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

- STAT 494: Statistical Genetics (1 section) 2022
- MATH/STAT 455: Mathematical Statistics (3 sections) 2020–present
- STAT 155: Introduction to Statistical Modeling (11 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
  (Intermediate Spanish I & II, Calculus I, Abstract Algebra I)
- Urban Schools and Communities Program, Participant 2012
- Department of Mathematics, Statistics, and Computer Science, Tutor 2011
  (Calculus I & II, Multivariable Calculus)

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.

    This paper is a collaboration with Macalester student Abdullgadir (AK) Hayir and researchers in the Department of Veterinary and Biomedical Sciences at the University of Minnesota. AK and I assisted with data visualization, creating one of the main figures in the paper (Figure 6) as well as an interactive version of the visualization that is available online [link]. This work appears in a special issue (*Next-Generation Technologies to Understand Mechanisms of Virus Infections*) of the journal *Viruses*, an Open Access journal of virology that is affiliated with numerous professional societies in the field (e.g., the American Society for Virology). *Viruses* has an impact factor of 5.712 and is in the top quartile of journals in infectious diseases (source: Scopus). As of August 11, 2022, this paper has 1 citation (source: Google Scholar).

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. "Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI Trans-Omics for Precision Medicine (TOPMed) consortium." *eBioMedicine* 63 (2021): 103157.

    This paper is a collaboration with the TOPMed Kidney Working Group and an application of some of the methods proposed in my graduate dissertation. I am a joint first-author on this paper. I designed, conducted analyses, and wrote all portions of the paper related to local ancestry inference, admixture mapping, and ancestry-specific allele frequency estimation. This work 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. *eBioMedicine* has an impact factor of 7.813 and is in the top 10 percent of journals in genetics and molecular biology (source: Scopus). As of August 11, 2022, this paper has 5 citations (source: 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.

    This paper is a collaboration with the TOPMed Hematology & Hemostasis Working Group and an application of some of the methods proposed in my graduate dissertation. I helped with the design, analyses, and writing of the portions of the paper related to admixture mapping. This work appears in the *Journal of Thrombosis and Haemostasis* (JTH), which is the official journal of the International Society on Thrombosis and Haemostasis. JTH has an impact factor of 13.274 and is in the top 5 percent of journals in hematology (source: Scopus). As of August 11, 2022, this paper has 13 citations (source: Google Scholar).

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.

    This paper presents results from an international collaboration to conduct a meta-analysis of genome-wide association studies (GWAS) of dental diseases and traits. I first conducted GWAS in collaboration with the Hispanic Community Health Study/Study of Latinos (HCHS/SOL) Dental Working Group and then contributed our HCHS/SOL results to this larger meta-analysis effort led by Dmitry Shungin. This work appears in *Nature Communications*, an Open Access journal that publishes work across the sciences and is part of the prestigious *Nature Research* portfolio of journals. *Nature Communications* has an impact factor of 15.405 and is ranked third among multidisciplinary journals (preceded only by *Nature* and *Science*) and fifth among journals in genetics and molecular biology (source: Scopus). As of August 11, 2022, this is my top-cited paper, with 104 citations (source: Google Scholar).

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.

    This paper proposes methods to address departures from normality in genetic association studies. The methods development was motivated in part by the analysis that I conducted in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL) for refereed journal article [9]. The HCHS/SOL analysis serves as one of the illustrative examples included in this paper. This work appears in *Genetic Epidemiology*, the official journal of the International Genetic Epidemiology Society. *Genetic Epidemiology* has an impact factor of 2.4 (source: Scopus) and is a primary journal for publishing work in statistical genetics. As of August 11, 2022, this paper has 43 citations (source: Google Scholar).

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.

    This paper proposes methods for estimating the number of generations since admixture and the genome-wide significance threshold for admixture mapping studies. It represents one of the major projects of my graduate dissertation. I developed the methods, derived the theoretical results, conducted all analyses (with the exception of local ancestry inference, which was conducted by my co-author Lisa Brown), and wrote the paper. This work

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 9.318 and ranks in the top five percent of journals in genetics and molecular biology (source: Scopus). As of August 11, 2022, this paper has 22 citations (source: Google Scholar).

