

CHARLES J. WOLOCK

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Department of Biostatistics, Epidemiology and Informatics, University of Pennsylvania
417 Blockley Hall, 423 Guardian Drive, Philadelphia, PA 19104

EDUCATION

University of Washington, Seattle, WA

Ph.D., Biostatistics

Advisors: Marco Carone, Ph.D. and Noah Simon, Ph.D.

Sept. 2018 - Aug. 2023

Harvard University

B.A., Organismic and Evolutionary Biology

Language citation, Spanish

Summa cum laude, Highest Honors

Sept. 2011 - May 2015

PROFESSIONAL POSITIONS

Postdoctoral Researcher

Department of Biostatistics, Epidemiology and Informatics

University of Pennsylvania

Supervisor: Yong Chen, Ph.D.

Sept. 2023 - present

Research Staff Associate

Institute for Genomic Medicine

Columbia University

Supervisors: Andrew S. Allen, Ph.D. and David B. Goldstein, Ph.D.

Nov. 2016 - July 2018

TEACHING EXPERIENCE

Instructor of Record

University of Washington

BIOST311: Regression Methods in the Health Sciences

Mar. 2022 - June 2022

Teaching Assistant

University of Washington

BIOST 511: Medical Biometry I (Lead TA)

Sept. 2020 - Dec. 2020

BIOST 310: Biostatistics for the Health Sciences (Lead TA)

Sept. 2021 - Dec. 2021

Research Mentor

Fred Hutchinson Cancer Center

Pathways Undergraduate Research Program

June 2021 - Aug. 2021

University of Washington

Directed Reading Program: Introduction to Prediction

Jan. 2023 - Mar. 2023

Guest Lecturer

University of Washington

BIOST 561: Computational Skills for Biostatistics

May 2023

AWARDS, HONORS, FELLOWSHIPS

University of Washington

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| NSF Graduate Research Fellowship | Sept. 2020 - Sept. 2023 |
| Thomas R. Fleming Excellence in Biostatistics Award | June 2023 |
| UW Biostatistics highest honor for Ph.D. students | |
| Donovan J. Thompson Award | Oct. 2020 |
| Best combined performance on the Ph.D. Applied and Theory qualifying exams | |
| NIH T32 Statistical Genetics Training Grant | Sept. 2018 - Sept. 2020 |

Harvard University

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| Phi Beta Kappa | May 2015 |
| Herchel Smith Research Fellowship | June 2014 - Aug. 2014 |
| Microbial Sciences Initiative Research Fellowship | June 2014 - Aug. 2014 |
| John Harvard Scholar | May 2013 |
| National Merit Scholarship | Sept. 2011 |

PROFESSIONAL SERVICE

Manuscript Reviewer

Bayesian Analysis
Biometrics
Biostatistics
Journal of Machine Learning Research
Scientific Reports
Statistics and Computing

Conference Session Chair

Next Generation Methods for Evidence Synthesis and Reproducibility (*JSM, Portland, Aug. 2024*)
Heterogeneous Treatment Effects (*ACIC, Seattle, May 2024*)

UNIVERSITY SERVICE

University of Washington, Department of Biostatistics

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| Faculty Search Committee | Sept. 2022 - Mar. 2023 |
| Student Seminar Coordinator | Sept. 2020 - June 2022 |
| Peer mentor | June 2019 - June 2022 |
| Admissions Committee | Sept. 2021 - Mar. 2022 |
| Education Policy and Teaching Evaluation Committee | Sept. 2020 - Sept. 2021 |
| Equity, Diversity, and Inclusion Committee | Sept. 2019 - June 2021 |
| Student-Faculty-Staff Relations Committee | Sept. 2019 - Sept. 2020 |

BIBLIOGRAPHY

(The * symbol denotes equal contribution.)

Refereed Journal Publications

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.

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.
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.
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.
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.
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.
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, Haeffliger 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.
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.
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.
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.
12. Heil J, **Wollock CJ**, Pierce NE, Pringle A, Bittleston LS. (2022). Pitcher plant-associated microbial communities differ primarily by host species across a longitudinal gradient. *Environmental Microbiology* 24(8): 3500–3516.
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.
14. Chen YT, Williamson BD, Okonek T, **Wollock 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.

15. Kohn M, **Wollock 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.
16. Bittleston LS*, **Wollock 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* e00812-23.
17. **Wollock 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.
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, **Wollock CJ**, Zainal HN, Stein MB, Ursano RJ, Kessler RC. (2024). Predicting Suicides Among US Army Soldiers After Leaving Active Service. *JAMA Psychiatry*.

Under Revision/Under Review

1. **Wollock CJ**, Gilbert PB, Simon N, Carone M. (2023+). Assessing variable importance in survival analysis using machine learning. [arXiv.2311.12726](https://arxiv.org/abs/2311.12726). Invited revision, *Biometrika*.
2. **Wollock 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. [medRxiv.2024.306260](https://medrxiv.org/lookup/doi/10.1101/2024.306260). Invited revision, *Journal of Biomedical Informatics*.
3. Wu Q, Pajor NM, Lu Y, **Wollock CJ**, Tong J, Lorman V, Johnson KB, Moore JH, Forrest CB, Asch DA, Chen Y. (2024+). Post-acute healthcare demands following SARS-CoV-2 infection in children and adolescents: a hospital-specific investigation through heterogeneous transfer learning. Invited revision, *Patterns*.
4. **Wollock CJ***, Jacob S*, Weil AA, Bennett JC, Elias-Warren A, O'Hanlon J, Kenny A, Jewell NP, Rotnitzky A, Chu HY, Carone M. (2024+). Investigating symptom duration using current status data: a case study of post-acute COVID-19 syndrome. [arXiv.2407.04214](https://arxiv.org/abs/2407.04214). Under review, *Epidemiology*.
5. Kenny A, **Wollock CJ**. (2024+). SimEngine: A Modular Framework for Statistical Simulations in R. [arXiv:2403.05698](https://arxiv.org/abs/2403.05698). Under review, *Journal of Statistical Software*.

In Preparation

1. **Wollock CJ***, Yan J*, Ning Y, Chen Y. (2024+) Transfer learning for model-free variable importance. In preparation.
2. **Wollock CJ**, Zhang B, Zhang D, Wu Q, Chen Y. (2024+) Estimating causal effects from electronic health records data with underreported exposure. In preparation.
3. Wollum A, Ralph L, Grossman D, **Wollock CJ**, Moseson H. (2024+) Evaluating a double list experiment to measure lifetime self-managed abortion attempts in the United States: analysis of a nationally representative cross-sectional survey in 2017. In preparation.
4. Morenz E*, **Wollock CJ***, Rotnitzky A, Carone M. (2024+) Debiased machine learning for survival functionals based on left-truncated right-censored data. In preparation.

SOFTWARE

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| 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

1. Estimating causal effects from electronic health records data with underreported exposure.
JSM, Portland, Aug. 2024. (contributed)
2. Nonparametric variable importance for time-to-event outcomes with application to prediction of HIV infection.
JSM, Toronto, Aug. 2023. (invited)
ENAR, Baltimore, Mar. 2024. (contributed)
3. Flexible estimation of the conditional survival function via observable regression models.
ENAR, Nashville, Mar. 2023. (contributed)
JSM, Washington, D.C., Aug. 2022. (contributed)
WNAR, virtual, June 2022. (contributed)

PROFESSIONAL AFFILIATIONS

American Statistical Association
International Biometric Society (ENAR)

SKILLS

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| Programming | Python, R, Bash, SQL |
| Other applications | \LaTeX , Git |
| Languages | English (native), Spanish (proficient) |