

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

September 2018 - August 2023

Ph.D., Biostatistics

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

Harvard University

September 2011 - May 2015

B.A., Organismic and Evolutionary Biology

Language citation, Spanish

Summa cum laude, Highest Honors

PROFESSIONAL POSITIONS

Postdoctoral Researcher

Department of Biostatistics, Epidemiology and Informatics

University of Pennsylvania

Supervisor: Yong Chen, Ph.D.

September 2023 - present

Research Staff Associate

Institute for Genomic Medicine

Columbia University

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

November 2016 - July 2018

TEACHING EXPERIENCE

Instructor of Record

University of Washington

BIOST311: Regression Methods in the Health Sciences

March 2022 - June 2022

Teaching Assistant

University of Washington

BIOST 511: Medical Biometry I (Lead TA)

September 2020 - December 2020

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

September 2021 - December 2021

Research Mentor

Fred Hutchinson Cancer Research Center

Pathways Undergraduate Research Program

June 2021 - August 2021

University of Washington

Directed Reading Program: Introduction to Prediction

January 2023 - March 2023

Guest Lecturer

University of Washington

BIOST 561: Computational Skills for Biostatistics

May 2023

AWARDS, HONORS, FELLOWSHIPS

University of Washington

NSF Graduate Research Fellowship	<i>September 2020 - September 2023</i>
Thomas R. Fleming Excellence in Biostatistics Award	<i>June 2023</i>
UW Biostatistics highest honor for PhD students	
Donovan J. Thompson Award	<i>October 2020</i>
Best combined performance on the PhD Applied and Theory qualifying exams	
NIH T32 Statistical Genetics Training Grant	<i>September 2018 - September 2020</i>

Harvard University

Phi Beta Kappa	<i>May 2015</i>
Herchel Smith Research Fellowship	<i>June 2014 - August 2014</i>
Microbial Sciences Initiative Research Fellowship	<i>June 2014 - August 2014</i>
John Harvard Scholar	<i>May 2013</i>
National Merit Scholarship	<i>September 2011</i>

PROFESSIONAL SERVICE

Manuscript Reviewer

Bayesian Analysis
Journal of Machine Learning Research

UNIVERSITY SERVICE

University of Washington, Department of Biostatistics

Faculty Search Committee	<i>September 2022 - March 2023</i>
Student Seminar Coordinator	<i>September 2020 - June 2022</i>
Peer mentor	<i>June 2019 - June 2022</i>
Admissions Committee	<i>September 2021 - March 2022</i>
Education Policy and Teaching Evaluation Committee	<i>September 2020 - September 2021</i>
Equity, Diversity, and Inclusion Committee	<i>September 2019 - June 2021</i>
Student-Faculty-Staff Relations Committee	<i>September 2019 - September 2020</i>

