JIAQI ZHANG

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EDUCATION

Brown University, United States

Sep. 2021 - June. 2026 (anticipated)

Ph.D., Computer Science

Southeast University, China

B.S., Software Engineering

Sep. 2015 - Jun. 2020

GPA: **3.56**/4.00

RESEARCH INTEREST

Bioinformatics: single-cell analysis, multi-modal integration, model interpretation, gene network Machine Learning: multi-modal learning, manifold learning, large-scale optimization, probabilistic graphical model

PUBLICATIONS

(★: conference paper; †: journal paper; △: preprint)

- △ **Jiaqi Zhang**, Manav Chakravarthy, and Ritambhara Singh. scMultiNODE: Integrative and Scalable Framework for Multi-Modal Temporal Single-Cell Data. *biorxiv*, 2024 (doi.org/10.1101/2024.10.27.620531).
- * Jiaqi Zhang, Erica Larschan, Jeremy Bigness, and Ritambhara Singh. scNODE: Generative Model for Temporal Single Cell Transcriptomic Data Prediction. 23rd European Conference on Computational Biology (ECCB) 2024 (Proceedings in Bioinformatics).
- ★ Jiaqi Zhang, Yiqin Wang, Meng Wang, and Beilun Wang. Sparse and Smooth Additive Isotonic Model in High-Dimensional Settings. *Machine Learning*, 2024 (in press).
- † **Jiaqi Zhang** and Ritambhara Singh. Investigating the Complexity of Gene Co-expression Estimation for Single-cell Data. *Journal of Machine Learning for Modeling and Computing*, 2023.
- † Beilun Wang, **Jiaqi Zhang**, Haoqing Xu, and Te Tao. Fast and scalable learning of sparse changes in high-dimensional graphical model structure. *Neurocomputing*, 2022.
- † Qianli Yang, Zhongqiao Lin, Wenyi Zhang, Jianshu Li, Xiyuan Chen, **Jiaqi Zhang**, and Tianming Yang. Monkey plays Pac-Man with compositional strategies and hierarchical decision-making. *Elife*, 2022.
- [†] Beilun Wang, **Jiaqi Zhang**, Yan Zhang, Meng Wang, and Sen Wang. Scalable Estimator for Multi-task Gaussian Graphical Models Based in an IoT Network. *ACM Transactions on Sensor Networks*, 17(3), June 2021.
- * Jiaqi Zhang, Meng Wang, Qinchi Li, Sen Wang, Xiaojun Chang, and Beilun Wang. Quadratic Sparse Gaussian Graphical Model Estimation Method for Massive Variables. *International Joint Conferences on Artificial Intelligence Organization (IJCAI)*, 2020.

AWARDS

2024 ECCB Travel Fellowship

2021-2022 Brown Graduate Fellowship

CONFERENCE AND TALKS

Title: scMultiNODE: Integrative and Scalable Framework for Multi-Modal Temporal Single-Cell Data

2024 ECCB: Poster Presentation

2024 CSHL Biological Data Science: Poster Presentation

2025 System Biology of Singel Cells (SysBioSC): Poster Presentation

<u>Title</u>: scNODE: Generative Model for Temporal Single Cell Transcriptomic Data Prediction

2023 MLCB, 2024 RECOMB: Poster Presentation

2024 ECCB: Selected Talk

Title: Quadratic Sparse Gaussian Graphical Model Estimation Method for Massive Variables

2020 IJCAI: Selected Talk & Poster Presentation

TECHNICAL SKILLS

Programming Language Python, R, C++, MATLAB, JAVA

Machine Learning Pytorch, Tensorflow, Pyro, Pytorch-Geometric (PyG), Python OT, Sklearn

Data Processing Numpy, Pandas, SciPy, AnnData

Bioinformatics ScanPy, Seurat

Data Visualization matplotlib, seaborn, ggplot

PROFESSIONAL COMMUNITY SERVICE

2025 Reviewer of ACM BCB conference.

2022 - 2025 Sub-reviewer of ICML, NeurIPS, ICLR, and RECOMB conferences.

TEACHING EXPERIENCE

Graduate Teaching Assistant (Brown University)

• CSCI2952G Deep Learning in Genomics (2025 Spring)

Lectured a few times, held discussion sessions and office hours, graded assignments.

Instructor: Ritambhara Singh, Ph.D.

SOFTWARE

scNODE

- A generative model that simulates and predicts realistic *in silico* single-cell gene expressions at any unmeasured timepoint.
- Link: https://github.com/rsinghlab/scNODE
- Reference: Zhang, Jiaqi, et al. "scNODE: generative model for temporal single cell transcriptomic data prediction." *Bioinformatics* 40.Supplement_2 (2024): ii146-ii154.

scMultiNODE

- An unsupervised integration model that combines gene expression and chromatin accessibility measurements in developing single cells, while preserving cell type variations and cellular dynamics.
- Link: https://github.com/rsinghlab/scMultiNODE

• Reference: Zhang, Jiaqi, Manav Chakravarthy, and Ritambhara Singh. "scMultiNODE: Integrative Model for Multi-Modal Temporal Single-Cell Data." bioRxiv (2024).

PROJECT EXPERIENCE

Dropout-Aware Weighted NMF on scRNA-seq Data

2022

♦ Course final project for CS2952Q Robust Algorithms for Machine Learning.

Disease Prediction Using Deep Learning Methods

2022

 \diamond Course final project for CS2470 Deep Learning, collaborated with Atishay Jain and Tassallah Amina Abdullahi.

A Distributed Repaying Loan Ability Evaluating System Based on Gradient Boosting Machine 2018

- ♦ Responsible for software architecture and backend modules implementation.
- ♦ Project for a seminar course; the third prize.

An Employee Management System

2017

- ♦ Responsible for software architecture and core modules implementation.
- ♦ Project for a seminar course; the third prize.