Cole Williams

Postdoctoral Scholar
Department of Medicine
University of California, San Francisco

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williamscole

Education

Brown University 2020–2025
Ph.D. in Computational Biology GPA: 4.0/4.0

- Advisor: Dr. Sohini Ramachandran
- National Science Foundation Graduate Research Fellow

University of California, Davis 2015–2019
B.Sc. in Genetics & Genomics with highest honors GPA: 3.99/4.0

- Advisor: Dr. Brenna Henn
- Thesis: A rapid, accurate approach to inferring pedigrees in endogamous populations

Awards & Fellowships

- National Science Foundation Graduate Research Fellow (2022)
- National Institutes of Health Predoctoral Training Program (T32) Fellow (2021)
- UC Davis College of Biological Sciences Undergraduate of the Year (2019)
- Citation for Outstanding Performance in Genetics and Genomics (2019)
- Molecular and Cellular Biology Departmental Citation (2019)
- Edward F. Kraft Prize (2015)

Research interests

Population and statistical genetics; complex traits; germline variation in cancer outcomes

Technical Skills

- **Programming:** Python (numpy, pandas, scikit-learn, pytorch), R, Bash
- **Tools & Technologies:** Git/Github, Apptainer/Singularity, Linux/Unix, workflow management (Nextflow, Snakemake)
- **Statistical Genetics:** GWAS, fine-mapping (SuSiE), genotype imputation (GLIMPSE2), phasing, IBD inference, HLA typing and imputation (HLA-HD, HIBAG, arcasHLA), polygenic risk scores
- **Data Types:** Array genotypes, exome/WGS, low-pass WGS, bulk and single-cell RNA-seq

Research experience

Postdoctoral Scholar 2025–
Department of Medicine, University of California, San Francisco

- Advisor: Dr. Elad Ziv
- Developing computational approaches to identify germline genetic predictors of cancer treatment outcomes, including immune-related adverse events and tumor-immune microenvironment phenotypes. Work spans HLA association studies, polygenic risk score development, and genotype imputation from tumor sequencing data.

Graduate student researcher 2020–2025
Center for Computational Molecular Biology, Brown University

- Advisor: Dr. Sohini Ramachandran
- Developed a method for inter-chromosomal haplotype phasing. Investigated the performance of existing phasing algorithms on non-European populations. Improved upon my previous work on kinship and pedigree inference. Mentored an undergraduate student at Brown on a genetic variation visualization project. Currently mentoring a masters student on a project that investigates the bias of close relatives on inferring demographic parameters.

Professional research assistant 2019–2020

Colorado Center for Personalized Medicine

- Supervisors: Dr. Christopher Gignoux and Dr. Ethan Lange
- Researched identity by descent (IBD) segments and their application to kinship inference, rare variant mapping, and various population genetics questions in the context of large biobank datasets (UK Biobank, Colorado Biobank) as well as smaller biomedical datasets from around the world.

Undergraduate researcher 2018–2019

Department of Anthropology, UC Davis

- Advisor: Dr. Brenna Henn
- Investigated the use of IBD segments in constructing pedigrees of inbred human populations. Wrote a machine learning algorithm in Python that uses qualities of IBD segments (number and position in genome) to infer pedigree relationships in inbred populations. Research was focused on southern African populations such as the San and the Himba from northern Namibia. Awarded the UC Davis College of Biological Sciences' Undergraduate of the Year—given to the college's top graduating senior—in part for research in Dr. Henn's lab.

Publications

* denotes equal first authorship; † denotes equal senior authorship

Ramanan, V.*, Vinod, R.*, **Williams, C.***, Ramachandran, S.†, & Venkatasubramanian, S.† Principles and Policy Recommendations for Comprehensive Genetic Data Governance. *Proceedings of the Eighth AAAI/ACM Conference on AI, Ethics, and Society (AIES 2025).* arXiv:2502.09716

Williams, C.M., O'Connell, J., Jewett, E., Freyman, W.A., Gignoux, C.R., Ramachandran, S.†, & Williams, A.L.† Phasing millions of samples achieves near perfect accuracy, enabling parent-of-origin analyses. *Human Genetics and Genomics Advances*, 6(4), October 2025. doi:10.1016/j.xhgg.2025.100479

