempia S, Bingham J, Maslo C, Toubkin M, Laubscher A, et al. Direct and Indirect Effects of the Coronavirus Disease 2019 Pandemic on Private Healthcare Utilization in South Africa, March 2020-September 2021. Clin Infect Dis. 2022;75(1):e1000-e10.
12. **Perofsky AC**, Ancel Meyers L, Abondano LA, Di Fiore A, Lewis RJ. Social groups constrain the spatiotemporal dynamics of wild sifaka gut microbiomes. Mol Ecol. 2021;30(24):6759-75.
13. McBride DS*, **Perofsky AC***, Nolting JM, Nelson MI, Bowman AS. Tracing the Source of Influenza A Virus Zoonoses in Interconnected Circuits of Swine Exhibitions. J Infect Dis. 2021;224(3):458-68. ***Co-first authors**
14. Viboud C, Gostic K, Nelson MI, Price GE, **Perofsky A**, Sun K, et al. Beyond clinical trials: Evolutionary and epidemiological considerations for development of a universal influenza vaccine. PLoS Pathog. 2020;16(9):e1008583.
15. **Perofsky AC**, Nelson MI. The challenges of vaccine strain selection. Elife. 2020;9.
16. Nelson MI, **Perofsky A**, McBride DS, Rambo-Martin BL, Wilson MM, Barnes JR, et al. A Heterogeneous Swine Show Circuit Drives Zoonotic Transmission of Influenza A Viruses in the United States. J Virol. 2020;94(24).
17. **Perofsky AC**, Lewis RJ, Meyers LA. Terrestriality and bacterial transfer: a comparative study of gut microbiomes in sympatric Malagasy mammals. ISME J. 2019;13(1):50-63.
18. Rakotomalala EJ, Rakotondraparany F, **Perofsky AC**, Lewis RJ. Characterization of the Tree Holes Used by Lepilemur ruficaudatus in the Dry, Deciduous Forest of Kirindy Mitea National Park. Folia Primatologica. 2017;88(1):28-41.
19. **Perofsky AC**, Lewis RJ, Abondano LA, Di Fiore A, Meyers LA. Hierarchical social networks shape gut microbial composition in wild Verreaux's sifaka. Proc Biol Sci. 2017;284(1868).
20. Berry BS, Magori K, **Perofsky AC**, Stallknecht DE, Park AW. Wetland cover dynamics drive hemorrhagic disease patterns in white-tailed deer in the United States. J Wildl Dis. 2013;49(3):501-9.

Preprints and Submitted Manuscripts

1. Iwu, CD, Elias-Warren, A, Bennett, JC, Logue, JK, Grindstaff, S, Stone, J, …, **Perofsky, AC**, …, et al. Clinical and genomic epidemiology of influenza viruses before and during the COVID-19 pandemic, Seattle, Washington USA. In review.
2. Bennet, JC, Elias-Warren, A, Wetzler, E, Starita, LM, Stone, J, Capodanno, …, **Perofsky, AC**, …, et al. RSV Molecular Epidemiology Pre- and Post-COVID-19 Pandemic Periods in Seattle, Washington, USA. In review.
3. Tran-Kiem C, **Perofsky AC**, Lessler J, Bedford T. Characterizing the informativeness of pathogen genome sequence datasets about transmission between population groups. medRxiv. 2025. In press, *Proc Biol Sci*
4. Srinivas Duddu A, Elgamal I, Camacho-Mateu J, Holubowska O, Rella SA, Bents SJ, …, **Perofsky AC**. Modeling the effects of COVID-19 mobility disruptions on RSV transmission in Seattle, Washington. medRxiv. 2024:2024.09.13.24313667. In prep.

