

Yi Jiang

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Education

Undergraduate, Shandong University	2019.09 – 2023.06
<i>Software Engineering</i>	<i>Jinan, Shandong, China</i>
<ul style="list-style-type: none">• Concentration: AI, Bioinformatics	
Biomedical Science Graduate Program, The Ohio State University	2023.06 – 2025.06
<i>Biomedical Science</i>	<i>Columbus, OH, U.S.</i>
<ul style="list-style-type: none">• Computational Biology, Bioinformatics• Plan to graduate as a master student	

Research Experience

Student Research Assistant	2020.04 – 2023.05
<i>Research Center of Software and Data Engineering, SDU, Leyi Wei</i>	
<ul style="list-style-type: none">• Prediction of peptide secondary structures is an intermediate step in predicting three-dimensional (3D) or tertiary structures; Using the deep learning method, the PHAT framework is proposed. In this framework, Hypergraph Multi-head Attention network and language model–ProtT5 are used to predict the peptide secondary structures only based on peptide sequences and obtain the state of the art.	
Graduate Research Assistant	2023.05 – 2025.05
<i>Bioinformatics and Mathematical Biosciences Lab, OSU, Qin Ma</i>	
<ul style="list-style-type: none">• My major focuses on the research of single-cell multi-omics data, aiming to develop cutting-edge computational tools to discover underlying mechanisms in diverse biological systems.	

Research Publications

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- Citations: 350+
- <https://scholar.google.com/citations?user=lUQuWLgAAAAJ>
- Explainable Deep Hypergraph Learning Modeling the Peptide Secondary Structure Prediction. **Y Jiang**, R Wang, et al. *Advanced Science*, 2023
 - DeepBIO is an automated and interpretable deep-learning platform for biological sequence prediction, functional annotation, and visualization analysis. R Wang, **Y Jiang**, et al. *Nucleic acids research (Breakthrough Article)*, 2023
 - AFP-MFL: accurate identification of antifungal peptides using multi-view feature learning. Y Fang, F Xu, L Wei, **Y Jiang**, et al. *Briefings in Bioinformatics*, 2023
 - scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. C Dai, **Y Jiang**, et al. *Nucleic acids research*, 2022
 - iDNA-ABF: multi-scale deep biological language learning model for the accurate and interpretable prediction of DNA methylations. J Jin, Y Yu, R Wang, X Zeng, P Chao, **Y Jiang**, et al. *Genome Biology*, 2022
 - Accelerating bioactive peptide discovery via mutual information-based meta-learning. W He, **Y Jiang**, et al. *Briefings in Bioinformatics*, 2022
 - DeepProSite: structure-aware protein binding site prediction using ESMFold and pretrained language model. Y Fang, **Y Jiang**, et al. *Bioinformatics*, 2023
 - ConPep: Prediction of peptide contact maps with pre-trained biological language model and multi-view feature extracting strategy. Q Wei, R Wang, **Y Jiang**, et al. *Computers in Biology and Medicine*, 2023
 - MVIL6: Accurate identification of IL-6-induced peptides using multi-view feature learning. R Wang, Y Feng, M Sun, **Y Jiang**, et al. *International Journal of Biological Macromolecules*, 2023

- MechRetro is a chemical-mechanism-driven graph learning framework for interpretable retrosynthesis prediction and pathway planning, Y Wang, C Pang, Y Wang, **Y Jiang**, arXiv, 2022
- Multi-view deep learning based molecule design and structural optimization accelerates the SARS-CoV-2 inhibitor discovery. C Pang, Y Wang, **Y Jiang**, et al. arXiv, 2022
- Delineating lymphocyte aggregates from tertiary lymphoid structures using spatial transcriptomics, J Krull, A Byappanahalli, **Y Jiang**, A Gunderson, et al. Cancer Research, 2024
- Graph Fourier transform for spatial omics representation and analyses of complex organs. Y Chang, J Liu, **Y Jiang**, et al. Nature Communication, 2024
- Harnessing the deep learning power of foundation models in single-cell omics. Q Ma, **Y Jiang**, et al. Nature Reviews Molecular Cell Biology, 2024
- scGNN+: Adapting ChatGPT for Seamless Tutorial and Code Optimization. **Y Jiang**, et al. bioRxiv, 2024

Conference Experience

2024 MCBIOS in Atlanta, Georgia, USA 2024.03

20th Annual Meeting of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS)

- Give a workshop presentation titled "HyperGRN: Elucidate Gene Regulatory Networks in the Spatial Context". Introduced a hypergraph-based approach for deciphering GRN spatial dynamics, enhancing the understanding of functional diversity among cells in under complex tissue environments.

2024 ISMB Conference in Montreal, Quebec, Canada 2024.06

2024 International Conference on Intelligent Systems for Molecular Biology (ISMB)

- Hands-on Practice in Single-Cell Multi-Omics and Spatial Transcriptomics Workshop: Participated in extensive coding practices and system demonstrations, covering the single-cell analysis pipeline and machine learning techniques for single-cell and spatial omics data.
- Poster Presentation titled "HyperGRN: Elucidating High-Order-Relation Gene Regulatory Networks in Spatial Context"

Projects

Second-hand market program based on Java Swing 2020.03 – 2020.05

Course Project

- A Second-hand market program; Trading and communicating based on socket connection and using Java Swing to design graphical user interface.
- Development tools: Java

iSDU applet based on Java system and React Framework 2020.06 – 2021.03

Widely used by SDU students

- A service platform that provides access to grades, class schedules, and school news and information; Personal information storage and information collection based on Springboot framework with MySQL and React with Javascript to design graphical clients.
- Development tools: Java(Springboot), Javascript(React.js), MySQL

A map applet showed in Shandong University Official Admissions Letter 2020.06 – 2020.07

Widely used by SDU first-year students for 2020 and 2021

- A service program to provide first-year students with maps of multiple campuses of Shandong University; Map image acquisition based on Springboot framework and Taro framework with React and Javascript to design graphical client.
- Development tools: Java(Springboot), Javascript(Taro.js), Python

DeepBIO: a deep-learning platform for biological sequence analysis 2021.12 – 2022.12

Retweeted by 138 tweets from 128 users, covering an upper bound of 300,000+ followers

- A first-of-its-kind automated and interpretable deep-learning platform for biological sequence functional analysis based on Springboot framework and Pytorch to run biological AI Model and React framework with Javascript to design web interface.
- Development tools: Java(Springboot), Javascript(React.js), Python(Pytorch)

Other Experience

- Minister of Research Department of Sharing-idea, School of Software, Shandong University
- Minister of Shandong University Student Online Technology Department
- Minister of AI Department of Microsoft Club of Shandong University

Awards & Honors

The 15th National University Student Software Innovation Competition Winning prize <i>Alliance of Model Software Institutes, China</i>	<i>2022</i>
The 14th National University Student Software Innovation Competition Winning prize <i>Alliance of Model Software Institutes, China</i>	<i>2021</i>
Ranked 37th in the second track of 2021 global AI innovation competition <i>Alibaba Cloud</i>	<i>2021</i>

Specialized Skills

Programming Languages: Python, Java, C++, Javascript, HTML, CSS, etc.
Modeling on Machine Learning and Deep Learning: Pytorch
Design framework figure: Power Point and Adobe Illustrator