

Yihe Yang, Ph.D.

Research Associate

Department of Population and Quantitative Health Sciences

Case Western Reserve University School of Medicine

yxy1234@case.edu · 216-304-0664 · GitHub · Google Scholar

Research Profile

- Statistician working on **causal inference, statistical genetics, and high-dimensional methods**, with applications to Mendelian randomization, gene prioritization, and personalized treatment policies.
- Author of **12 published, accepted, or in-press articles**, including eight as first, co-first, sole, or corresponding author, with publications in *Nature Communications*, *Genome Biology*, *Biometrics*, and other statistical and genomic journals.
- Current methodological work includes robust multivariable and multi-ancestry Mendelian randomization, transcriptome-wide association analysis, and sparse policy learning for continuous treatments.
- Sole or lead developer of **four open-source R packages** translating statistical methodology into tools for genetic and genomic research.

Employment

- **Research Associate**
Case Western Reserve University School of Medicine, Cleveland, OH Mar. 2026 – Present
- **Postdoctoral Scholar**
Case Western Reserve University School of Medicine, Cleveland, OH Mar. 2022 – Feb. 2026

Education

- **Doctor of Philosophy (Ph.D.) in Statistics**
Sichuan University, Chengdu, P.R. China Sep. 2015 – Dec. 2021
- **Bachelor of Science in Mathematics**
Wuhan University, Wuhan, P.R. China Sep. 2011 – Jun. 2015

Selected Honors and Awards

- **Featured Plenary Abstract Presentation — ASHG Annual Meeting, Montréal, Canada, 2026.**
Selected for one of 12 abstract-driven plenary talks, the meeting's most selective abstract presentation category.
Recognized work: "Fine-mapping gene-gene and gene-environment interactions at phenotype-associated loci."
- **Best of *AJHG* and *HGG Advances* — Cell Press, 2024 and 2025.**
Editorial selection recognizing the most impactful papers published across the two flagship journals of the American Society of Human Genetics, in two consecutive years; also listed as a highlighted publication in the ASHG 2024–2025 Annual Report.
Recognized work: "MRBEE: A bias-corrected multivariable Mendelian randomization method" (*HGG Advances*, 2024).

First-, Co-First-, Sole-, and Corresponding-Author Publications and Manuscripts

† co-first author; * corresponding author.

- Bian, Z.[†], **Yang, Y.**[†], Moodie, E. E. M., & Wang, L. (2026). Learning parsimonious policies for continuous treatments with an application to optimizing sleep recommendations for college students. Submitted to *Journal of the American Statistical Association*.
- **Yang, Y.**, Lee, D., Chakravarti, A.* , & Zhu, X.* (2026). Partitioned blood pressure polygenic risk reveals differential genetic effects of tissue-specific enhancers and their interactions on cardiovascular disease. *Nature Genetics*, under review. Preprint
- **Yang, Y.**, Lin, Z., Xue, H., & Zhu, X.* (2026). Recalibrating Mendelian randomization under winner's curse, sample structure and polygenicity. *The American Journal of Human Genetics*, under review.
- **Yang, Y.** & Lin, Z.* (2026). Dissecting shared and trait-specific causal factors with a robust multi-exposure and multi-outcome Mendelian randomization framework. Submitted to *JASA*.
- **Yang, Y.*** & Zhu, X. (2026). Testing parametric structure in genetic age-effect curves: A GAM-based framework with application to the UK Biobank. *Journal of the American Statistical Association*, under review (minor revision invited). *Sole first author and corresponding author*. Preprint
- **Yang, Y.** & Zhu, X.* (2026). MRBEE-TL: Improving causal effect estimation in multi-ancestry multivariable Mendelian randomization with transfer learning. *Genome Biology*, published 30 Mar. 2026.
- **Yang, Y.*** (2026). Factor-augmented group effect selection with application to gene set analysis. *Statistics Innovation*, 3(1). *Sole author*.
- **Yang, Y.**, Lorincz-Comi, N., & Zhu, X.* (2025). Uncovering causal gene-tissue pairs and variants through a multivariate TWAS controlling for infinitesimal effects. *Nature Communications*, 16(1), 6098.
- **Yang, Y.**, Lorincz-Comi, N., Li, M., & Zhu, X.* (2025). Cis-MRBEE: A multivariable cis-Mendelian randomization method robust to weak instrument bias and horizontal pleiotropy bias. *Briefings in Bioinformatics*, 26(3), bbaf250.
- Lorincz-Comi, N.[†], **Yang, Y.**[†], Li, G., & Zhu, X.* (2024). MRBEE: A bias-corrected multivariable Mendelian randomization method. *Human Genetics and Genomics Advances*, 5(3). *Selected as Best of Cell Press, 2024 and 2025*.
- **Yang, Y.**, Lorincz-Comi, N., & Zhu, X.* (2024). Estimation of a genetic Gaussian network using GWAS summary data. *Biometrics*, 80(4), ujae148.
- **Yang, Y.**, Dai, H., & Pan, J.* (2023). Block-diagonal precision matrix regularization for ultra-high dimensional data. *Computational Statistics & Data Analysis*, 179, 107630.
- **Yang, Y.**, Zhou, J., & Pan, J.* (2021). Estimation and optimal structure selection of high-dimensional Toeplitz covariance matrix. *Journal of Multivariate Analysis*, 184, 104739.

