Michael A. Martin, PhD

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Catonsville, MD 21228

RESEARCH & PROFESSIONAL EXPERIENCE

Johns Hopkins Bloomberg School of Public Health Department of Epidemiology Baltimore, MD
Postdoctoral Research Fellow (w/ Dr. Derek Cummings) June 2025 - Present

Johns Hopkins School of Medicine Department of Pathology Baltimore, MD
Postdoctoral Research Fellow (w/ Dr. M. Kate Grabowski) August 2022 - June 2025

Emory University Department of Biology Atlanta, GA
Doctor of Philosophy Candidate (w/ Dr. Katia Koelle) Sept. 2018 - July 2022

Association of Public Health Laboratories Denver, CO
COVID Genomic Data Specialist, Colorado Department of Public Health & Environment June 2021 - Dec. 2021

Emory University School of Medicine Atlanta, GA
Rotation Student (w/ Dr. Tim Read) Nov. 2018 - Jan. 2019

Harvard T.H. Chan School of Public Health Boston, MA
Research Assistant (w/ Dr. Bill Hanage) Jan. 2017 - July 2018

Boston Biomedical Consultants (IQVIA) Waltham, MA
Associate Market Analyst June 2014 - June 2016

Johns Hopkins University Bloomberg School of Public Health Baltimore, MD
Undergraduate Research Assistant (w/ Dr. Jrgen Bosch) May 2012 - Dec. 2013

PUBLICATIONS

[*] *contributed equally*
[c] *corresponding author*
[†] *undergradaute mentee*

Articles in peer-reviewed journals

Martin, M.A., Reynolds, S.J., Foley, B.T., Nalugoda, F., Quinn, T.C., Kemp, S.A., Nakalanzi, M., Kankaka, E.N., Kigozi, G., Ssekubugu, R., Gupta, R.K., Abeler-Dörner, L., Kagaayi, J., Ratmann, O., Fraser, C., Galiwango, R.M., Bonsall, D., Grabowski, M.K., on behalf of the PANGEA-HIV Consortium and the Rakai Health Sciences Program. (2024). HIV drug resistance during antiretroviral therapy scale-up in Uganda, 2012-19: a population-based, longitudinal study. *Lancet Microbe.* In press (pre-print: 10.1101/2023.10.14.23297021).

Martin, M.A.[c], Brizzi, A., Xiaoyue, Xi, Galiwango, R.M., Moyo, Sikhulile, Ssemwanga, D., Blenkinsop, A., Redd, A.D., Abeler-Drner, L., Fraser, C., Reynolds, S.J., Quinn, T.C., Kagaayi, J., Bonsall, D., Serwadda, D., Nakigozi, G., Kigozi, G., Grabowski, M.K.[c], Ratmann, O.[c], with the PANGEA-HIV Consortium and the Rakai Health Sciences Program. (2025). Quantifying prevalence and risk factors of HIV multiple infection in Uganda from population-based deep-sequence data. *PLOS Pathogens.* 10.1371/journal.ppat.1013065.

Kim, S.[c], Kigozi, G., **Martin, M.A.**, Galiwango, R.M., Quinn, T.C., Redd, A.D., Ssekubugu, R., Bonsall, D., Ssemwanga, D., Rambaut, A., Herbeck, J.T., Reynolds, S.J., Foley, B., Abeler-Dörner, L. Fraser, C., Ratmann, O., Kagaayi, J., Laeyendecker, O., Grabowski, M.K. (2024). Intra- and inter-subtype HIV diversity between 1994 and 2018 in southern Uganda: a longitudinal population-based study. *Virus Evolution.* 10.1093/ve/veae065.

Martin, M.A.[c], Berg, N.[†], Koelle, K. (2024). Influenza A genomic diversity during human infections underscores the strength of genetic drift and the existence of tight transmission bottlenecks. *Virus Evolution.* 10.1093/ve/veae042.

