

Kelsey Erin Grinde

CONTACT	Mathematics, Statistics, & Computer Science Macalester College Saint Paul, MN 55105	763-567-8325 kgrinde@macalester.edu kegrinde.github.io
EDUCATION	Ph.D. in Biostatistics University of Washington, Seattle, WA Dissertation: Statistical inference in admixed populations 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	Courses Taught <ul style="list-style-type: none">• STAT 155: Introduction to Statistical Modeling (5 sections) Macalester College, Saint Paul, MN• MATH/STAT 455: Mathematical Statistics Macalester College, Saint Paul, MN• BIOST 311: Regression Methods in the Health Sciences University of Washington, Seattle, WA (co-taught with Brian Williamson)	2019–2020 2020 2018

Teaching Assistantships

- BIOST 310: Biostatistics for the Health Sciences 2017
University of Washington, Seattle, WA
- BIOST 570: Regression Methods for Independent Data 2016
University of Washington, Seattle, WA

Other Teaching Experience

- Guest Lecturer (2 first year graduate courses) 2017
University of Washington, Seattle, WA
- Co-Instructor, First Year Statistical Theory Exam review sessions 2016
University of Washington, Seattle, WA
- Grader, STAT 322: Statistical Theory 2013
St. Olaf College, Northfield, MN
- Academic Assistant & Tutor, math and Spanish (all levels) 2011–2012
St. Olaf College, Northfield, MN
- Urban Schools and Communities Program 2012
St. Olaf College Off-Campus Studies, Minneapolis, MN

**HONORS &
AWARDS****Fellowships, Scholarships, and Grants**

- Graduate Research Fellowship 2016–2019
National Science Foundation
- Gertrude M. Cox Scholarship 2018
American Statistical Association
- Achievement Rewards for College Scientists Fellowship 2014–2017
ARCS Foundation Seattle Chapter
- Statistical Genetics Training Grant 2015–2016
National Institutes of Health
- Buntrock Scholarship 2010–2014
St. Olaf College

Teaching, Service, and Leadership Awards

- 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
- Service Leadership Scholar 2010–2014
St. Olaf College

Academic Honors and Awards

- Thomas R. Fleming Excellence in Biostatistics Award 2019
University of Washington Department of Biostatistics
(highest honor given to a graduating Ph.D. student)
- Donovan J. Thompson Award 2016
University of Washington Department of Biostatistics
(best combined score on Ph.D. qualifying exams)
- Statistically Significant Award 2014
St. Olaf College

- Phi Beta Kappa 2013
St. Olaf College
- Pi Mu Epsilon 2013
St. Olaf College

Research Communication and Travel Awards

- Travel Grant 2018
University of Washington Graduate and Professional Student Senate
- Distinguished Oral Presentation Award 2018
Western North American Region of the International Biometric Society
- Conference Travel Award 2018
University of Washington Department of Biostatistics
- Travel Award 2017
University of Washington Graduate School Fund for Excellence and Innovation
- Honorable Mention 2014
USRESP Undergraduate Research Project Competition

PUBLICATIONS

- 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.
- 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.
- 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., Munsani, 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.
- 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.
- 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.

(Selected as the International Genetic Epidemiology Society Communications Committee's highlight from this issue of *Genetic Epidemiology*.)
- 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.

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.
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.
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.
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.

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 gastrointestinal bleeding.” *Gastrointestinal Endoscopy* 87.6S (2018): AB418–AB419.

SUBMITTED MANUSCRIPTS

2. Lin, B.*, **Grinde, K.***, Brody, J., Raffield, L., Thornton, T., ..., & Franceschini, N. “Discovery of rare genetic variants from whole genome sequencing analyses of kidney function (eGFR) in 23,732 participants from multi-ethnic populations: the Trans-Omics for Precision Medicine (TOPMed) program.”

*joint first authors

1. Snyder, J.M., Iwata, T., **Grinde, K.**, & Treuting, P.M. “Review and comparison of age-associated pathology in male Fischer 344 and Long Evans rats.”