Williams, C.M., Scelza, B.A., Slack, S.D., Font-Porterias, N., Al-Hindi, D.R., Mathias, R.A., Watson, H., Barnes, K.C., Lange, E., Johnson, R.K., Gignoux, C.R., Ramachandran, S., & Henn, B.M. A rapid accurate approach to inferring pedigrees in endogamous populations. *Genetics*, iyaf094, May 2025. doi:10.1093/genetics/iyaf094

Moody, N.M., **Williams, C.M.**, Ramachandran, S., & Fuxjager, M.J. Social mates dynamically coordinate aggressive behavior to produce flexible territorial strategies. *PLOS Computational Biology*, in revision.

Wiley, L.K., Shortt, J.A., Roberts, E.R., Lowery, J., Kudron, E., Lin, M., Mayer, D., Wilson, M., Brunetti, T.M., Chavan, S., Phang, T.L., Pozdeyev, N., Lesny, J., Wicks, S.J., Moore, E.T., Morgenstern, J.L., Roff, A.N., Shalowitz, E.L., Stewart, A., **Williams, C.M.**, Edelmann, M.N., Hull, M., Patton, J.T., Axell, L., Ku, L., Lee, Y.M., Jirikowitz, J., Tanaka, A., Todd, E., White, S., Peterson, B., Hearst, E., Zane, R., Greene, C.S., Mathias, R., Coors, M., Taylor, M., Ghosh, D., Kahn, M.G., Brooks, I.M., Aquilante, C.L., Kao, D., Rafaels, N., Crooks, K.R., Hess, S., Barnes, K.C., & Gignoux, C.R. Building a vertically integrated genomic learning health system: The biobank at the Colorado Center for Personalized Medicine. *The American Journal of Human Genetics*, 111(1):11–23, January 2024.

Swinford, N.A., Prall, S.P., Gopalan, S., **Williams, C.M.**, Sheehama, J., Scelza, B.A., & Henn, B.M. Increased homozygosity due to endogamy results in fitness consequences in a human population. *Proceedings of the National Academy of Sciences*, 120(43):e2309552120, October 2023.

Gopalan, S., Berl, R.E.W., Myrick, J.W., Garfield, Z.H., Reynolds, A.W., Bafens, B.K., Belbin, G., Mastoras, M., **Williams, C.**, Daya, M., Negash, A.N., Feldman, M.W., Hewlett, B.S., & Henn, B.M. Hunter-gatherer genomes reveal diverse demographic trajectories during the rise of farming in Eastern Africa. *Current Biology*, 32(8):1852–1860.e5, April 2022.

Conference Presentations

Williams, C.M. and Ramachandran S. Rethinking identity-by-descent through demographic lenses. Poster presentation at the American Society for Human Genetics (ASHG) Annual Meeting, Boston, MA, October 2025.

Williams, C.M., O'Connell, J., 23andMe Research Team, Gignoux, C.R., Ramachandran, S., & Williams, A.L. Phasing of millions of samples achieves near perfect accuracy, enabling parent-of-origin classification of variants. Poster presentation at the American Society for Human Genetics (ASHG) Annual Meeting, Washington, D.C., November 2023.

Williams, C.M., 23andMe Research Team, Gignoux, C.R., Ramachandran, S., & Williams, A.L. Parent of origin classification of identity by descent segments. Poster presentation at the Probabilistic Modeling in Genomics Meeting, Cold Spring Harbor, NY, March 2023.

Williams, C.M., Scelza, B.A., Shortt, J.A., Lange, E., Rafaels, N., Crooks, K., Barnes, K.C., Gignoux, C., & Henn, B.M. A rapid, accurate approach to inferring pedigrees in endogamous populations. Poster presentation at the American Society for Human Genetics (ASHG) Annual Meeting, Houston, TX, October 2019.

Williams, C.M., Scelza, B., & Henn, B.M. A rapid, accurate approach to inferring pedigrees in endogamous populations. Talk presented at the Bay Area Population Genomics Meeting, Palo Alto, CA, June 2019.