

CHARLES J. WOLOCK

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Department of Biostatistics and Computational Biology, University of Rochester
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EDUCATION

University of Washington

Ph.D., Biostatistics

Advisors: Marco Carone and Noah Simon

Seattle, WA

2018 – 2023

Harvard University

B.A., Organismic and Evolutionary Biology

Language citation, Spanish

Summa cum laude, Highest Honors

Cambridge, MA

2011 – 2015

PROFESSIONAL POSITIONS

University of Rochester

Assistant Professor

Department of Biostatistics and Computational Biology

Rochester, NY

2025–present

University of Pennsylvania

Postdoctoral Researcher

Department of Biostatistics, Epidemiology and Informatics

Host: Yong Chen

Philadelphia, PA

2023–2025

Columbia University

Research Staff Associate

Institute for Genomic Medicine

New York, NY

2016 – 2018

TEACHING AND MENTORING

University of Washington

Instructor of Record

BIOST 311: Regression Methods in the Health Sciences

Seattle, WA

2022

Teaching Assistant

BIOST 310: Biostatistics for the Health Sciences

2021

BIOST 511: Medical Biometry I

2020

Research Mentor

Directed Reading Program: Introduction to Prediction

2023

Pathways Undergraduate Research Program

2021

Guest Lecturer

BIOST 561: Computational Skills for Biostatistics

2023

AWARDS, HONORS, FELLOWSHIPS

NSF Graduate Research Fellowship	2020 – 2023
Thomas R. Fleming Excellence in Biostatistics Award (University of Washington)	2023
Donovan J. Thompson Award (University of Washington)	2020
NIH T32 Statistical Genetics Training Grant (University of Washington)	2018 – 2020
Phi Beta Kappa (Harvard University)	2015
Herchel Smith Research Fellowship (Harvard University)	2014
Microbial Sciences Initiative Research Fellowship (Harvard University)	2014
John Harvard Scholar (Harvard University)	2013

PROFESSIONAL SERVICE

Manuscript Reviewer

Bayesian Analysis
Biometrics
Biostatistics
Journal of Machine Learning Research
Journal of the Royal Statistical Society: Series B
Scientific Reports
Statistics and Computing
Statistics in Biopharmaceutical Research

Conference Session Chair

Exploring Frontiers in Functional Data Analysis and Applications (*ENAR, New Orleans, 2025*)
Next Generation Methods for Evidence Synthesis and Reproducibility (*JSM, Portland, 2024*)
Heterogeneous Treatment Effects (*ACIC, Seattle, 2024*)

Paper Competition Reviewer

ICSA Applied Statistics Symposium Student Paper Competition (2025)

UNIVERSITY SERVICE

University of Washington, Department of Biostatistics	Seattle, WA
Faculty Search Committee	2022 – 2023
Student Seminar Coordinator	2020 – 2022
Admissions Committee	2021 – 2022
Education Policy and Teaching Evaluation Committee	2020 – 2021
Equity, Diversity, and Inclusion Committee	2019 – 2021

BIBLIOGRAPHY

(* equal contribution)

Refereed Research Articles

1. Sperling EA, **Wolock CJ**, Morgan AS, Gill BC, Kunzmann M, Halverson GP, Macdonald FA, Knoll AH, Johnston DT. (2015). Statistical analysis of iron geochemical data suggests limited late Proterozoic oxygenation. *Nature* 523: 451–454. doi:[10.1038/nature14589](https://doi.org/10.1038/nature14589)

