

Jean Morrison

Postdoctoral Scholar
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Department of Human Genetics

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Education

- 2016 PHD BIOSTATISTICS, University of Washington
Advisor: Noah Simon, Department of Biostatistics
- 2009 BA MATHEMATICS, University of Chicago

Professional Positions

- DEPARTMENT OF HUMAN GENETICS, UNIVERSITY OF CHICAGO
- 10.2016–
Present *Postdoctoral Scholar*
Supervisor: Xin He and Mathew Stephens
- DEPARTMENT OF BIOSTATISTICS, UNIVERSITY OF WASHINGTON
- 12.2013–
8.2016 *Research Assistant*
Supervisor: Noah Simon
Statistical methods for spatially structured genomic data and high dimensional studies.
- 6.2014–9.2015 *Research Assistant*, Genetic Analysis Center
Supervisor: Cathy Laurie
Genome wide association analysis of blood cell and dental traits for the Hispanic Community Health Study/ Study of Latinos, a large multi-ethnic study of Latino populations.
- 6.2011–6.2014 *Research Assistant*
Supervisor: Bruce Weir and Tim Thornton
Investigations of population structure and its effects in genetic association studies.
- DEPARTMENT OF MEDICINE, SECTION OF GENETICS, UNIVERSITY OF CHICAGO
- 7.2009–6.2011 *Research Assistant*

Supervisor: Nancy Cox

Genome wide association analysis, quality control and imputation for the Hyperglycemia and Adverse Pregnancy Outcomes (HAPO) study. QC and programming support for other genetic analysis projects.

Honors, Awards

2019	Nan Xiao Prize for Computational Reproducibility
2016	ASA Section on Genetics and Genomics Student Paper Award
	University of Washington School of Public Health Gilbert S. Omenn Award for Academic Excellence
2016	Ruth L. Kirschstein Predoctoral Individual National Research Service Award, National Institutes of Health
2016	Biostatistics Statistical Genetics Training Grant, National Institutes of Health
2011–2014	

Publications

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

Zhang, Z., Luo, K., Zou, Z., Qiu, M., Tian, J., Sieh, L., (2020). "Genetic analyses support the contribution of mRNA N 6-methyladenosine (m6A) modification to human disease heritability". *Nature Genetics*.

Burkart, K. M., Sofer, T., London, S. J., Manichaikul, A., Hartwig, F. P., Yan, Q., (2018). "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* 198.2, pp. 208–219.

Liu, Y., Liang, Y., Cicek, A., Li, Z., Li, J., Muhle, R., (2018). "A Statistical Framework for Mapping Risk Genes from De Novo Mutations in Whole-Genome-Sequencing Studies". *American Journal of Human Genetics* 12.6, pp. 1031–1047.

Morrison, J., Simon, N., (2018). "Rank Conditional Coverage and Confidence Intervals in High Dimensional Problems". *Journal of Computational and Graphical Statistics* 27.3, pp. 648–656.

Hodonsky, C., Jain, D., Schick, U., **Morrison, J.**, Brown, L., McHugh, C., (2017). "Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos". *PLoS Genetics* 13.4.

- Jain, D., Hodonsky, C. J., Schick, U. M., **Morrison, J. V.**, Brown, L., Schurmann, C., (2017). "Genome-Wide Association of White Blood Cell Counts in Hispanic/Latino Americans: The Hispanic Community Health Study/Study of Latinos". *Human Molecular Genetics* 26.6, pp. 1193–1204.
- Morrison, J.**, Witten, D., Simon, N., (2016). "Simultaneous detection and estimation of trait associations with genomic phenotypes". *Biostatistics* 18.1, pp. 147–164.
- Schick, U. M., Jain, D., Hodonsky, C. J., **Morrison, J. V.**, Davis, J. P., Brown, L., (Jan. 2016). "Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans". English. *The American Journal of Human Genetics* 98, pp. 229–242.
- Morrison, J.**, Laurie, C. C., Marazita, M. L., Sanders, A. E., Offenbacher, S., Salazar, C. R., (Dec. 2015). "Genome-wide association study of dental caries in the Hispanic Communities Health Study/Study of Latinos (HCHS/SOL)." *Human Molecular Genetics* 25.4, pp. 807–816.
- Hayes, M. G., Urbanek, M., Hivert, M. F., Armstrong, L. L., **Morrison, J.**, Guo, C., (Sept. 2013). "Identification of HKDC1 and BACE2 as genes influencing glycemic traits during pregnancy through genome-wide association studies". *Diabetes* 62.9, pp. 3282–3291.
- Morrison, J.** (Sept. 2013). "Characterization and correction of error in genome-wide ibd estimation for samples with population structure". *Genetic Epidemiology* 37.6, pp. 635–641.
- Urbanek, M., Hayes, M. G., Armstrong, L. L., **Morrison, J.**, Lowe, L. P., Badon, S. E., (Sept. 2013). "The chromosome 3q25 genomic region is associated with measures of adiposity in newborns in a multi-ethnic genome-wide association study". *Human Molecular Genetics* 22.17, pp. 3583–3596.
- Below, J. E., Gamazon, E. R., **Morrison, J. V.**, Konkashbaev, A., Pluzhnikov, A., McK-eigue, P. M., (Aug. 2011). "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* 54.8, pp. 2047–2055.

