

# Qingyang Yin

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## Education

Department of Quantitative and Computational Biology, University of Southern California

Los Angeles, CA, USA

*Ph.D. Student in Computational Biology and Bioinformatics*

*Aug. 2021-present*

Berkeley Global Access Program, University of California, Berkeley

Berkeley, CA, USA

*Visiting Student, GPA: 4.0/4.0*

*Aug. 2019-Dec. 2019*

Department of Automation, Xiamen University

Xiamen, Fujian, China

*B.E. in Automation, GPA: 90.85/100, Ranking: 1/81*

*Sep. 2017-Jun. 2021*

## Publications

- Yin, Q., Wang, Y., Guan, J. & Ji, G. (2021). scIAE: an Integrative Autoencoder-based Ensemble Classification Framework for Single-cell RNA-seq Data. *Briefings in Bioinformatics*, accepted.
- Guan, J., Wang, Y., Lin, Y., Yin, Q., Zhuang, Y. & Ji, G. (2021). Cell Type-Specific Predictive Models Perform Prioritization of Genes and Gene Sets Associated with Autism. *Frontiers in Genetics*, 11, 1778.

## Research Interests

Single-cell RNA sequencing data analysis and its application in brain disorders

## Research & Project Experiences

Transcriptomics Analysis of Brain Development and Neurodegenerative Diseases

*Aug. 2021-present*

- Performed cell-type composition analysis by deconvolution in a dataset of Alzheimer's disease
- Tried deconvolution methods such as DWLS, OLS, SVR etc.
- Analyzing cell types with significant differences between control group and disease group

Autoencoder-based Ensemble Classification Framework for Single-cell RNA-seq Data

*Apr. 2020-Jun. 2021*

- Developed scIAE, an integrative autoencoder-based ensemble classification framework for single-cell RNA-seq data
- Compared scIAE with common feature extraction methods to show scIAE can perform robust feature extraction
- Showed scIAE's great classification power in cell type annotation and disease status prediction by comparing with existing general and single-cell specific classification methods

Cell Type-specific Predictive Models Associated with Autism Spectrum Disorder (ASD)

*Jan. 2020-Jul. 2020*

- Extracted differential expression genes by constructing the predictive models using PLS
- Performed recursive feature elimination with cross-validation (RFECV) to select the genes for prediction
- Compared the model performances using edgeR genes, SFARI ASD genes and RFE genes

## Skills

- **Programming:** Python, R, C, SQL
- **Frameworks & Tools:** Unix/Linux, MATLAB, TensorFlow, Keras, LaTeX, Git

## Awards & Honors

- Outstanding graduate at Xiamen University (top 10%) *Jun. 2021*
- Jixin-Engine special scholarship (top 1%) *Apr. 2021*
- Meritorious Winner of 2020 Mathematical Contest in Modeling *Apr. 2020*
- Zhongxian Huang scholarship (top 5%) *Mar. 2020*
- First Prize of Fujian Province of Contemporary Undergraduate Mathematical Contest in Modeling *Dec. 2019*
- National scholarship (top 2%) *Sep. 2018*