

# Jiacheng Miao

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## Research interests

My research interests lie in developing generic statistical methods and computational tools to analyze human genetics data. Currently, I am working on gene-environment interactions, genetic risk prediction, and multi-ancestry analysis.

## Education

### **Ph.D. in Biomedical Data Science**

University of Wisconsin-Madison, Sep. 2020- present  
Advisor: Prof. Qiongshi Lu and Prof. Lauren Schmitz

### **M.S. in Statistics**

University of Wisconsin-Madison, Sep. 2019 - May. 2020

### **B.S. in Statistics**

Nanjing University, Sep. 2015 - Jun. 2019

## Awards

Distinguished Student Paper Award, Section on Statistical Genomics and Genetics of the American Statistical Association (ASA), 2022

Reviews' Choice Award, American Society of Human Genetics (ASHG) Annual Meeting, 2021

Second-Class Scholarship for Students (top 10%), Nanjing University, 2018

## Papers and preprints

\* junior authors with equal contribution; † senior authors with equal contribution

### – **Lead-authored**

- [1] **Miao, J.**, Wu Y., Lu Q. (2023). Statistical Methods for Gene-environment Interaction Analysis. (Review) *Submitted*.

- [2] **Miao, J.**, Song G., Wu Y., Hu J., Wu Y., Basu S., Andrews J., Schaumberg K., Fletcher J., Schmitz L., Lu Q. (2022). Reimagining Gene-Environment Interaction Analysis for Human Complex Traits. *Submitted. (preprint available on bioRxiv)* [\[Preprint\]](#) [\[Software\]](#)
- [3] **Miao, J.\***, Guo, H.\* , Song, G., Zhao, Z., Lin, H.<sup>†</sup>, and Lu, Q.<sup>†</sup> (2023). Quantifying portable genetic effects and improving cross-ancestry genetic prediction with GWAS summary statistics. *Nature Communications* [\[Journal\]](#) [\[Preprint\]](#) [\[Software\]](#)
- [4] **Miao J.** and Lu Q. (2022). Identifying genetic loci associated with complex trait variability. *Handbook of Statistical Bioinformatics (2nd Edition)*. Springer (Book Chapter) [\[Book Chapter\]](#)
- [5] **Miao, J.**, Lin, Y., Wu, Y., Zheng, B., Schmitz, L. L., Fletcher, J. M., and Lu, Q. (2022). A quantile integral linear model to quantify genetic effects on phenotypic variability. *Proceedings of the National Academy of Sciences (PNAS)* [\[Journal\]](#) [\[Preprint\]](#) [\[Software\]](#)
  - This work wins **Distinguished Student Paper Award** from the Section on Statistical Genomics and Genetics of the American Statistical Association (ASA), 2022.
  - This work wins **Reviews' Choice Award** from American Society of Human Genetics Meeting (ASHG) Annual Meeting, 2021.
- **Collaborative & co-authored**
- [6] IGVF Consortium (2023). The impact of genomic variation on function (IGVF) consortium. *Submitted. (preprint available on arXiv)*
- [7] He, Q., Keding, T., Zhang, Q., **Miao J.**, Herringa, R., Lu, Q., Travers, B., & Li, J. J. (2022). Neurogenetic Mechanisms of Risk for ADHD: Examining Associations of Functionally-Annotated Polygenic Scores and Brain Volumes in a Population Cohort. *Submitted. (preprint available on medRxiv)*
- [8] Deming Y., Vasiljevic E., Morrow A., **Miao, J.**, Van Hulle C., Jonaitis E., Ma Y., Whitenack V., Kollmorgen G., Wild N., Suridjan I., Shaw L., Asthana S., Carlsson C., Johnson S., Zetterberg H., Blennow K., Bendlin B., Lu Q., Engelman C., the Alzheimer's Disease Neuroimaging Initiative (2022). Neuropathology-based APOE genetic risk score better quantifies Alzheimer's risk. *Alzheimer's & Dementia*
- [9] Zhao, Z., Gruenloh, T., Wu, Y., Sun, Z., **Miao, J.**, Wu, Y., Song, J., Lu, Q. (2022). Optimizing and benchmarking polygenic risk scores with GWAS summary statistics. *Submitted. (preprint available on bioRxiv)*
- [10] Song, J., Zou Y., Wu, Y., **Miao, J.**, Yu, Z., Fletcher, J., Lu, Q. (2022). Decomposing heritability and genetic covariance by direct and indirect effect paths. *PLOS Genetics* [\[Journal\]](#)
- [11] Schmitz, L. L., Zhao, W., Ratliff, S. M., Goodwin, J., **Miao, J.**, Lu, Q., ..., and Smith, J. A. (2021). The Socioeconomic Gradient in Epigenetic Ageing Clocks: Evidence from the Multi-Ethnic Study of Atherosclerosis and the Health and Retirement Study. *Epigenetics*, 1-23. [\[Journal\]](#)
- [12] Schmitz, L. L., Goodwin, J., **Miao, J.**, Lu, Q., and Conley, D. (2021). The impact of late-career job loss and genetic risk on body mass index: Evidence from variance polygenic scores. *Scientific reports*, 11(1), 1-15. [\[Journal\]](#)