Collaborative Publications

- Zhu, X.* , **Yang, Y.**, et al. (2024). An approach to identify gene-environment interactions and reveal new biological insight in complex traits. *Nature Communications*, 15(1), 3385.
- Lorincz-Comi, N., **Yang, Y.**, Zhu, X.* , et al. (2025). HORNET: Tools to find genes with causal evidence and their regulatory networks using eQTLs. *Bioinformatics Advances*, 5(1), vbaf068.
- Lorincz-Comi, N., **Yang, Y.**, & Zhu, X.* (2024). simmrdr: An open-source tool to perform simulations in Mendelian randomization. *Genetic Epidemiology*, 48(2), 59–73.
- Peng, C., **Yang, Y.**, Zhou, J., & Pan, J.* (2022). Latent Gaussian copula models for longitudinal binary data. *Journal of Multivariate Analysis*, 189, 104940.

Research Funding and Grant Applications

- **NIH/NHGRI K99/R00 Pathway to Independence Application, 2026.**

“Statistical Methods for Discerning Shared and Population-Specific Genetic Architectures of Complex Traits.”

Principal Investigator. Reviewed and discussed by study section.

- **NIH/NHGRI R01 HG011052** (X. Zhu, PI), 2020–2028.

“Statistical analysis of large genomic data sets.”

Key Investigator. Contributed core statistical methodology to the majority of publications produced under this grant, including two *Nature Communications* papers and the *Human Genetics and Genomics Advances* paper selected as Best of Cell Press 2024.

- **NIH/NHLBI R01 HL086694** (A. Chakravarti, PI; X. Zhu, sub-contract PI), 2023–2027.

“From GWAS Loci to Blood Pressure Genes, Variants and Mechanisms (FEHGAS4).”

Key Investigator. Lead statistical contributor to the project component on partitioned blood pressure polygenic risk scores and the differential genetic effects of tissue-specific enhancers and gene–environment interactions on cardiovascular disease.

Editorial and Peer Review Service

- **Youth Editorial Board Member, *Statistics Innovation***, 2025–present.

- **Peer reviewer for twelve international scientific journals**, having completed multiple rounds of review for: *Nature Communications* (2023, 3 rounds; 2025, 1 round); *Cell Genomics* (2026, 1 round); *PLoS Genetics* (2024, 2 papers; 2025, 2 papers; 2026, ongoing); *Statistics in Medicine* (2026, 2 papers, ongoing); *Biometrics* (2024, 2 rounds; 2025, 1 round); *Journal of Genetics and Genomics* (2025, 2 rounds); *Human Genetics and Genomics Advances* (2024, 2 rounds); *Bioinformatics* (2025, 1 round); *Clinical Epidemiology* (2025, 1 round); *Statistics Innovation* (2025, 1 round); *Pediatric Research* (2024, 2 rounds); *Clinical, Cosmetic and Investigational Dermatology* (2024, 1 round).

Open-Source Software Contributions

All packages implement novel statistical methods developed in the candidate’s published research.

- **TGVIS** — *Sole developer*. R package implementing the multivariate TWAS method controlling for infinitesimal effects published in *Nature Communications* (2025).

github.com/harryiheyang/TGVIS

- **MRBEE** — *Sole developer*. R package implementing the cis-MRBEE and MRBEE-TL methods published in *Briefings in Bioinformatics* (2025) and *Genome Biology* (2026).

github.com/harryiheyang/MRBEE

- **EGG** — *Sole developer*. R package implementing the genetic Gaussian network estimation method published in *Biometrics* (2024).

github.com/harryiheyang/EGG

- **MRBEE** — *Co-developer* (with N. Lorincz-Comi). R package implementing the bias-corrected multivariable Mendelian randomization method published in *HGG Advances* (2024) and selected as Best of Cell Press 2024.

github.com/noahlorinczcomi/MRBEE

Selected International Conference Presentations

- **ASHG Annual Meeting**, Montréal, Canada, 2026. Fine-mapping gene-gene and gene-environment interactions at phenotype-associated loci. (*Featured Plenary Oral Presentation*)
- **ASHG Annual Meeting**, Boston, MA, 2025. Partitioning polygenic risk scores using tissue-CREs and their impacts on cardiovascular disease. (Poster)
- **IGES Annual Meeting**, Cologne, Germany, 2025. Improving causal effect estimation in multi-ancestry Mendelian randomization with transfer learning. (*Selected Oral Presentation*)
- **ASHG Annual Meeting**, Denver, CO, 2024. Uncovering causal gene-tissue pairs and variants: A multi-variable TWAS method that controls for infinitesimal effects. (*Reviewers' Choice Poster*)
- **IGES Annual Meeting**, Denver, CO, 2024. Selecting associated variants as instrument variables can bias multivariable Mendelian randomization. (Poster)
- **ASHG Annual Meeting**, Washington D.C., 2023. Multivariable Mendelian randomization reveals potential causal genes that contribute to blood pressure traits in diverse populations. (*Reviewers' Choice Poster*)
- **IGES Annual Meeting**, Nashville, TN, 2023. Joint selection of exposures and horizontal pleiotropy in multivariable Mendelian randomization with application to causal gene identification. (*Selected Oral Presentation; Neel Award Finalist*)
- **ASHG Annual Meeting**, Los Angeles, CA, 2022. Improving the accuracy and interpretation of polygenic risk scores through modeling pathways of disease and multiple risk factors. (Poster)

Teaching Experience

- **Teaching Assistant for a Graduate Statistics Course**, Case Western Reserve University. Assisted Dr. Xiaofeng Zhu during postdoctoral training.

Mentoring

- Co-mentoring two PhD students in the Zhu Laboratory at Case Western Reserve University, providing day-to-day supervision on methodological projects in transcriptome-wide association studies (TWAS) and rare variant association testing.

Professional Memberships

- Member, American Society of Human Genetics (ASHG), 2022–present.
- Member, International Genetic Epidemiology Society (IGES), 2023–present.