Kelsey E. Grinde

CONTACT

Mathematics, Statistics, & Computer Science
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EDUCATION

Ph.D. in Biostatistics 2019
University of Washington, Seattle, WA

Dissertation: *Statistical inference in admixed populations*
Advisor: Sharon Browning, Ph.D.

B.A. in Mathematics, Concentration in Statistics 2014
St. Olaf College, Northfield, MN

Graduated *summa cum laude* with Distinction in Statistics
Advisor: Paul Roback, Ph.D.

WORK EXPERIENCE

Assistant Professor 2020–present
Department of Mathematics, Statistics, & Computer Science
Macalester College, Saint Paul, MN

Postdoctoral Teaching Fellow 2019–2020
Department of Mathematics, Statistics, & Computer Science
Macalester College, Saint Paul, MN

Graduate Research Assistant 2014–2019
Browning Statistical Genetics Lab
University of Washington, Seattle, WA

Graduate Research Assistant 2015–2016
Genetic Analysis Center
University of Washington, Seattle, WA

Undergraduate Research Assistant 2013, 2014
Summer Research Program in Statistical Genetics & Biostatistics
Dordt College, Sioux Center, IA

Undergraduate Research Fellow 2013–2014
Center for Interdisciplinary Research
St. Olaf College, Northfield, MN

TEACHING EXPERIENCE

Macalester College

- MATH/STAT 455: Mathematical Statistics (3 sections) 2020–present
- STAT 155: Introduction to Statistical Modeling (10 sections) 2019–present

University of Washington

- BIOST 311: Regression Methods in the Health Sciences, Co-Instructor 2018
- BIOST 310: Biostatistics for the Health Sciences, Teaching Assistant 2017
- BIOST 561: Computational Skills for Biostatistics, Guest Lecturer 2017
- BIOST 550: Statistical Genetics I, Guest Lecturer 2017

- BIOST 570: Regression Methods for Independent Data, Teaching Asst. 2016
- First Year Statistical Theory Exam Review Sessions, Co-Instructor 2016

St. Olaf College

- STAT 322: Statistical Theory, Grader 2013
- Academic Support Center, Tutor & Academic Assistant 2011–2012
- Urban Schools and Communities Program, Participant 2012

PUBLICATIONS

* *denotes an undergraduate student*

\+ *denotes joint first authors*

Refereed Journal Articles

12. Zucko, D., Hayir, A.*, **Grinde, K.**, & Boris-Lawrie, K. "Circular RNA Profiles in Viremia and ART Suppression Predict Competing circRNA–miRNA–mRNA Networks Exclusive to HIV-1 Viremic Patients." *Viruses* 14.4 (2022): 683.

    Explores circular RNA profiles in patients with HIV-1 before and after antiretroviral therapy. Appears in the *Next-Generation Technologies to Understand Mechanisms of Virus Infections* special issue of journal *Viruses*, an open access journal of virology affiliated with the American, Spanish, Canadian, Italian, and Australasian Societies of Virology. *Viruses* has an impact factor of 5.048 and ranks in the second quartile (Q2) of virology journals according to Journal Citation Reports and the top quartile (Q1) of infectious disease journals according to CiteScore. I advised Macalester student Abdullgadir Hayir in creating an interactive circos plot to visualize the study findings (see Figure 6).

11. Lin, B.+, **Grinde, K.**+, Brody, J., Breeze, C., Raffield, L., Mychaleckyj, J., Thornton, T., Perry, J., Baier, L., de Las Fuentes, L., Guo, X., Heavner, B., Hanson, R., Hung, Y.-J., Qian, H., Hsiung, C., Hwang, S.-J., Irvin, M., Jain, D., Kelly, T., Kobes, S., Lange, L., Lash, J., Li, Y., Liu, X., Mi, X., Musani, X., Papanicolaou, G., Parsa, A., Reiner, A., Salimi, S., Sheu, W., Shuldiner, A., Taylor, K., Smith, A., Smith, J., Tin, A., Vaidya, D., Wallace, R., Yamamoto, K., Sakaue, S., Matsuda, K., Kamatani, Y., Momozawa, Y., Yanek, L., Young, B., Zhao, W., Okada, Y., Abecasis, G., Psaty, B., Arnett, D., Boerwinkle, E., Cai, J., Chen, I., Correa, A., Cupples, L.A., He, J., Kardia, S., Kooperberg, C., Mathias, R., Mitchell, B., Nickerson, D., Turner, S., Ramachandran, V., Rotter, J., Levy, D., Kramer, H., Köttgen, A., Rich, S., Lin, D.-Y., Browning, S., Franceschini, N., & TOPMed Kidney Working Group. "Discovery of rare genetic variants from whole genome sequencing analyses of kidney function (eGFR) in 23,732 participants from multi-ethnic populations: the Trans-Omics for Precision Medicine (TOPMed) program." *eBioMedicine* 63 (2021): 103157.

