

# Zhentao He

[jameshezt@gmail.com](mailto:jameshezt@gmail.com)  
[github.com/JimmyTauH](https://github.com/JimmyTauH)

## EDUCATION

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### Fudan University

Ph.D.

Shanghai, China

Sept. 2025 - June 2030

### Wuhan University

B.E. in Computer Science & Technology

Wuhan, Hubei Province, China

Sept. 2021 - June 2025

- Hongyi Honor College Student
- GPA: 3.91/4.00
- Outstanding Student Award
- Operational command of English (IELTS Band 7)

## PUBLICATIONS

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- Interpretable Data Integration for Single Cell and Spatial Multi-Omics. CELL-SYSTEMS. Yang, Chenghui and He, Zhentao and Nie, Qing and Zhang, Lihua [Link](#)

## CURRENTLY RESEARCH FOCUS

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Bioinformatics [Multiomics Analysis, Perturbation Prediction], AI for Medicine

## EXPERIENCE

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### PhD Student Researcher

*Lab of Data Mining and Intelligent Information Processing, ISTBI, Fudan University*

Sept. 2025 - June 2030

Advisor: Prof. Shanfeng Zhu

- Integration and analysis of spatial multiomics data.

### Undergraduate Researcher

*BIOD Lab, School of Computer Science, Wuhan University*

July 2022 - June 2025

Advisor: Prof. Lihua Zhang

- Develop methods single-cell multiomics data integration and analysis.
- Predict the impact of drug and genetic perturbations on cell states.
- Studied metabolic pathway design and molecular feature representation techniques.

### iGEM Team Member (Head of Model Team)

*WHU-China, CRISPRReporter*

Nov. 2022 - Nov. 2023

Advisor: Dr. Lei Bai, Prof. Zhixiong Xie & Prof. Lihua Zhang

- **Gold Medal**; Nomination for Best Foundational Advance Project, etc.
- A novel multi-level DNA memory device with CRISPR technology and **its software suite**. [Description](#)

## PROJECTS

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- **CRISPRReporter: model and software suit** [Model](#) [Our Gitlab](#)  
sgRNA generator utilizing machine learning techniques and sequence alignment technologies, predicts the on-target and off-target rates of sgRNAs, providing experimental teams with high-quality sgRNA sequences.  
**Editing simulator** is designed to emulate the temporal relationships between multi-level signal recordings, enabling precise logging through the appropriate setting of biological oscillator cycles and recording system thresholds.
- **Multiomics integration via feature-guided optimal transport** [FGOT](#)  
We use feature-guided optimal transport for the integration of cells across different modalities. My contributions encompass a portion of the coding, experiments, and the co-authorship of the manuscript.

## COMPETENCIES & SKILLS

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**Programming Languages:** Python, C++, R

**Libraries and Tools:** PyTorch, Git, Docker; Scanpy, Seurat, etc.

**ML Architectures:** VAE, GNN, GAN, OT (Neural Optimal Transport), Transformer, etc.