

# QINGYANG YIN

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## Education

### University of Southern California

08/2021 – 05/2026 (Expected)

*Doctor of Philosophy in Computational Biology and Bioinformatics (GPA: 3.97/4.0)*

Los Angeles, CA, USA

*Courses: Algorithms, Machine learning, Artificial intelligence, Database systems, Computational Molecular Biology.*

### Xiamen University

09/2017 – 06/2021

*Bachelor of Engineering in Automation (GPA: 3.81/4.0, Ranking: 1/81)*

Xiamen, China

*Courses: Software fundamentals (Data structure), Principles of computer, Computer networks, Case analysis for big data.*

## Skills

**Programming languages:** Python, C, C++, Java, HTML/CSS, JavaScript, SQL, bash, R, MATLAB

**Tools:** TensorFlow, Keras, PyTorch, Node.js, MapReduce, Hadoop, Linux, Git, LaTeX

**Others:** deep learning (DNN, CNN, RNN, autoencoder, XAI, transformer, GPT, etc.), bioinformatics (next-generation sequencing toolsets, molecular biology, etc.), automatic control (Simulink, PID, etc.)

## Experience & Selected Projects

### University of Southern California, Los Angeles, CA, USA | Research Assistant

08/2021 – Present

#### Project 1: Cancer driver gene and mutation detection with XAI | Python

06/2023 – Present

- Utilized **explainable AI** techniques to detect cancer driver genes and mutations with **Keras and TensorFlow**.
- Built a novel **explainable DNN** model to predict the mutation status of genes based on the DepMap cancer dependency data. The AUROC can reach 0.96 for some candidate cancer driver genes.
- Designed and implemented a knowledge-primed **autoencoder** to generate driver-like artificial mutations.
- Used **activation values** of neural network neurons to find important pathways of cancer.

#### Project 2: Cell type identification with XAI | Python, R

08/2021 – 06/2023

- Developed CellTICS, an **explainable DNN** for cell-type identification and pathway finding in scRNA-seq data.
- Compared the classification performance of CellTICS with other state-of-the-art methods using 6 datasets, demonstrating superior performance with macro F1 scores ranging between 0.9406 and 0.9993.

#### Project 3: Dimensionality reduction of images | MATLAB, Python

05/2022 – 08/2022

- Implemented the **sparsity and geometry preserving graph embedding (SGPGE)** algorithm for dimensionality reduction of images.
- Resolved the issue of the non-positive definiteness in the eigenvalue problem.
- Compared SGPGE with traditional methods (**PCA, LDA, LPP, SPP**) and its variants using **kNN** classification on the ORL face dataset. Achieved an accuracy of 0.94 with SGPGE.

#### Project 4: Development and application of Burrows–Wheeler Transform | C++

01/2022 – 05/2022

- Used the **DC3 algorithm** to construct the suffix array of input strings.
- Implemented the **Burrows–Wheeler transform** and conducted a query using the compression to determine the exact match count of the pattern in the input string.
- Validated the results by comparing with those obtained from the **KMP algorithm** and checked for linear complexity.

### Xiamen University, Xiamen, China | Undergraduate Researcher

01/2020 – 06/2021

#### Project 1: Feature extraction and classification for scRNA-seq data | R, Python

06/2020 – 06/2021

- Employed **stacked denoising sparse autoencoders** with **Keras and TensorFlow** for feature extraction and built an **ensemble learning** model to predict cell types and ASD status. Developed a framework called scIAE.
- Evaluated scIAE against 11 other feature extraction methods through **t-SNE** visualization, **clustering**, and **SVM** classification. scIAE ranked first in SVM classification performance.
- Compared scIAE with 15 other classification tools using accuracy, mean F1 score, and median F1 score metrics. Paired t-tests indicated that scIAE had greater classification power than most of the other methods.

#### Project 2: Cell-type-specific predictive models for ASD | R

01/2020 – 06/2020

- Performed **recursive feature elimination** with cross-validation to select ASD-related genes.
- Used **partial least squares** to predict ASD status. The average AUROC can reach 0.85 for all cell types.

## Publications

- [1] **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.
- [2] **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.
- [3] 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, 628539.