2. Raghavan NS, Brickman AM, Andrew H, Manly JJ, Schupf N, Lantigua R, The Alzheimer's Disease Sequencing Project, **Wollock CJ**, Kamalakaran S, Petrovski S, Tosto G, Vardarajan BN, Goldstein DB, Mayeux R. (2018). Whole exome sequencing in 20,197 individuals identifies ultra-rare SORL1 loss-of-function variants in late-onset Alzheimer's disease. *Annals of Clinical and Translational Neurology* 5(7): 832–842. doi:[10.1002/acn3.582](https://doi.org/10.1002/acn3.582)
3. Bittleston LS, **Wollock CJ**, Bakhtiar EY, Chan XY, Chan KG, Pierce NE, Pringle A. (2018). Convergence between the microcosms of Southeast Asian and North American pitcher plants. *eLife* 7. doi:[10.7554/eLife.36741](https://doi.org/10.7554/eLife.36741)
4. Hayeck TJ, Stong N, **Wollock CJ**, Copeland B, Kamalakaran S, Goldstein DB, Allen AS. (2019). Improved Pathogenic Variant Localization using a Hierarchical Model of Sub-regional Intolerance. *American Journal of Human Genetics* 104(2): 299–309. doi:[10.1016/j.ajhg.2018.12.020](https://doi.org/10.1016/j.ajhg.2018.12.020)
5. **Wollock CJ**, Stong N, Ma F, Nagasaki T, Lee W, Tsang SH, Kamalakaran S, Goldstein DB, Allikmets R. (2019). A case-control collapsing analysis identifies retinal dystrophy genes associated with ophthalmic disease in patients with no pathogenic ABCA4 mutations. *Genetics in Medicine* 21: 2336–2344. doi:[10.1038/s41436-019-0495-0](https://doi.org/10.1038/s41436-019-0495-0)
6. Gelfman S, Dugger SA, Moreno CAM, Ren Z, **Wollock CJ**, Shneider NA, Phatnani H, Cirulli ET, Lasseigne BN, Harris T, Maniatis T, Rouleau GA, Brown RH, Gitler AD, Myers RM, Petrovski S, Allen AS, Harms MB, Goldstein DB. (2019). A new approach for rare variation collapsing on functional protein domains implicates specific genic regions in ALS. *Genome Research* 29(5): 809–818. doi:[10.1101/gr.243592.118](https://doi.org/10.1101/gr.243592.118)
7. Cameron-Christie S, **Wollock CJ**, Groopman E, Petrovski S, Kamalakaran S, Povysil G, Zhang M, Fleckner J, Mar. RE, Gelfman S, Marasa M, Li Y, Sanna-Cherchi S, Kiryluk K, Allen AS, Fellström B, Haefliger C, Platt A, Goldstein DB, Gharavi A. (2019). Exome-based rare-variant analyses in chronic kidney disease. *Journal of the American Society of Nephrology* 30(6): 1109–1122. doi:[10.1681/ASN.2018090909](https://doi.org/10.1681/ASN.2018090909)
8. Ma CJ, **Wollock CJ**, Stong N, Nagasaki T, Lee W, Goldstein DB, Allikmets R. (2019). Case-control collapsing analysis identifies genes mimicking Stargardt/ABCA4 disease. *Investigative Ophthalmology & Visual Science* 60(9): 2935–2935.
9. Eade K, Gantner ML, Hostyk JA, Nagasaki T, Giles S, Harkins-Perry S, Fallon R, Baldini M, Schepke L, Dorrell MI, Cai C, Baugh EH, **Wollock CJ**, Wallace M, Berlow RB, Goldstein DB, Metallo CM, Friedlander M, Allikmets R. (2021). Serine biosynthesis defect due to haploinsufficiency of phosphoglycerate dehydrogenase (PHDGH) causes retinal disease. *Nature Metabolism* 3(3): 366–377. doi:[10.1038/s42255-021-00361-3](https://doi.org/10.1038/s42255-021-00361-3)
10. Bansal A, Heagerty PJ, Inoue LYT, Veenstra DL, **Wollock CJ**, Basu A. (2021). A Value of Information Framework for Personalizing the Timing of Surveillance Testing. *Medical Decision Making* 42(4): 474–486. doi:[10.1177/0272989x211049213](https://doi.org/10.1177/0272989x211049213)
11. Wasser SK, **Wollock CJ**, Kuhner MK, Brown JE, Morris C, Horowitz R, Wong A, Fernandez CJ, Otiende MY, Hoareau Y, Kaliszewska ZA, Jeon E, Han KL, Weir BS. (2022). Elephant genotypes reveal the size and connectivity of transnational ivory traffickers. *Nature Human Behaviour* 6(3): 371–382. doi:[10.1038/s41562-021-01267-6](https://doi.org/10.1038/s41562-021-01267-6)
12. Heil J, **Wollock CJ**, Pierce NE, Pringle A, Bittleston LS. (2022). *Sarracenia* pitcher plant-associated microbial communities differ primarily by host species across a longitudinal gradient. *Environmental Microbiology* 24(8): 3500–3516. doi:[10.1111/1462-2920.15993](https://doi.org/10.1111/1462-2920.15993)
13. Alfieri J, Coble MD, Conroy C, Dahl A, Hares D, Weir BS, **Wollock CJ**, Zhao E, Kingston H, Zolandz T.

