Jean Morrison

John G Searl Assistant Professor
University of Michigan
Department of Biostatistics

jvmorr@umich.edu
https://jean997.github.io

Education

PhD Biostatistics, University of Washington 2016
Advisor: Noah Simon, Department of Biostatistics

BA Mathematics, University of Chicago 2009

Professional Positions

Assistant Professor, Department of Biostatistics, University of Michigan Sept 2020 to Present
Postdoctoral Scholar, Department of Human Genetics, University of Chicago Oct 2016 to Sept 2020
Supervisors: Xin He and Mathew Stephens

Pre-Prints

1. **Li**, **J.** & Morrison, J. Mind the gap: characterizing bias due to population mismatch in two-sample Mendelian randomization. en. Under review at AJHG (Aug. 2025).
2. Shi, R. & **Morrison**, **J.** Multivariable Mendelian Randomization adjusting for heritable confounding analyzes the causal effects of C-reactive protein on multiple diseases. Under Review at International Journal of Epidemiology (Jan. 2025).
3. Moolhuijsen, L. M. E., Zhu, J., Mullin, B. H., Pujol-Gualdo, N., Actkins, K. V., Mack, J. A., Rao, H., Trivedi, B., Kentistou, K. A., Zhao, Y., Westergard, D., Tyrmi, J. S., Thorleifsson, G., Zhang, Y., Wittemans, L., DeVries, A., Brewer, K., Sisk, R., Danning, R., Preuss, M. H., Jones, M. R., Ruth, K. S., Andersen, M., Azziz, R., Banasik, K., Boehnke, M., Broer, L., Brunak, S., Chan, Y.-M., Chasman, D. I., Daly, M., Ehrmann, D. A., Fauser, B. C., Fritsche, L. G., Hayes, M. G., He, C., Huang, H., Kowalska, I., Kraft, P., Legro, R. S., Lin, N., Loos, R. J., Louwers, Y. V., Magi, R., McCarthy, M. I., Morin-Papunen, L., **Morrison**, **J. V.**, Morton, C., Nadkarni, G. N., Neale, B. M., Nielsen, H. S., Nyegaard, M., Ostrowski, S. R., Pedersen, O. B. V., Sørensen, E., Mikkelsen, C., Erikstrup, C., Kaspersen, K. A., Bruun, M. T., Aagaard, B., Ullum, H., Obermayer-Pietsch, B., Palotie, A., Reeve, M. P., Salumets, A., Saxena, R., Spector, T. D., Stuckey, B. G. A., Thorsteinsdottir, U., Uitterlinden, A. G., Urbanek, M., Zollner, S., Team, G. H̃. R., Consortium, D. G., Team, 2. R., Heel, D. A. V., Hirschhorn, J. N., Stefansson, K., Perry, J. R. B., Styrkarsdottir, U., Wilson, S. G., Piltonen, T., Laisk, T., Jarvelin, M.-R., Burns, K., Justice, A. E., Laivuori,

H., Ong, K. K., Goodarzi, M. O., Davis, L. K., Dunaif, A., Lindgren, C. M., Laven, J. S. E., Franks, S., Visser, J. A., Welt, C. K., Karaderi, T. & Day, F. R. Genomic and proteomic evidence for hormonal and metabolic foundations of polycystic ovary syndrome. Under Revision at Nature Genetics (Apr. 2024).

4. **Morrison**, **J.**, Willwerscheid, J., Sylvertooth, D., He, X. & Stephens, M. Genetic Factor Analysis for Characterizing Phenome-Wide Patterns of Genetic Pleiotropy. Under Revision at Nature Genetics (July 2024).
5. Okamoto, J., Yin, X., Ryan, B., Chiou, J., Luca, F., Pique-Regi, R., Im, H. K., **Morrison**, **J.**, Burant, C., Fauman, E. B., Laakso, M., Boehnke, M. & Wen, X. Probabilistic Fine-mapping of Putative Causal Genes (Oct. 2024).