    Collaboration with the TOPMed Kidney Working Group that identifies ancestry-specific rare genetic variants associated with kidney function. Appears in *eBioMedicine*, an open access journal for translational biomedical research that is one of two open access offerings in the *Lancet* (a top medical journal) family, has an impact factor of 8.143, and ranks 17th (out of 140) among research and experimental medicine journals according to Journal Citation Reports. I am a joint first-author on this paper, contributing all aspects of the study related to genetic ancestry (ancestry inference, admixture mapping, and ancestry-specific allele frequency estimation). This paper has been cited 5 times since publication. (Note: this and all following citation counts come from Google Scholar.)

10. Raffield, L., Lu, A., Szeto, M., Little, A., **Grinde, K.**, Shaw, J., Auer, P., Cushman, M., Horvath, S., Irvin, M., Lange, E., Lange, L., Nickerson, D., Thornton, T., Wilson, J., Wheeler, M., NHLBI TOPMed Consortium, TOPMed Hematology & Hemostasis Working Group, Zakai, N., & Reiner, A. "Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence

and epigenome-wide analysis in African Americans." *Journal of Thrombosis and Haemostasis* 18.6 (2020): 1335–1347.

Collaboration with the TOPMed Hematology & Hemostasis Working Group that confirms associations between the blood-clotting protein Factor VIII (FVIII), cardiovascular disease, and mortality in African American adults, as well as identifying genetic variants associated with FVIII. Appears in the *Journal of Thrombosis and Haemostasis* (JTH), the official journal of the International Society on Thrombosis and Haemostasis. JTH has an impact factor of 5.824 and ranks 17th (out of 76) in hematology journals and 9th (out of 65) in peripheral vascular disease according to Journal Citation Reports. I assisted with the admixture mapping portion of the paper, with primary responsibility for inferring local and global ancestry and estimating a genome-wide significance threshold for the admixture mapping study. Cited 12 times since publication.

9. Shungin, D., Haworth, S., Divaris, K., Agler, C., Kamatani, Y., Lee, M.K., **Grinde, K.**, Hindy, G., Alaraudanjoki, V., Pesonen, P., Temuer, A., Holtfreter, B., Sakaue, S., Hirata, J., Yu, Y.H., Ridker, P., Giulianini, F., Chasman, D., Magnusson, P., Sudo, T., Okada, Y., Voelker, U., Kocher, T., Anttonen, V., Laitala, M.L., Orho-Melander, M., Sofer, T., Shaffer, J., Vieira, A., Marazita, M., Kubo, M., Furuichi, Y., North, K., Offenbacher, S., Ingelsson, E., Franks, P., Timpson, N., Johansson, I. "Genome-wide analysis of dental caries and periodontal disease combining clinical and self-reported data." *Nature Communications* 10.1 (2019): 2773.

   An international, collaborative endeavor to conduct a meta-analysis of genome-wide association studies of dental disease and traits. Appears in *Nature Communications*, an open access journal that publishes work across the sciences and is part of *Nature Research* portfolio of journals (including the prestigious *Nature*). *Nature Communications* has an impact factor of 14.919. I contributed genome-wide association study results from the Hispanic Community Health Study/Study of Latinos, the only study of Hispanics/Latinos included in the meta-analysis. This is my top-cited paper to date, with 96 citations.