- (2022). A new implementation of a semi-continuous method for DNA mixture interpretation. *Forensic Science International: Reports* 6: 100281. doi:[10.1016/j.fsir.2022.100281](https://doi.org/10.1016/j.fsir.2022.100281)
14. Chen YT, Williamson BD, Okonek T, **Wolock CJ**, Spieker AJ, Hee Wai TY, Hughes JP, Emerson SS, Willis AD. (2022). rigr: Regression, Inference, and General Data Analysis Tools in R. *The Journal of Open Source Software* 7(80): 4847. doi:[10.21105/joss.04847](https://doi.org/10.21105/joss.04847)
 15. Kohn M, **Wolock CJ**, Poulson I, Fernando N. (2023). A meta-analysis of outcomes of patients with chronic hepatitis C vs. patients without chronic hepatitis C undergoing total hip or total knee arthroplasty. *EFORT Open Reviews* 8(4): 180–188. doi:[10.1530/eor-22-0117](https://doi.org/10.1530/eor-22-0117)
 16. Bittleston LS*, **Wolock CJ***, Maeda J, Infante V, Ané JM, Pierce NE, Pringle, A. (2023). Carnivorous *Nepenthes* pitchers with less acidic fluid house nitrogen-fixing bacteria. *Applied and Environmental Microbiology* 89(7): e00812-23. doi:[10.1128/aem.00812-23](https://doi.org/10.1128/aem.00812-23)
 17. **Wolock CJ**, Gilbert PB, Simon N, Carone M. (2024). A framework for leveraging machine learning tools to estimate personalized survival curves. *Journal of Computational and Graphical Statistics* 33(3): 1098–1108. doi:[10.1080/10618600.2024.2304070](https://doi.org/10.1080/10618600.2024.2304070)
 18. Kennedy CJ, Kearns JC, Geraci JC, Gildea SM, Hwang IH, King AJ, Liu H, Luedtke A, Marx BP, Panini S, Petukhova MV, Sampson NA, Smoller JW, **Wolock CJ**, Zainal HN, Stein MB, Ursano RJ, Kessler RC. (2024). Predicting Suicides Among US Army Soldiers After Leaving Active Service. *JAMA Psychiatry* 81(12): 1215-1224. doi:[10.1001/jamapsychiatry.2024.2744](https://doi.org/10.1001/jamapsychiatry.2024.2744)
 19. Wu Q, Pajor NM, Lu Y, **Wolock CJ**, Tong J, Lorman V, Johnson KB, Moore JH, Forrest CB, Asch DA, Chen Y. (2024). A latent transfer learning method for estimating hospital-specific post-acute healthcare demands following SARS-CoV-2 infection. *Patterns* 5(11): 101079. doi:[10.1016/j.patter.2024.101079](https://doi.org/10.1016/j.patter.2024.101079)
 20. **Wolock CJ**, Williamson BD, Shortreed SM, Simon GE, Coleman KJ, Yeargans R, Ahmedani BK, Daida Y, Lynch FL, Rossom RC, Ziebell RA, Cruz M, Wellman RD, Coley RY. (2024). Importance of variables from different time frames for predicting self-harm using health system data. *Journal of Biomedical Informatics* 160: 104750. doi:[10.1016/j.jbi.2024.104750](https://doi.org/10.1016/j.jbi.2024.104750)
 21. **Wolock CJ**, Gilbert PB, Simon N, Carone M. (2025). Assessing variable importance in survival analysis using machine learning. *Biometrika* 112(2). doi:[10.1093/biomet/asae061](https://doi.org/10.1093/biomet/asae061)
 22. **Wolock CJ***, Jacob S*, Bennett JC, Elias-Warren A, O'Hanlon J, Kenny A, Jewell NP, Rotnitzky A, Cole SR, Weil AA, Chu HY, Carone M. (2025). Investigating symptom duration using current status data: a case study of post-acute COVID-19 syndrome. *Epidemiology*. doi:[10.1097/EDE.0000000000001882](https://doi.org/10.1097/EDE.0000000000001882)
 23. Zhang D, Zhang B, Wang H, Lu Y, **Wolock CJ**, Hu W, Wang L, Hripcsak G, Chen Y. (2025) Negative control-calibrated difference-in-difference analyses: addressing unmeasured confounding in real-world data with application to quantifying the impact of pandemic on racial/ethnic differences. *npj Digital Medicine* 8: 452. doi:[10.1038/s41746-025-01821-w](https://doi.org/10.1038/s41746-025-01821-w)
 24. Kenny A, **Wolock CJ**. (2025+). SimEngine: A Modular Framework for Statistical Simulations in R. [arXiv:2403.05698](https://arxiv.org/abs/2403.05698). To appear in *The R Journal*.
 25. Frivold C, Cox SN, Starita L, Babu TM, Hoffman KL, Carone M, Lockwood CM, Kuntz JL, Mularski RA, Varga A, Han PD, Reed J, Piliper EA, Mohamed Bakhsh SAK, Greninger AL, Clark E, Stone J, Grindstaff S, Boisvert CL, Yetz N, Lo NK, Hatchie TL, Marshall G, **Wolock CJ**, Feldstein LR, Weil AA, Englund JA, Naleway AL, Chu HY. (2025+). Correlates of Risk of Respiratory Syncytial Virus Disease: A Prospective Cohort Study. To appear in *Nature Communications*.

