

Kelsey E. Grinde

CONTACT	Mathematics, Statistics, and Computer Science Macalester College 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 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	2019 2014
WORK EXPERIENCE	Assistant Professor Department of Mathematics, Statistics, & Computer Science Macalester College, Saint Paul, MN Postdoctoral Teaching Fellow Department of Mathematics, Statistics, & Computer Science Macalester College, Saint Paul, MN Graduate Research Assistant Browning Statistical Genetics Lab University of Washington, Seattle, WA Graduate Research Assistant Genetic Analysis Center University of Washington, Seattle, WA Undergraduate Research Assistant Summer Research Program in Statistical Genetics & Biostatistics Dordt College, Sioux Center, IA Undergraduate Research Fellow Center for Interdisciplinary Research St. Olaf College, Northfield, MN	2020–present 2019–2020 2014–2015, 2016–2019 2013, 2014 2013–2014
TEACHING EXPERIENCE	Macalester College <ul style="list-style-type: none">STAT 253: Statistical Machine Learning Sections Taught: Fall 2024 (×3), Spring 2025, Fall 2025 (×3)STAT 494: Statistical Genetics Sections Taught: Fall 2022, Spring 2025MATH/STAT 455: Mathematical Statistics Sections Taught: Spring 2020, Spring 2021, Spring 2022, Spring 2023STAT 155: Introduction to Statistical Modeling Sections Taught: Fall 2019 (×2), Spring 2020, Fall 2020 (×2), Spring 2021, Fall 2021 (×2), Spring 2022 (×2), Fall 2022, Spring 2023 (×2)	2024–present 2022, 2025 2020–2023 2019–2023

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 Assistant 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
(Anderson Elementary School [1st Grade], Waite House Afterschool Programs [K–8th Grade])
- 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., Wijisman, 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-Arviso, 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 gastrointestinal bleeding.” *Gastrointestinal Endoscopy* 87.6S (2018): AB418–AB419. [\[link\]](#)

Open Education Resources

3. **Grinde, K.**, Heggeseth, B., Johnson, A., & Myint, L. “STAT 253: Statistical Machine Learning Course Notes.” Online course text (2025): [\[link\]](#).
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): [\[link\]](#).

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

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): [\[link\]](#).
3. Hayir, A.^{*}, & **Grinde, K.** “Interactive Circos Tool.” R shiny application (2022): [\[link\]](#).
2. Huang, Z.^{*}, & **Grinde, K.** “Significance Threshold Estimation for Admixture Mapping using Rcpp.” R package (2020): [\[link\]](#).
1. **Grinde, K.** “STEAM: Significance Threshold Estimation for Admixture Mapping.” R package (2019): [\[link\]](#).

RESEARCH TALKS

Presentations at International or National Venues

11. UPCOMING: Big Data Summer Institute Concluding Symposium, University of Michigan Department of Biostatistics, Ann Arbor, MI. (July 2025.) (**Invited, Keynote**)
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.
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.
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

25. UPCOMING: MSCS Colloquium, Department of Mathematics, Statistics, and Computer Science, St. Olaf College. (September 2025.) **(Invited)**
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. Department of Mathematics and Statistics, Carleton College. Northfield, MN. 2023. **(Invited)**
22. Statistical genetics in populations with mixed ancestry. Department of Mathematics, Creighton University. Omaha, NE. 2022. **(Invited)**
21. What's our work: statistical genetics. Department of Mathematics, Statistics, and Computer Science, Macalester College. Saint Paul, MN. 2021.
20. Genome-wide significance thresholds for admixture mapping studies. Interdisciplinary Biostatistics Training in Genetics and Genomics Journal Club, University of Minnesota. Virtual. 2021. **(Invited)**
19. Statistical genetics in populations with mixed ancestry. Mathematics Colloquium, Augsburg University. Virtual. 2020. **(Invited)**
18. Statistical methods for genome-wide admixture mapping studies. Division of Pediatric Epidemiology and Clinical Research, University of Minnesota. Virtual. 2020. **(Invited)**
17. Statistical genetics in populations with mixed ancestry. Department of Mathematics, Statistics, and Computer Science, Macalester College. 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, University of Washington. Seattle, WA. 2019. **(Invited)**
14. Adjusting for population structure in genetic association studies: new insights and the potential pitfalls of using PCs. Population Genetics (PopGen) Lunch, University of Washington. Seattle, WA. 2019. **(Invited)**
13. Statistical inference in populations with mixed ancestry. Biostatistics Colloquium, University of Washington. 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. Department of Biostatistics, University of Michigan. 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. Department of Biostatistics, University of Michigan. 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. Natural Sciences and Mathematics Honors' Day Poster Session, St. Olaf College. Northfield, MN. 2014. **(Poster)**
2. Predicting donors at Red Cross blood drives. Mathematics, Statistics, and Computer Science Colloquium, St. Olaf College. 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. Summer Research Showcase, Macalester College. Saint Paul, MN. 2024. **(Poster)**
8. Chen, T. Evaluating the power of admixture mapping: a literature review and simulation study. Summer Research Showcase, Macalester College. Saint Paul, MN. 2024. **(Poster)**
7. Barragan, S. Genetic ancestry, gene expression, and survival in children with B-ALL. Pediatric Research, Education, & Scholarship Symposium. Minneapolis, MN. 2022. **(Poster)**
6. Barragan, S. 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, S. 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, S. Statistical methods for pediatric leukemia: gene expression & ancestry in B-cell acute lymphoblastic leukemia. Summer Research Showcase, Macalester College. 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. Summer Research Showcase, Macalester College. 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