8. Sofer, T., Zheng, X., Gogarten, S.M., Laurie, C.A., **Grinde, K.**, Shaffer, J.R., Shungin, D., O'Connell, J.R., Durazo-Arvizo, R.A., Raffield, L., Lange, L., Musani, S., Vasan, R.S., Cupples, L.A., Reiner, A.P., Laurie, C.C., Rice, K.M. "A fully-adjusted two-stage procedure for rank normalization in genetic association studies." *Genetic Epidemiology* 43.3 (2019): 263–275.

   Proposes methods to address departures from normality, thus reducing type I error and improving power, in genetic association studies. Appears in *Genetic Epidemiology*, the flagship journal of the International Genetic Epidemiology Society and one of the primary journals for publishing work in statistical genetics. *Genetic Epidemiology* has an impact factor of 2.135. I worked on the genome-wide association analysis of the number of teeth in the Hispanic Community Health Study/Study of Latinos, which is one of the illustrative examples included in the paper. Has been cited 45 times.

7. **Grinde, K.**, Brown, L., Reiner, A., Thornton, T., Browning, S. "Genome-wide significance thresholds for admixture mapping studies." *American Journal of Human Genetics* 104 (2019): 454–465.

   Proposes methods to estimate the number of generations since admixture and the genome-wide significance threshold for admixture mapping studies. Appears in the *American Journal of Human Genetics* (AJHG), the official journal of the American Society of Human Genetics. AJHG has an impact factor of 10.5 and is one of the top-ranked journals in genetics and a primary journal for publishing work in statistical genetics. I was the lead author of this paper and was responsible for all analyses (with the exception of local ancestry inference, which was conducted by my co-author Lisa Brown), theoretical derivations, and writing. This paper has 20 citations thus far.

6. **Grinde, K.**, Qi, Q., Thornton, T., Liu, S., Shadyab, A.H., Chan, K.H.K., Reiner, A.P., & Sofer, T. "Generalizing polygenic risk scores from Europeans to Hispanics/Latinos." *Genetic Epidemiology* 43.1 (2019): 50–62.

Proposes and compares methods for constructing polygenic risk scores (used to predict complex diseases/traits) in admixed populations. Appears in *Genetic Epidemiology*, the flagship journal of the International Genetic Epidemiology Society (IGES) and one of the primary journals for publishing work in statistical genetics. *Genetic Epidemiology* has an impact factor of 2.135. I was the lead author of this paper, and along with senior author Tamar Sofer was the primary contributor to the data analyses, simulation studies, and writing. This paper was selected as the IGES Communication Committee's Highlight from this issue of *Genetic Epidemiology* and is a top-cited article of the journal as of April 2021. With 60 citations, this is my top-cited first-author paper to date.

5. **Grinde, K.**, Green, A., Arbet, J., O'Connell, M., Valcarcel, A., Westra, J., & Tintle, N. "Illustrating, quantifying and correcting for bias in post-hoc analysis of gene-based rare variant tests of association." *Frontiers in Genetics* 8.117 (2017): 1–11.

   Proposes methods for addressing bias that arises, due to the phenomenon of *winner's curse*, when estimating genetic effect sizes for individual variants after a significant gene-based test. Appears in the *Statistical Genetics and Methodology* section of *Frontiers in Genetics*, an open access journal publishing work across the fields of genetics and genomics that uses a unique, transparent peer-review system with reviewer names listed on the published article. *Frontiers in Genetics* has an impact factor of 4.274. Initial analyses, simulation studies, and methods development were conducted collaboratively with undergraduate co-authors over the course of two summers, but I took the lead in continuing the work and writing the manuscript with supervisor Nathan Tintle after the conclusion of our summer research program. This paper has 4 citations.

4. Browning, S.R., **Grinde, K.**, Plantinga, A., Gogarten, S.M., Stilp, A.M., Kaplan, R.C., Avilés-Santa, L., Browning, B.L., & Laurie, C.C. "Local ancestry inference in a large US-based Hispanic/Latino study: Hispanic Community Health Study/Study of Latinos (HCHS/SOL)." *G3: Genes|Genomes|Genetics* 6.6 (2016): 1525–1534.

