

Qingyang Yin

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Education

Department of Quantitative and Computational Biology, University of Southern California	Los Angeles, CA, USA
<i>Ph.D. Student in Computational Biology and Bioinformatics, GPA: 3.97/4.0</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., Chen, L. (2023). CellTICS: an explainable neural network for cell-type identification and interpretation based on single-cell RNA-seq data. Under review.
- 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
- Biologically interpretable deep learning

Research & Project Experiences

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

- Developed CellTICS, an explainable neural network for cell-type identification for single-cell RNA-seq data
- Compared CellTICS with other cell type annotation methods to show the accuracy and robustness of CellTICS
- Discovered important pathways for aging process and autism spectrum disorder
- Revealed the mechanism of expression stochasticity in important pathway discovery

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

Skills

- **Programming:** Python, R, C/C++, MATLAB, SQL, TensorFlow, LaTeX, Linux
- **Language:** Chinese, English

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*