

Qingyang Yin

Phone: +1 (213) 431 9881 Email: yinq@usc.edu Personal Website: <https://qyyin0516.github.io/>

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

Education

Department of Quantitative and Computational Biology, University of Southern California	Los Angeles, CA, USA
<i>Ph.D. Student in Computational Biology and Bioinformatics</i>	<i>Aug. 2021-present</i>
Berkeley Global Access Program, University of California, Berkeley	Berkeley, CA, USA
<i>Visiting Student, GPA: 4.0/4.0</i>	<i>Aug. 2019-Dec. 2019</i>
Department of Automation, Xiamen University	Xiamen, Fujian, China
<i>B.E. in Automation, GPA: 90.85/100, Ranking: 1/81</i>	<i>Sep. 2017-Jun. 2021</i>

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	<i>Aug. 2021-present</i>
● 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	<i>Apr. 2020-Jun. 2021</i>
● 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)	<i>Jan. 2020-Jul. 2020</i>
● 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%) | <i>Jun. 2021</i> |
| ● Jixin-Engine special scholarship (top 1%) | <i>Apr. 2021</i> |
| ● Meritorious winner of 2020 mathematical contest in modeling | <i>Apr. 2020</i> |
| ● Zhongxian Huang scholarship (top 5%) | <i>Mar. 2020</i> |
| ● First prize of Fujian province of contemporary undergraduate mathematical contest in modeling | <i>Dec. 2019</i> |
| ● National scholarship (top 2%) | <i>Sep. 2018</i> |