   Presents results and lessons learned from inferring local ancestry in a large study of Hispanics/Latinos, including a comparison of different approaches for local ancestry inference on chromosome X. Appears in the journal *G3: Genes|Genomes|Genetics*, an open access journal affiliated with the Genetics Society of America (along with its companion journal, *GENETICS*). *G3*'s current impact factor is 3.154. I contributed all portions of the paper (methods development, data analysis, writing) related to chromosome X. Citations: 55.

3. Greco, B., Hainline, A., Arbet, J., **Grinde, K.**, Benitez, A., & Tintle, N. "A general approach for combining diverse rare variant association tests provides improved robustness across a wider range of genetic architectures." *European Journal of Human Genetics* 24 (2016): 767–773.

   Proposes a method to combine gene-based tests (e.g., burden tests, variance components tests) that perform well in different settings to improve power across a wider range of scenarios. Appears in the *European Journal of Human Genetics* (EJHG), the official journal of the European Society of Human Genetics. EJHG has an impact factor of 4.246 and ranks 60th (out of 175) in genetics and heredity and 126th (out of 298) in biochemistry and molecular biology according to Journal Citation Reports. I assisted with the simulation studies, figure creation, and writing, but was brought onto the project after the methods had been developed. Cited 12 times since publication in 2016.

2. Green, A., Cook, K., **Grinde, K.**, Valcarcel, A., & Tintle, N. "A general method for combining different family-based rare-variant tests of association to improve power and robustness of a wide range of genetic architectures." *BioMed Central Proceedings* 10.7.23 (2016): 165–170.

   Similar to Greco et al., 2016 but with a focus on combining family-based tests that account for relatedness across individuals. Appears in *BioMed Central (BMC) Proceedings* as part of the conference proceedings for the 19th Genetic Analysis Workshop, a conference focused on evaluating and comparing statistical methods using a common dataset across

all participants. I assisted with initial data processing, but did not take a leading role in methods development or simulation studies. This paper has 4 citations.

1. Valcarcel, A., **Grinde, K.**, Cook, K., Green, A., & Tintle, N. "A multistep approach to single nucleotide polymorphism–set analysis: An evaluation of power and type I error of gene-based tests of association after pathway-based association tests." *BioMed Central Proceedings* 10.7.16 (2016): 349–355.

   Proposes and evaluates a multi-step approach for conducting genetic association tests: first at the higher-level pathway level, and then at the finer-scale gene level. Appears in *BioMed Central (BMC) Proceedings* as part of the conference proceedings for the 19th Genetic Analysis Workshop (see also Green et al., 2016). I contributed to methods development, simulation studies, and writing jointly with the first-author Alessandra Valcarcel. Has received 1 citation since publication.

Published Abstracts

1. Jensen-Otsu, E., **Grinde, K.**, Baxi, A., Harms, M., Teng, B., Strate, L.L., & Ko, C.W. "Anesthesia professional-delivered sedation is associated with similar outcomes compared to nurse administered sedation in patients admitted with acute upper gastrointenstinal bleeding." *Gastrointenstinal Endoscopy* 87.6S (2018): AB418–AB419.

   Compares upper endoscopy surgery outcomes between patients whose anethesia was administered by a nurse versus an anesthesiologist. Published in *Gastrointenstinal Endoscopy*, a journal focused on endoscopic procedures with an impact factor of 9.427. This abstract is the result of a consulting project with physician Elsbeth Jensen-Otsu — I conducted all statistical analyses and contributed to the writing. In some areas of medicine, conference abstracts are the primary form of disseminating scholarship.

Other Writing

1. Heggeseth, B., Myint, L., & **Grinde, K.** "Stat 155 Notes." Online text (2021): https://bcheggeseth.github.io/Stat155Notes/.

   Online, open-source textbook for *STAT 155: Introduction to Statistical Modeling*. My colleagues Brianna Heggeseth and Leslie Myint created the first draft of this text, but I have contributed to updates to notation and organization since then.

SUBMITTED MANUSCRIPTS

1. Barragan, F.*, Mills, L., Raduski, A., Marcotte, E., **Grinde, K.**, Spector, L., & Williams, A. "Genetic ancestry, differential gene expression, and survival in pediatric b-cell acute lymphoblastic leukemia." Submitted to *Cancer*.

