YUHUA ZHANG

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SUMMARY

Yuhua Zhang is a third year Ph.D. candidate at the Biostatistics Department, University of Michigan, whose research focuses on high-dimensional statistical inference with an emphasis on large-scale social network data and exome sequencing data.

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
Selected Coursework: **L**inear Regression, **S**tatistical Inference, **B**ayesian Modeling, **N**umerical Linear Algebra, **S**tatistical Computing, **S**tochastic Process, **L**inear Programming, **M**achine Learning

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

Statistical Inference for High Dimensional Data, Graph Clustering, Bayesian Nonparametric Method, Large-scale Network Data Analysis, Causal Inference in 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 Methods
· Statistical Inference
· (Generalized) Linear Regression Model

Data Experience
· Large-scale Network Data
—- Interaction data of 1.1 million users 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 provides proper supports to certain users.
· Searched for potential genetic markers for bipolar disorder to improve the clinical diagnosis in the Prechter research program.
· Analyzed the longitudinal data collected from 1,159 bipolar patients over 15 years and identified patterns of multiple clinical outcomes.

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., ... Wen, X. (2020). PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. Genome biology, 21(1), 1-26.

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 (Preview)

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