PRE-PRINTS AND ARTICLES UNDER REVIEW

- Sakabe, N., Aneas, I., Knoblauch, N., Sobreira, D., Clark, N., Paz, C., (2020). "Transcriptome and regulatory maps of decidua-derived stromal cells inform gene discovery in preterm birth".

Conference Presentations

INVITED AND CONTRIBUTED TALKS

- Morrison, J.**, Knoblauch, N., Marcus, J., Stephens, M., He, X., (2019b). "Mendelian Randomization Accounting for Horizontal and Correlated Pleiotropy Using Genome-Wide Summary Statistics". In: *The Western North American Region of the International Biometric Society*. Portland, Oregon.
- Morrison, J.**, Knoblauch, N., Marcus, J., Stephens, M., He, X., (2018). "Accounting for confounding in Mendelian randomization using genome wide summary statistics". In: *Probabilistic Modeling in Genomics*. Cold Spring Harbor Laboratories.
- Morrison, J.**, Simon, N., (2017). "Adaptive discovery of signal regions in spatially structured genomic data with false discovery rate control". In: *The Western North American Region of the International Biometric Society*. Santa Fe, NM.
- Morrison, J.**, Simon, N., Witten, D., (2016). "Simultaneous Detection and Estimation of Trait Associations with Genomic Phenotypes". In: *Joint Statistical Meetigs*. Chicago, IL.

POSTERS

- Morrison, J.**, Knoblauch, N., Marcus, J., Stephens, M., He, X., (2019a). "Mendelian Randomization Accounting for Correlated and Uncorrelated Pleiotropy Using Genome Wide Summary Statistics". In: *American Society for Human Genetics Meetings*. Houston, Texas.
- Morrison, J.**, Marcus, J., Knoblauch, N., He, X., Stephens, M., (2017). "Integrative analysis of eQTL and GWAS summary statistics to identify functional relationships." In: *American Society for Human Genetics Meetings*. Orlando, Florida.
- Morrison, J.**, Sandstrom, R., Simon, N., (2015). "Locally adaptive comparison of DNase I profiles to detect fine scale differences in regulatory activity." In: *American Society for Human Genetics Meetings*. Baltimore, MD.
- Morrison, J.**, Witten, D., Simon, N., (2014). "JADE: A tool for comparative analysis of spatially smooth genomic data." In: *American Society for Human Genetics Meetings*. San Deigo, CA.
- Morrison, J.** (2012). "Overestimation of relatedness in admixed and ancestrally heterogeneous populations using method of moments estimation." In: *American Society for Human Genetics Meetings*. San Francisco, CA.
- Morrison, J.**, Scheftner, D., Pluzhnikov, A., Lowe, L., Ackerman, C., Armstrong, L., (2011). "SNPs near CCNL1 associated with infant adiposity in multi-ethnic mega-analysis with strongest effect observed in European ancestry newborns". In: *International Congress on Human Genetics meeting*. Montreal, Quebec.

Morrison, J., Pluzhnikov, A., Hayes, M., Lee, H., Levine, D., McHugh, C., (2010). "G6PC2 associated with fasting glucose levels in pregnant women of European ancestry." In: *American Society for Human Genetics Meetings*. Washington, DC.

Software

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>

Teaching Experience

- Fall 2014 *Teaching Assistant*, BIOS T 536: Categorical Data Analysis in Epidemiology
Supervisor: Scott Emerson
- Spring 2014 *Teaching Assistant*, BIOS T 540: Correlated Data Analysis
Supervisor: Ken Rice
- 9.2008–5.2009 *Teaching Assistant for SESAME Algebra*, University of Chicago
Algebra for middle grade teachers.
- 9.2006–9.2007 *Young Scholars Program Counselor/Teaching Assistant*, University of Chicago
Math enrichment program for middle schoolers.

Professional Service

- 9.2015–8.2016 *Member*, Biostatistics Department Curriculum Committee
- 9.2014–5.2015 *Member*, Biostatistics Department Student, Faculty Relations Committee