   Investigates associations between genetic ancestry, gene expression, and survival in children with b-cell acute lymphoblastic leukemia. Submitted to the journal *Cancer* (impact factor 6.860) in June 2022. I advised Macalester student Freddy Barragan in all aspects concerning genetic ancestry, as well as figure creation and writing. As the paper was just submitted recently, we are still awaiting review. A version of this work, with more emphasis on statistical methodology, was published in April 2022 as Freddy's Honors Thesis.

MANUSCRIPTS IN PROGRESS

1. **Grinde, K.**, Browning, B., & Browning, S. "Adjusting for principal components can induce spurious associations in genome-wide association studies."

   Compares methods for controlling for ancestral heterogeneity in genome-wide association studies and demonstrates potential pitfalls of widely-used approaches based on principal component analysis. All analyses are finished and writing is nearly complete, with the goal of submitting in Summer 2022 to the *American Journal of Human Genetics*, a top journal in genetics. I designed and implemented the simulations studies, derived theoretical results, and have taken the lead role in writing the manuscript.

SOFTWARE

2. Huang, Z.*, & **Grinde, K.** "Significance Threshold Estimation for Admixture Mapping using `Rcpp`." R package (2020): https://github.com/GrindeLab/STEAMcpp.

   A faster version of the `STEAM` package (see below) that uses `Rcpp` to integrate R and C++ code. Available via GitHub, a popular website for version control and collaborative software development, and one of the primary sites for sharing code/software with others. I advised Macalester student Zuofu Huang in the creation of this package.

1. **Grinde, K.** "`STEAM`: Significance Threshold Estimation for Admixture Mapping." R package (2019): https://github.com/kegrinde/STEAM.

   An open-source R package that estimates the generations since admixture and genome-wide significance thresholds for admixture mapping studies (see Grinde et al., 2019). Also available on GitHub. I created, and now maintain, this package individually.

RESEARCH TALKS

Presentations at International or National Venues

10. Adjusting for principal components can induce spurious associations in genome-wide association studies in admixed populations. International Genetic Epidemiology Society Annual Meeting. Virtual. 2021. (Presentation Award Winner)
9. Deriving significance thresholds for genome-wide admixture mapping studies. International Genetic Epidemiology Society Annual Meeting. San Diego, CA. 2018.
8. Controlling for multiple testing in genome-wide admixture mapping studies. Western North American Region of the International Biometric Society Meeting. Edmonton, Canada. 2018. (Presentation Award Winner)
7. Admixture mapping: controlling for false positives in the presence of population structure. American Society of Human Genetics Annual Meeting. Orlando, FL. 2017. (Poster)
6. Generalizing genetic risk scores from Europeans to Hispanics/Latinos. International Genetic Epidemiology Society Annual Meeting. Cambridge, United Kingdom. 2017. (Poster)
5. Illustrating, quantifying, and correcting for bias in post-hoc analysis of gene-based rare variant tests of association. Joint Statistical Meetings. Seattle, WA. 2015. (Poster)
4. A hierarchical approach to SNP-set analysis: an evaluation of power and type I error of gene-based tests of association after pathway-based analysis. Genetic Analysis Workshop 19. Vienna, Austria. 2014.
3. Accounting for variability in paleoecological mixing models. National Conference for Undergraduate Research. Lexington, KY. 2014.
2. What now? Post-hoc approaches for gene-based, rare variant tests of association. American Society of Human Genetics Annual Meeting. Boston, MA. 2013. (Poster)
1. General approaches for combining multiple rare variant association tests provide improved power across a wider range of genetic architectures. American Society of Human Genetics Annual Meeting. Boston, MA. 2013. (Poster)

Presentations at Regional or Local Venues

21. What's our work: statistical genetics. Macalester College Mathematics, Statistics, and Computer Science Seminar. Saint Paul, MN. 2021.
20. Genome-wide significance thresholds for admixture mapping studies. University of Minnesota Interdisciplinary Biostatistics Training in Genetics and Genomics Journal Club. Virtual. 2021. (Invited)
19. Statistical genetics in populations with mixed ancestry. Augsburg University Mathematics Colloquium. Virtual. 2020. (Invited)

