Kelsey E. Grinde

CONTACT

Mathematics, Statistics, & Computer Science
Macalester College
1600 Grand Avenue
Saint Paul, MN 55105

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(651)-696-6976
kegrinde.github.io

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 253: Statistical Machine Learning (4 sections) 2024–2025
- STAT 494: Statistical Genetics (2 sections) 2022, 2025
- STAT 155: Introduction to Statistical Modeling (13 sections) 2019–2023
- MATH/STAT 455: Mathematical Statistics (4 sections) 2020–2023

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

15. **Grinde, K.**, Browning, B., Reiner, A., Thornton, T., & Browning, S. "Adjusting for principal components can induce collider bias in genome-wide association studies." *PLOS Genetics* 20.12 (2024): e1011242. [link]
14. 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]
13. 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]
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. [link]
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. [link]

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. [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-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. [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 gastrointenstinal bleeding." *Gastrointenstinal Endoscopy* 87.6S (2018): AB418–AB419. [link]

Open Education Resources

2. **Grinde, K**. "Rethinking grading systems in introductory and advanced statistics courses." *Consortium for the Advancement of Undergraduate Statistics Education Resources for JEDI-Informed Teaching of Statistics* (2025): [link].
1. Heggeseth, B., Myint, L., & **Grinde, K.** "Stat 155 Notes." Online textbook (2021): https://bcheggeseth.github.io/Stat155Notes/.

Other Writing

2. **Grinde, K.**$^{+}$, Theobold, A.$^{+}$, & Myint, L^{+}. "Beyond Achievement: Access, Identity, and Power in Alternative Grading." *Grading for Growth* (2024): [link].
1. **Grinde, K.** "Statistical Inference in Admixed Populations." Doctoral dissertation, University of Washington. 2019. [link].

SOFTWARE & APPLICATIONS

* *denotes an undergraduate student, as above*

4. Chen, T.*$^{+}$, McClure, K.*$^{+}$, Ohr, S.*$^{+}$, Huang, Z., & **Grinde, K.** "`STEAM`: Significance Threshold Estimation for Admixture Mapping." R package version 0.2.0 (2024): https://github.com/GrindeLab/STEAM.
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

24. Using PCA to infer and adjust for population structure: What can go wrong? Twin Cities Pop/EvoGen Group, University of Minnesota. Minneapolis, MN. 2024. **(Invited)**

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. 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

11. Ohr, S. Significance threshold estimation for admixture mapping (STEAM), an R package. Midstates Consortium Undergraduate Research Symposium. St. Louis, MO. 2024. (Poster)
10. Chen, T. Evaluating the power of admixture mapping: a literature review and simulation study. StatFest. New York, NY. 2024. (Poster)
9. McClure, K. and Ohr, S. Significance threshold estimation for admixture mapping (STEAM), an R package. Macalester Summer Research Showcase. Saint Paul, MN. 2024. (Poster)
8. Chen, T. Evaluating the power of admixture mapping: a literature review and simulation study. Macalester Summer Research Showcase. Saint Paul, MN. 2024. (Poster)
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 Undergraduate 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

22. Heysse, K. and **Grinde, K.** LaTeXAdvanced Workshop. Macalester College. St. Paul, MN. 2024.
21. Teaching careers roundtable. BIOS 834: Pedagogical Methods for Biostatistics Courses, University of Michigan. Virtual. 2024. **(Invited)**
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)

GRANTS

Funded by National Organizations

3. Safo, S. and **Grinde, K.** "Conference: STATGEN25." (pending)
   Submitted November 2024. Results pending.
   Amount: $49,440
   Funder: National Science Foundation (Program No. 21-541)
2. Graduate Research Fellowship 2016–2019
   Amount: $138,000
   Funder: National Science Foundation (Program No. 24-591)
1. Statistical Genetics Training Grant 2015–2016
   Amount: $22,476
   Funder: National Institutes of Health (T32 Training Grant)

Funded by Local Organizations

6. Collaborative Summer Research Award 2024
   Amount: $13,461
   Funder: Macalester College
5. Article Processing Charge Grant (for Refereed Journal Article [12]) 2022
   Amount: $1,466
   Funder: Macalester College Dewitt Wallace Library Open Access Fund
4. Collaborative Summer Research Award, 2020
   Amount: $5,500
   Funder: Macalester College
3. Travel Grant 2018
   Amount: $300
   Funder: University of Washington Graduate and Professional Student Senate
2. Conference Travel Award 2018
   Amount: $1,000
   Funder: University of Washington (UW) Department of Biostatistics
1. Travel Award 2017
   Amount: $500
   Funder: UW Graduate School Fund for Excellence and Innovation

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
- 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 — 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
  (for best score on Ph.D. qualifying exams)

Undergraduate Awards

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

SERVICE

Professional Service

- American Statistical Association (ASA) Section on Statistics in Genomics and Genetics (SSGG)
  - Co-Chair, STATGEN 2025 Local Organizing Committee — 2024–present
  - Invited Panelist, ASA SSGG Webinar Series — 2021 & 2023
    (see National Teaching/Outreach/Mentoring Talks # 2 and 4)
  - Contributor, ASA SSGG Quarterly Newsletter [link] — 2021
    ("Reflections and Tips from Recent Grads on the Job Search Experience")
- Review Editor for *Frontiers in Genetics* — 2021–present
  (Statistical Genetics and Methodology section)

- Peer Reviewer for *Cell Genomics*, *GENETICS* (x2), *Nature Communications*, *PLOS Computational Biology*, *Scientific Reports*, and *SIAM Undergraduate Research Online* — 2018–present

Macalester College

- Service to the College
  - Serie Center Book Club Co-Coordinator — 2025
    (Book: *Grading for Growth* by D. Clark and R. Talbert)
  - Faculty Liaison to Admissions — 2022–2024
  - AAC&U Open Educational Resources Institute Team Member — 2022–2023
  - Mid-Course Interview Scribe — ~~2020~~*, 2021
    (*canceled due to COVID-19)
- Service to the Department of Mathematics, Statistics, and Computer Science
  - Academic Planning Committee — 2022–2023, 2024–present
  - MSCS Honors Seminar — 2021–2023, 2024–present
    (Co-Creator and Coordinator)
  - Statistics Visiting/Postdoc Search Committee — 2020–2022, 2024–present
    (hired Bryan Martin [2021], James Normington and Laura Lyman [2022])
  - DataFest Mentor — 2021, 2022, 2023
  - Statistics Tenure Track Search Committee — 2022
    (hired Taylor Okonek)

University of Washington Department of Biostatistics

- Diversity Committee — 2017–2019
- Women in Biostatistics and Statistics (Leadership Team) — 2017–2018
- Admissions Committee — 2017–2018
- Peer Mentoring Program (Founding Member) — 2016–2018
- Educational Policy and Teaching Evaluation Committee — 2016–2017
- Biostatistics Outreach Working Group — 2015

St. Olaf College

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

OTHER PROFESSIONAL ACTIVITIES

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

- Tina Chen. Power analysis for admixture mapping studies. 2024–2025
- 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

- Paige Tomer. An investigation into the causes of home field advantage in professional soccer. 2024
- 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

- Tina Chen 2024
  (Funded by Local Grant #6)
- Sydney Ohr 2024
  (Funded by Local Grant #6)
- Katelyn McClure 2024
  (Funded by start-up funds)
- Freddy Barragan 2021
  (Funded by Macalester Mann-Hill Fellowship for Student-Faculty Research)
- Zuofu Huang 2020
  (Funded by Local Grant #4)

LAST UPDATE January 8, 2025