Shuguang (Scott) Wang

Ph.D. Candidate in Bioinformatics

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Research Highlights

- Co-first authored **two *Nature Methods*** studies that systematically defined evaluation standards for single-cell multi-modal integration and perturbation response prediction.
- Contributed to the development of deep generative models for multi-omics integration (***Genome Biology***).
- Built reproducible, end-to-end computational pipelines across diverse omics modalities (genomic, transcriptomic, epigenomic, and spatial transcriptomic), from raw sequencing reads to biological interpretation.
- **National Doctoral Scholarship** recipient (top 0.2% nationwide).

Education

Tongji University — Ph.D. Candidate in Bioinformatics — *Shanghai, China*
Advisor: Prof. Qi Liu — *Sep. 2022 – Jun. 2026 (Expected)*
- Research Focus: Single-cell Multi-omics Integration, Deep Generative Models, & Systematic Benchmarking

Tongji University — M.S. in Bioinformatics (Transferred to Ph.D.) — *Shanghai, China*
Advisors: Prof. Qi Liu & Prof. Yawei Gao — *Sep. 2020 – Jun. 2022*

BGI Research — Visiting Research Student (Joint Training Program) — *Shenzhen, China*
Advisor: Prof. Hai-Xi Sun — *Oct. 2019 – Jul. 2020*

Huazhong Agricultural University — B.S. in Bioinformatics — *Wuhan, China*
Advisor: Prof. Jingbo Xia — *Sep. 2016 – Jun. 2020*
- Outstanding Graduation Thesis

Publications

Selected Publications (First / Co-first Author)

Fu, S.*, **Wang, S.***, Si, D., Li, G., Gao, Y., Liu, Q. 2025. Benchmarking Single-Cell Multi-Modal Data Integrations. *Nature Methods*, 22(11): 2437–2448. [GitHub]

Wei, Z.*, Wang, Y.*, Gao, Y.*, **Wang, S.***, Li, P., Si, D., et al. 2025. Benchmarking Algorithms for Generalizable Single-Cell Perturbation Response Prediction. *Nature Methods*, 1–14. [GitHub]

Wang, S.*, Meng, X.*, Wang, Y., Liu, Y., Xia, J. 2019. HPO-Shuffle: An Associated Gene Prioritization Strategy and Its Application in Drug Repurposing for the Treatment of Canine Epilepsy. *Bioscience Reports*, 39(9). [GitHub]

** denotes co-first authorship*

Selected Co-authored Publications

Li, G., Fu, S., **Wang, S.**, et al. 2022. A Deep Generative Model for Multi-View Profiling of Single-Cell RNA-seq and ATAC-seq Data. *Genome Biology*, 23(1): 20.

Dong, K., ..., **Wang, S.**, et al. 2025. Benchmarking Multi-Slice Integration and Downstream Applications in Spatial Transcriptomics Data Analysis. *Genome Biology*, 26(1): 318.

Bai, Z., Chang, Z., **Wang, S.**, et al. 2025. Revealed the Regulatory Role of CCN1 to Microglia Distribution through Region-Specific Cellular Interactions. *Genes & Diseases*, 101969.

Tang, C., ..., **Wang, S.**, et al. 2023. Personalized Tumor Combination Therapy Optimization Using the Single-Cell Transcriptome. *Genome Medicine*, 15(1): 105.

Manuscripts in Preparation

Wang, S., et al. Systematic Evaluation of RNA Velocity and Spatiotemporal Dynamics Inference Methods in Single-Cell Biology. *(Manuscript in preparation)*

Research Experience

Tongji University — Lab of Prof. Qi Liu *Shanghai, China*

Graduate Research Assistant *Sep. 2020 – Present*

- Designed and led two comprehensive benchmarking studies that established evaluation standards and revealed critical failure modes across the landscape of single-cell integration and perturbation prediction methods (Two *Nature Methods* publications).
- Contributed to the design and implementation of a deep generative model for joint profiling of scRNA-seq and scATAC-seq data, enabling cross-modal biological discovery (Published in ***Genome Biology***).
- Built end-to-end analysis pipelines spanning genomic, transcriptomic, epigenomic, and spatial data modalities. Applied spatial transcriptomics to reveal that CCN1 knockout disrupts microglia spatial organization (Published in ***Genes & Diseases***).

BGI Research *Shenzhen, China*

Visiting Research Student (Joint Training Program) *Oct. 2019 – Jul. 2020*

- Pioneered bioinformatics pipelines for lentiviral lineage tracing and developed the SCTCA tool to resolve FACS heterogeneity, securing Software Copyright (No. 2021SR2046800).
- Identified key stemness regulators and predicted Retinoic Acid efficacy via computational modeling (Published in ***Clinical and Translational Medicine***).

Huazhong Agricultural University — Lab of Prof. Jingbo Xia *Wuhan, China*

Undergraduate Research Assistant *Sep. 2017 – Jun. 2020*

- Developed "HPO-Shuffle", a gene prioritization algorithm integrating multi-modal data (GWAS, transcriptomics, phenotype ontologies). Applied to drug repurposing via CMap analysis (First author, Published in ***Bioscience Reports***).

Skills

Core Expertise	Establishing gold-standard and large-scale evaluation frameworks for single-cell computational methods; Implementing deep learning architectures for multi-omics data integration; Integrating multi-modal biological data across scales — from raw data to biological discovery.
Programming	Python, R, Shell, LaTeX, Git
Deep Learning	PyTorch, VAE, GANs
Bioinformatics	Experienced across the scverse and Seurat ecosystems; proficient in spatial transcriptomics analysis and multi-omics data integration
Engineering	Snakemake, Docker, WDL, HPC Computing

Honors & Awards

Oct. 2025 **National Scholarship for Doctoral Students**, Ministry of Education of China *Top 0.2%*