18. Statistical methods for genome-wide admixture mapping studies. University of Minnesota Division of Pediatric Epidemiology and Clinical Research. Virtual. 2020. (Invited)
17. Statistical genetics in populations with mixed ancestry. Macalester College Department of Mathematics, Statistics, and Computer Science. Saint Paul, MN. 2019. (Invited)
16. Statistial inference in populations with mixed ancestry. Department of Mathematics, Statistics, and Computer Science, St. Olaf College. Northfield, MN. 2019. (Invited)
15. Adjusting for principal components can induce spurious associations in genome-wide association studies. Genetic Analysis Center. Seattle, WA. 2019. (Invited)
14. Adjusting for population structure in genetic association studies: new insights and the potential pitfalls of using PCs. University of Washington Popgen Lunch. Seattle, WA. 2019. (Invited)
13. Statistical inference in populations with mixed ancestry. University of Washington Biostatistics Colloquium. Seattle, WA. 2018. (Invited)
12. Admixture mapping in TOPMed. NHLBI Trans-Omics for Precision Medicine (TOPMed) Kidney Working Group. Virtual. 2018.
11. Admixture mapping: controlling for false positives in the presence of population structure. Biostatistics Department Retreat, University of Washington. Seattle, WA. 2017. (Poster)
10. Issues in implementation of local ancestry inference on the X chromosome. Omics in Latinos Genetic Analysis Center Meeting. Seattle, WA. 2015.
9. Estimating genetic maps with large data sets. Biostatistics Department Retreat, University of Washington. Blaine, WA. 2015. (Poster)
8. Identifying and correcting for bias in post-hoc ranking strategies: an application to gene-based rare variant tests of association. Dordt College Summer Seminar. Sioux Center, IA. 2014.
7. A hierarchical approach to SNP-set analysis: evaluation of power and type I error of gene-based tests of association after pathway-based analysis. Dordt College Summer Seminar. Sioux Center, IA. 2014.
6. Identifying and correcting for bias in post-hoc ranking strategies: an application to gene-based rare variant tests of association. University of Michigan Department of Biostatistics. Ann Arbor, MI. 2014.
5. A hierarchical approach to SNP-set analysis: evaluation of power and type I error of gene-based tests of association after pathway-based analysis. University of Michigan Department of Biostatistics. Ann Arbor, MI. 2014.
4. What now? Post-hoc approaches for gene-based, rare variant tests of association. Great Plains R-Users Group Conference. Sioux Center, IA. 2014. (Poster)
3. Accounting for variability in paleoecological mixing models. St. Olaf Natural Sciences and Mathematics Honors' Day Poster Session. Northfield, MN. 2014. (Poster)
2. Predicting donors at Red Cross blood drives. St. Olaf Mathematics, Statistics, and Computer Science Colloquium. Northfield, MN. 2014.
1. Predicting donors at Red Cross blood drives. American Red Cross. Saint Paul, MN. 2014.

Student Presentations of Joint Work

6. Barragan, F. Genetic ancestry, gene expression, and survival in children with B-ALL. Pediatric Research, Education, & Scholarship Symposium. Minneapolis, MN. 2022. (Poster)

5. Barragan, F. Gene expression differences by race and genetic ancestry in B-cell acute lymphoblastic leukemia. American Society of Human Genetics Annual Meeting. Virtual. 2021. (Poster)
4. Barragan, F. Characterizing racial disparities in pediatric cancer: ancestry, gene expression, and survival disparities in B-cell acute lymphoblastic leukemia. Underrepresented Students in STEM Symposium. Minneapolis, MN. 2021. (Poster)
3. Barragan, F. Statistical methods for pediatric leukemia: gene expression & ancestry in B-cell acute lymphoblastic leukemia. Macalester Summer Research Showcase. Saint Paul, MN. 2021. (Poster)
2. Huang, Z. Statistical methods for genetic association studies in populations with mixed ancestry. Midstates Consortium Research Symposium. Virtual. 2020.
1. Huang, Z. Using Rcpp to speed up tool for controlling for multiple testing in genetic studies. Electronic Undergraduate Statistics Research Conference. Virtual. 2020.