Conferences

Podium presentations

2025 NetSci International Conference on Network Science, Maastricht, The Netherlands *Modelling the effects of COVID-19 mobility disruptions on RSV transmission in Seattle, Washington.*

2024 NetSci International Conference on Network Science, Québec City, Canada *Impacts of human mobility on the citywide transmission dynamics of respiratory viruses in pre- and post-COVID-19 pandemic years.*

2023 Epidemics^9 International Conference on Infectious Disease Dynamics, Bologna, Italy *Are changes in population mobility predictive of respiratory virus transmission? Insights from high resolution mobile phone data in the pre- and post-COVID-19 pandemic periods in Seattle, Washington.*

2023 EpiMob Satellite* ("Epidemic control: from mobility data to public health"), NetSci International Conference on Network Science, Vienna, Austria *Are changes in population mobility predictive of respiratory virus transmission? Insights from high resolution mobile phone data in the pre- and post-COVID-19 pandemic periods in Seattle, Washington.* * **Invited keynote speaker**

2022 NIH/FDA COVID-19 Research Workshop (Virtual) *The impact of COVID-19 restrictions and mobility behavior on respiratory pathogen transmission in Seattle, Washington.*

2022 Options XI for the Control of Influenza, Belfast, Northern Ireland *Impact of antigenic drift on influenza A/H3N2 vaccine effectiveness in the United States.*

2022 NIH Modeling of Infectious Disease Agent Study (MIDAS) Annual Meeting, Bethesda, MD *The impact of social distancing on respiratory pathogen transmission in Seattle, Washington.*

2021 NIH Modeling of Infectious Disease Agent Study (MIDAS) Annual Meeting (Virtual) *Impact of antigenic drift on influenza A/H3N2 vaccine effectiveness in the United States.*

2021 NIH NIAID Centers of Excellence for Influenza Research and Surveillance (CEIRS) Annual Meeting (Virtual) *Impact of antigenic drift on influenza A/H3N2 vaccine effectiveness in the United States.*

2020 NIH/FDA COVID-19 Research Workshop (Virtual) *Utilizing Respiratory Syndromic Surveillance Data to Monitor COVID-19 Activity in South Africa.*

2019 Epidemics^7 International Conference on Infectious Disease Dynamics, Charleston, SC *Impact of influenza antigenic evolution on disease dynamics in the United States.*

2019 Options X for the Control of Influenza, Singapore *Impact of influenza antigenic evolution on disease dynamics in the United States.*

2018 American Association of Physical Anthropologists (AAPA) Conference, Austin, TX *Gut microbiome diversity across sympatric mammal populations of Madagascar reflects diet, substrate use, and host phylogeny.*

2016 NSF BEACON Annual Congress, Michigan State University, East Lansing, MI *Social network structure shapes gut microbial communities in wild Verreaux's sifaka.*

Poster presentations

2020 European Scientific Working group on Influenza (ESWI) Conference (Virtual) *Impact of influenza antigenic evolution on disease dynamics in the United States.*

2019 Ecology and Evolution of Infectious Diseases (EEID) Conference, Princeton, NJ *Impact of influenza antigenic evolution on disease dynamics in the United States.*

2017 Society of Molecular Biology and Evolution (SMBE) Conference, Austin, TX *Hierarchical social networks shape gut microbial composition in wild Verreaux's sifaka.*

2017 Ecology and Evolution of Infectious Diseases (EEID) Conference, Isla Vista, CA *Hierarchical social networks shape gut microbial composition in wild Verreaux's sifaka.*

2015 Epidemics^5 International Conference on Infectious Disease Dynamics, Clearwater Beach, FL *Social network structure shapes gut microbial communities in wild Verreaux's sifaka.*

Seminar presentations (post-graduate)

Invited talks

2025 Bouvé College of Health Sciences, Northeastern University (Virtual) *Elucidating the Ecological, Evolutionary, and Behavioral Drivers of Respiratory Virus Outbreaks*

2024 Yale School of Public Health, New Haven, CT *Impacts of human mobility on the citywide transmission dynamics of respiratory viruses: Insights from the Seattle Flu Study and high-resolution mobile phone data.*

2024 Network Science Institute, Northeastern University, Boston, MA. *Impacts of human mobility on the citywide transmission dynamics of respiratory viruses in pre- and post-COVID-19 pandemic years.*

