

CHARLES J. WOLOCK

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Department of Biostatistics, University of Washington
3980 15th Avenue NE, Box 351617, Seattle, WA 98195

EDUCATION

University of Washington, Seattle, WA

September 2018 - present

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

RESEARCH EXPERIENCE

Research Assistant

University of Washington, Department of Biostatistics

Supervisor: Bruce S. Weir, Ph.D.

September 2018 - September 2020

Research Staff Associate

Columbia University, Institute for Genomic Medicine

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

September 2020 - present

Thomas R. Fleming Excellence in Biostatistics Award

June 2023

UW Biostatistics highest honor for PhD students

Donovan J. Thompson Award

October 2020

Best combined performance on the PhD Applied and Theory qualifying exams

NIH T32 Statistical Genetics Training Grant

September 2018 - September 2020

Harvard University

Phi Beta Kappa

May 2015

Herchel Smith Research Fellowship

June 2014 - August 2014

Microbial Sciences Initiative Research Fellowship

June 2014 - August 2014

John Harvard Scholar

May 2013

National Merit Scholarship

September 2011

PROFESSIONAL SERVICE

Manuscript Reviewer

Bayesian Analysis

Journal of Machine Learning Research

UNIVERSITY SERVICE

University of Washington, Department of Biostatistics

Faculty Search Committee

September 2022 - March 2023

Student Seminar Coordinator

September 2020 - June 2022

Peer mentor

June 2019 - June 2022

Admissions Committee

September 2021 - March 2022

Education Policy and Teaching Evaluation Committee

September 2020 - September 2021

Equity, Diversity, and Inclusion Committee

September 2019 - June 2021

Student-Faculty-Staff Relations Committee

September 2019 - September 2020

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. Statistical analysis of iron geochemical data suggests limited late Proterozoic oxygenation. *Nature* 523: 451–454, 2015.
2. Raghavan N.S., Brickman A.M., Andrew H., Manly J.J., Schupf N., Lantigua R., The Alzheimer's Disease Sequencing Project, **Wolock C.J.**, Kamalakaran S., Petrovski S., Tosto G., Vardarajan B.N., Goldstein D.B., Mayeux R. 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, 2018.
3. Bittleston L.S., **Wolock C.J.**, Bakhtiar E.Y., Chan X.Y., Chan K.G., Pierce N.E., Pringle A. Convergence between the microcosms of Southeast Asian and North American pitcher plants. *eLife* 7, 2018.
4. Hayeck T.J., Stong N., **Wolock C.J.**, Copeland B., Kamalakaran S., Goldstein D.B., Allen A.S. Improved Pathogenic Variant Localization using a Hierarchical Model of Sub-regional Intolerance. *American Journal of Human Genetics* 104(2): 299-309, 2019.
5. **Wolock C.J.**, Stong N., Ma F., Nagasaki T., Lee W., Tsang S.H., Kamalakaran S., Goldstein D.B., Allikmets R. 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, 2019.
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. A new approach for rare variation collapsing on functional protein domains implicates specific genic regions in ALS. *Genome Research* 29(5): 809-818, 2019.
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. Exome-based rare-variant analyses in chronic kidney disease. *Journal of the American Society of Nephrology* 30(6): 1109-1122, 2019.
 8. Ma C.J., **Wolock C.J.**, Stong N., Nagasaki T., Lee W., Goldstein D.B., Allikmets R. Case-control collapsing analysis identifies genes mimicking Stargardt/ABCA4 disease. *Investigative Ophthalmology & Visual Science* 60(9): 2935-2935, 2019.
 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. Serine biosynthesis defect due to haploinsufficiency of phosphoglycerate dehydrogenase (PHGDH) causes retinal disease. *Nature Metabolism* 3(3): 366-377, 2021.
 10. Bansal A., Heagerty P.J., Inoue L.Y.T., Veenstra D.L., **Wolock C.J.**, Basu A. A Value of Information Framework for Personalizing the Timing of Surveillance Testing. *Medical Decision Making* 42(4): 474-486, 2021.
 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. Elephant genotypes reveal the size and connectivity of transnational ivory traffickers. *Nature Human Behaviour* 6(3): 371-382, 2022.
 12. Heil J., **Wolock C.J.**, Pierce N.E., Pringle A., Bittleston L.S. Pitcher plant-associated microbial communities differ primarily by host species across a longitudinal gradient. *Environmental Microbiology* 24(8): 3500-3516, 2022.
 13. Alfieri J., Coble M.D., Conroy C., Dahl A., Hares D., Weir B.S., **Wolock C.J.**, Zhao E., Kingston H., Zolanz T. A new implementation of a semi-continuous method for DNA mixture interpretation. *Forensic Science International: Reports* 6, 2022.
 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. **rigr**: Regression, Inference, and General Data Analysis Tools in R. *The Journal of Open Source Software* 7(80): 4847, 2022.
 15. Kohn M., **Wolock C.J.**, Poulson I., Fernando N. 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, 2023.
 16. Bittleston L.S.* , **Wolock C.J.***, Maeda J., Infante V., Ané J.M., Pierce N.E., Pringle, A. Carnivorous *Nepenthes* pitchers with less acidic fluid house nitrogen-fixing bacteria. *Applied and Environmental Microbiology* e00812-23, 2023. *equal contribution

SUBMITTED/IN PREPARATION

1. **Wolock C.J.**, Gilbert P.B., Simon N., Carone M. A framework for leveraging machine learning tools to estimate personalized survival curves. [arXiv.2211.03031](https://arxiv.org/abs/2211.03031). Under review.
2. **Wolock C.J.**, Simon N., Carone M. Nonparametric variable importance for time-to-event outcomes with application to prediction of HIV seroconversion. In preparation.

- Morenz E., **Wolock C.J.**, Carone M. Debiased machine learning for survival functionals based on left-truncated right-censored data. In preparation.

SOFTWARE

<code>survML</code>	Conditional survival function estimation using machine learning (<code>cre</code> , <code>aut</code>)
<code>SimEngine</code>	Framework for reproducible statistical simulations in R (<code>aut</code>)
<code>rigr</code>	Regression, inference, and general data analysis tools for R (<code>aut</code>)

PRESENTATIONS

Extramural

- ENAR.** Flexible estimation of the conditional survival function via observable regression models. Nashville, TN. March 2023.
- JSM.** Flexible estimation of the conditional survival function via observable regression models. Washington, D.C. August 2022.
- WNAR.** Flexible estimation of the conditional survival function via observable regression models. Virtual. June 2022.

Intramural

- Biostatistics Student Seminar Series.** Flexible estimation of the conditional survival function via observable regression models. University of Washington, Department of Biostatistics. April 2022.
- Statistical Learning Applied to Biostatistics (SLAB) Lab.** Flexible estimation of the conditional survival function via observable regression models. University of Washington. March 2022.
- Biostatistics Student Seminar Series.** Concordance-based variable importance for right-censored data. University of Washington, Department of Biostatistics. November 2021.

PROFESSIONAL AFFILIATIONS

American Statistical Association
International Biometric Society (WNAR)

SKILLS

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