Farjo, M., Koelle, K., **Martin, M.A.**, Gibson, L.L., Walden, K.K.O., Rendon, G., Fields, C.J., Alnaji, F.G., Gallagher, N., Luo, C.H., Mostafa, H.H., Manabe, Y.C., Pekosz, A., Smith, R.L., McManus, D.D., Brooke, C.B.[c] (2024). Within-host evolutionary dynamics and tissue compartmentalization during acute SARS-CoV-2 infection. *Journal of Virology.* 10.1128/jvi.01618-23.

Shi, T., Harris, J.D., **Martin, M.A.**, Koelle, K.[c] (2024). Transmission bottleneck size estimation from de novo viral genetic variation. *Molecular Biology and Evolution*. 10.1093/molbev/msad286.

Park, Y., **Martin, M.A.**, Koelle, K.[c] (2023). Epidemiological inference for emerging viruses using segregating sites. *Nature Communications*. 10.1038/s41467-023-38809-7.

Bianco, C.M., Moustafa, A.M., O'Brien, K., **Martin, M.A.**, Read, T.D., Kreiswirth, B.N., Planet, P.J.[c] (2023). Pre-epidemic evolution of the MRSA USA300 clade and a molecular key for classification. *Frontiers in Cellular and Infection Microbiology*. 10.3389/fcimb.2023.1081070.

Koelle, K.[c], **Martin, M.A.**, Antia, R., Lopman, B., Dean, N.E. (2022). The changing epidemiology of SARS-CoV-2. *Science*. 10.1126/science.abm4915.

Babiker, A.[*], **Martin, M.A.**[*], Marvil, C., Bellman, S., Pettit III, R.A., Bradler, H.L., Sittleburg, V.D., Kunkes, A., Ingersoll, J., Kraft, C.S., Read, T.D., Waggoner, J., Koelle, K., Piantadosi, A.[c] (2022). Unrecognized introductions of SARS-CoV-2 into the state of Georgia shaped the early epidemic. *Virus Evolution*. 10.1093/ve/veac011.

Martin, M.A., Koelle, K.[c] (2021). Comment on "Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2." *Science Translational Medicine*. 10.1126/scitranslmed.abh1803.

Martin, M.A., VanInsberghe, D., Koelle, K.[c] (2021). Insights from SARS-CoV-2 sequences. *Science*, 371(6528). 10.1126/science.abf3995.

Moreno, G.K.[*], Braun, K.M.[*], Riemersma, K.K.[*], **Martin, M.A.**, Halfmann, P.J., Crooks, C.M., Prall, T., Baker, D., Baczenas, J.J., Heffron, A.S., Ramuta, M., Khubbar, M., Weiler, A.M., Accola, M.A., Rehrauer, W.M., O'Connor, S.L., Safdar, N., Pepperell, C.S., Dasu, T., Bhattacharyya, S., Kawaoka, Y., Koelle, K., O'Connor, D.H., Friedrich, T.C.[c] (2020). Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introductions and spread. *Nature Communications*, 11(5558). 10.1038/s41467-020-19346-z.

Miller, D.[*], **Martin, M.A.**[*], Harel, N.[*], Tirosh O.[*], Kustin, T.[*], Meir, M., Sorek, N., Gefen-Halevi, S., Amit, S., Vorontsov, O., Shaag, A., Wolf, D., Peretz, A., Shemer-Avni, Y., Roif-Kaminsky, D., Kopelman, N.M., Huppert, A., Koelle, K., Stern, A.[c] (2020). Full genome viral sequences inform patterns of SARS-CoV-2 spread into and within Israel. *Nature Communications*, 11(5518). 10.1038/s41467-020-19248-0.

Martin, M.A., Lee, R.S.[c], Cowley, L.A., Gardy, J.L., & Hanage, W.P.[c] (2018). Within-host *Mycobacterium tuberculosis* diversity and its utility for inferences of transmission. *Microbial genomics*, 4(10). 10.1099/mgen.0.000217.