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.

   This paper proposes and evaluates methods for constructing polygenic risk scores in admixed populations. Along with senior author Tamar Sofer, I was the primary contributor to the methods development, data analyses, simulation studies, and writing. This work appears in *Genetic Epidemiology*, the official journal of the International Genetic Epidemiology Society (IGES). *Genetic Epidemiology* has an impact factor of 2.4 (source: Scopus) and is a primary journal for publishing work in statistical genetics. This paper was selected as the "IGES Communication Committee Highlight" from its issue of *Genetic Epidemiology* and is among the journal's ten most highly cited recent articles (source: Top-cited *Genetic Epidemiology* Articles [link]). As of August 11, 2022, this is my top-cited first-author paper, with 70 citations (source: Google Scholar).

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.

   This paper proposes methods to address the phenomenon of *winner's curse* when estimating genetic effect sizes after gene-based testing. Initial analyses, simulation studies, and methods development were conducted collaboratively with fellow undergraduate coauthors. I took the lead in continuing the work and writing the manuscript with supervisor Nathan Tintle after the conclusion of the summer undergraduate research program. This work 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. *Frontiers in Genetics* has an impact factor of 4.365 and ranks in the second quartile of journals in genetics and molecular biology (source: Scopus). As of August 11, 2022, this paper has 4 citations (source: Google Scholar).

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.

   This paper presents methods and results related to inferring local ancestry in a large study of Hispanics/Latinos. It includes a comparison of methods for local ancestry inference on chromosome X that stems from my graduate dissertation. I contributed all portions of the paper (methods development, data analysis, writing) related to chromosome X. This work appears in the journal *G3: Genes|Genomes|Genetics*, an Open Access journal affiliated with the Genetics Society of America (along with its highly-ranked companion journal, *GENETICS*). *G3* has an impact factor of 3.083 and ranks in the second quartile of journals in genetics and molecular biology (source: Scopus). As of August 11, 2022, this paper has 55 citations (source: Google Scholar).

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.

   This paper proposes methods to combine different types of gene-based tests to improve power across a wide range of scenarios. I began this work as an undergraduate research assistant, contributing to the simulation studies and data visualization, and then continued my work after the conclusion of the summer research program to assist with manuscript writing and editing. This work 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 4.706 and ranks in the top quartile of journals in genetics and molecular

biology (source: Scopus). As of August 11, 2022, this paper has 12 citations (source: Google Scholar).

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.

   This paper stems from refereed article [3], with a particular focus on tests that account for relatedness across individuals. I advised on methods development and assisted with initial data cleaning. This work 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. *BMC Proceedings* has an impact factor of 2.067 (source: Scopus). As of August 11, 2022, this paper has 4 citations (source: Google Scholar).

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.

   This paper proposes a multi-step method for conducting genetic association tests (first at the higher-level pathway level, and then at the gene level) and stems from the same undergraduate research program as refereed journal articles [2], [3], and [5]. Although it is not listed as such, I contributed to methods development, simulation studies, and writing jointly with the first author Alessandra Valcarcel. This work appears in *BioMed Central (BMC) Proceedings* as part of the conference proceedings for the 19th Genetic Analysis Workshop. *BMC Proceedings* has an impact factor of 2.067 (source: Scopus). As of August 11, 2022, this paper has 1 citation (source: Google Scholar).

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.

   This abstract is the result of a consulting project with physician Elsbeth Jensen-Otsu to compare upper endoscopy surgery outcomes between patients whose anesthesia was administered by a nurse versus an anesthesiology. I conducted all statistical analyses and contributed to the writing of methods and results. This work is published in *Gastrointenstinal Endoscopy*, a journal focused on endoscopic procedures. *Gastrointenstinal Endoscopy* has an impact factor of 3.943 and ranks in the top ten percent of journals in gastroenterology (source: Scopus). In some areas of medicine, conference abstracts (rather than journal articles) are a primary vehicle for disseminating scholarship.

