Yuxin Li

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EDUCATION

Fudan University   Sep. 2022 – Jun. 2026 (Expected)
B.S. in Data Science, GPA: 3.72/4.0 (93/100)   *Shanghai, China*

PUBLICATIONS

Li, Y., Lu, Z., & Lin, X. (2025). Adaptive Partial Conjunction Hypothesis: Identifying Pleiotropy Across Heterogeneous Effect Units. *bioRxiv* (preprint). https://doi.org/10.1101/2025.11.25.690340

RESEARCH EXPERIENCE

Adaptive Partial Conjunction Hypothesis: Identifying Pleiotropy Across Heterogeneous Effect Units

Advisor: Xiaolei Lin, School of Data Science, Fudan University   Aug. 2024 – Present

– Formulated detection of pleiotropy across effects (SNPs, genes) and features (traits, tissues) as a large-scale partial conjunction hypothesis problem with rigorous FDR control on selected subsets.
– Built a hierarchical shrinkage model that ties adaptive shrinkage (ash) priors to joint significance patterns across features while accommodating correlated noise.
– Designed a greedy, level-by-level inference procedure based on multivariate local FDR.
– Conducted simulation studies with OPERA, Repfdr, ASSET, and CPBayes, showing the highest power and well-calibrated FDR across most settings (with heterogeneous effect sizes and noise correlation).
– Applied the method to five T2D-related GWAS traits, identifying loci with co-occurring significance patterns.
– Developed the R package APCH with parallelization and other optimizations for large-scale problems (likelihood factorization, ash grid distillation).

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Preprint   R package

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Multi-tissue Transcriptomic Responses to Partitioned Polygenic Risk in Type 2 Diabetes

Advisor: Xin He, Department of Human Genetics, University of Chicago   Apr. 2025 – Present

– Leading a project integrating partitioned polygenic scores for T2D with GTEx v8 multi-tissue RNA-seq expression data to study tissue-specific responses to distinct components of genetic liability.
– Viewed the setting as a multi-condition (partitioned polygenic scores), multi-tissue transcriptomic experiment and focused the analysis on how distinct genetic deficits underlying insulin resistance shape responses and crosstalk among key metabolic tissues.
– Built a unified enrichment framework that starts from GO GSEA and then uses semantic and network-based clustering to distill highly redundant gene sets into cross-condition, cross-tissue comparable pathway themes.
– Used genes driving enrichment signals across conditions and tissues to nominate tissue-specific biomarker candidates and construct protein–protein interaction networks defining cross-tissue insulin resistance modules.

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Project page

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RELEVANT COURSEWORK

Mathematical Statistics (Honors) (A); Causal Inference (A); Stochastic Processes (A); Statistical Computing (A); Multivariate Statistics (A); Big Data Statistics for Medical Treatment (A); Artificial Intelligence (in progress)

HONORS & AWARDS

Fudan Undergraduate Research Opportunities Program Grant	2025
China Undergraduate Mathematical Contest in Modeling, First Prize (Provincial Level)	2024
Fudan University Undergraduate Outstanding Student Scholarship	2023, 2024
High School Biology Olympiad, First Prize (Provincial Level)	2021

SKILLS

Languages: Mandarin (native), English (TOEFL 107)
Programming: R, C++, Python, LaTeX