Submitted and in-prep manuscripts

Martin, M.A., Blenkinsop, A., Moffa, M., Reynolds, S.J., Nalugoda, F., Quinn, T.C., Kigozi, G., Ssekubugu, R., Gupta, R.K., Grayson, N.E., MacIntyre-Cockett, G., Kagaayi, J., Nakigozi, G., Abeler-Drner, L., Fraser, C., Ratmann, O., Tobian, A.A.R., Laeyendecker, O., Moyo, S., Kennedy, C.E., Bonsall, D.[*], Galiwango, R.M.[*], Grabowski, M.K.[c,*] (2025). Patterns of HIV-1 viral load suppression and drug resistance during the dolutegravir transition: a population-based longitudinal study. *medRxiv*. 10.1101/2025.09.01.25334862.

Shi, Y.K., **Martin, M.A.**, Weissman, D.B., Koelle, K.[c] (2025). Genetic drift acts strongly on within-host influenza virus populations during acute infection but does not act alone. *bioRxiv*. 10.1101/2025.08.27.672713. *under review*.

Martin, M.A., Woods, C.W., Koelle, K. (2019). The dynamics of influenza A H3N2 defective viral genomes from a human challenge study. *bioRxiv*. 10.1101/814673. *under revision*.

Text books

Martin, M.A., Rodriguez-Barraquer, I., Grabowski, M.K., "Genomic Epidemiology." *Infectious Disease Epidemiology, Fourth Edition*, edited by Gurley, E. & Williams, C.M., Jones & Bartlett Learning. In press.

PRESENTATIONS

Invited Oral Presentations

Martin, M.A. (2024). Using genomic data to provide insights into pathogen evolutionary and epidemiological dynamics. Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health. Baltimore, MD, United States.

Martin, M.A. (2024). Beyond SNVs: using influenza A defective viral genomes to better understand viral evolutionary dynamics within- and between- human hosts. Centers of Excellence for Influenza Research and Response Computational Modeling Core Seminar. Virtual

Martin, M.A. (2024). HIV multiple infections in the Rakai Community Cohort Study. Machine Learning and Global Health Network. Virtual.

Martin, M.A. (2024). Leveraging genomic data to gain insights into viral evolution and spread across biological scales. Department of Biomedical Informatics, Ohio State University. Columbus, Ohio, United States.

Martin, M.A. (2023). An introduction to infectious disease phylodynamics. Taming the BEAST. Squamish, British Columbia, Canada.

Martin, M.A., Berg, N., Koelle, K. (2022) Defective viral genomes for understanding IAV dynamics within- and between-hosts. Milner Center for Evolution Seminar Series. Bath, Somerset, England.

Submitted Oral Presentations

Martin, M.A., Blenkinsop, A., Moffa, M., Reynolds, S.J., Nalugoda, F., Quinn, T.C., Kigozi, G., Ssekubugu, R., Gupta, R.K., Kagaayi, J., Nakigozi, G., Abeler-Drner, L., Fraser, C., Ratmann, O., Tobian, A.A.R., Laeyendecker, O., Moyo, S., Kennedy, C.E., Bonsall, D., Galiwango, R.M., Grabowski, M.K. (2025). Patterns of HIV-1 viral load suppression and drug resistance during the dolutegravir transition: a population-based longitudinal study. International Workshop on HIV Drug Resistance and Treatment Strategies. Virtual.

Martin, M.A., Brizzi, A., Galiwango, R.M., Moyo, S., Ssemwanga, D., Blenkinsop, A., Redd, A.D., Abeler-Dörner, L., Fraser, C., Reynolds, S.J., Quinn, T.C., Kagaayi, J., Bonsall, D., Serwadda, D., Nakigozi, G., Kigozi, G., Grabowski, M.K., Ratmann, O. (2024). Quantifying prevalence and risk factors of HIV multiple infection in Uganda from population-based deep-sequence data. MIDAS Annual Meeting. Silver Spring, Maryland, United States.

Martin, M.A., Brizzi, A., Kagaayi, J., Wymant, C., Kigozi, G., Ssekubugu, R., Galiwango, R., Ratmann, O., Fraser, C., Grabowski, M.K. (2023). Epidemiological Implications of HIV-1 multiple infections in Uganda. Dynamics & Evolution of Human Viruses. Heidelberg, Baden-Württemberg, Germany.