Publications

1. **Morrison**, **J.** GWASBrewer: An R Package for Simulating Realistic GWAS Summary Statistics. *Genetic Epidemiology* **49,** e22594 (Feb. 2025).
2. Okamoto, J., Yin, X., Ryan, B., Chiou, J., Luca, F., Pique-Regi, R., Im, H. K., **Morrison**, **J.**, Burant, C., Fauman, E. B., Laakso, M., Boehnke, M. & Wen, X. Multi-INTACT: integrative analysis of the genome, transcriptome, and proteome identifies causal mechanisms of complex traits. *Genome Biology* **26,** 19 (Feb. 2025).
3. Terman, S. W., Josephson, C. B., Goyal, P., Gonzalez-Izquierdo, A., **Morrison**, **J.**, Denaxas, S. & Wiebe, S. Lamotrigine and Cardiac Arrhythmias: A Target Trial Approach. *Neurology.* Accepted (Mar. 2025).
4. Yin, X., Li, J., Bose, D., Okamoto, J., Kwon, A., Jackson, A. U., Fernandes Silva, L., Oravilahti, A., Chu, X., Stringham, H. M., Liu, L., Peng, R., Xia, Z., Ripatti, S., Daly, M., Palotie, A., Scott, L. J., Burant, C. F., Fauman, E. B., Wen, X., Boehnke, M., Laakso, M. & **Morrison**, **J.** Assessing the potential causal effects of 1099 plasma metabolites on 2099 binary disease endpoints. en. *Nature Communications* **16.** Publisher: Nature Publishing Group, 3039 (Mar. 2025).
5. Kundu, R., Shi, X., **Morrison**, **J.**, Barrett, J. & Mukherjee, B. A Framework for Understanding Selection Bias in Real-World Healthcare Data. *Accepted, Journal of the Royal Statistical Society: Series A* (Mar. 2024).
6. Wang, L., Wen, X. & **Morrison**, **J.** Imperfect gold standard gene sets yield inaccurate evaluation of causal gene identification methods. *Communications Biology* **7.** Publisher: Nature Publishing Group, 1–5 (July 2024).
7. Burgess, S., Davey Smith, G., Davies, N. M., Dudbridge, F., Gill, D., Glymour, M. M., Hartwig, F. P., Kutalik, Z., Holmes, M. V., Minelli, C., **Morrison**, **J. V.**, Pan, W., Relton, C. L. & Theodoratou, E. Guidelines for performing Mendelian randomization investigations: update for summer 2023. *Wellcome Open Research* **4,** 186 (Aug. 2023).
8. Harlan, E. A., Venkatesh, S., **Morrison**, **J.**, Cooke, C. R., Iwashyna, T. J., Ford, D. W., Moscovice, I. S., Sjoding, M. W. & Valley, T. S. Rural-urban differences in mortality for mechanically ventilated patients in intensive care and intermediate care. *Accepted, Annals of the American Thoracic Society* (Dec. 2023).

9. Okamoto, J., Wang, L., Yin, X., Luca, F., Pique-Regi, R., Helms, A., Im, H. K., **Morrison**, **J.** & Wen, X. Probabilistic integration of transcriptome-wide association studies and colocalization analysis identifies key molecular pathways of complex traits. *The American Journal of Human Genetics* **110.** PMCID: PMC9892769, 44–57 (Jan. 2023).

10. Sanderson, E., Glymour, M. M., Holmes, M. V., Kang, H., **Morrison**, **J.**, Munafò, M. R., Palmer, T., Schooling, C. M., Wallace, C., Zhao, Q. & Davey Smith, G. Mendelian randomization. en. *Nature Reviews Methods Primers* **2.** PMCID: PMC7614635, 1–21 (Feb. 2022).

11. Yin, X., Bose, D., Kwon, A., Hanks, S. C., Jackson, A. U., Stringham, H. M., Welch, R., Oravilahti, A., Fernandes Silva, L., Locke, A. E., Fuchsberger, C., Service, S. K., Erdos, M. R., Bonnycastle, L. L., Kuusisto, J., Stitziel, N. O., Hall, I. M., **Morrison**, **J.**, Ripatti, S., Palotie, A., Freimer, N. B., Collins, F. S., Mohlke, K. L., Scott, L. J., Fauman, E. B., Burant, C., Boehnke, M., Laakso, M. & Wen, X. Integrating transcriptomics, metabolomics, and GWAS helps reveal molecular mechanisms for metabolite levels and disease risk. en. *The American Journal of Human Genetics* **109.** PMCID: PMC9606383, 1727–1741 (Oct. 2022).