2023 US CDC Technical Outreach and Assistance to States (TOAST) Office Hours (Virtual) *Are changes in population mobility predictive of respiratory virus transmission? Insights from high resolution mobile phone data in the pre- and post-COVID-19 pandemic periods in Seattle, Washington.*

2023 Pierre Louis Institute of Epidemiology and Public Health (IPLESP), French National Institute of Health and Medical Research (INSERM), Paris, France *Are changes in population mobility predictive of respiratory virus transmission? Insights from high resolution mobile phone data in the pre- and post-COVID-19 pandemic periods in Seattle, Washington.*

2023 Infectious Disease Modeling Working Group, World Health Organization (Virtual) *Antigenic drift and subtype interference shape A/H3N2 epidemic dynamics in the United States.*

2023 California Department of Public Health COVID-19 Modeling Team Open House (Virtual) *A time series approach for short-term forecasts and long-term scenario projections of influenza hospitalizations.*

2023 NIH NIAID Centers of Excellence for Influenza Research and Response (CEIRR) (Virtual) *Antigenic drift and subtype interference shape A/H3N2 epidemic dynamics in the United States.*

2023 Infectious Disease Forecasting Call, organized by US CDC and NIH MIDAS (Virtual) *Impact of influenza antigenic evolution on A/H3N2 epidemics and vaccine effectiveness in the United States.*

2023 Center for the Ecology of Infectious Diseases, University of Georgia (Virtual) *The impact of physical distancing on respiratory pathogen transmission in Seattle, Washington.*

2021 Influenza Research Group, National Animal Disease Center, US Department of Agriculture (Virtual) *Impact of influenza antigenic evolution on A/H3N2 vaccine effectiveness in the United States.*

2018 Fogarty International Center, National Institutes of Health, Bethesda, MD *Drivers of gut microbial composition and transmission within and among wild lemur populations.*

Internal seminars

2023 Respiratory Virus Interest Group, National Institutes of Health, Bethesda, MD (Hybrid) *The impact of influenza antigenic drift on A/H3N2 vaccine effectiveness in the United States.*

2019 Influenza Interest Group, National Institutes of Health, Bethesda, MD *Impact of influenza antigenic evolution on disease dynamics in the United States.*

Operational involvement in the COVID-19 pandemic response and disease predictions

2022 – Contributor to the US CDC FluSight Forecasting Collaboration. Submitted weekly short-term forecasts of flu hospitalizations during the 2022-23, 2023-24, and 2024-25 seasons.

2022 – Contributor to the US Influenza Scenario Modeling Hub. Submitted long-term scenario projections of flu hospitalizations during the 2022-23, 2023-24, and 2024-25 seasons.

2023 – 2024 Public dashboard of SARS-CoV-2 variant forecasts for Washington and other US states, Seattle Flu Alliance, https://seattleflu.org/sars-cov-2-forecasts (In collaboration with Nextstrain)

2020 – 2022 Led the analysis and provided technical support to South Africa's National Institute for Communicable Diseases for their COVID-19 Private Consultations Excess Respiratory Encounters Report. Reports were updated on a bi-weekly or monthly basis.

2019 – 2022 Contributor to the US Department of Defense Forecasting Collaboration. Submitted weekly short-term forecasts of influenza-like illness and COVID-like illness cases on US military bases during the 2019-20, 2020-21, and 2021-22 seasons.

Professional activities

2026 – Member, Task Force for University-wide Center for Public Health Technology, Northeastern University

2026 – Co-organizer, Early Career Investigator Series, Roux Institute, Northeastern University

2026 Abstract reviewer, NetSci International Conference on Network Science

2025 Lead organizer, EpiMob Satellite (*Epidemic control: from mobility data to public health*), NetSci International Conference on Network Science, Maastricht, The Netherlands

2024 Co-organizer, EpiMob Satellite (*Epidemic control: from mobility data to public health*), NetSci International Conference on Network Science, Québec City, Canada

2023 Working group, *The use of human mobility data in infectious disease modeling*, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD

2022 – Abstract reviewer, NIH Modeling of Infectious Disease Agent Study (MIDAS) Annual Meeting