Martin, M.A., Berg, N., Koelle, K. (2022) Defective viral genomes for understanding IAV dynamics within- and between-hosts. European Conference on Mathematical and Theoretical Biology. Heidelberg, Baden-Württemberg, Germany.

Martin, M.A., Berg, N., Koelle, K. (2022) Defective viral genomes as a genomic barcode for understanding evolutionary dynamics within- and between-hosts. American Society for Virology Annual Meeting. Madison, Wisconsin, United States.

Martin, M.A., Lin, J., Park, Y., Kraay, A., Koelle, K. (2022). Evolutionary dynamics giving rise to Norovirus GII.4 variants. Dynamics & Evolution of Human Viruses. San Diego, California, United States.

Martin, M.A., Berg, N., Park, Y., Koelle, K. (2022). Leveraging genomic and genetic diversity to gain insights into viral evolution and spread. Social Viruses. Oxford, England, United Kingdom.

Martin, M.A., Koelle, K. (2021). Deep sequencing data points towards a a small SARS-CoV-2 transmission bottleneck: implications for evolution and epidemiology. 2021 MIDAS Network Annual Meeting (Rapid Fire). Virtual.

Martin, M.A., Koelle, K. (2021). Re-analysis of deep-sequencing data from Austria points towards a small SARS-CoV-2 transmission bottleneck on the order of one to three virions. 28th Annual Dynamics & Evolution of Human Viruses. Virtual.

Martin, M.A., Koelle, K., Stern, A. (2020). Phylodynamics of SARS-CoV-2 in Israel. Emory Population Biology, Ecology, and Evolution Seminar Series. Virtual.

Poster Presentations

Martin, M.A., Reynolds, S.J., Foley, B.T., Nalugoda, F., Quinn, T.C., Kigozi, G., Ssekubugu, R., Gupta, R.K., Kagaayi, J., Ratmann, O., Fraser, C., Galiwango, R.M., Bonsall, D., Grabowski, M.K., on behalf of the Rakai Health Sciences Program. (2025). Population-Based Longitudinal Dynamics of HIV Drug Resistance During Dolutegravir Roll-Out in Uganda. Conference on Retroviruses and Opportunistic Infections. San Francisco, California, United States.

Martin, M.A., Berg, N., Koelle, K. (2022). Leveraging genomic diversity to gain insights into viral evolution and spread. Ecology and Evolution of Infectious Diseases. Atlanta, Georgia, United States.

Martin, M.A., Koelle, K. (2021). Estimating the SARS CoV-2 transmission bottleneck using deep sequencing data. 2021 Virus Genomics and Evolution. Virtual.

Martin, M.A., Koelle, K. (2019). Stochastic processes dominate the within-host dynamics of influenza A defective interfering particles. Epidemics[7]. Charleston, South Carolina, United States.

Martin, M.A., Koelle, K. (2019). The within-host dynamics of influenza defective interfering particles in humans. Jacques Monod conference: Virus evolution on the mutualist - parasite continuum. Roscoff, France.

Martin, M.A., Boucher, L., Paul, C., Bosch, J. (2012). Analyzing the Interaction Between *Pf*SUB1 and its Prodomain p31. Johns Hopkins University Biophysics Retreat.

EDUCATION

Emory University Atlanta, GA
Doctor of Philosophy, Population Biology, Ecology, and Evolution; GPA: 3.98 Sept. 2018 - June 2022
<u>Thesis</u>: Leveraging genomic and genetic diversity to gain insights into viral evolution and spread

Harvard T.H. Chan School of Public Health Boston, MA
Master of Science, Infectious Disease Epidemiology; GPA: 3.84 Sept. 2016 - May 2018
<u>Thesis</u>: Identification of heterogeneity within *Mycobacterium tuberculosis* infection in single hosts

Johns Hopkins University Baltimore, MD
Bachelor of Arts, Biophysics; GPA: 3.42 Sept. 2010 - Dec. 2013

