Amanda C. Perofsky, Ph.D.

Brotman Baty Institute for Precision Medicine, University of Washington, Seattle, Washington
Fogarty International Center, National Institutes of Health, Bethesda, Maryland
Email: amanda.perofsky@nih.gov • Website: https://aperofsky.github.io

Research interests

My research focuses on the ecological, evolutionary, and behavioral drivers of respiratory virus infections, with aims to improve infectious disease surveillance and better understand and predict recurring and emerging outbreaks. I apply a variety of statistical and computational approaches to diverse data sets (surveillance, genomic, serology, and mobility) to characterize respiratory virus transmission patterns and epidemiology, with a particular focus on influenza and SARS-CoV-2. I also produce 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

Professional experience

2021 – **Research Scientist,** University of Washington
Seattle Flu Alliance, Brotman Baty Institute for Precision Medicine

Guest Researcher, Fogarty International Center, National Institutes of Health
Division of International Epidemiology and Population Studies
Supervisor: Cécile Viboud

2018 – 2021 **Postdoctoral Research Fellow,** Fogarty International Center, National Institutes of Health
Division of International Epidemiology and Population Studies
Supervisor: Cécile Viboud

2010 – 2011 **Postbaccalaureate IRTA Fellow,** National Institute of Dental and Craniofacial Research, National Institutes of Health
Adeno-Associated Virus Biology Section, Molecular Physiology and Therapeutics Branch
Supervisor: John Chiorini

2009 **Research Assistant,** Odum School of Ecology, University of Georgia
Supervisor: Andrew Park

Fellowships and awards

2023 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*, Fogarty International Center, NIH

2020, 2021 Director's Group Merit Award, *For outstanding modeling work to support the COVID-19 pandemic response domestically and internationally,* Fogarty International Center, NIH

2020 Young Scientist Award, European Scientific Working group on Influenza (ESWI) Conference

2019 Director's Individual Merit Award, *For outstanding efforts to forecast weekly influenza-like illness activity in 27 US military facilities in collaboration with DoD*, Fogarty International Center, NIH

2017, 2018 Graduate School Summer Semester Continuing Fellowship, UT-Austin

2017 Graduate Student Professional Development Award, College of Natural Sciences, UT-Austin

2012 – 2017 NSF Graduate Research Fellowship, National Science Foundation

2011 – 2012 Department of Integrative Biology Graduate Recruitment Fellowship, UT-Austin

2010 – 2011 Postbaccalaureate IRTA Fellowship, National Institutes of Health

2008 Elected, Phi Beta Kappa Honors Society

2007 Honors International Scholarship, UGA Honors Program

2005 – 2009 National Merit Scholarship, UGA

2005 – 2009 Georgia HOPE Scholarship (full tuition)

Submitted manuscripts

2024 Kostandova, N., Corgel, R., Bansal, S., Bérubé, S., Cleary, E., Hansen, C., Hitchings, M. D. T., García-Carreras, B., Gardner, L., Kraemer, M. U. G., Lai, S., Li, Y., **Perofsky, A. C.**, Pullano, G., Read, J. M., Ribeiro dos Santos, G., Salje, H., Takahashi, S., Viboud, C., Wang, J., Cummings, D. A. T., Wesolowski, A. Data and model needs for generalizable inferences linking human mobility and infectious disease transmission.

2024 Tran-Kiem, C., Paredes, M. I., **Perofsky, A. C.**, . . . Viboud, C., Bedford, T. Fine-scale spatial and social patterns of SARS-CoV-2 transmission from identical pathogen sequences. *medRxiv*, 2024.05.24.24307811. DOI

2023 Mathis, S. M., Webber, A. E., León, T. M., . . . , **Perofsky, A. C.**, . . . Biggerstaff, M., Borchering, R. K. Evaluation of FluSight influenza forecasting in the 2021-22 and 2022-23 seasons with a new target laboratory-confirmed influenza hospitalizations. *medRxiv*, 2023.12.08.23299726. DOI

