

# Jean Morrison

Assistant Professor  
University of Michigan  
Department of Biostatistics

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<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 and In Preparation

1. Kundu, R., Shi, X., **Morrison, J.**, Barrett, J. & Mukherjee, B. A Framework for Understanding Selection Bias in Real-World Healthcare Data. *arXiv*. arXiv: [2304.04652\[stat\]](https://arxiv.org/abs/2304.04652) (Aug. 2023).
2. **Morrison, J.** Empirical Shrinkage Multivariable Mendelian Randomization. *In Preparation* (Oct. 2023).
3. **Morrison, J.**, Sylvertooth, D., Willwerscheid, J., He, X. & Stephens, M. Factor Analysis of Phenome-Wide Genetic Associations Reveals Biological Pathways. *In Preparation* (Oct. 2023).
4. Wang, L., Wen, X. & **Morrison, J.** Imperfect gold standard gene sets yield inaccurate evaluation of causal gene identification methods. en. *bioRxiv*: 2023.05.04.539407. Under consideration at Nature Communications (May 2023).
5. Yin, X., Li, J., Bose, D., Okamoto, J., Kwon, A., Jackson, A. U., Fernandes, L. F., Oravilahti, A., Stringham, H. M., Ripatti, S., Daly, M., Palotie, A., Scott, L. J., Burant, C. F., Fauman, E. B., Wen, X., Boehnke, M., Laakso, M. & **Morrison, J.** Metabolome-wide Mendelian randomization characterizes heterogeneous and shared causal effects of metabolites on human health. *MedRxiv*: 2023.06.26.23291721. Under revision for Nature Communications (June 2023).

## Publications

1. 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. 4, 2023).
2. 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).
  3. 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).
  4. 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., Stitzel, 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).
  5. 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., Stitzel, 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).
  6. **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).
  7. 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).
  8. 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<sup>6</sup>-methyladenosine (m<sup>6</sup>A) modification to human disease heritability. en. *Nature Genetics* **52**. PMCID: PMC7483307, 939–949 (Sept. 2020).
  9. 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**. PMID: PMC6058984, 208–219 (2018).
10. 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**. PMID: PMC5992125, 1031–1047 (2018).
  11. **Morrison, J.** & Simon, N. Rank Conditional Coverage and Confidence Intervals in High Dimensional Problems. *Journal of Computational and Graphical Statistics* **27**. PMID: PMC6364309, 648–656 (2018).
  12. 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**. PMID: PMC5428979 (2017).
  13. 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**. PMID: PMC5968624, 1193–1204 (2017).
  14. **Morrison, J.**, Witten, D. & Simon, N. Simultaneous detection and estimation of trait associations with genomic phenotypes. *Biostatistics* **18**. PMID: PMC6082590, 147–164 (Aug. 2016).
  15. 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**. PMID: PMC4746331, 229–242 (Jan. 2016).
  16. **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**. PMID: PMC4743689, 807–816 (Dec. 2015).
  17. 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**. PMID: PMC3749326, 3282–3291 (Sept. 2013).
18. **Morrison, J.** Characterization and correction of error in genome-wide ibd estimation for samples with population structure. *Genetic Epidemiology* **37**. PMID: PMC4001853, 635–641 (Sept. 2013).
  19. 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**. PMID: PMC3736865, 3583–3596 (Sept. 2013).
  20. 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**. PMID: PMC3761075, 2047–2055 (Aug. 2011).

## Presentations

### CONFERENCE PRESENTATIONS

#### **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 Shrinkage 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 Shrinkage 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

**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

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 esti-

mates <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%
- European Commission (PI Ju); \$766,326 Jan 2024 - Dec 2027  
*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-May 2026  
*NEPTUNE Public-Private Partnership*  
Role: Biostatistician; FTE: 10%
- 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%

### COMPLETED

- 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: Biostatistician

## Teaching

### UNIVERSITY OF MICHIGAN, DEPT OF BIostatISTICS

- BIOST 881: Advanced Topics in Causal Inference Winter 2022, 2023  
[https://jean997.github.io/BIOST\\_881\\_causal\\_inference/](https://jean997.github.io/BIOST_881_causal_inference/)
- BIOST 699: Analysis of Biostatistical Investigations Winter 2021, 2022, 2023
- Big Data Summer Institute: Introduction to Genetics 2022, 2023
- Reproducible Research Lecture Annual since 2020  
[https://jean997.github.io/rr\\_tools/](https://jean997.github.io/rr_tools/)
- Introduction to Snakemake Workshop 2023  
[https://jean997.github.io/snakemake\\_tutorial/](https://jean997.github.io/snakemake_tutorial/)

UNIVERSITY OF WASHINGTON, DEPT OF BIostatISTICS

*Teaching Assistant*, BIOS 536: Categorical Data Analysis in Epidemiology Fall 2014  
Instructor of Record: Scott Emerson

*Teaching Assistant*, BIOS 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

**GSTP Training Grant Advisor**

Jack Li Sept 2022 to Present

Jasmine Mack Sept 2020 to May 2021

**GSRA Supervisor**

Stefan Eng Sept 2023 to Present

Jueyi Liu Sept 2023 to Present

Dhajanae Sylvertooth Sept 2021 to May 2023

Scott (Chenhao) Shangguan Summer 2021, Winter 2022

Co-Supervised with Laura Mariani

**PhD Committee Member**

Dan Ciotlos 2024 (anticipated)

Jeffrey Okamoto 2024 (anticipated)

Boran Gao 2024 (anticipated)

Kevin Liao 2023 (anticipated)

Keitan Yu 2023 (anticipated)

Ying Ma Graduated 2023

Pedro Orozco Graduated 2022

Abhay Hukku Graduated 2021

## Service Activities

### COMMITTEES

Faculty Advisor, STATCOM University of Michigan	Sept 2022 to Present
70th Anniversary Planning Committee University of Michigan	Winter 2022
Hiring Committee University of Michigan	Fall 2021
Chair, Seminar Committee University of Michigan	Sept 2020 to May 2022
Faculty Advisor, Student Brownbag Seminar University of Michigan	Sept 2020 to May 2022
Member, Biostatistics Department Curriculum Committee University of Washington	Sept 2015 to Aug 2016
Member, Biostatistics Department Student, Faculty Relations Committee University of Washington	Sept 2014 to May 2015

### PEER REVIEW

Ad-hoc peer review for:

- American Journal of Human Genetics
- Annals of Applied Statistics
- Biometrics
- Frontiers in Genetics
- Genetics
- 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

Reviewer, National Institutes of Health NHGRI, Loan Repayment Program	March 2021
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## **Honors, Awards**

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