12. Yin, X., Chan, L. S., Bose, D., Jackson, A. U., VandeHaar, P., Locke, A. E., Fuchsberger, C., Stringham, H. M., Welch, R., Yu, K., Fernandes Silva, L., Service, S. K., Zhang, D., Hector, E. C., Young, E., Ganel, L., Das, I., Abel, H., Erdos, M. R., Bonnycastle, L. L., Kuusisto, J., Stitziel, N. O., Hall, I. M., Wagner, G. R., Kang, J., **Morrison**, **J.**, Burant, C. F., Collins, F. S., Ripatti, S., Palotie, A., Freimer, N. B., Mohlke, K. L., Scott, L. J., Wen, X., Fauman, E. B., Laakso, M. & Boehnke, M. Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. en. *Nature Communications* **13.** PMCID: PMC8960770, 1644 (Mar. 2022).

13. **Morrison**, **J.**, Knoblauch, N., Marcus, J. H., Stephens, M. & He, X. Mendelian randomization accounting for correlated and uncorrelated pleiotropic effects using genome-wide summary statistics. en. *Nature Genetics* **52.** PMCID: PMC7343608, 740–747 (July 2020).

14. Sakabe, N. J., Aneas, I., Knoblauch, N., Sobreira, D. R., Clark, N., Paz, C., Horth, C., Ziffra, R., Kaur, H., Liu, X., Anderson, R., **Morrison**, **J.**, Cheung, V. C., Grotegut, C., Reddy, T. E., Jacobsson, B., Hallman, M., Teramo, K., Murtha, A., Kessler, J., Grobman, W., Zhang, G., Muglia, L. J., Rana, S., Lynch, V. J., Crawford, G. E., Ober, C., He, X. & Nóbrega, M. A. Transcriptome and regulatory maps of decidua-derived stromal cells inform gene discovery in preterm birth. en. *Science Advances* **6.** PMCID: PMC7710387, eabc8696 (Dec. 2020).

15. Zhang, Z., Luo, K., Zou, Z., Qiu, M., Tian, J., Sieh, L., Shi, H., Zou, Y., Wang, G., **Morrison**, **J.**, Zhu, A. C., Qiao, M., Li, Z., Stephens, M., He, X. & He, C. Genetic analyses support the contribution of mRNA N 6 -methyladenosine (m 6 A) modification to human disease heritability. en. *Nature Genetics* **52.** PMCID: PMC7483307, 939–949 (Sept. 2020).

16. Burkart, K. M., Sofer, T., London, S. J., Manichaikul, A., Hartwig, F. P., Yan, Q., Artigas, S., Avila, L., Chen, W., Thomas, S. D., Diaz, A. A., Hall, I. P., Horta, B. L., Kaplan, R. C., Laurie, C. C., Menezes, A. M., **Morrison**, **J. V.**, Oelsner, E. C., Rastogi, D., Rich, S. S., Soto-quiros, M., Stilp, A. M., Tobin, M. D., Wain, L. V., Celed, J. C. & Barr, R. G. A Genome-Wide Association Study in Hispanics/Latinos Identifies Novel Signals for Lung Function The Hispanic Community Health Study/Study of Latinos. *American Journal of Respiratory and Critical Care Medicine* **198.** PMCID: PMC6058984, 208–219 (2018).

17. Liu, Y., Liang, Y., Cicek, A., Li, Z., Li, J., Muhle, R., Krenzer, M., Mei, Y., Wang, Y., Knoblauch, N., **Morrison**, **J.**, Zhao, S., Jiang, Y., Geller, E., Ionita-Laza, I., Wu, J., Xia, K., Noonan, J., Sun, Z. & He, X. A Statistical Framework for Mapping Risk Genes from De Novo Mutations in Whole-Genome-Sequencing Studies. *American Journal of Human Genetics* **12.** PMCID: PMC5992125, 1031–1047 (2018).

18. **Morrison**, **J.** & Simon, N. Rank Conditional Coverage and Confidence Intervals in High Dimensional Problems. *Journal of Computational and Graphical Statistics* **27.** PMCID: PMC6364309, 648–656 (2018).

19. Hodonsky, C., Jain, D., Schick, U., **Morrison**, **J.**, Brown, L., McHugh, C., Schurmann, C., Chen, D., Liu, Y., Auer, P., Laurie, C., Taylor, K., Browning, B., Li, Y., Papanicolaou, G., Rotter, J., Kurita, R., Nakamura, Y., Browning, S., Loos, R., North, K., Laurie, C., Thornton, T., Pankratz, N., Bauer, D., Sofer, T. & Reiner, A. Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. *PLoS Genetics* **13.** PMCID: PMC5428979 (2017).

