Kelsey E. Grinde

CONTACT   Mathematics, Statistics, & Computer Science   kgrinde@macalester.edu
Macalester College   (651)-696-6976
1600 Grand Avenue   kegrinde.github.io
Saint Paul, MN 55105

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 *summa cum laude* 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

Macalester College
- MATH/STAT 455: Mathematical Statistics (4 sections)   2020–present
- STAT 155: Introduction to Statistical Modeling (13 sections) 2019–present
- STAT 494: Statistical Genetics (1 section)   2022

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 Asst.   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
- 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

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* (2022): 1–12.

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., 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.

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-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.

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 gastrointenstinal bleeding." *Gastrointenstinal Endoscopy* 87.6S (2018): AB418–AB419.

Open Education Resources

1. Heggeseth, B., Myint, L., & **Grinde, K.** "Stat 155 Notes." Online text (2021): https://bcheggeseth.github.io/Stat155Notes/.

MANUSCRIPTS IN PROGRESS

2. Horimoto, A., Boyken, L., Blue, E., **Grinde, K.**, Nafikov, R., Sohi, H., Nato, A., Bis, J., Brusco, L., Morelli, L., Ramirez, A., Dalmasso, C., ..., Mayeux, R., Browning, S., Seshadri, S., Wijsman, E., & Thornton, T. "Admixture mapping implicates *LIG4*, *MYO16*, and *FAM155A* at 13q33.3 as ancestry-of-origin loci for Alzheimer's disease in multiplex U.S. Caribbean Hispanic Families."

1. **Grinde, K.**, Browning, B., Reiner, A., Thornton, T., & Browning, S. "Adjusting for principal components can induce spurious associations in genome-wide association studies."

SOFTWARE

2. Huang, Z.*, & **Grinde, K.** "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 TALKS

Presentations at International or National Venues

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. **(Presentation Award Winner)**

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. **(Presentation Award Winner)**

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

22. Statistical genetics in populations with mixed ancestry. Creighton University Department of Mathematics. Omaha, NE. 2022. **(Invited)**

21. What's our work: statistical genetics. Macalester College Mathematics, Statistics, and Computer Science Seminar. Saint Paul, MN. 2021.

20. Genome-wide significance thresholds for admixture mapping studies. University of Minnesota Interdisciplinary Biostatistics Training in Genetics and Genomics Journal Club. Virtual. 2021. **(Invited)**

19. Statistical genetics in populations with mixed ancestry. Augsburg University Mathematics Colloquium. Virtual. 2020. **(Invited)**

18. Statistical methods for genome-wide admixture mapping studies. University of Minnesota Division of Pediatric Epidemiology and Clinical Research. Virtual. 2020. **(Invited)**

17. Statistical genetics in populations with mixed ancestry. Macalester College Department of Mathematics, Statistics, and Computer Science. Saint Paul, MN. 2019. **(Invited)**

16. Statistial 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. Seattle, WA. 2019. **(Invited)**

14. 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)**

13. Statistical inference in populations with mixed ancestry. University of Washington Biostatistics Colloquium. 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. University of Michigan Department of Biostatistics. 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. University of Michigan Department of Biostatistics. 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. St. Olaf Natural Sciences and Mathematics Honors' Day Poster Session. Northfield, MN. 2014. (Poster)

2. Predicting donors at Red Cross blood drives. St. Olaf Mathematics, Statistics, and Computer Science Colloquium. Northfield, MN. 2014.

1. Predicting donors at Red Cross blood drives. American Red Cross. Saint Paul, MN. 2014.

Student Presentations of Joint/Supervised Work

6. Barragan, F. Genetic ancestry, gene expression, and survival in children with B-ALL. Pediatric Research, Education, & Scholarship Symposium. Minneapolis, MN. 2022. (Poster)

5. Barragan, F. Gene expression differences by race and genetic ancestry in B-cell acute lymphoblastic leukemia. American Society of Human Genetics Annual Meeting. Virtual. 2021. (Poster)

4. Barragan, F. 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)

3. Barragan, F. Statistical methods for pediatric leukemia: gene expression & ancestry in B-cell acute lymphoblastic leukemia. Macalester Summer Research Showcase. Saint Paul, MN. 2021. (Poster)

2. Huang, Z. Statistical methods for genetic association studies in populations with mixed ancestry. Midstates Consortium Research Symposium. Virtual. 2020.

1. Huang, Z. Using Rcpp to speed up tool for controlling for multiple testing in genetic studies. Electronic Undergraduate Statistics Research Conference. Virtual. 2020.