Open Education Resources

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

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

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." In revision at *Cancer Medicine*.

   This paper is a collaboration with Macalester student Freddy Barragan and investigators in the Division of Epidemiology and Clinical Research at the Unviersity of Minnesota. I advised Macalester student Freddy Barragan in all aspects of the project concerning

genetic ancestry, as well as general figure creation and writing. We have received initial reviews and are in the process of revising the manuscript for re-submission. This work is in revision at *Cancer Medicine*, an Open Access journal that publishes work related to cancer research, biology, and prevention, as well as bioinformatics. *Cancer Medicine* has an impact factor of 4.548 and ranks in the top quartile of oncology journals and second quartile of journals in cancer research (source: Scopus). A version of this work, with additional emphasis on statistical methodology, was included in Freddy's Honors Thesis (successfully defended April 2022).

MANUSCRIPTS IN PROGRESS

2. Horimoto, A., Boyken, L., Blue, E., **Grinde, K.**, Nafikov, R., Sohi, H., Nato, A., Bis, J., Brusco, L., Morelli, L., Ramirez, A., Dalmasso, C., ..., Mayeux, R., Browning, S., Seshadri, S., Wijsman, E., & Thornton, T. "Admixture mapping implicates *LIG4*, *MYO16*, and *FAM155A* at 13q33.3 as ancestry-of-origin loci for Alzheimer's disease in multiplex U.S. Caribbean Hispanic Families."

   This paper proposes a method for conducting admixture mapping studies with a binary trait and applies the method to a study of Alzheimer's disease. I consulted on various aspects of the methods used in this paper, including genetic ancestry inference, model design, and adjustment for multiple testing. All analyses are complete and a draft of the manuscript has been circulated to co-authors for final checks before submission. I anticipate that we will submit the paper sometime in the next month or so.

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

   This paper stems from the final project of my graduate dissertation. It 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. I conducted all data analyses, designed and implemented the simulations studies, derived theoretical results, and wrote the manuscript. All analyses are complete and a draft of the manuscript has been approved by my co-authors. The paper uses data from the Women's Health Initiative (WHI) and Trans-Omics for Precision Medicine (TOPMed) studies, both of which require that manuscripts be submitted to their publications committee prior to journal submission. Our paper is currently under review by the WHI publications committee and will be submitted to TOPMed shortly. Upon approval from both studies, we will submit the paper to the *American Journal of Human Genetics*, a top journal in genetics.

SOFTWARE

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

   This is a faster version of the `STEAM` package (see below) that uses `Rcpp` to integrate R and C++ code. The package was created in collaboration with Macalester student Zuofu Huang. It is 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.

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

   This is an open-source R package that implements the methods proposed in refereed journal article [7]. I am the sole creator and maintainer of this package. Like `STEAMcpp`, this R package is also available on GitHub.

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

22. ~~Statistical genetics in populations with mixed ancestry. Creighton University Department of Mathematics. Omaha, NE. 2021. (Invited)~~ (postponed to 2022 due to illness)
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/Supervised 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. **(Invited)**
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
  (for International Research Talk [10])
- Top Cited Article — 2021
  Genetic Epidemiology Journal
  (for Refereed Journal Article [6])
- 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
  (for International Research Talk [8])
- 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

- Member, Statistics Tenure Track Search Committee 2022–present
- 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

- Alayna Johnson 2022–present
- Marshall Roll (primary) 2022–present
- Michael Nadeau (primary) 2022–present
- Kristy Ma 2022–present
- Eli Ivanov (primary) 2022–present
- Yunyang Zhong (primary) 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
  (funded by NIH Research Supplement to Promote Diversity in Health-Related Research)
- 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 Mann-Hill Fellowship for Student-Faculty Research)
- Zuofu Huang 2020
  (funded by Macalester Collaborative Summer Research Award)

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