20. Jain, D., Hodonsky, C. J., Schick, U. M., **Morrison**, **J. V.**, Brown, L., Schurmann, C., Liu, Y., Auer, P. L., Laurie, C. A., Taylor, K. D., Browning, B., Papanicolaou, G., Browning, S. R., Loos, R. J., North, K. E., Thyagarajan, B., Laurie, C. C., Thornton, T. A., Sofer, T. & Reiner, A. P. Genome-Wide Association of White Blood Cell Counts in Hispanic/Latino Americans: The Hispanic Community Health Study/Study of Latinos. *Human Molecular Genetics* **26.** PMCID: PMC5968624, 1193–1204 (2017).

21. **Morrison**, **J.**, Witten, D. & Simon, N. Simultaneous detection and estimation of trait associations with genomic phenotypes. *Biostatistics* **18.** PMCID: PMC6082590, 147–164 (Aug. 2016).

22. Schick, U. M., Jain, D., Hodonsky, C. J., **Morrison**, **J. V.**, Davis, J. P., Brown, L., Sofer, T., Conomos, M. P., Schurmann, C., McHugh, C. P., Nelson, S. C., Vadlamudi, S., Stilp, A., Plantinga, A., Baier, L., Bien, S. A., Gogarten, S. M., Laurie, C. A., Taylor, K. D., Liu, Y., Auer, P. L., Franceschini, N., Szpiro, A., Rice, K., Kerr, K. F., Rotter, J. I., Hanson, R. L., Papanicolaou, G., Rich, S. S., Loos, R. J., Browning, B. L., Browning, S. R., Weir, B. S., Laurie, C. C., Mohlke, K. L., North, K. E., Thornton, T. A. & Reiner, A. P. Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. English. *The American Journal of Human Genetics* **98.** PMCID: PMC4746331, 229–242 (Jan. 2016).

23. **Morrison**, **J.**, Laurie, C. C., Marazita, M. L., Sanders, A. E., Offenbacher, S., Salazar, C. R., Conomos, M. P., Thornton, T., Jain, D., Laurie, C. A., Kerr, K. F., Papanicolaou, G., Taylor, K., Kaste, L. M., Beck, J. D. & Shaffer, J. R. Genome-wide association study of dental caries in the Hispanic Communities Health Study/Study of Latinos (HCHS/SOL). *Human Molecular Genetics* **25.** PMCID: PMC4743689, 807–816 (Dec. 2015).

24. Hayes, M. G., Urbanek, M., Hivert, M. F., Armstrong, L. L., **Morrison**, **J.**, Guo, C., Lowe, L. P., Scheftner, D. A., Pluzhnikov, A., Levine, D. M., McHugh, C. P., Ackerman, C. M., Bouchard, L., Brisson, D., Layden, B. T., Mirel, D., Doheny, K. F., Leya, M. V., Lown-Hecht, R. N., Dyer, A. R., Metzger, B. E., Reddy, T. E., Cox, N. J. & Lowe, W. L. Identification of HKDC1 and BACE2 as genes influencing glycemic traits during pregnancy through genome-wide association studies. *Diabetes* **62.** PMCID: PMC3749326, 3282–3291 (Sept. 2013).

25. **Morrison**, **J.** Characterization and correction of error in genome-wide ibd estimation for samples with population structure. *Genetic Epidemiology* **37.** PMCID: PMC4001853, 635–641 (Sept. 2013).

26. Urbanek, M., Hayes, M. G., Armstrong, L. L., **Morrison**, **J.**, Lowe, L. P., Badon, S. E., Scheftner, D., Pluzhnikov, A., Levine, D., Laurie, C. C., McHugh, C., Ackerman, C. M., Mirel, D. B., Doheny, K. F., Guo, C., Scholtens, D. M., Dyer, A. R., Metzger, B. E., Reddy, T. E., Cox, N. J. & Lowe, W. L. The chromosome 3q25 genomic region is associated with measures of adiposity in newborns in a multi-ethnic genome-wide association study. *Human Molecular Genetics* **22.** PMCID: PMC3736865, 3583–3596 (Sept. 2013).