2022 Invited panelist, *Reflections on COVID-19*, NIH MIDAS Annual Meeting, Bethesda, MD

2020 Poster Judge, NIH Annual Graduate Student Research Symposium, Bethesda, MD

2020 – Member, NIH MIDAS

2019 – 2021 Essay editor, Science Policy for All (policy blog with contributors from the Washington, DC area)

2017 Invited Panelist, NSF BEACON Public Engagement Workshop, Austin, TX

Teaching and mentoring experience

2024	Tutor, *Complexity 72h: Interdisciplinary workshop for young researchers in complex systems*, Carlos III University of Madrid, Spain. Led a team of 5 graduate students in carrying out a research project within 3 days (i.e., 72h). Project title: "Impacts of COVID-19 restrictions on mobility networks and the spread of endemic respiratory viruses."
2020	Completed 9-week NIH pedagogy course *Scientists Teaching Science* on best practices for teaching and learning in STEM subjects at the undergraduate level.
2019	Co-Instructor, *FIC-DIVERGE Training Workshop on RSV Genomics and Evolution*, Fogarty International Center, National Institutes of Health, Bethesda, MD
2018	Co-Instructor, *FIC-NICD Training Workshop on Infectious Disease Dynamics and Evolution*, National Institutes of Communicable Diseases, Johannesburg, South Africa
Fall 2016, 2017	Graduate Teaching Assistant, *Scientific Inquiry Across Disciplines*, UT-Austin
Summer 2016	Master's student mentoring in primate field ecology, Department of Animal Biology, University of Antananarivo, Madagascar. Safidy Rasolonjatovo, *Verreaux's sifaka scent marking behavior*, Kirindy Mitea National Park
2015	Guest Lecture, *Biological Networks and Social Network Analysis*, Introduction to Biological Statistics Course, Center for Computational Biology and Bioinformatics, UT-Austin
2014	Guest Lecture, *Introduction to Networks*, Introduction to Biological Statistics Course, Center for Computational Biology and Bioinformatics, UT-Austin
Spring 2013	Graduate Teaching Assistant, *Social Networks and Infectious Diseases*, UT-Austin
Summer 2012	Master's student mentoring in primate field ecology, Department of Animal Biology, University of Antananarivo, Madagascar. Elvis Rakotomalala, *Lepilemur tree hole characteristics*, Kirindy Mitea National Park

Science communication and outreach

2024	*Elife* podcast interview, *Flu virus evolution: Combining antibody responses and genetic data can help gauge the threats posed by evolving flu strains* Link
2021	Science Policy for All blogpost, *Can the United States achieve herd immunity? Vaccine mandates and other policies to increase COVID-19 vaccination* Link
2020	Science Policy for All blogpost, *The Use of COVID-19 Prediction Models in Guiding Policy Decisions* Link
2019 – 2021	Member, National Institutes of Health Science Policy Discussion Group, Bethesda, MD. NIH SPDG is a fellow-led and run self-governing organization that brings together fellows with a shared passion for understanding the intersection of scientific research and legislative policy.
2018	Selected speaker, American Association for the Advancement of Science (AAAS) Classroom Science Days, Austin, TX. Outreach lecture (*Meet the Lemurs*) to middle school students.
2016	Public outreach lecture (*Meet the Lemurs*), Science Under the Stars, Austin, TX.
2016	NSF BEACON "Researchers at Work" essay, *How lemur social networks shape microbial transmission* Link
2011 – 2018	Radio DJ and Science Talk Show Co-host, They Blinded Me with Science, KVRX 91.7FM, UT-Austin, Austin, TX. TBMWS was a weekly educational talk show that interviewed both UT-based and visiting researchers and reviewed current science publications and news. I recruited guests, conducted interviews, and produced podcasts.
2011 – 2017	Co-organizer and Volunteer, Science Under the Stars, Austin, TX. SUTS is a free, monthly public outreach lecture series founded and organized by graduate students in the Department of Integrative Biology at UT-Austin.