MENTORING, TEACHING, & OUTREACH TALKS	**Presentations at International or National Venues**

Presentations at International or National Venues

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

16. Keynotes: studies, statistics, and serial killers. The Abstract Podcast. Virtual. 2021. **(Invited)**

15. Inclusivity in teaching panel. Radical MacACCESS, Macalester College. Virtual. 2021. **(Invited)**

14. Pathways into science outreach panel. Fred Hutchinson Cancer Research Center Hutch United Outreach Committee & Wallin Education Partners Program. 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. St. Olaf College Biostatistics Class. Northfield, MN. 2019. **(Invited)**

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. **(Invited)**

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. **(Invited)**

2. Graduate and professional student panel. Healthcare Exploration for Youth Program. 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)

HONORS & AWARDS	

Professional Awards and Recognition

- Poster/Lightning Talk Award, 2nd Place (for International Research Talk [10]) 2021
International Genetic Epidemiology Society Annual Meeting

- Top Cited Article (for Refereed Journal Article [6]) 2021
Genetic Epidemiology Journal

- Thomas R. Fleming Excellence in Biostatistics Award 2019
University of Washington Department of Biostatistics

- Gertrude M. Cox Scholarship 2018
American Statistical Association

- 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

- Distinguished Oral Presentation Award (for International Research Talk [8]) 2018
Western North American Region of the International Biometric Society

- Achievement Rewards for College Scientists (ARCS) Fellowship 2014–2017
ARCS Foundation, Seattle Chapter

- Donovan J. Thompson Award (for best score on Ph.D. qualifying exams) 2016
University of Washington Department of Biostatistics

Grants and Other Research Funding

- Collaborative Summer Research Award 2020
Macalester College

- Graduate Research Fellowship 2016–2019
National Science Foundation

- Travel Grant 2018
University of Washington Graduate and Professional Student Senate

- Conference Travel Award 2018
University of Washington Department of Biostatistics

- Travel Award 2017
University of Washington Graduate School Fund for Excellence and Innovation

- Statistical Genetics Training Grant 2015–2016
National Institutes of Health

Undergraduate Awards

- Undergraduate Research Project Competition Honorable Mention 2014
Consortium for Advancement of Undergraduate Statistics Education

- Statistically Significant Award 2014
St. Olaf College

- Buntrock Scholarship 2010–2014
St. Olaf College

• Service Leadership Scholarship St. Olaf College	2010–2014
• Phi Beta Kappa National Honor Society	2013
• Pi Mu Epsilon National Honor Society	2013

SERVICE

Macalester College Service

• Faculty Liaison, Admissions	2022–present
• Member, MSCS Academic Planning Committee	2022–present
• Team Member, AAC&U Open Educational Resources Institute	2022–present
• Co-Creator and Coordinator, MSCS Honors Seminar	2021–present
• Member, Statistics Tenure Track Search Committee	2022
• Mentor, DataFest	2021, 2022
• Member, Statistics Visiting/Postdoc Search Committee	2020–2022
• Scribe, Mid-Course Interview	2021
• ~~Scribe, Mid-Course Interview~~ (canceled due to COVID-19)	2020

University of Washington Department of Biostatistics Service

• 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 Service

• 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 Editorial Board Positions and Peer Review

• Review Editor for the *Statistical Genetics and Methodology* section of *Frontiers in Genetics*	2021–present
• Peer-Reviewer for *GENETICS*, *PLOS Computational Biology*, *Scientific Reports*, and *SIAM Undergraduate Research Online*	2018–present

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 Trans-Omics for Precision Medicine Whole Genome Sequencing Program	2018–2021

- Dental Genetics Working Group   2016
  Hispanic Community Health Study/Study of Latinos

ADVISING **Honors Thesis Advisor**
- Freddy Barragan. Statistical genetics for pediatric leukemia: char-   2021–2022
  acterizing racial disparities in pediatric acute lymphoblastic leukemia.
  (funded by NIH Research Supplement to Promote Diversity in Health-Related Research)

- Zuofu Huang. Estimating significance thresholds and the number   2020–2021
  of generations since admixture in admixture mapping studies.

Honors Thesis Committee Member
- Zhaoheng Li. A comparison of stacking methods to estimate survival   2022
  using residual lifetime data from prevalent cohort studies.

Summer Research Supervisor
- Freddy Barragan   2021
  (funded by Mann-Hill Fellowship for Student-Faculty Research)

- Zuofu Huang   2020
  (funded by Macalester Collaborative Summer Research Award)

LAST UPDATE January 9, 2023