27. Below, J. E., Gamazon, E. R., **Morrison**, **J. V.**, Konkashbaev, A., Pluzhnikov, A., McKeigue, P. M., Parra, E. J., Elbein, S. C., Hallman, D. M., Nicolae, D. L., Bell, G. I., Cruz, M., Cox, N. J. & Hanis, C. L. Genome-wide association and meta-analysis in populations from Starr County, Texas, and Mexico City identify type 2 diabetes susceptibility loci and enrichment for expression quantitative trait loci in top signals. *Diabetologia* **54.** PMCID: PMC3761075, 2047–2055 (Aug. 2011).

Presentations

Conference Presentations

***Invited Talk*, June 2024** *Network Mendelian Randomization.* Mendelian Radomization Conference, Bristol UK

***Invited Talk*, May 2024** *An efficient method for network Mendelian randomization allows network structure discovery and effect estimation.* STATGEN 2024: Conference on Statistics in Genomics and Genetics, Pittsburgh, PA

***Invited Talk*, January 2024** *Introducing the OpenMR Project* Mendelian Randomization Meeting, Bristol, UK

***Contributed Poster*, March 2023** *Efficient, Scalable Multivariable Mendelian Randomization with Reduced Weak Instrument Bias* Probabilistic Modeling in Genomics, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY

***Contributed Poster*, Oct. 2022** *Efficient Multivariable Mendelian Randomization for Confounder Adjustment* American Society for Human Genetics, Los Angeles, CA

***Invited Talk*, Sept 2022** *Empirical Shirnkage Multivariable Mendelian Randomization* Pacific Causal Inference Conference, virtual

***Invited Talk*, August 2022** *Identifying Unobserved Genetic Mediators Using Empirical Bayes Matrix Decomposition* Joint Statistical Meetings, Washington DC

***Contributed Talk*, May 2022** *Empirical Shirnkage Multivariable Mendelian Randomization* American Causal Inference Conference, Berkeley, CA

***Contributed Talk*, March 2022** *Variable selection for automatic confounder adjustment in Mendelian randomization using public GWAS databases* Eastern North American Region of the International Biometric Society, Dallas, TX/virtual

***Invited Talk*, Dec 2021** *Variable Selection for Automatic Confounder Adjustment in Mendelian Randomization* University of North Carolina Functional Genomics Group, virtual

***Contributed Poster*, Oct 2021** *Exploiting public GWAS databases to identify and adjust for heritable confounders in Mendelian randomization studies.* American Society for Human Genetics, virtual

***Invited Talk*, Sept 2021** *Exploiting public GWAS databases to identify and adjust for heritable confounders in Mendelian randomization studies.* International Chinese Statistical Association, virtual

***Contributed Talk*, March 2021** *Sparse Factor Decomposition Accounting for Correlated Errors Aids Biological Discovery From Phenome-Wide Analysis of Genetic Associations.* Eastern North American Region of the International Biometric Society, virtual

***Invited Talk*, 2019** *Mendelian Randomization Accounting for Horizontal and Correlated Pleiotropy Using Genome-Wide Summary Statistics* Western North American Region of the International Biometric Society, Portland, OR

***Invited Talk*, 2018** *Accounting for confounding in Mendelian randomization using genome wide summary statistics* Probabilistic Modeling in Genomics, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY

***Invited Talk*, 2017** *Adaptive discovery of signal regions in spatially structured genomic data with false discovery rate control* The Western North American Region of the International Biometric Society, Santa Fe, NM

***Contributed Talk*, 2016** *Simultaneous Detection and Estimation of Trait Associations with Genomic Phenotypes*, Joint Statistical Meetings, Chicago IL

Seminars and Workshops

***Invited Seminar*, March 2025** *Genetic Factor Analysis Aids Biological Discovery in High Dimensional Phenotypes*, Channing Division of Network Medicine (CDNM) Genomics Seminar, Brigham and Women's Hospital

***Roundtable*, January 2025** *Value of a Postdoc Panel Discussion*, ASA SSGG, Online

***Invited Seminar*, October 2024** *Network Mendelian Randomization*, Statistical Genetics Seminar, Johns Hopkins University

***Invited Seminar*, April 2024** *Applications of Genetic Factor Analysis for High Dimensional Phenotypes*, D2C2 Seminar Series, Department of Anaesthesiology, University of Michigan