RESEARCH PRESENTATIONS

22. Statistical genetics in populations with mixed ancestry. Mathematics, Statistics, and Computer Science Colloquium, Augsburg University. Minneapolis, MN, 2020. (*Invited Speaker*) (**postponed due to COVID-19**)
21. Statistical genetics in populations with mixed ancestry. Department of Mathematics, Statistics, and Computer Science, Macalester College. Saint Paul, MN, 2019. (*Invited Speaker*)
20. Adjusting for principal components can induce spurious associations in genome-wide association studies. Genetic Analysis Center, University of Washington. Seattle, WA, 2019. (*Invited Speaker*)
19. Adjusting for population structure in genetic association studies: new insights and the potential pitfalls of using PCs. Popgen Lunch, University of Washington. Seattle, WA, 2019. (*Invited Speaker*)
18. Statistical inference in populations with mixed ancestry. Biostatistics Colloquium, University of Washington. Seattle, WA, 2018. (*Invited Speaker*)
17. Deriving significance thresholds for genome-wide admixture mapping studies. International Genetic Epidemiology Society Annual Meeting. San Diego, CA, 2018.

16. Controlling for multiple testing in genome-wide admixture mapping studies. Western North American Region of the International Biometric Society Meeting. Edmonton, Canada, 2018. (*Oral Presentation Award Winner*)
15. Admixture mapping: controlling for false positives in the presence of population structure. American Society of Human Genetics Annual Meeting. Orlando, FL, 2017. (*Poster*)
14. Generalizing genetic risk scores from Europeans to Hispanics/Latinos. International Genetic Epidemiology Society Annual Meeting. Cambridge, United Kingdom, 2017. (*Poster*)
13. 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*)
12. 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.
11. 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.
10. 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.
9. 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.
8. 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.
7. What now? Post-hoc approaches for gene-based, rare variant tests of association. Great Plains R-Users Group Conference. Sioux Center, IA, 2014. (*Poster*)
6. Accounting for variability in paleoecological mixing models. St. Olaf Natural Sciences and Mathematics Honors' Day Poster Session. Northfield, MN, 2014. (*Poster*)
5. Accounting for variability in paleoecological mixing models. National Conference for Undergraduate Research. Lexington, KY, 2014.
4. Predicting donors at Red Cross blood drives. St. Olaf Mathematics, Statistics, and Computer Science Colloquium. Northfield, MN, 2014.
3. Predicting donors at Red Cross blood drives. American Red Cross. St. Paul, MN, 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*)

OUTREACH & MENTORING PRESENTATIONS

12. (Bio)statistics PhD programs: application tips and research opportunities. Biostatistics Class, St. Olaf College. Northfield, MN, 2019.
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.
8. Travel grants and conference funding. University of Washington Department of Biostatistics. Seattle, WA, 2017.
7. What is Biostatistics? Science Research Class, Forest Ridge School of the Sacred Heart. 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, Distance Learning Center & 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. Seattle, WA, 2016.
2. Graduate and professional student panel. Healthcare Exploration for Youth Program. Seattle, WA, 2015.
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*)

SERVICE & LEADERSHIP

Macalester College

- Scribe, Mid-Course Interview (**postponed due to COVID-19**) 2020

University of Washington, Department of Biostatistics

- 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

- 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 Peer Review

- GENETICS 2020
- SIAM Undergraduate Research Online (SIURO) 2020
- PLOS Computational Biology 2019
- Scientific Reports 2018

Working Groups

- Kidney Working Group 2018–present
- NHLBI Trans-Omics for Precision Medicine Whole Genome Sequencing Program

- Dental Genetics Working Group 2016
- Hispanic Community Health Study/Study of Latinos (HCHS/SOL)

Professional Organization Membership

- American Society of Human Genetics
- American Statistical Association
- Caucus for Women in Statistics
- International Genetic Epidemiology Society
- Western North American Region of the International Biometric Society

**COMPUTING
EXPERIENCE** R, highly proficient
Unix/Linux, proficient
Python, familiar

SOFTWARE *STEAM*: Significance Threshold Estimation for Admixture Mapping (R package)
• Available on GitHub: <https://github.com/kegrinde/STEAM>

LANGUAGES English, fluent/native
Spanish, highly proficient

**RESEARCH
INTERESTS** Statistical genetics
Biostatistics
Multiple testing

LAST UPDATE August 12, 2020