

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	August 2019
	University of Washington, Seattle, WA	
	Dissertation: Statistical inference in admixed populations	
	Advisor: Sharon Browning, Ph.D.	
	B.A. in Mathematics , Concentration in Statistics	May 2014
	St. Olaf College, Northfield, MN	
	Graduated <i>summa cum laude</i> with Distinction in Statistics	
	Advisor: Paul Roback, Ph.D.	
WORK EXPERIENCE	Postdoctoral Teaching Fellow	2019–present
	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 (2 sections)	2019
	Macalester College, Saint Paul, MN	
	• BIOST 311: Regression Methods in the Health Sciences	2018
	University of Washington, Seattle, WA	
	Overall Median Course Evaluation: 4.9/5.0	
	Co-Instructor: 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 (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

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

Fellowships, Scholarships, and Training 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

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

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.

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

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.

SUBMITTED MANUSCRIPTS

3. Raffield, L., Lu, A., Little, A., **Grinde, K.**, et al. "Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenome-wide analysis in African Americans." (Submitted to *Journal of Thrombosis and Haemostasis*.)
2. Jensen-Otsu, E., **Grinde, K.**, Teng, B.J., Baxi, A.C., Harms, M.A., 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." (Submitted to *Gastrointestinal Endoscopy*.)
1. Snyder, J., Iwata, T., Patil, K., Tryon, V., **Grinde, K.**, Mizumori, S., Treuting, & Treuting, P. "Comparison of end-of-life pathology in aged male Fischer 344 and Long Evans rats." (Submitted to *Journal of Comparative Pathology*.)

WORKS IN PREPARATION

2. "Whole genome sequencing of kidney traits: the Trans-Omics for Precision Medicine (TOPMed) Project."
1. "Adjusting for principal components can induce spurious associations in genome-wide association studies."

RESEARCH PRESENTATIONS

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	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	
	• 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	
COMPUTING EXPERIENCE	R, highly proficient	
	Unix/Linux, proficient	
	Python, familiar	
SOFTWARE	<i>STEAM</i> : 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	September 29, 2019	