

YUHUA ZHANG

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EDUCATION

University of Michigan, Ann Arbor, Michigan

2019.9-2023(expected)

Ph.D. in Biostatistics

Dissertation Topic: Statistical Modeling of Large-scale Social Network Data

Supervised by: Dr. Walter Dempsey & Dr. Sebastian Zoellner

University of Michigan, Ann Arbor, Michigan

2017.9-2019.4

M.S. in Biostatistics

Shanghai Jiaotong University, Shanghai, China

2013.9-2017.6

B.S. in Biology

Thesis: Identifying Causal Variants of Complex Diseases Based on GWAS Data

RESEARCH INTERESTS

Social Network Modeling, Large-scale Network Data Analysis, Bayesian Nonparametric Method, Statistical Inference for High Dimensional Data, Statistical Genetics

PROFESSIONAL SKILLS SUMMARY

Computing Skills

- Computing language: Python, R, SQL
- Able to work under Linux environment
- Able to learn new tools in a decent amount of time

Statistical Modeling

- Bayesian Nonparametric Method
- Statistical Inference
- (Generalized) Linear Regression Model

Data Experience

- Large-scale Network Data - Interaction data from the TalkLife Platform
- High dimensional data/ Genomic Data - Exome sequence data from Prechter Project and MGI Project

Communication Skills

- Demonstrated ability to present the research work and analysis results clearly and precisely
- Experience with collaborating and communicating efficiently with team members

Language:

- Chinese (native), English (working)

PROFESSIONAL EXPERIENCE

University of Michigan, Ann Arbor

Graduate Student Research Assistant

2018.9 – present

- Identified the underlying community structures of the network data from TalkLife to help the platform provide proper supports to certain users.
- Pre-processed and analyzed the exome sequence data in Prechter Project for Bipolar Disorder.
- Analyzed the 15-yr longitudinal data collected from 1,159 bipolar patients to improve clinical diagnosis.

Yale University

Research Assistant

2016.9 – 2017.5

- Integrated functional annotation to prioritize GWAS summary stats.
- Proposed an innovative fine-mapping model under Bayesian framework.
- Compared polygenic risk scores in different simulation settings.

PUBLICATIONS

Ryan, K. A., Han, P., **Zhang, Y.**, Marshall, D. F., Yocum, A. K., McInnis, M. G., Zöllner, S. (2021). Stability of personality traits in bipolar disorder: Findings from a longitudinal cohort. *Journal of Affective Disorders*, 283, 1-10.

Zhang, Y., Quick, C., Yu, K., Barbeira, A., Luca, F., Pique-Regi, R., ... & GTEx Consortium. (2019). Investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. *bioRxiv*, 808295.

Hu, Y., Lu, Q., Liu, W., **Zhang, Y.**, Li, M., & Zhao, H. (2017). Joint modeling of genetically correlated diseases and functional annotations increases accuracy of polygenic risk prediction. *PLoS genetics*, 13(6), e1006836.

Manuscripts in Preparation

Zhang, Y., Dempsey, W. An edge exchangeable model based community detection method for large-scale network data

Zhang, Y., Zoellner, S. Integrating gene co-expression network communities into the effect size estimation

LEADERSHIP AND SERVICE

Department of Biostatistics, University of Michigan, Ann Arbor

- Co-founder and member of the DEI Student Committee, August 2020- April 2021
- Co-founder and member of the Student Research Conflict Committee, August 2020- April 2021
- Departmental DEI committee member, January 2019- June 2020