CHEN, Yiru

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Education

B.S. **Zhejiang University–University of Edinburgh (ZJE) Institute**
Zhejiang University, China
2022–2026 (expected)

- **Degree:** Dual-Award Bachelor of Science in Bioinformatics
- **Academic Performance:** GPA: 85.7/100 (Rank: 10/46; Top 20%)
- **Selected Coursework:** Computational Modelling & Machine Learning, Advanced Mathematics, Applied Data Science, Database & Software Technology, Genomics & Proteomics, Biomedical Genetics.

Publications & Presentations

*†Co-first authors; *Corresponding authors; #Presenter*

I. Published:

Xue Z., Wu L., Gao B., Tian R., **Chen Y.**, Qi Y., Dong T., Bai Y., Zhao Y., He B., Wang L., Liu Z., Yao J., Lu L., Liu W. A pan-disease and population-level single-cell TCR$\alpha\beta$ repertoire reference. *Cell Discovery*, 2025, 11: 82. Availiable at: `https://www.nature.com/articles/s41421-025-00836-7`

Tian R.†, Xue Z.†, **Chen Y.**, Qi Y., Zhang J., Yuan J., Ruan D., Lin J., Liu J., Wang D., Ye Y., Liu W.* Integrating Cross-Sample and Cross-Modal Data for Spatial Transcriptomics and Metabolomics with SpatialMETA. *Nature Communications*, 2025, 16: 8855. Avaliable at: `https://www.nature.com/articles/s41467-025-63915-z`

II. Submitted/Under Review:

Chen Y., Xie M., Hu Y., Yuan W., Sarkar H., Li B., Zhang L.*, Zhou X.M.* From features to slice: parameter-cloud modeling of spatial transcriptomics for simulation and 3D interpolatory augmentation. 2025. [Submitted for Publication]. Github: `https://github.com/maiziezhoulab/FEAST`

Pan X., **Chen Y.**, Zhang X.* Integrative Inference of Spatially Resolved Cell Lineage Trees using LineageMap. 2025. [Submitted for Publication]. GitHub: `https://github.com/ZhangLabGT/LineageMap`

Yu Z., Chen Y., **Chen Y.**, Qi Y., Liu W.* Recent Advances in Single-Cell Isoform Profiling. 2025. [Review; Submitted for Publication].

III. Conference Presentations:

Tian R.†, **Chen Y.**†#, Qi Y.†, Xue Z., Yu Z., Liu W.* SpatialTCR: An integrated platform for high-resolution spatial sequencing of T cell receptor repertoires. *GPB Omics & Bioinformatics Frontiers Symposium*, Zhejiang, China, 2025. (Best Poster Presentation Award).

Pan X., Danies-Lopez A., **Chen Y.**, Zhang X.* Mapping lineage-resolved scRNA-seq data with spatial transcriptomics using TemSOMap. *Pacific Symposium on Biocomputing (PSB)*, 2026. (Accepted for Presentation).

Highlighted Research Experience

SpatialTCR: An integrated platform for high-resolution spatial sequencing of T cell receptor repertoires

Active Project; Expected co-first author

Prof. Wanlu Liu
ZJU-UoE Institute
Zhejiang University, China
Jan. 2025 – Present
On-site

- Co-developed a novel spatial TCR sequencing method in collaboration with wet-lab researchers.
- **My contribution:** Engineered the computational pipeline from upstream raw data processing to the downstream TCR-omics analysis and visualization toolkit.

FEAST: Simulation and interpolation of spatial transcriptomics from statistical feature cloud

Independent Research Project; Submitted as First Author

Prof. Maizie Zhou
BME & CS Department
Vanderbilt University, U.S.
Aug. 2024 – Nov. 2025
Hybrid (Remote & On-site)

- Developed a statistical model for single and multi-slice 3D Spatial Transcriptomics

(ST) simulation using vine-copula modeling on parameter space.
- Implemented interpolation algorithms using optimal transport-driven geodesic paths.
- **My contribution:** Led the full research lifecycle including literature review, model formulation, algorithm implementation, benchmarking, and manuscript preparation.

SpatialMETA: Integrating Cross-Sample and Cross-Modal Data for Spatial Transcriptomics and Metabolomics

Research Assistant; Published in Nature Communications as 3rd co-author

Prof. Wanlu Liu
ZJU-UoE Institute
Zhejiang University, China
Nov. 2024 – Spring 2025
On-site

- Contributed to algorithm development using Conditional Variational Autoencoders (CVAE) to integrate spatial transcriptomics and metabolomics.
- **My contribution:** Designed and executed comprehensive benchmarks and metrics for the multimodal spatial integration task.

TemSOMap and LineageMap: Spatially resolved lineage mapping and tracing inference

Active Projects

Prof. Xiuwei Zhang
College of Computing
Georgia Institute of Technology, U.S.
Apr. 2024 – Present
Remote

- **TemSOMap:** Infer a cell-to-spot mapping matrix by minimizing a loss function based on expression and lineage. Expected 3rd co-author. [GitHub ↗]
- **LineageMap:** Novel integrative inference of spatially informed cell lineage trees. Expected 2nd co-author[GitHub ↗]
- **My contribution:** Assisted in framework design and testing, performed downstream analyses and benchmarking, and drafted sections of the manuscript.

Mechanism of intermittent fasting to promote skeletal muscle injury repair

Active Project; Expected co-first author

Prof. Di Wang
& Prof. Zhexu Chi
School of Medicine
Zhejiang University, China
Aug. 2025 – Present
On-site

- Investigating the impact of intermittent fasting on skeletal muscle regeneration using robust bioinformatic analysis (Bulk RNA-seq, scRNA-seq, and spatial omics).
- **My contribution:** Led the computational experimental design, performed statistical analysis of results, and coordinated with wet-lab activities. Currently scRNA analysis results are guiding the next step of wet lab experiments.

General Technical Skills

Programming & Development

- **Coding Languages:** Python, R, Bash/Shell (Advanced); Java, SQL, JavaScript, C++ (Familiar).
- **Development Environment:** Linux HPC/Server, Git, Docker, Conda, Vim.
- **Web Development:** General full-stack experience (Frontend emphasis), especially for bioinformatics databases and visualization.
- **Other Open-Source Contributions**: FDTranSearcher ↗ (Functional DNA transposons searcher); PyRAMA ↗ (Protein Ramachandran plot generator).

Computational Biology & Bioinformatics Toolbox

- **Machine Learning:** Classical ML (Scikit-learn, Ski-image; OpenCV); Deep learning (PyTorch) for multi-omics (GCN, VAE, Transformers).
- **Statistical Methods:** Bayesian Inference, Maximum Likelihood Estimation, Hidden Markov Models (HMM), Monte Carlo simulations, Vine Copula modeling.
- **Wet Lab Foundation:** Solid biomedicine knowledge and foundations on wet lab protocols; experiences in wet lab experimental design.

Languages & Other Skills

- **English:** TOEFL iBT 105 (R30, L28, S23, W24); All-in-English Courses.
- **Content Creation:** LaTeX, Adobe Illustrator (Professional Scientific Figures), Adobe Premiere Pro.