

Kelsey Erin Grinde

CONTACT	Mathematics, Statistics, & Computer Science	763-567-8325
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	Saint Paul, MN 55105	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 <i>summa cum laude</i> 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	Courses Taught	
	• STAT 155: Introduction to Statistical Modeling (10 sections)	2019–present
	Macalester College, Saint Paul, MN	
	• MATH/STAT 455: Mathematical Statistics (3 sections)	2020–present
	Macalester College, Saint Paul, MN	
	• BIOST 311: Regression Methods in the Health Sciences	2018
	University of Washington, Seattle, WA	
	(co-taught with Brian Williamson)	

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, BIOST 550: Statistical Genetics I and 2017
BIOST 561: Computational Skills for Biostatistics
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

PUBLICATIONS

+ denotes joint first authors

* denotes an undergraduate student

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.
11. 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.” *EBioMedicine* 63 (2021): 103157.
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.
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.
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.

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.
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.
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.
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

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.”

OTHER WRITING

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

SOFTWARE

2. Grinde, K., & Huang, Z.* “**STEAMcpp**: 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 PRESENTATIONS

26. What's our work: statistical genetics. Macalester College Mathematics, Statistics, and Computer Science Seminar. Saint Paul, MN. 2021.
25. Adjusting for principal components can induce spurious associations in genome-wide association studies in admixed populations. International Genetic Epidemiology Society Annual Meeting. Virtual. 2021. (*2nd Place Award Winner*)
24. Genome-wide significance thresholds for admixture mapping studies. University of Minnesota Interdisciplinary Biostatistics Training in Genetics and Genomics Journal Club. Minneapolis, MN. 2021. (*Invited Speaker*)
23. Statistical genetics in populations with mixed ancestry. Augsburg University Mathematics Colloquium. Minneapolis, MN. 2020. (*Invited Speaker*)
22. Statistical methods for genome-wide admixture mapping studies. University of Minnesota Division of Pediatric Epidemiology and Clinical Research. Minneapolis, MN. 2020. (*Invited Speaker*)
21. Statistical genetics in populations with mixed ancestry. Macalester College Department of Mathematics, Statistics, and Computer Science. Saint Paul, MN. 2019. (*Invited Speaker*)
20. Adjusting for principal components can induce spurious associations in genome-wide association studies. Genetic Analysis Center. Seattle, WA. 2019. (*Invited Speaker*)
19. 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 Speaker*)
18. Statistical inference in populations with mixed ancestry. University of Washington Biostatistics Colloquium. 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. Saint 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, &
TEACHING
PRESENTATIONS**

16. Panel on Time Management, Research Strategy, and Health Habits for Graduate Students. American Statistical Association Section on Statistics in Genomics and Genetics. 2021.
15. Radical MacAccess Inclusivity in Teaching Panel. Macalester College. 2021.
14. Pathways into Science Outreach Panel. Sponsored by Hutch United (educational outreach committee of the Fred Hutchinson Cancer Research Center) for students from the Wallin Education Partners program. 2021.
13. Graduate programs in (bio)statistics. Electronic Undergraduate Statistics Research Conference (eUSR). 2020.
12. (Bio)statistics PhD programs: application tips and research opportunities. St. Olaf College Biostatistics Class. Northfield, MN. 2019.
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.
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.

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*)

HONORS & AWARDS

Fellowships, Scholarships, and Grants

- Collaborative Summer Research Award (1 student) 2020
Macalester College
- 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

Research Communication and Travel Awards

- Poster/Lightning Talk Award, 2nd Place 2021
International Genetic Epidemiology Society Annual Meeting
- Top Cited Article 2021
Genetic Epidemiology Journal
- 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

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)

	<ul style="list-style-type: none"> Donovan J. Thompson Award University of Washington Department of Biostatistics (best combined score on Ph.D. qualifying exams) 	2016
	<ul style="list-style-type: none"> Statistically Significant Award St. Olaf College 	2014
	<ul style="list-style-type: none"> Phi Beta Kappa St. Olaf College 	2013
	<ul style="list-style-type: none"> Pi Mu Epsilon St. Olaf College 	2013
SERVICE & LEADERSHIP	<p>Macalester College</p> <ul style="list-style-type: none"> Coordinator, MSCS Honors Seminar Scribe, Mid-Course Interview Scribe, Mid-Course Interview (canceled due to COVID-19) <p>University of Washington, Department of Biostatistics</p> <ul style="list-style-type: none"> Member, Diversity Committee Leadership Team, Women in Biostatistics and Statistics Member, Admissions Committee Founding Member, Peer Mentoring Program Member, Educational Policy and Teaching Evaluation Committee Member, Biostatistics Outreach Working Group <p>St. Olaf College</p> <ul style="list-style-type: none"> President, Spanish Honor House Volunteer Teaching Assistant & Tutor, Northfield Public Schools Volunteer Teaching Assistant, Wayzata High School 	2020–present 2021 2020 2017–2019 2017–2018 2017–2018 2016–2018 2016–2017 2015 2013–2014 2011–2014 2011
PROFESSIONAL ACTIVITIES	<p>Journal Editorial Board Positions and Peer Review</p> <ul style="list-style-type: none"> Review Editor on Editorial Board for <i>Frontiers in Genetics</i> (Statistical Genetics and Methodology Section) Reviewer for <i>GENETICS</i>, <i>PLOS Computational Biology</i>, <i>Scientific Reports</i>, <i>SIAM Undergraduate Research Online</i> <p>Working Groups</p> <ul style="list-style-type: none"> Kidney Working Group NHLBI Trans-Omics for Precision Medicine Whole Genome Sequencing Program Dental Genetics Working Group Hispanic Community Health Study/Study of Latinos (HCHS/SOL) <p>Professional Organization Membership</p> <ul style="list-style-type: none"> American Society of Human Genetics American Statistical Association Caucus for Women in Statistics International Genetic Epidemiology Society 	2021–present 2018–2020 2018–2021 2016
COMPUTING EXPERIENCE	R, highly proficient Unix/Linux, proficient Python, familiar	

LANGUAGES English, fluent/native
 Spanish, proficient

RESEARCH Statistical genetics
INTERESTS Biostatistics

LAST UPDATE April 14, 2022