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 — 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 *summa cum laude* 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 Colllege, 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

- STAT 322: Statistical Theory (*grader*) 2013
  St. Olaf College, Northfield, MN

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
- 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 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

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
  (awarded to one graduating statistics student)
- Phi Beta Kappa 2013
  St. Olaf College
- Pi Mu Epsilon 2013
  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-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.
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.

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 gastrointenstinal bleeding." (Submitted to *Gastrointenstinal 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
- 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 September 14, 2019