REFEREED JOURNAL PUBLICATIONS

1. Sperling E.A., **Wolock C.J.**, Morgan A.S., Gill B.C., Kunzmann M., Halverson G.P., Macdonald F.A., Knoll A.H., Johnston D.T. (2015). Statistical analysis of iron geochemical data suggests limited late Proterozoic oxygenation. *Nature* 523: 451–454.
2. Raghavan N.S., Brickman A.M., Andrew H., Manly J.J., Schupf N., Lantigua R., The Alzheimers Disease Sequencing Project, **Wolock C.J.**, Kamalakaran S., Petrovski S., Tosto G., Vardarajan B.N., Goldstein D.B., Mayeux R. (2018). Whole exome sequencing in 20,197 individuals identifies ultra-rare SORL1 loss-of-function variants in late-onset Alzheimers disease. *Annals of Clinical and Translational Neurology* 5(7): 832-842.
3. Bittleston L.S., **Wolock C.J.**, Bakhtiar E.Y., Chan X.Y., Chan K.G., Pierce N.E., Pringle A. (2018). Convergence between the microcosms of Southeast Asian and North American pitcher plants. *eLife* 7.
4. Hayeck T.J., Stong N., **Wolock C.J.**, Copeland B., Kamalakaran S., Goldstein D.B., Allen A.S. (2019). Improved Pathogenic Variant Localization using a Hierarchical Model of Sub-regional Intolerance. *American Journal of Human Genetics* 104(2): 299-309.
5. **Wolock C.J.**, Stong N., Ma F., Nagasaki T., Lee W., Tsang S.H., Kamalakaran S., Goldstein D.B., 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 S.A., Moreno C.A.M., Ren Z., **Wolock C.J.**, Shneider N.A., Phatnani H., Cirulli E.T., Lasseigne B.N., Harris T., Maniatis T., Rouleau G.A., Brown R.H., Gitler A.D., Myers R.M., Petrovski S., Allen A.S., Harms M.B., Goldstein D.B. (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., **Wolock C.J.**, Groopman E., Petrovski S., Kamalakaran S., Povysil G., Zhang M., Fleckner J., March R.E., Gelfman S., Marasa M., Li Y., Sanna-Cherchi S., Kiryluk K., Allen A.S., Fellström B., Haefliger C., Platt A., Goldstein D.B., 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 C.J., **Wolock C.J.**, Stong N., Nagasaki T., Lee W., Goldstein D.B., 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 M.L., Hostyk J.A., Nagasaki T., Giles S., Harkins-Perry S., Fallon R., Baldini M., Schepke L., Dorrell M.I., Cai C., Baugh E.H., **Wolock C.J.**, Wallace M., Berlow R.B., Goldstein D.B., Metallo C.M., 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 P.J., Inoue L.Y.T., Veenstra D.L., **Wolock C.J.**, Basu A. (2021). A Value of Information Framework for Personalizing the Timing of Surveillance Testing. *Medical Decision Making* 42(4): 474-486.
 11. Wasser S.K., **Wolock C.J.**, Kuhner M.K., Brown J.E., Morris C., Horowitz R., Wong A., Fernandez C.J., Otiende M.Y., Hoareau Y., Kaliszewska Z.A., Jeon E., Han K.L., Weir B.S. (2022). Elephant genotypes reveal the size and connectivity of transnational ivory traffickers. *Nature Human Behaviour* 6(3): 371-382.
 12. Heil J., **Wolock C.J.**, Pierce N.E., Pringle A., Bittleston L.S. (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 M.D., Conroy C., Dahl A., Hares D., Weir B.S., **Wolock C.J.**, 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 Y.T., Williamson B.D., Okonek T., **Wolock C.J.**, Spieker A.J., Hee Wai T.Y., Hughes J.P., Emerson S.S., Willis A.D. (2022). **rigr**: Regression, Inference, and General Data Analysis Tools in R. *The Journal of Open Source Software* 7(80): 4847.
 15. Kohn M., **Wolock C.J.**, 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 L.S.^{*}, **Wolock C.J.**^{*}, Maeda J., Infante V., Ané J.M., Pierce N.E., Pringle, A. (2023). Carnivorous *Nepenthes* pitchers with less acidic fluid house nitrogen-fixing bacteria. *Applied and Environmental Microbiology* e00812-23. ^{*}equal contribution
 17. **Wolock C.J.**, Gilbert P.B., Simon N., Carone M. (2024). A framework for leveraging machine learning tools to estimate personalized survival curves. *Journal of Computational and Graphical Statistics*, in press.

SUBMITTED/IN PREPARATION

1. **Wolock C.J.**, Gilbert P.B., Simon N., Carone M. Nonparametric variable importance for time-to-event outcomes with application to prediction of HIV infection. [arXiv.2311.12726](#). Preprint.
2. Morenz E., **Wolock C.J.**, Carone M. Debiased machine learning for survival functionals based on left-truncated right-censored data. In preparation.

SOFTWARE

survML	Conditional survival function estimation using machine learning (<code>cre</code> , <code>aut</code>)
SimEngine	Framework for reproducible statistical simulations in R (<code>aut</code>)
rigr	Regression, inference, and general data analysis tools for R (<code>aut</code>)
vimp	Inference on algorithm-agnostic variable importance (<code>ctb</code>)

PRESENTATIONS

1. Nonparametric variable importance for time-to-event outcomes with application to prediction of HIV infection.
JSM, Toronto, August 2023. (invited)
2. Flexible estimation of the conditional survival function via observable regression models.
ENAR, Nashville, March 2023. (contributed)
JSM, Washington, D.C., August 2022. (contributed)
WNAR, virtual, June 2022. (contributed)

PROFESSIONAL AFFILIATIONS

American Statistical Association
International Biometric Society (ENAR)

SKILLS

Programming	Python, R, Bash, SQL
Other applications	L ^A T _E X, Git
Languages	English (native), Spanish (proficient)