Publications

2024 **Perofsky, A. C.**, Hansen, C., Burstein, R., . . . Bedford, T., Chu, H. Y., Englund, J. A., Starita, L. M., Viboud, C. Impacts of human mobility on the citywide transmission dynamics of 18 respiratory viruses in pre- and post-COVID-19 pandemic years. *Nature Communications, 15,* 4164. DOI *Featured in Editors' Highlights for "Public Health"

2024 Paredes, M. I., **Perofsky, A. C.**, Frisbie, L., . . . Müller, N. F., Bedford, T. Local-scale phylodynamics reveal differential community impact of SARS-CoV-2 in a metropolitan US county. *PLOS Pathogens*, *20*(3), e1012117. DOI

2024 **Perofsky, A. C.**, Huddleston, J., Hansen, C., . . . Kondor, R., Wentworth, D. E., Lewis, N., . . . Sullivan, S. G., Barr, I. G., Subbarao, K., Krammer, F., Bedford, T., Viboud, C. Antigenic drift and subtype interference shape A(H3N2) epidemic dynamics in the United States. *Elife*, *13*, RP91849. DOI *Featured on *eLife*'s podcast

2022 **Perofsky, A. C.**, Tempia, S., Bingham, J., Maslo, C., Toubkin, M., Laubscher, A., Walaza, S., Pulliam, J. R. C., Viboud, C., & Cohen, C. Direct and Indirect Effects of the Coronavirus Disease 2019 Pandemic on Private Healthcare Utilization in South Africa, March 2020-September 2021. *Clinical Infectious Diseases*, *75*(1), e1000-e1010. DOI

2022 Hansen, C., **Perofsky, A. C.**, Burstein, R., . . . Bedford, T., Chu, H. Y., Starita, L. M., Viboud, C. 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 Network Open*, *5*(12), e2245861. DOI

2021 **Perofsky, A. C.**, Meyers, L. A., Abondano, L. A., Di Fiore, A., & Lewis, R. J. Social groups constrain the spatiotemporal dynamics of wild sifaka gut microbiomes. *Molecular Ecology*, *30*(24), 6759-6775. DOI

2021 McBride, D. S.†, **Perofsky, A. C.**†, Nolting, J. M., Nelson, M. I., & Bowman, A. S. Tracing the Source of Influenza A Virus Zoonoses in Interconnected Circuits of Swine Exhibitions. *Journal of Infectious Diseases*, *224*(3), 458-468. DOI (†co-first authors)

2020 **Perofsky, A. C.**, & Nelson, M. I. Seasonal influenza: The challenges of vaccine strain selection. *Elife*, *9*, e62955. DOI

2020 Viboud, C., Gostic, K., Nelson, M. I., Price, G. E., **Perofsky, A.**, Sun, K., Sequeira Trovao, N., Cowling, B. J., Epstein, S. L., & Spiro, D. J. Beyond clinical trials: Evolutionary and epidemiological considerations for development of a universal influenza vaccine. *PLOS Pathogens*, *16*(9), e1008583. DOI

2020 Nelson, M. I., **Perofsky, A.**, McBride, D. S., Rambo-Martin, B. L., Wilson, M. M., Barnes, J. R., van Bakel, H., Khan, Z., Dutta, J., Nolting, J. M., & Bowman, A. S. A Heterogeneous Swine Show Circuit Drives Zoonotic Transmission of Influenza A Viruses in the United States. *Journal of Virology*, *94*(24). DOI

2019 **Perofsky, A. C.**, Lewis, R. J., & Meyers, L. A. Terrestriality and bacterial transfer: a comparative study of gut microbiomes in sympatric Malagasy mammals. *The ISME Journal*, *13*(1), 50-63. DOI

2017 Rakotomalala, E. J., Rakotondraparany, F., **Perofsky, A. C.**, & Lewis, R. J. Characterization of the Tree Holes Used by *Lepilemur ruficaudatus* in the Dry, Deciduous Forest of Kirindy Mitea National Park. *Folia Primatologica*, *88*(1), 28-41. DOI

