

Michael A. Martin, PhD

mmart108@jhmi.edu | (860) 249-4445 | m-a-martin.github.io
600 N. Wolfe Street, Baltimore, MD 21287

RESEARCH & PROFESSIONAL EXPERIENCE

Johns Hopkins School of Medicine Department of Pathology Post Doctoral Research Fellow, Grabowski Laboratory	Baltimore, MD August 2022 - Current
Emory University Department of Biology Doctor of Philosophy Candidate, Koelle Laboratory	Atlanta, GA Sept. 2018 - July 2022
Association of Public Health Laboratories COVID Genomic Data Specialist, Colorado Department of Public Health & Environment	Denver, CO June 2021 - Dec. 2021
Emory University School of Medicine Rotation Student, Read Laboratory	Atlanta, GA Nov. 2018 - Jan. 2019
Harvard T.H. Chan School of Public Health Research Assistant, Hanage Laboratory	Boston, MA Jan. 2017 - July 2018
Boston Biomedical Consultants (IQVIA) Associate Market Analyst	Waltham, MA June 2014 - June 2016
Johns Hopkins University Bloomberg School of Public Health Undergraduate Research Assistant, Bosch Lab	Baltimore, MD May 2012 - Dec. 2013

PUBLICATIONS

* *contributed equally*

Articles in peer-reviewed journals

- Martin, M.A.**, Berg, N., Koelle, K. (2023). 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. (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. (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. (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. (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., **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. (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. (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. (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. (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. (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., Cowley, L.A., Gardy, J.L., & Hanage, W.P. (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

- Kim, S., 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). Increasing intra- and inter-subtype HIV diversity despite declining HIV incidence in Uganda. *medRxiv*. 10.1101/2024.03.14.24303990. *under review*.
- Martin, M.A.**, Reynolds, S.J., Ssuuna, C., 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. (2023). Population dynamics of HIV drug resistance among pre-treatment and treatment- experienced persons with HIV during treatment scale-up in Uganda: a population- based longitudinal study. *medRxiv*. 10.1101/2023.10.14.23297021. *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). 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.**, 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. 28th Annual 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

- 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. Epidemics⁷. 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 *PfSUB1* 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
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

NIH Loan Repayment Program (NIAID) (\$39,638/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

Johns Hopkins University	Baltimore, MD
Organizer, Infectious Disease Dynamics Group Meeting	2023 - Present
Emory University	Atlanta, GA
Planning Committee, Ecology & Evolution of Infectious Disease Conference 2022	2021 - Present
Social Committee, Population Biology, Ecology, and Evolution Graduate Program	2019 - Present
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

SKILLS

Bioinformatics

Proficient in commonly used bioinformatics techniques including read mapping (Bowtie/Bowtie2, BWA, SMALT, STAR), variant calling (FreeBayes, GATK, iVar, SAMtools/BCFTools, VarScan), multiple sequence alignment (MAFFT) phylogenetics (IQ-Tree, RAxML), and GWAS (treeWAS).

Computing

Proficient in Bash and Python (including packages such as NumPy, and Pandas); Experienced with git, L^AT_EX, Nextflow, R (including packages such as dplyr), SAS, and STATA.

Data Visualization

Proficient in data visualization in R (ggplot2) and Python (Matplotlib); Proficient in the visualization of phylogenetic trees and associated metadata (Baltic and ggtree).

Modeling

Proficient in the implementation of deterministic and stochastic models for infectious disease dynamics; Experienced in implementing methods used to fit stochastic partially observable markov process models to observational data including particle MCMC and maximum likelihood by iterated filtering; Experienced in implementing Bayesian statistical models in Stan.

Phylodynamics

Proficient in BEAST/BEAST2, including methods and implementation of exponential growth, skyline, and structured (e.g. MASCOT, PhyDyn) coalescent models; Proficient in the use of TreeTime.