MENTORING, TEACHING, & OUTREACH TALKS

Presentations at International or National Venues

2. Time management, research strategy, and healthy habits for graduate students. American Statistical Association Section on Statistics in Genomics and Genetics. Virtual. 2021. (Invited)
1. Graduate programs in (bio)statistics. Electronic Undergraduate Statistics Research Conference. Virtual. 2020. (Invited)

Presentations at Regional or Local Venues

16. Keynotes: studies, statistics, and serial killers. The Abstract Podcast. Virtual. 2021. (Invited)
15. Inclusivity in teaching panel. Radical MacACCESS, Macalester College. Virtual. 2021. (Invited)
14. Pathways into science outreach panel. Fred Hutchinson Cancer Research Center Hutch United Outreach Committee & Wallin Education Partners Program. Virtual. 2021. (Invited)
13. Genetic testing: how does it work? (a statistician's perspective). Department of Mathematics, Statistics, and Computer Science, St. Olaf College. Northfield, MN. 2019. (Invited)
12. (Bio)statistics PhD programs: application tips and research opportunities. St. Olaf College Biostatistics Class. Northfield, MN. 2019. (Invited)
11. Fellowships, scholarships, and grants. University of Washington Biostatistics Student Seminar. Seattle, WA. 2018.
10. Admixture mapping: controlling for false positives in the presence of population structure. StatNorthwest. Seattle, WA. 2018. (Poster)
9. Graduate student panel. StatNorthwest. Seattle, WA. 2018.
8. Travel grants and conference funding. University of Washington Department of Biostatistics. Seattle, WA. 2017.
7. What is Biostatistics? Forest Ridge School of the Sacred Heart Science Research Class. Bellevue, WA. 2017.
6. NSF Graduate Research Fellowship Program information session. University of Washington Department of Biostatistics. Seattle, WA. 2017.
5. What is Biostatistics? 7th and 8th Grade STEM PREP Project. Seattle, WA. 2017.
4. Applying for outside funding opportunities. University of Washington Biostatistics Student Seminar. Seattle, WA. 2016.

3. Graduate and professional student panel. Healthcare Exploration for Youth Program. Seattle, WA. 2016. (Invited)
2. Graduate and professional student panel. Healthcare Exploration for Youth Program. Seattle, WA. 2015. (Invited)
1. What now? Post-hoc approaches for gene-based, rare variant tests of association. Inter-Disciplinary Explorations Across the Sciences. Sioux Center, IA. 2014. (Poster)

HONORS & AWARDS

Professional Awards and Recognition

- Poster/Lightning Talk Award, 2nd Place — 2021
  International Genetic Epidemiology Society Annual Meeting
- Top Cited Article — 2021
  Genetic Epidemiology Journal
- Thomas R. Fleming Excellence in Biostatistics Award — 2019
  University of Washington Department of Biostatistics
  (highest honor awarded to a graduating Ph.D. student)
- Gertrude M. Cox Scholarship — 2018
  American Statistical Association
  (national scholarship for women pursuing graduate studies in statistics)
- Dorothy L. Simpson Leadership Award — 2018
  Achievement Rewards for College Scientists Foundation, Seattle Chapter
  (first recipient of this award recognizing leadership and community service)
- Excellence in Teaching Award — 2018
  University of Washington Department of Biostatistics
- Distinguished Oral Presentation Award — 2018
  Western North American Region of the International Biometric Society
- Achievement Rewards for College Scientists (ARCS) Fellowship — 2014–2017
  ARCS Foundation, Seattle Chapter
- Donovan J. Thompson Award — 2016
  University of Washington Department of Biostatistics
  (awarded to student with best score on Ph.D. qualifying exams)

Grants and Other Research Funding

- Collaborative Summer Research Award — 2020
  Macalester College
- Graduate Research Fellowship — 2016–2019
  National Science Foundation
- Travel Grant — 2018
  University of Washington Graduate and Professional Student Senate
- Conference Travel Award — 2018
  University of Washington Department of Biostatistics
- Travel Award — 2017
  University of Washington Graduate School Fund for Excellence and Innovation
- Statistical Genetics Training Grant — 2015–2016
  National Institutes of Health

