Qingyang Yin

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Address: 1050 Childs Way, RRI 416A, Los Angeles, CA 90089

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. (2022). scIAE: an Integrative Autoencoder-based Ensemble Classification Framework for Single-cell RNA-seq Data. *Briefings in Bioinformatics,* 23(1): bbab508.
- 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
- Deep learning in transcriptome analysis

Research & Project Experiences

Cell Type Annotation for Single-cell RNA-seq Data with Interpretable Deep Learning   *Aug. 2021-present*

- Extracted marker genes and marker cells in a mouse brain dataset
- Constructing a neural network for cell type annotation using information of hierarchical biological pathways

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/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*