

CHEN Yiru

PhD Student, Quantitative Biology and Medicine Programme

Duke-NUS Medical School, National University of Singapore

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Education

Duke-NUS Medical School, National University of Singapore , Singapore PhD in Quantitative Biology and Medicine	2026–Present
Zhejiang University , Zhejiang University–University of Edinburgh Institute, China Bachelor of Science in Bioinformatics	2022–2026
The University of Edinburgh , United Kingdom Bachelor of Science with Honours in Biomedical Informatics <i>First Class Honours</i>	2022–2026

Research Interests

Computational biology; single-cell and spatial omics; spatial perturbation and pharmacology; statistical simulation and benchmarking; multimodal representation learning.

Publications

† *Equal contribution*; * *Corresponding author*.

Peer-Reviewed Journal Articles

1. R. Tian[†], Z. Xue[†], **Y. Chen**, Y. Qi, J. Zhang, J. Yuan, D. Ruan, J. Lin, J. Liu, D. Wang, Y. Ye, and W. Liu^{*}. Integrating Cross-Sample and Cross-Modal Data for Spatial Transcriptomics and Metabolomics with SpatialMETA. *Nature Communications*, 16, 8855, 2025.
2. Z. Xue, L. Wu, B. Gao, R. Tian, **Y. Chen**, Y. Qi, T. Dong, Y. Bai, Y. Zhao, B. He, L. Wang, Z. Liu, J. Yao, L. Lu, and W. Liu. A Pan-Disease and Population-Level Single-Cell TCR $\alpha\beta$ Repertoire Reference. *Cell Discovery*, 11, 82, 2025.

Peer-Reviewed Conference Papers

3. X. Pan, **Y. Chen**, and X. Zhang. Integrative Inference of Spatially Informed Cell Lineage Trees using LineageMap. Accepted at the *30th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2026)*, 2026.

Preprints

4. **Y. Chen**[†], M. Xie[†], Y. Hu, W. Yuan, H. Sarkar, B. Li, L. Zhang^{*}, and X. M. Zhou^{*}. From Parameter Clouds to Virtual Slices: Layout-Aware Simulation and Benchmark Construction for Spatial Transcriptomics. Preprint, 2025.

Selected Conference Presentations

R. Tian[†], **Y. Chen**[†] (presenter), Y. Qi[†], Z. Xue, Z. Yu, and W. Liu^{*}. “SpatialTCR: An Integrated Platform for High-Resolution Spatial Sequencing of T Cell Receptor Repertoires.” Poster presented at the *GPB Omics & Bioinformatics Frontiers Symposium*, Zhejiang, China, 2025. **Best Poster Presentation Award**.

Honors & Awards

Khoo Pre-Doctoral Fellowship Duke-NUS Medical School	2026
Outstanding Graduate of Zhejiang University University-level graduate distinction, Zhejiang University	2026

Technical Skills

Programming: Python, R, and Bash/Shell; working knowledge of Java, SQL, and JavaScript.

Machine Learning and Statistical Computing: PyTorch, PyTorch Geometric, scikit-learn, scvi-tools, graph neural networks, variational autoencoders, transformers, generalized linear models, Bayesian inference, maximum-likelihood estimation, Monte Carlo methods, and copula modeling.

Computational Biology: Scanpy, AnnData, Bioconductor, single-cell RNA sequencing, spatial transcriptomics, bulk RNA sequencing, TCR repertoire analysis, and multimodal omics integration.

Research Computing: Linux and HPC environments, Git, Docker, Conda, Snakemake, and Python package development.