***Invited Seminar*, March 2024** *New Directions in Mendelian Randomization*, Norwegian University of Science and Technology (NTNU) HUNT Center for Molecular and Clinical Epidemiology

***Shortcourse*, Feb 2024** *An Introduction to Mendelian Randomization*, ASA Section on Statistics in Genomics and Genetics

***Workshop*, Feb 2023** *Introduction to K99 Pathway to Independence Award* Early Career Grant Applications Workshop, University of Michigan

***Invited Seminar*, Dec 2022** *Cross-Phenotype Analysis for Causal Inference and Biological Discovery* University of Michigan Statistics Student Seminar Series

***Workshop*, Nov 2022** *Mendelian Randomization* Computational Modeling and Prediction Workshop, IGVF Consortium, virtual

***Symposium Talk*, Sept 2022** *Investigating Selection Bias In the Michigan Genomics Initiative* MGI 10th Anniversary Symposium, University of Michigan

***Invited Seminar*, May 2022** *Cross-Phenotype Analysis for Causal Inference and Biological Discovery* UCLA Bioinformatics Seminar Series

***Invited Seminar*, Feb 2021** *Insights and opportunities from cross-phenome analysis of genome-wide association studies* UC Berkely Biostatistics Seminar Series, virtual

***Invited Seminar*, Dec 2020** *Sparse factor decomposition accounting for correlated errors applied to phenome-wide analysis of genetic associations.* University of Washington Biostatistics Seminar Series, virtual

Software

`Genetic Factor Analysis`: Estimate latent low dimensional structure from GWAS summary statistics. https://jean997.github.io/GFA/

`GWASBrewer`: Realistic simulation of GWAS summary statistics. https://jean997.github.io/GWASBrewer/

`CAUSE`: Mendelian randomization accounting for unmeasured confounding using genome-wide summary statistics. https://jean997.github.io/cause/

`FRET`: Association testing with one dimensional spatially correlated data such as DNase-seq and other genomic phenotypes https://github.com/jean997/fret

`jadeTF`: Differential visualizations and function fitting for one dimensional spatially correlated data https://github.com/jean997/jadeTF

`RCC`: Confidence intervals controlling the rank conditional coverage for high dimensional parameter estimates https://cran.r-project.org/web/packages/rcc/index.html

Funding

Current

R01 HG013104 NIH/NHGRI (PI **Morrison**); $\$1,780,768$ Aug 2023-June 2028

Mendelian randomization for modern data: Integrating data resources to improve accuracy of causal estimates
Role: PI, FTE: 28%

Completed

R01 HG011031 NIH/NHGRI (PI: Zoellner); $\$1,442,296$ Jan 2023 - June 2024

Leveraging long-range haplotypes in sequencing data to advance large scale genetic studies
Role: Biostatistician; FTE: 5%

Elizabeth Caroline Crosby Award (PI **Morrison**); $\$5,000$ Jan 2022 - Sept 2022

Characterizing cross-trait patterns of genetic regulation across anthropometric traits, metabolic dysregulation, and cardiovascular disease.
Role: PI

P30-DK081943 NIH/NIDDK (PI Pennathur); $\$2,906,848$ Jan 2021 - July 2023

University of Michigan O'Brien Kidney Translational Core Center
Role: Biostatsistician

European Commission (PI Ju); $\$766,326$ Jan 2024 - Aug 2024

PRIME-CKD Personalized drug Response: IMplementation and Evaluation in CKD
Role: Co-I, FTE: 17%

Boehringer Ingelheim International (PI: Kretzler); $\$2,295,000$ Jan 2021-Aug 2024

NEPTUNE Public-Private Partnership
Role: Biostatistician; FTE: 10%

Teaching

University of Michigan, Dept of Biostatistics

BIOST 881: Advanced Topics in Causal Inference Winter 2022, 2023, 2024, 2025

https://jean997.github.io/BIOST_881_causal_inference/

BIOST 699: Analysis of Biostatistical Investigations Winter 2021, 2022, 2023, 2025

Big Data Summer Institute: Introduction to Genetics 2022, 2023

Reproducible Research Lecture Annual since 2020

https://jean997.github.io/rr_tools/

Introduction to Snakemake Workshop 2023

https://jean997.github.io/snakemake_tutorial/

University of Washington, Dept of Biostatistics

Teaching Assistant, BIOST 536: Categorical Data Analysis in Epidemiology Fall 2014

Instructor of Record: Scott Emerson

Teaching Assistant, BIOST 540: Correlated Data Analysis Spring 2014

Instructor of Record: Ken Rice

University of Chicago

Teaching Assistant for SESAME Algebra, University of Chicago — Sept 2008 to May 2009
Algebra for middle grade teachers.