Undergraduate Awards

- Undergraduate Research Project Competition Honorable Mention — 2014
  Consortium for Advancement of Undergraduate Statistics Education

- Statistically Significant Award 2014
  St. Olaf College
  (awarded to one graduating statistics student)
- Buntrock Scholarship 2010–2014
  St. Olaf College
  (top academic scholarship at St. Olaf)
- Service Leadership Scholarship 2010–2014
  St. Olaf College
- Phi Beta Kappa National Honor Society 2013
- Pi Mu Epsilon National Honor Society 2013
  (mathematics honor society)

SERVICE

Membership in Professional Societies

- Caucus for Women in Statistics (CWS) 2018–present
- International Genetic Epidemiology Society (IGES) 2016–present
- American Society of Human Genetics (ASHG) 2013–present
- American Statistical Association (ASA) 2013–present
- Western North American Region (WNAR) of the International Biometric Society (IBS) 2015–2019

Working Groups

- Kidney Working Group 2018–2021
  Trans-Omics for Precision Medicine Whole Genome Sequencing Program
- Dental Genetics Working Group 2016
  Hispanic Community Health Study/Study of Latinos

Journal Editorial Board Positions and Peer Review

- Review Editor for the *Statistical Genetics and Methodology* section of *Frontiers in Genetics* 2021–present
- Peer-Reviewer for *GENETICS*, *PLOS Computational Biology*, *Scientific Reports*, and *SIAM Undergraduate Research Online* 2018–present

Macalester College Service

- Team Member, AAC&U Open Educational Resources Institute 2022–present
- Co-Creator and Coordinator, MSCS Honors Seminar 2021–present
- Mentor, DataFest 2021, 2022
- Member, Statistics Visiting/Postdoc Search Committee 2020–2022
- Scribe, Mid-Course Interview 2021
- ~~Scribe, Mid-Course Interview~~ (canceled due to COVID-19) 2020

University of Washington Department of Biostatistics Service

- Member, Diversity Committee 2017–2019
- Leadership Team, Women in Biostatistics and Statistics 2017–2018
- Member, Admissions Committee 2017–2018
- Founding Member, Peer Mentoring Program 2016–2018
- Member, Educational Policy and Teaching Evaluation Committee 2016–2017

- Member, Biostatistics Outreach Working Group 2015

St. Olaf College Service

- President, Spanish Honor House 2013–2014
- Volunteer Teaching Assistant & Tutor, Northfield Public Schools 2011–2014
- Volunteer Teaching Assistant, Wayzata High School 2011

ADVISING

Academic Advisor

- Marshall Roll 2022–present
- Michael Nadeau 2022–present
- Kristy Ma 2022–present
- Eli Ivanov 2022–present
- Yunyang Zhong 2020–2022

Capstone Advisor

(×2) denotes a double major (i.e., two talks were supervised)

- Chen Yu, Freddy Barragan, Jasper Corey-Flatau, Kate Liberko (×2), Isabella Light, Roman Bactol 2022
- Corey Pieper (×2), Jack Tan (×2), Liam Purkey, Redi Kurti (×2) 2021
- Blair Cha, Christina Cai, Quinn Rafferty, Sofia Pozsonyiova 2020

Honors Thesis Advisor

- Freddy Barragan. Statistical genetics for pediatric leukemia: characterizing racial disparities in pediatric acute lymphoblastic leukemia. 2022
- Zuofu Huang. Estimating significance thresholds and the number of generations since admixture in admixture mapping studies. 2021

Honors Thesis Committee Member

- Zhaoheng Li. A comparison of stacking methods to estimate survival using residual lifetime data from prevalent cohort studies. 2022

Internship Faculty Supervisor

- Connie Zhang 2021
- Freddy Barragan 2021

Summer Research Supervisor

- Freddy Barragan 2021
  (funded by the Mann-Hill Fellowship for Student-Faculty Research)
- Zuofu Huang 2020
  (funded by a Macalester Collaborative Summer Research Award)

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