2017 **Perofsky, A. C.**, Lewis, R. J., Abondano, L. A., Di Fiore, A., & Meyers, L. A. Hierarchical social networks shape gut microbial composition in wild Verreaux's sifaka. *Proceedings of the Royal Society B*, 284(1868). DOI

2013 Berry, B. S., Magori, K., **Perofsky, A. C.**, Stallknecht, D. E., & Park, A. W. Wetland cover dynamics drive hemorrhagic disease patterns in white-tailed deer in the United States. *Journal of Wildlife Diseases*, *49*(3), 501-509. DOI

Conference presentations

Talks

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

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.*

Posters

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

Invited talks

2024 Yale School of Public Health Modeling Seminar Series, New Haven, CT (upcoming, November 2024)

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, 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) Computational Modeling Core (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.*

2016 Kirindy Mitea National Park headquarters, Belo Sur Mer, Madagascar. *Bacteria transmission dynamics among wildlife in Kirindy Mitea National Park.*

2012 Kirindy Mitea National Park headquarters, Morondava, Madagascar. *Infectious disease transmission in a wild lemur population.*

Internal seminars

2023 Respiratory Virus Interest Group, National Institutes of Health (Virtual) *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.*

2017 NSF BEACON weekly seminar, University of Texas at Austin, Austin, TX. (Hybrid) *Gut microbiome diversity across sympatric mammal populations of Madagascar reflects diet, substrate use, and host phylogeny.*

2016 NSF BEACON weekly seminar, University of Texas at Austin, Austin, TX. S*ocial networks shape the gut microbial communities of wild Verreaux's sifaka.*

2015 Department of Integrative Biology, University of Texas at Austin, Austin, TX. *Social networks shape the gut microbial communities of wild Verreaux's sifaka.*

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

2023 – 2024 Dashboard of SARS-CoV-2 variant forecasts for Washington and other US states, Seattle Flu Alliance (In collaboration with Nextstrain team)

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

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

2020 – 2022 Developed the analysis, drafted the first report, and provided technical support to South Africa's National Institute for Communicable Diseases for their COVID-19 Private Consultations Excess Respiratory Encounters Report. Reports tracked excess respiratory encounters at hospitals, emergency departments, and primary care providers across age groups and provinces.

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.

Research support

2018 Research Exchange Grant, NSF Infectious Disease Evolution Across Scales Research Coordination Network, *How does influenza evolution impact the epidemiology of annual epidemics?* $2800

2015 DBI-0939454, NSF BEACON Center for the Study of Evolution in Action, *Factors that influence gut microbiota diversity and intestinal bacteria transmission dynamics in wild lemurs* $16,000
Co-PI, with PIs Lauren Ancel Meyers and Rebecca Lewis

2015 Ecology, Evolution, and 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, and Behavior Startup Grant, UT-Austin $2000

2008 NSF Research Experiences for Undergraduates (REU) Internship, NSF Coweeta Long Term Ecological Research Program, Otto, NC

Workshop scholarships

2017 Network Modeling for Epidemics Course Fellowship, University of Washington, Seattle, WA

2014, 2015 Summer Institute in Statistics and Modeling in Infectious Diseases (SISMID) Scholarship and Travel Award, University of Washington, Seattle, WA

2011 Meaningful Modeling of Epidemiological Data (MMED) Clinic Scholarship and Travel Award, African Institute for Mathematical Sciences, Cape Town, South Africa

2010, 2011 Ecology and Evolution of Infectious Diseases (EEID) Conference Workshop Scholarship and Travel Award, Cornell University (2010) and University of California, Santa Barbara (2011)

Professional activities

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 on the use of human mobility data in infectious disease modeling, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD

2022, 2023 Abstract reviewer, NIH MIDAS Annual Meeting

2022 – Coordinate and lead monthly Data Analysis meetings for Seattle Flu Alliance research groups

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 Modeling of Infectious Disease Agent Study (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

