Cole Williams

Ph.D. candidate
Center for Computational Molecular Biology
Brown University

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⌨ williamscole

Education

Brown University   2020–

Ph.D. in Computational Biology
M.Sc. in Computational Biology (2024)   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

Demographic inference; kinship and genealogy; population genetics; statistical genetics; complex traits

Programming languages

Python, R, Bash

Research experience

Graduate student researcher   2020–

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

- Nicole M. Moody, Cole M. Williams, Sohini Ramachandran, and Matthew J. Fuxjager. Social mates dynamically coordinate aggressive behavior to produce flexible territorial strategies. *in revision at PLOS Computational Biology*

- Cole M. Williams, Jared O'Connell, William A. Freyman, 23andMe Research Team, Christopher R. Gignoux, Sohini Ramachandran, and Amy L. Williams. Phasing millions of samples achieves near perfect accuracy, enabling parent-of-origin classification of variants. *bioRxiv*, May 2024

- Cole M. Williams, Brooke A. Scelza, Sarah D. Slack, Rasika A. Mathias, Harold Watson, Kathleen C. Barnes, Ethan Lange, Randi K. Johnson, Christopher R. Gignoux, Sohini Ramachandran, and Brenna M. Henn. A rapid, accurate approach to inferring pedigrees in endogamous populations. *bioRxiv*, July 2024

- Laura K. Wiley, Jonathan A. Shortt, Emily R. Roberts, Jan Lowery, Elizabeth Kudron, Meng Lin, David Mayer, Melissa Wilson, Tonya M. Brunetti, Sameer Chavan, Tzu L. Phang, Nikita Pozdeyev, Joseph Lesny, Stephen J. Wicks, Ethan T. Moore, Joshua L. Morgenstern, Alanna N. Roff, Elise L. Shalowitz, Adrian Stewart, Cole Williams, Michelle N. Edelmann, Madelyne Hull, J. Tacker Patton, Lisen Axell, Lisa Ku, Yee Ming Lee, Jean Jirikowic, Anna Tanaka, Emily Todd, Sarah White, Brett Peterson, Emily Hearst, Richard Zane, Casey S. Greene, Rasika Mathias, Marilyn Coors, Matthew Taylor, Debashis Ghosh, Michael G. Kahn, Ian M. Brooks, Christina L. Aquilante, David Kao, Nicholas Rafaels, Kristy R. Crooks, Steve Hess, Kathleen C. Barnes, and Christopher R. Gignoux. 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

- Natalie A. Swinford, Sean P. Prall, Shyamalika Gopalan, Cole M. Williams, Jacob Sheehama, Brooke A. Scelza, and Brenna M. Henn. 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

- Shyamalika Gopalan, Richard E.W. Berl, Justin W. Myrick, Zachary H. Garfield, Austin W. Reynolds, Barnabas K. Bafens, Gillian Belbin, Mira Mastoras, Cole Williams, Michelle Daya, Akmel N. Negash, Marcus W. Feldman, Barry S. Hewlett, and Brenna M. Henn. 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 abstracts

- **Cole M. Williams**, Jared O'Connell, 23andMe Research Team, Christopher R. Gignoux, Sohini Ramachandran, Amy L. Williams. 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

- **Cole M. Williams**, 23andMe Research Team, Christopher R. Gignoux, Sohini Ramachandran, Amy L. Williams. Parent of origin classification of identity by descent segments. Poster presentation at the Probabilistic Modeling in Genomics meeting. Cold Spring Harbor, NY. March 2023

- **Cole M. Williams**, Brooke A. Scelza , Johnathan A. Shortt, Ethan Lange, Nicholas Rafaels, Kristy Crooks, Kathleen C. Barnes, Christopher Gignoux, Brenna M. Henn. 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

- **Cole M. Williams**, Brooke Scelza , Brenna M. Henn. A rapid, accurate approach to inferring pedigrees in endogamous populations. Talk presented at the Bay Area Population Genomics meeting. Palo Alto, CA. June 2019