TEACHING EXPERIENCE

Emory University Atlanta, GA
Teaching Assistant, Evolutionary Biology, Dr. Katia Koelle Sept. 2019 - Dec. 2019

Harvard T.H. Chan School of Public Health Boston, MA
Teaching Assistant, Analysis of Case Control and Cohort Studies, Dr. Lori Chibnik Jan. 2018 - May 2018
Teaching Assistant, Evolutionary Epidemiology of Infectious Disease, Dr. Bill Hanage Sept. 2017 - Dec. 2017

FELLOWSHIPS, AWARDS, & RESEARCH FUNDING

NIH Loan Repayment Program (NIAID) ($42,500 year 1, $21,250 year 2)	2025 - 2027
Conference on Retroviruses and Opportunistic Infections New Investigator Scholarship	2025
NIH R21 Exploratory/Developmental Grant 1R21AI189301-01 (Key Personnel, PI: Grabowski)	2025-2027
NIH Loan Repayment Program (NIAID) ($40,000/yr)	2023 - 2025
Emory University Department of Biology Graduate Research Award	2022
Emory University Population Biology, Ecology, and Evolution Graduate Program Scholar of the Year	2021
NIH NRSA F31 Predoctoral Fellowship (NIAID) ($46,036/yr)	2021 - 2022
Emory University Laney Graduate School Fellowship ($2,500/yr)	2018 - 2022
Emory University Infectious Disease Across Scales Training Program Award of Distinction ($1000)	2020

SERVICE

Pathoplexus pathoplexus.org
Data Curator Nov. 2024 - Present

Johns Hopkins University Baltimore, MD
Organizer, Infectious Disease Dynamics Group Meeting 2023 - 2024

Emory University Atlanta, GA
Planning Committee, Ecology & Evolution of Infectious Disease Conference 2022 2021 - 2022
Social Committee, Population Biology, Ecology, and Evolution Graduate Program 2019 - 2022
Undergraduate Student Mentor (Nicholas Berg), Koelle Laboratory 2018 - 2021

Manuscript review
AIDS Research and Human Retroviruses, eLife, Epidemics, G3: Genes, Genomes, Genetics, The Journal of Infectious Diseases, Journal of Virology, Microbiology Spectrum, Molecular Biology and Evolution, Nature Communications, PLOS Computational Biology, Virus Evolution

PROFESSIONAL SOCIETIES

Society for Modeling and Theory in Population Biology
Member 2024 - Present

TECHNICAL SKILLS

Languages: Bash, Git/GitHub, LaTeX, MatLab, NextFlow, Python (BioPython, ETEToolkit, MatPlotLib, Numba, NumPy, Pandas, PyEnv, PyPiper, SciPy, SciKit-Learn, Seaborn), R (CmdStanR, Emmeans, Geepack, Tidyverse), SAS, SLURM, Snakemake, Stan, STATA.

Modeling: Clustered data models (general estimating equations), deterministic and stochastic ODE-based compartmental models, dimensionality reduction (PCA), generalized linear models, hierarchical/random effects models, latent class mixture models, partially observable Markov process models, parameter inference (maximum likelihood, Markov chain/Hamiltonian Monte Carlo, iterated filtering), variable selection (Bayesian shrinkage priors).

Bioinformatics: NGS quality control (FastQC, MultiQC), read trimming (FastP, Trimmomatic), metagenomic classification (Kraken2), read mapping (Bowtie/2, BWA, STAR), genome assembly (IVA, Shiver), variant calling (deepSNV, GATk, IRMA, LoFreq), structural variant calling (ViReMa), multiple sequence alignment (MAFFT).

Data Visualization: Visualization of high-dimensional continuous and discrete data and parameter estimates for presentations and written reports. Visualization of large phylogenetic trees and associated metadata.

Phylogenetics: Maximum likelihood phylogenetics (IQ-TRee2, RAxML, TreeTime), within-host phylogenetics (Phyloscanner), Bayesian phylogenetics (BEAST/2), Bayesian coalescent models (Skyline, Skygrid), and structured coalescent models (MASCOT, PhyDyn).