Ad-hoc peer review: American Journal of Epidemiology, American Journal of Primatology, Animal Behaviour, BMJ Global Health, Ecology Letters, Ecology and Evolution, Epidemics, The ISME Journal, Molecular Ecology, Nature Communications, Nature Ecology and Evolution, Nature Physics, PLOS Computational Biology, PNAS Nexus

Teaching and mentoring experience

2024 Tutor, *Complexity 72h: Interdisciplinary workshop for young researchers in complex systems*, Carlos III University of Madrid, Spain. Led and mentored 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, *Fogarty International Center-DIVERGE Training Workshop on RSV Genomics and Evolution,* National Institutes of Health, Bethesda, MD.

2018 Co-Instructor, *Fogarty International Center-NICD Training Workshop on Infectious Disease Dynamics and Evolution*, National Institutes of Communicable Diseases, Johannesburg, South Africa.

Summer 2016 Master's student mentoring, Department of Animal Biology, University of Antananarivo. Trained Safidy Rasolonjatovo in field research techniques, data collection, and specimen preservation. Guided an independent project on sifaka scent marking behavior at Ankoatsifaka Research Station in Kirindy Mitea National Park, Madagascar.

Fall 2016, 2017	Graduate Teaching Assistant, *Scientific Inquiry Across Disciplines*, UT-Austin, Austin, TX.
2015	Guest Lecture, *Biological Networks and Social Network Analysis*, Introduction to Biological Statistics Course, Center for Computational Biology and Bioinformatics, UT-Austin, Austin, TX.
2014	Guest Lecture, *Introduction to Networks*, Introduction to Biological Statistics Course, Center for Computational Biology and Bioinformatics, UT-Austin, Austin, TX.
Spring 2013	Graduate Teaching Assistant, *Social Networks and Infectious Diseases*, UT-Austin, Austin, TX.
Summer 2012	Master's student mentoring, Department of Animal Biology, University of Antananarivo. Trained Elvis Rakotomalala in field research techniques, data collection, and specimen preservation. Guided an independent project on *Lepilemur* tree hole characteristics at Ankoatsifaka Research Station in Kirindy Mitea National Park, Madagascar.

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*
2021	Science Policy for All blogpost, *Can the United States achieve herd immunity? Vaccine mandates and other policies to increase COVID-19 vaccination*
2020	Science Policy for All blogpost, *The Use of COVID-19 Prediction Models in Guiding Policy Decisions*
2019 – 2021	Member, National Institutes of Health Science Policy Discussion Group, Bethesda, MD. Biweekly seminar series for early-career scientists focused on the intersection of scientific research and legislative policy. Delivered science policy presentations, invited two guest speakers, and wrote and edited articles for the "Science Policy for All" blog.
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. AAAS article
2016	Public outreach lecture (*Meet the Lemurs*), Science Under the Stars, Austin, TX. Daily Texan article
2016	NSF BEACON "Researchers at Work" essay, *How lemur social networks shape microbial transmission*
2011 – 2018	Radio DJ and Science Talk Show Co-host, They Blinded Me with Science, KVRX 91.7FM, UT-Austin, Austin, TX. Co-hosted a weekly educational talk show that interviewed UT-based and visiting researchers and reviewed science publications and news. Recruited guests, conducted interviews, and produced podcasts.
2011 – 2017	Co-organizer and Volunteer, Science Under the Stars, Austin, TX. Monthly public outreach lecture series founded and organized by graduate students in the Department of Integrative Biology.

References

1. Cécile Viboud, Senior Staff Scientist
   Fogarty International Center, National Institutes of Health
   Division of International Epidemiology and Population Studies
   Email: viboudc@mail.nih.gov

2. David Spiro, Division Director
   Fogarty International Center, National Institutes of Health
   Division of International Epidemiology and Population Studies
   Email: david.spiro@nih.gov

3. Trevor Bedford, Professor
   Fred Hutchinson Cancer Center
   Vaccine and Infectious Disease, Human Biology, and Public Health Sciences Divisions
   Email: trevor@bedford.io