

# Michael A. Martin, PhD

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Baltimore, MD 21205

## RESEARCH & PROFESSIONAL EXPERIENCE

<b>Johns Hopkins Bloomberg School of Public Health Department of Epidemiology</b> Postdoctoral Research Fellow (w/ Dr. Derek Cummings)	Baltimore, MD June 2025 - Present
<b>Johns Hopkins School of Medicine Department of Pathology</b> Postdoctoral Research Fellow (w/ Dr. M. Kate Grabowski)	Baltimore, MD August 2022 - June 2025
<b>Emory University Department of Biology</b> Doctor of Philosophy Candidate (w/ Dr. Katia Koelle)	Atlanta, GA Sept. 2018 - July 2022
<b>Association of Public Health Laboratories</b> COVID Genomic Data Specialist, Colorado Department of Public Health & Environment	Denver, CO June 2021 - Dec. 2021
<b>Emory University School of Medicine</b> Rotation Student (w/ Dr. Tim Read)	Atlanta, GA Nov. 2018 - Jan. 2019
<b>Harvard T.H. Chan School of Public Health</b> Research Assistant (w/ Dr. Bill Hanage)	Boston, MA Jan. 2017 - July 2018
<b>Boston Biomedical Consultants (IQVIA)</b> Associate Market Analyst	Waltham, MA June 2014 - June 2016
<b>Johns Hopkins University Bloomberg School of Public Health</b> Undergraduate Research Assistant (w/ Dr. Jürgen Bosch)	Baltimore, MD May 2012 - Dec. 2013

## PUBLICATIONS

\* *contributed equally*

<sup>c</sup> *corresponding author*

† *undergraduate mentee*

### Articles in peer-reviewed journals

- Gotthold, Z., Epstein-Shuman, A., Kigozi, G., Lamers, S.L., Ssempijja, V., Quiros, G., **Martin, M.A.**, Grabowski, M.K., Fernandez, R.E., Chang, L.W., Galiwango, R.M., Nakigozi, G., Reynolds, S.J., Scully, E., Redd, A.D., Laeyendecker, O.<sup>c</sup> (2026). Pre-ART Vertical HIV-1 Transmission Risk in Uganda Varies by Sex of Child and Maternal Viral Subtype. *The Journal of Infectious Diseases*. 10.1093/infdis/jiag198.
- Shi, Y.K., **Martin, M.A.**, Weissman, D.B., Koelle, K.<sup>c</sup> (2026). Genetic drift acts strongly on influenza virus populations within acute human infections but is obscured by other factors within acutely infected swine. *Virus Evolution*. 10.1093/ve/veag021.
- 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.<sup>c,\*</sup> (2026). Patterns of HIV-1 viral load suppression and drug resistance during the dolutegravir transition: a population-based longitudinal study (Editor's Choice). *Clinical Infectious Diseases*. 10.1093/cid/ciag161.
- 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*. 10.1016/j.lanmic.2025.101218.
- Martin, M.A.**<sup>c</sup>, 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.<sup>c</sup>, Ratmann, O.<sup>c</sup>, 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.<sup>c</sup>, 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.**<sup>c</sup>, Berg, N.<sup>†</sup>, 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.<sup>c</sup> (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.<sup>c</sup> (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.<sup>c</sup> (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.<sup>c</sup> (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.<sup>c</sup>, **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.<sup>c</sup> (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.<sup>c</sup> (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.<sup>c</sup> (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., Rehauer, 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.<sup>c</sup> (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.<sup>c</sup> (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.<sup>c</sup>, Cowley, L.A., Gardy, J.L., & Hanage, W.P.<sup>c</sup> (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

- Bell, Griffin J.\*<sup>c</sup>, Grabowski, M.K.\* , Mpagazi, J., Di Lauro, F., Khalifa, A., Ndyanabo, A., Nakawooya, H., Kagaayi, J., Kigozi, G., Nakigozi, G., Galiwango, R.M., Kigozi, G., **Martin, M.A.**, Ferretti, L., Fraser, C., Bonsall, D., Abeler-Dörner, L., Golubchik, T., Tobian, A.A.R., Beres, L.K., Kennedy, C., Lessler, J., Quinn, T.C., Reynolds, S.J., Wawer, M.J., Gray, R.H., Serwadda, D., Chang, L.W.\* , Ssekubugu, R.\* (2026). HIV Transmission in a Declining African Epidemic. MedRxiv. 10.64898/2026.04.29.26350859.
- 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.** (2026). Next-generation data science methods for precision infectious disease epidemiology. Lunenfeld-Tanenbaum Research Institute, Sinai Health. Toronto, ON, Canada.
- Martin, M.A.** (2026). Next-generation methods for precision infectious disease epidemiology. Department of Medical Epidemiology and Biostatistics, Karolinska Institutet. Solna, Sweden.
- 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**

- Anderson, T., **Martin, M.A.**, Alexandre, M., Hsu Hnin Mon, S., Kankaka, E., Nakigozi, G., Serwadda, D., Quinn, T.C., Kigozi, G., Reynolds, S.J., Chang, L., Fraser, C., Galiwango, R.M., Grabowski, M.K., Hill, A.L. (2026). Quantifying Uncertainty in HIV Transmission Risk from Persons with Low-Level Viremia. Conference on Retroviruses and Opportunistic Infections (Themed Discussion: Precision Comes to Public Health). Denver, Colorado, United States.
- 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-Dörner, 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 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. Dynamics & Evolution of Human Viruses. Virtual.

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

### Poster Presentations

Anderson, T., **Martin, M.A.**, Alexandre, M., Hsu Hnin Mon, S., Kankaka, E., Nakigozi, G., Serwadda, D., Quinn, T.C., Kigozi, G., Reynolds, S.J., Chang, L., Fraser, C., Galiwango, R.M., Grabowski, M.K., Hill, A.L. (2026). Quantifying Uncertainty in HIV Transmission Risk from Persons with Low-Level Viremia. Conference on Retroviruses and Opportunistic Infections. Denver, Colorado, United States.

**Martin, M.A.**, Kim, S., Galiwango, R.M., Moyo, Sikhulile, Abeler-Drner, L., Fraser, C., Ratmann, O., Serwadda, D., Nakigozi, G., Bonsall, D., Reynolds, S.J., Grabowski, M.K., on behalf of the Rakai Health Sciences Program. (2026). Genetically Inferred Patterns of Transmitted HIV Pre-Treatment Resistance in Southern Uganda. Conference on Retroviruses and Opportunistic Infections. Denver, Colorado, United States.

**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. 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<sup>(7)</sup>. 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. Baltimore, Maryland, United States.

### EDUCATION

**Emory University** Atlanta, GA  
 Doctor of Philosophy, Population Biology, Ecology, and Evolution; GPA: 3.98 Sept. 2018 - June 2022  
Thesis: 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  
Thesis: 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

Conference on Retroviruses and Opportunistic Infections New Investigator Scholarship 2026  
 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 (Co-Author, 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 Infectious Disease Across Scales Training Program Award of Distinction (\$1000)	2020

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## SERVICE

<b>Pathoplexus</b>	pathoplexus.org
Data Curator	Nov. 2024 - Present
<b>Johns Hopkins University</b>	Baltimore, MD
Organizer, Infectious Disease Dynamics Group Meeting	2023 - 2024
<b>Emory University</b>	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

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## PROFESSIONAL SOCIETIES

<b>Society for Modeling and Theory in Population Biology</b>	
Member	2024 - Present

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## TECHNICAL SKILLS

**Languages:** Bash, Git/GitHub, L<sup>A</sup>T<sub>E</sub>X, 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).