Young Scholars Program Counselor, University of Chicago — Sept 2006 to Sept 2007
Math enrichment program for middle school students.

Mentoring and Advising

PhD Supervision

Rouyao Shi	Jan 2022 to Present
Jack Li	Sept 2022 to Present
Jiongming Wang	Jan 2024 to Present

GSTP Training Grant Advisor

Jack Li	Sept 2022 to Aug 2025
Jasmine Mack	Sept 2020 to May 2021

GSRA or Research Supervisor

Ruixuan Wang	May 2025 to Present
Yize Hao	May 2025 to Present
Stefan Eng	Sept 2023 to Present
Brady Ryan	Oct 2024 to Present
Jueyi Liu	Sept 2023 to July 2024
Dhajanae Sylvertooth	Sept 2021 to May 2023
Scott (Chenhao) Shangguan Co-Supervised with Laura Mariani	Summer 2021, Winter 2022

PhD Committee Member

Nam Nguyen-Hoang	2027 (anticipated)
Brady Ryan	2026 (anticipated)
Jiacong Du	2025 (anticipated)
Alicia Dominguez	2025 (anticipated)
Kiran Kumar	2025 (anticipated)
Zheng Li	2025 (anticipated)
Elysia Chou	2025 (anticipated)
Dan Ciotlos	2025 (anticipated)
Guanghao Zhang	2025 (anticipated)

Jeffrey Okamoto	Graduated 2024
Boran Gao	Graduated 2024
Kevin Liao	Graduated 2023
Keitan Yu	Graduated 2023
Ying Ma	Graduated 2023
Pedro Orozco	Graduated 2022
Abhay Hukku	Graduated 2021

Service Activities

ACIC 2025 Program Committee — Sept 2024 to May 2025
University of Michigan

CSG Meeting Organizer — Sept 2024 to Present
University of Michigan

Faculty Advisor, STATCOM — Sept 2022 to May 2024
University of Michigan

70th Anniversary Planning Committee — Winter 2022
University of Michigan

Hiring Committee — Fall 2021, 2024
University of Michigan

Chair, Seminar Committee — Sept 2020 to May 2022
University of Michigan

Faculty Advisor, Student Brownbag Seminar — Sept 2020 to May 2022
University of Michigan

Member, Biostatistics Department Curriculum Committee — Sept 2015 to Aug 2016
University of Washington

Member, Biostatistics Department Student, Faculty Relations Committee — Sept 2014 to May 2015
University of Washington

Peer Review

Ad-hoc peer review for:

- American Journal of Human Genetics
- Annals of Applied Statistics
- Bioinformatics
- Biometrics
- Frontiers in Genetics
- Genetics
- Genetic Epidemiology
- HGG Advances
- Journal of Allergy and Clinical Immunology
- Journal of the American Statistical Association
- Journal of Machine Learning Research
- Nature Communications
- Nature Genetics
- PLOS Computational and Molecular Biology
- PLOS Genetics

Associate Editor PLOS Genetics	2025-Present
Guest Associate Editor for PLOS Genetics	2024
Associate Editor HGG Advances	2024-Present
Reviewer, National Institutes of Health	
NHGRI, Loan Repayment Program	March 2021
NHGRI, F31 Review Group	June 2024

Honors, Awards

John G Searl Assistant Professorship (University of Michigan)	2024-2025
Nan Xiao Prize for Computational Reproducibility (University of Chicgao)	2019
ASA Section on Genetics and Genomics Student Paper Award	2016
Gilbert S. Omenn Award for Academic Excellence (University of Washington)	2016
Ruth L. Kirschstein Predoctoral Individual National Research Service Award, NIH	2016
Biostatistics Statistical Genetics Training Grant, National Institutes of Health	2011 to 2014

Professional Memberships

American Society of Human Genetics	Since 2011
International Biometric Society	
Eastern North American Region	Since 2021
Western North American Region	2017-2019
Society for Causal Inference	Since 2023