# 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, GPA: 3.97/4.0

Aug. 2021-present

Additional: 5 computational classes taken from M.S. in Computer Science.

Berkeley Global Access Program, University of California, Berkeley

Berkeley, CA, USA Aug. 2019-Dec. 2019

Visiting Student, GPA: 4.0/4.0

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., Chen, L. (2024). CellTICS: an explainable neural network for cell-type identification and interpretation based on single-cell RNA-seq data. *Briefings in Bioinformatics*, 25(1): bbad449.

- 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**

- High-throughput sequencing data analysis
- Biologically interpretable deep learning

## Experience

## Teaching assistant, University of Southern California

Jan. 2024-present

 Holding weekly discussion sessions, holding office hours, and grading homework and exams for QBIO 305: Statistics for Biological Sciences

#### Research assistant, University of Southern California

Aug. 2022-present

- Developed CellTICS, an explainable neural network for cell-type identification for single-cell RNA-seq data
- Working on analyzing cancer dependency data to identify cancer driver mutations and genes

#### Part-time student supervisor, Xiamen University

Jul. 2020-Jun. 2021

• Dealt with student affairs as a helper of full-time student supervisor.

## Undergraduate researcher, Xiamen University

Feb. 2020-Jun. 2021

Developed scIAE, an integrative autoencoder-based ensemble classification framework for single-cell RNA-seq data

## **Skills**

- **Programming:** Python, C/C++, Java, SQL
- Frameworks & Tools: TensorFlow, PyTorch, Keras, R, MATLAB, Unix/Linux, LaTex, Git

#### Awards and 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