Zhaotong Lin

401 Statistics Building Department of Statistics, Florida State University

Employment

Florida State University Assistant Professor, Department of Statistics

Education

University of MinnesotaMinneapolis, United StatesPhD in BiostatisticsJune 2023Thesis: Robust Mendelian Randomization Methods Based on Constrained Maximum Likelihood for Causal InferenceSun Yat-sen UniversitySun Yat-sen UniversityGuangzhou, ChinaB.Sc. in Applied MathematicsJune 2019

Research Interests

Statistical genetics, Mendelian randomization, polygenic risk scores prediction, GWAS, TWAS, gene prioritization and drug discovery

PUBLICATIONS

- L. Fang, H. Xue, Z. Lin, and W. Pan, "Multivariate proteome-wide association study to identify causal proteins for alzheimer disease," *The American Journal of Human Genetics*, vol. 112, no. 2, pp. 291–300, 2025.
- [2] P. Wang, Z. Lin, and W. Pan, "Unbiased causal inference with mendelian randomization and covariate-adjusted gwas data," *Human Genetics and Genomics Advances*, vol. 6, no. 2, p. 100412, 2025.
- [3] Z. Lin, I. Pan, and W. Pan, "On network deconvolution for undirected graphs," *Biometrics*, vol. 80, p. ujae112, 10 2024.
- [4] Z. Lin, "A novel framework with automated horizontal pleiotropy adjustment in mendelian randomization," Human Genetics and Genomics Advances, vol. 5, no. 4, 2024.
- [5] Z. Lin and W. Pan, "A robust cis-mendelian randomization method with application to drug target discovery," *Nature Communications*, vol. 15, no. 1, p. 6072, 2024.
- [6] P. Wang, Z. Lin, H. Xue, and W. Pan, "Collider bias correction for multiple covariates in gwas using robust multivariable mendelian randomization," *Plos Genetics*, vol. 20, no. 4, p. e1011246, 2024.
- [7] S. H. Kwak, ..., Z. Lin, ..., J. Rotter, J. Meigs, and Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium, "Time-to-event genome-wide association study for incident cardiovascular disease in people with type 2 diabetes," *Diabetes Care*, vol. 47, pp. 1042–1047, 04 2024.
- [8] A. Patel, T. Ye, H. Xue, Z. Lin, S. Xu, B. Woolf, A. M. Mason, and S. Burgess, "Mendelianrandomization v0. 9.0: updates to an r package for performing mendelian randomization analyses using summarized data," Wellcome Open Research, vol. 8, 2023.
- [9] S. Chen, Z. Lin, X. Shen, L. Li, and W. Pan, "Inference of causal metabolite networks in the presence of invalid instrumental variables with gwas summary data," *Genetic Epidemiology*, 2023.
- [10] J. Ren, Z. Lin, and W. Pan, "Integrating gwas summary statistics, individual-level genotypic and omic data to enhance the performance for large-scale trait imputation," *Human Molecular Genetics*, p. ddad097, 2023.
- [11] Z. Lin, H. Xue, and W. Pan, "Combining mendelian randomization and network deconvolution for inference of causal networks with gwas summary data," *PLoS genetics*, vol. 19, no. 5, p. e1010762, 2023.
- [12] J. Ren, Z. Lin, R. He, X. Shen, and W. Pan, "Using gwas summary data to impute traits for genotyped individuals," *Human Genetics and Genomics Advances*, vol. 4, no. 3, 2023.
- [13] Z. Lin, H. Xue, and W. Pan, "Robust multivariable mendelian randomization based on constrained maximum likelihood," *The American Journal of Human Genetics*, vol. 110, no. 4, pp. 592–605, 2023.
- [14] R. He, M. Liu, Z. Lin, Z. Zhuang, X. Shen, and W. Pan, "Delivr: a deep learning approach to iv regression for testing nonlinear causal effects in transcriptome-wide association studies," *Biostatistics*, vol. 25, no. 2, pp. 468–485, 2024.
- [15] Z. Lin, K. A. Knutson, and W. Pan, "Leveraging omics data to boost the power of genome-wide association studies," *Human Genetics and Genomics Advances*, vol. 3, no. 4, 2022.

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Tallahassee, United States August 2023 - Present

- [16] Z. Lin, I. Pan, and W. Pan, "A practical problem with egger regression in mendelian randomization," *PLoS genetics*, vol. 18, no. 5, p. e1010166, 2022.
- [17] Z. Lin, S. Seal, and S. Basu, "Estimating snp heritability in presence of population substructure in biobank-scale datasets," *Genetics*, vol. 220, no. 4, p. iyac015, 2022.
- [18] Z. Lin, H. Xue, M. M. Malakhov, K. A. Knutson, and W. Pan, "Accounting for nonlinear effects of gene expression identifies additional associated genes in transcriptome-wide association studies," *Human molecular* genetics, vol. 31, no. 14, pp. 2462–2470, 2022.
- [19] Z. Lin, Y. Deng, and W. Pan, "Combining the strengths of inverse-variance weighting and egger regression in mendelian randomization using a mixture of regressions model," *PLoS genetics*, vol. 17, no. 11, p. e1009922, 2021.

PRESENTATIONS

- A robust cis-Mendelian randomization method with application to drug target discovery Invited presentation, PCIC, Shanghai (virtual), July 2024 Invited presentation, ICSA Canada chapter, Niagara Falls, Jun 2024 Invited presentation, STATGEN, Pittsburg, May 2024 Invited presentation, MCBIOS, Atalanta, March 2024 Poster presentation, ASHG, Washington DC, Nov 2023 Platform presentation, IGES, Nashville, Nov 2023
- Inference of causal networks using bi-directional Mendelian randomization and network deconvolution with GWAS summary data Contributed talk, ENAR, Nashville, Mar 2023 Platform presentation, ASHG, Los Angeles, Oct 2022
- Combining the strengths of inverse-variance weighting and Egger regression in Mendelian randomization using a mixture of regressions model Contributed talk, ENAR, Houston, Mar 2022 Poster presentation, ASHG, Virtual, Oct 2021 Platform presentation, IGES, Virtual, Oct 2021

Awards and Scholarships

- Jacob E. Bearman Student Achievement Award, University of Minnesota, 2023
- Biostatistics Research Assistant Award, University of Minnesota, 2021, 2022
- Williams Award Finalist, International Genetic Epidemiology Society, 2021, 2023
- Dean's PhD Scholars Award, University of Minnesota, 2019
- Outstanding Graduate, Sun Yat-sen University, 2019
- National Scholarship, China, 2016, 2017

ACADEMIC SERVICE

• Reviewer for Nature Mental Health, Nature Communications, American Journal of Human Genetics, PLoS Genetics, Frontiers in Genetics, Bioinformatics, BMC Genomics, PLoS ONE, Statistics in Biosciences, Genetic Epidemiology