

Kelsey E. Grinde

CONTACT	Mathematics, Statistics, & Computer Science Macalester College 1600 Grand Avenue Saint Paul, MN 55105	kgrinde@macalester.edu (651)-696-6976 kegrinde.github.io
EDUCATION	Ph.D. in Biostatistics University of Washington, Seattle, WA Dissertation: <i>Statistical inference in admixed populations</i> Advisor: Sharon Browning, Ph.D.	2019
	B.A. in Mathematics , Concentration in Statistics St. Olaf College, Northfield, MN Graduated <i>summa cum laude</i> with Distinction in Statistics Advisor: Paul Roback, Ph.D.	2014
WORK EXPERIENCE	Assistant Professor Department of Mathematics, Statistics, & Computer Science Macalester College, Saint Paul, MN	2020–present
	Postdoctoral Teaching Fellow Department of Mathematics, Statistics, & Computer Science Macalester College, Saint Paul, MN	2019–2020
	Graduate Research Assistant Browning Statistical Genetics Lab University of Washington, Seattle, WA	2014–2019
	Graduate Research Assistant Genetic Analysis Center University of Washington, Seattle, WA	2015–2016
	Undergraduate Research Assistant Summer Research Program in Statistical Genetics & Biostatistics Dordt College, Sioux Center, IA	2013, 2014
	Undergraduate Research Fellow Center for Interdisciplinary Research St. Olaf College, Northfield, MN	2013–2014
TEACHING EXPERIENCE	Macalester College <ul style="list-style-type: none">• STAT 155: Introduction to Statistical Modeling (13 sections)• MATH/STAT 455: Mathematical Statistics (4 sections)• STAT 494: Statistical Genetics (1 section)	2019–2023 2020–2023 2022
	University of Washington <ul style="list-style-type: none">• BIOST 311: Regression Methods in the Health Sciences, Co-Instructor• BIOST 310: Biostatistics for the Health Sciences, Teaching Assistant• BIOST 561: Computational Skills for Biostatistics, Guest Lecturer	2018 2017 2017

- BOST 550: Statistical Genetics I, Guest Lecturer 2017
- BOST 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

- Horimoto, A., Boyken, L., Blue, E., **Grinde, K.**, Nafikov, R., Sohi, H., Nato, A., Bis, J., Brusco, L., Morelli, L., Ramirez, A., Dalmasso, M., Temple, S., Satizabal, C., 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 disease in Hispanic and Latino populations.” *HGG Advances* 4.3 (2023): 1000207. [\[link\]](#)
- 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.” *Cancer Medicine* 12.4 (2023): 4761–4772. [\[link\]](#)
- 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. [\[link\]](#)
- 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. [\[link\]](#)
- 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. [\[link\]](#)

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. [\[link\]](#)
8. Sofer, T., Zheng, X., Gogarten, S.M., Laurie, C.A., **Grinde, K.**, Shaffer, J.R., Shungin, D., O’Connell, J.R., Durazo-Arviso, R.A., Raffield, L., Lange, L., Musani, S., Vasani, 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. [\[link\]](#)
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. [\[link\]](#)
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. [\[link\]](#)
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. [\[link\]](#)
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. [\[link\]](#)
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. [\[link\]](#)
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. [\[link\]](#)
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. [\[link\]](#)

Refereed 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 gastrointestinal bleeding.” *Gastrointestinal Endoscopy* 87.6S (2018): AB418–AB419. [\[link\]](#)

Open Education Resources

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

SUBMITTED MANUSCRIPTS

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

SOFTWARE & APPLICATIONS

3. Hayir, A. *, & **Grinde, K.** “Interactive Circos Tool.” R shiny application (2022): <https://kblcircosgraph.shinyapps.io/circos/>
2. Huang, Z. *, & **Grinde, K.** “Significance Threshold Estimation for Admixture Mapping using Rcpp.” R package (2020): <https://github.com/GrindeLab/STEAMcpp>.
1. **Grinde, K.** “STEAM: Significance Threshold Estimation for Admixture Mapping.” R package (2019): <https://github.com/kegrinde/STEAM>.