## Presentations

- [1] Talk, 2023 Frontiers of Economic Analysis with Genetic Data, UChicago Mar. 2023  
*Reimagining Gene-Environment Interaction Analysis for Human Complex Traits.*
- [2] Poster, 2022 American Society of Human Genetics Annual Meeting Oct. 2022  
*Quantifying portable genetic effects and improving cross-ancestry genetic prediction with GWAS summary statistics.*
- [3] Talk, 2022 Integrating Genetics and the Social Sciences conference Sep. 2022  
*Reimagining Gene-Environment Interaction Analysis for Human Complex Traits*
- [4] Student paper award winner talk, 2022 Joint Statistical Meetings. Aug. 2022  
*A quantile integral linear model to quantify genetic effects on phenotypic variability.*
- [5] Poster, Annual Center for Genomic Science Innovation Retreat, UW-Madison. June 2022  
*Reimagining Gene-Environment Interaction Analysis for Human Complex Traits*
- [6] Poster, Annual CIBM and BDS Retreat, UW-Madison. June 2022  
*Quantifying portable genetic effects and improving cross-ancestry genetic prediction with GWAS summary statistics.*
- [7] Talk, the 35th New England Statistics Symposium, UConn. (Virtual) May 2022  
*Quantifying portable genetic effects and improving cross-ancestry genetic prediction with GWAS summary statistics.*
- [8] Talk, 2021 Integrating Genetics and the Social Sciences conference Oct. 2021  
*A quantile integral linear model to quantify genetic effects on phenotypic variability.*
- [9] Poster, 2021 American Society of Human Genetics Annual Meeting (Virtual) Oct. 2021  
*A quantile integral linear model to quantify genetic effects on phenotypic variability.*
- [10] Poster, 2020 American Society of Human Genetics Annual Meeting (Virtual) Oct. 2020  
*A quantile regression framework to identify genetic loci affecting phenotypic variability.*
- [11] Talk, 2019 Integrating Genetics and the Social Sciences conference Sep. 2019  
*Testing gene-environment interactions without measuring the environment.*

## Software

- **PIGEON** for polygenic gene-environment interaction inference.  
<https://github.com/qlu-lab/PIGEON>
- **X-Wing** for improving cross-population polygenic prediction.  
<https://github.com/qlu-lab/X-Wing>
- **QUAIL** for estimating genetic effects on the variance of quantitative traits.  
<https://github.com/qlu-lab/QUAIL>
- **SGEGG** for fitting the linear mixed model to identify genome-wide gene-environment or gene-gene interactions for repeated measures.  
<https://github.com/jmiao24/SGEGG>

## Teaching

- **Teaching Assistant**
  - BMI826: Statistics in Human Genetics, Spring 2022-2023.
- **Guest Lecturer**
  - BMI826: Statistics in Human Genetics, Spring 2022-2023.

## Professional activities and Mentoring

- **Reviewer for Journals:** Behaviour Genetics, BMC Genomics
- **Review Editor:** Frontiers in Genetics
- **Research Mentor**
  - Yixuan Wu (05/2022 - present) Undergraduate student in computer science at UW-Madison, Winner of Hilldale Undergraduate/Faculty Research Award
  - Gefei Song (07/2020 - 06/2022) Undergraduate student in biology and statistics at UW-Madison, Winner of Hilldale Undergraduate/Faculty Research Award

## Industry experience

- **Summer 2023, Regeneron, Tarrytown, NY**
  - Ph.D. intern in Regeneron Genetics Center