Other Refereed Scholarly Publications

26. Coates MM, **Wolock CJ**, Arah OA. (2025+) Re: Pre-diagnostic exposures and cancer survival: Can a meaningful causal estimand be specified? To appear in *Epidemiology*.

Submitted Manuscripts and Preprints

27. Carone M, **Wolock CJ**, Olivas-Martinez A, Rotnitzky A, Gilbert PB. (2025+). Immune Correlates and Vaccine Immunobridging: Statistical Innovations, Challenges and Opportunities. Invited revision, *The Journal of Infectious Diseases*.
28. Wollum A, Ralph L, Grossman D, **Wolock CJ**, Moseson H. (2025+) Evaluating a double list experiment to measure the population proportion of people who have attempted a self-managed abortion in the United States: analysis of a nationally representative cross-sectional survey in 2017. Invited revision, *AJE Advances: Research in Epidemiology*.
29. He H, Li L, Zhang D, Wang H, Zhang B, Lu Y, **Wolock CJ**, Shen Y, Alemayehu D, Chu H, Schuemie M, Suchard M, Ryan P, Hripcsak G, Xu H, Zou J, Asch DA, Chen Y. (2025+) RWE-Transformer: A pretrained transformer model with negative control outcomes for debiased real-world evidence. Under review, *Nature Communications*.
30. Hoffman KL, Marshall G, Frivold C, Acker Z, Arnould IS, Babu TM, Barnes SR, Briggs-Hagen M, Casto A, Clark E, Cox SN, Drummond M, Ehmen B, Englund JA, Gamboa L, Greninger AL, Grindstaff S, Grioni H, Han P, Hatchie T, Hollcroft M, Kuntz JL, Lo NK, Lockwood CM, McAllister KD, McCormick CJ, MacMillan MP, Midgley CM, Nguyen D, Plumb ID, Reed JC, Reich S, Roychoudhury P, Schmidt M, Starita LM, Stone J, Varga A, Weil AA, **Wolock CJ**, Yetz N, Gilbert PB, Naleway AL, Chu HY, Carone M. (2025+) Immune Correlates of Risk for SARS-CoV-2 Infection in Children. Under review, *Nature Medicine*.
31. Morenz ER*, **Wolock CJ***, Carone M. (2025+) Debiased machine learning for survival functionals based on left-truncated right-censored data. [arXiv.2411.09017](https://arxiv.org/abs/2411.09017).

SOFTWARE

survML	Tools for flexible survival analysis using machine learning (cre, aut)
SimEngine	Framework for reproducible statistical simulations in R (aut)
rigr	Regression, inference, and general data analysis tools for R (aut)
vimp	Inference on algorithm-agnostic variable importance (ctb)

PRESENTATIONS

(^{*}invited, [†]upcoming)

Institute of Mathematical Statistics New Researchers Conference^{*†} <i>Nonparametric approaches to assessing variable importance using health data</i>	Nashville, TN 2025
ICSA Applied Statistics Symposium[*] <i>Nonparametric approaches to assessing variable importance using health data</i>	Storrs, CT 2025
ENAR Spring Meeting <i>Transfer learning for model-free variable importance</i>	New Orleans, LA 2025

Columbia University Biostatistics Levin Lecture* <i>Nonparametric approaches to assessing variable importance using health data</i>	New York, NY 2025
University of Rochester Biostatistics and Computational Biology Seminar* <i>Nonparametric approaches to assessing variable importance using health data</i>	Rochester, NY 2024
University of Minnesota Biostatistics Seminar* <i>Nonparametric approaches to assessing variable importance using health data</i>	Minneapolis, MN 2024
Joint Statistical Meetings (JSM) <i>Estimating causal effects from electronic health records data with underreported exposure</i>	Portland, OR 2024
ENAR Spring Meeting <i>Nonparametric variable importance for time-to-event outcomes with application to prediction of HIV infection</i>	Baltimore, MD 2024
Joint Statistical Meetings (JSM)* <i>Nonparametric variable importance for time-to-event outcomes with application to prediction of HIV infection</i>	Toronto, Canada 2023
ENAR Spring Meeting <i>Flexible estimation of the conditional survival function via observable regression models</i>	Nashville, TN 2023
Joint Statistical Meetings (JSM) <i>Flexible estimation of the conditional survival function via observable regression models</i>	Washington, DC 2022
WNAR Annual Meeting <i>Flexible estimation of the conditional survival function via observable regression models</i>	virtual 2022

PROFESSIONAL AFFILIATIONS

American Statistical Association
International Biometric Society (ENAR)
Institute of Mathematical Statistics