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

23. Statistical methods for genetic studies in admixed populations. Carleton College Math/Stats Colloquium. Northfield, MN. 2023. (**Invited**)
22. Statistical genetics in populations with mixed ancestry. Creighton University Department of Mathematics. Omaha, NE. 2022. (**Invited**)
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. Statistical 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

7. Barragan, F. Genetic ancestry, gene expression, and survival in children with B-ALL. Pediatric Research, Education, & Scholarship Symposium. Minneapolis, MN. 2022. (Poster)
6. 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)
5. 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)
4. 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)
3. Huang, Z. Statistical methods for genetic association studies in populations with mixed ancestry. Midstates Consortium Research Symposium. Virtual. 2020.
2. Huang, Z. Using Rcpp to speed up tool for controlling for multiple testing in genetic studies. Electronic Undergraduate Statistics Research Conference. Virtual. 2020.
1. Huang, Z.* "Statistical methods for genetic association studies in populations with mixed ancestry." Macalester Summer Research Showcase. Virtual. 2020. (Poster)

TEACHING, OUTREACH, & MENTORING TALKS

Presentations at International or National Venues

4. Panel discussion on academic careers and job search. American Statistical Association Section on Statistics in Genomics and Genetics. Virtual. 2023. **(Invited)**
3. Rethinking (and then rethinking some more) grading systems in introductory and advanced statistics courses. Joint Statistical Meetings. Toronto, Canada. 2023. **(Invited)**
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

20. Career discussion. Gender Minorities in Math and Statistics (GeMMS), Carleton College. Northfield, MN. 2024. **(Invited)**
19. Alternative grading strategies. MSCS Inclusive Pedagogy Summit, Macalester College. St. Paul, MN. 2023. **(Invited)**
18. Faculty panel. Preparing Future Faculty Practicum, University of Minnesota. Virtual. 2023. **(Invited)**
17. Tips and tricks with R/RStudio. MSCS Student Advisory Board Skill-Building Sessions, Macalester College. St. Paul, MN. 2023. **(Invited)**
16. Open Educational Resources and textbook affordability: Macalester environmental scan and survey results. Jan Serie Center for Scholarship and Teaching, Macalester College. St. Paul, MN. 2023.
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 (for International Research Talk [10]) 2021
International Genetic Epidemiology Society Annual Meeting
- Top Cited Article (for Refereed Journal Article [6]) 2021
Genetic Epidemiology Journal
- Thomas R. Fleming Excellence in Biostatistics Award 2019
University of Washington Department of Biostatistics
- Gertrude M. Cox Scholarship 2018
American Statistical Association
- Dorothy L. Simpson Leadership Award 2018
Achievement Rewards for College Scientists Foundation, Seattle Chapter
- Excellence in Teaching Award 2018
University of Washington Department of Biostatistics
- Distinguished Oral Presentation Award (for International Research Talk [8]) 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 (for best score on Ph.D. qualifying exams) 2016
University of Washington Department of Biostatistics

Grants and Other Research Funding

- Article Processing Charge Grant (for Refereed Journal Article [12])
Macalester College Dewitt Wallace Library Open Access Fund 2022
- Collaborative Summer Research Award
Macalester College 2020
- Graduate Research Fellowship
National Science Foundation 2016–2019
- Travel Grant
University of Washington Graduate and Professional Student Senate 2018
- Conference Travel Award
University of Washington Department of Biostatistics 2018
- Travel Award
University of Washington Graduate School Fund for Excellence and Innovation 2017
- Statistical Genetics Training Grant
National Institutes of Health 2015–2016

Undergraduate Awards

- Undergraduate Research Project Competition Honorable Mention
Consortium for Advancement of Undergraduate Statistics Education 2014
- Statistically Significant Award
St. Olaf College 2014
- Buntrock Scholarship
St. Olaf College 2010–2014
- Service Leadership Scholarship
St. Olaf College 2010–2014
- Phi Beta Kappa National Honor Society 2013
- Pi Mu Epsilon National Honor Society 2013

SERVICE

Macalester College Service

- Team Member, AAC&U Open Educational Resources Institute 2022–2023
- Faculty Liaison, Admissions 2022–2023
- Member, MSCS Academic Planning Committee 2022–2023
- Co-Creator and Coordinator, MSCS Honors Seminar 2021–2023
- Mentor, DataFest 2021, 2022, 2023
- Member, Statistics Tenure Track Search (hired Taylor Okonek) 2022
- Member, Statistics Visiting/Postdoc Search Committee
(hired Bryan Martin [2021], James Normington and Laura Lyman [2022]) 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

PROFESSIONAL ACTIVITIES 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

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

ADVISING

Honors Thesis Advisor

- Freddy Barragan. Statistical genetics for pediatric leukemia: characterizing racial disparities in pediatric acute lymphoblastic leukemia. 2021–2022
(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. 2020–2021

Honors Thesis Committee Member

- Erin Franke. Gentrification and crime in the Twin Cities: insights and challenges through a statistical lens 2023
- Zhaoheng Li. A comparison of stacking methods to estimate survival using residual lifetime data from prevalent cohort studies. 2022

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)

LAST UPDATE January 26, 2024