23. UPCOMING: Center for Interdisciplinary Research, St. Olaf College. (September 2025.) **(Invited)**
22. L^AT_EX Advanced 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. Hutch United Outreach Committee & Wallin Education Partners Program, Fred Hutchinson Cancer Research Center. 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. STAT 284: Biostatistics, St. Olaf College. Northfield, MN. 2019. **(Invited)**
11. Fellowships, scholarships, and grants. Biostatistics Student Seminar, University of Washington. 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. Department of Biostatistics, University of Washington. 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. Department of Biostatistics, University of Washington. Seattle, WA. 2017.
5. What is Biostatistics? 7th and 8th Grade STEM PREP Project, University of Washington. Seattle, WA. 2017.
4. Applying for outside funding opportunities. Biostatistics Student Seminar, University of Washington. Seattle, WA. 2016.
3. Graduate and professional student panel. Healthcare Exploration for Youth Program, University of Washington. Seattle, WA. 2016. **(Invited)**
2. Graduate and professional student panel. Healthcare Exploration for Youth Program, University of Washington. 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

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| 3. Safo, S. and Ginde, K. "Conference: STATGEN25." | 2025 |
| Amount: \$19,104 | |
| 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

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| 6. Collaborative Summer Research Award | 2024 |
| Amount: \$13,461 | |
| Funder: Macalester College | |
| 5. Article Processing Charge Grant | Amount: \$1,466 |
| Funder: Macalester College Dewitt Wallace Library Open Access Fund | |
| (for Refereed Journal Article [12]) | |
| 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 | |

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| 2. | Conference Travel Award
Amount: \$1,000
Funder: University of Washington (UW) Department of Biostatistics | 2018 |
| 1. | Travel Award
Amount: \$500
Funder: UW Graduate School Fund for Excellence and Innovation | 2017 |

HONORS & AWARDS

Professional Awards and Recognition

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|---|--|-----------|
| • | Poster/Lightning Talk Award, 2nd Place
International Genetic Epidemiology Society Annual Meeting
(for International Research Talk [10]) | 2021 |
| • | Top Cited Article
Genetic Epidemiology Journal
(for Refereed Journal Article [6]) | 2021 |
| • | Thomas R. Fleming Excellence in Biostatistics Award
University of Washington Department of Biostatistics | 2019 |
| • | Gertrude M. Cox Scholarship
American Statistical Association | 2018 |
| • | Dorothy L. Simpson Leadership Award
Achievement Rewards for College Scientists Foundation, Seattle Chapter | 2018 |
| • | Excellence in Teaching Award
University of Washington Department of Biostatistics | 2018 |
| • | Distinguished Oral Presentation Award
Western North American Region of the International Biometric Society
(for International Research Talk [8]) | 2018 |
| • | Achievement Rewards for College Scientists (ARCS) Fellowship
ARCS Foundation, Seattle Chapter | 2014–2017 |
| • | Donovan J. Thompson Award
University of Washington Department of Biostatistics | 2016 |

Undergraduate Awards

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|---|---|-----------|
| • | Honorable Mention, Undergraduate Research Project Competition
Consortium for Advancement of Undergraduate Statistics Education | 2014 |
| • | Honorable Mention, Graduate Research Fellowship Program
National Science Foundation | 2014 |
| • | Statistically Significant Award
St. Olaf Department of Mathematics, Statistics, and Computer Science | 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

Professional Service

- American Statistical Association Section on Statistics in Genomics and Genetics
 - STATGEN 2026 Review Committee 2025–present
 - Co-Chair, STATGEN 2025 Local Organizing Committee 2024–2025
 - Contributor, ASA SSGG Quarterly Newsletter [\[link\]](#) 2021
("Reflections and Tips from Recent Grads on the Job Search Experience")
- *Frontiers in Genetics* Statistical Genetics and Methodology Section
 - Community Reviewer 2025–present
 - Review Editor 2021–2025
- Ad Hoc Peer Reviewer for *Cell Genomics*, *GENETICS*, *Nature Communications*, *PLOS Computational Biology*, *Scientific Reports*, and *SIAM Undergraduate Research Online* 2018–present

Macalester College

- Service to the College
 - Opening Convocation Committee 2025–present
 - Co-Coordinator, Serie Center Reading Group 2025
(Book: *Grading for Growth* by D. Clark and R. Talbert)
 - Faculty Liaison to Admissions 2022–2024
 - AAC&U Open Educational Resources Institute Team 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 Coordinator 2021–2023, 2024–present
 - Statistics Tenure Track Search Committee 2022, 2025
 - Statistics Visiting/Postdoc Search Committee 2020–2022, 2024–2025
 - DataFest Judge 2025
 - DataFest Mentor 2021, 2022, 2023

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 & Mentor 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
- Liberal Arts Program in Seville, Orientation Leader 2013
- 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	Summer Research Supervisor	
	• Tina Chen	2024
	(Funded by Local Grant [6])	
	• Sydney Ohr	2024
	(Funded by Local Grant [6])	
	• Katelyn McClure	2024
	(Funded by Faculty Start-Up Funds)	
	• Sofia Barragan	2021
	(Funded by Macalester Mann-Hill Fellowship for Student-Faculty Research)	
	• Zuofu Huang	2020
	(Funded by Local Grant [4])	
	Honors Thesis Advisor	
	• Tina Chen. Evaluating the power of admixture mapping.	2024–2025
	• Sofia 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	
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