Jiahao Huang

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EDUCATION

Massachusetts Institute of Technology — *Sep 2022 - Present*
Ph.D. in Chemical Biology, Department of Chemistry — Cambridge, United States

Georgetown University — *Aug 2017 - Aug 2018*
M.S. in Bioinformatics, Department of Biochemistry, Molecular & Cellular Biology — Washington D.C., United States

Purdue University — *Jan 2013 - May 2016*
B.S. in Biochemistry, College of Agriculture — West Lafayette, United States

RESEARCH DOMAIN

AI for Science, Spatial Transcriptomics, Biomedical Imaging, Large Language Model, Agentic System, Bioinformatics, Data/Figure Automation, Production-grade Tooling.

PROFESSIONAL EXPERIENCE

Massachusetts Institute of Technology — *Sep 2022 - Present*
Research Assistant, Supervisor: Prof. Xiao Wang — Cambridge, MA

- **Spatial transcriptomic and translatomic co-profiling of Schizophrenia:** Employed single-cell resolved spatial transcriptomics (STARmap) combined with translatomics (RIBOmap) to generate an atlas of transcriptional and translational states in the Grin2a+/- mouse model of SCZ. Identified Grin2a-dependent translation downregulation of synaptic plasticity/function regulators and co-variational gene programs. [Ongoing]
- **End-to-end analysis toolkit for spatial transcriptomics (Starfinder):** Built a modularized E2E pipeline for image-based *in-situ* sequencing assays with Snakemake. Integrated SOTA tools covering image denoising, registration, segmentation, and alignment. Created a standardized IO & workflow configuration format for better reproducibility. Productionized on in-house HPC/SLURM with job orchestration, containerized via Docker. 5X faster vs. legacy baseline, providing a technical foundation for organism-level spatial profiling. [Nature Protocols 2025]
- **Spatially resolved single-cell translatomics (RIBOmap):** Designed DNA probe sets for a new spatial translatomics assay. Implemented density peak clustering strategy for cell detection with RNA point clouds. Trained KNN classifiers for automated quality assessment and cell type annotation. Integrated spatial transcriptome and translatome to characterize gene modules with different translational efficiency across cell types/brain regions. [Science 2023]

Broad Institute for Harvard and MIT — *Sep 2019 - Aug 2022*
Associate Computational Biologist — Cambridge, MA

- **Integrative in-situ mapping of mouse brain (STARmap PLUS):** Developed an analysis pipeline for a spatial transcriptomics assay with multi-modalities. Employed a U-Net model to achieve SOTA cell segmentation. Characterized disease-associated glial cell subpopulations with spatial variable gene expression and modeled their distribution in AD. Created a spatial atlas of the mouse CNS covering 1.09 million cells and 11,844 genes. [Nature Neuroscience 2023] [Nature 2023]

SELECTED PUBLICATIONS [🎓]

*CO-FIRST AUTHORS

1. Ren, J.*, Zeng, H.*, **Huang, J.***, Shi, H., Sui, X., ... & Wang, X. Spatially resolved in situ profiling of mRNA life cycle at transcriptome scale in intact cells and tissues. Nature Protocols 2025
2. Zeng, H.*, **Huang, J.***, Ren, J.*, Wang, C.K., Tang, Z., ... & Wang, X. Spatially resolved single-cell translatomics at molecular resolution. Science 2023
3. Zeng, H.*, **Huang, J.***, Zhou, H.*, Meilandt, W.J., ... & Sheng, M., Wang, X. Integrative in situ mapping of single-cell transcriptional states and tissue histopathology in a mouse model of Alzheimers disease. Nature Neuroscience 2023
4. He, Y., Tang, X., **Huang, J.**, Ren, J., Zhou, H., Chen, K., Liu, A., Shi, H., Lin, Z., Li, Q., Aditham, A., ... & Liu, J., Wang, X. ClusterMap for multi-scale clustering analysis of spatial gene expression. Nature Communications 2021
5. Shi, H., He, Y., Zhou, Y., **Huang, J.**, Maher, K., Wang, B., Tang, Z., Luo, S., Tan, P., Wu, M., ... & Wang, X. Spatial atlas of the mouse central nervous system at molecular resolution. Nature 2023
6. Tang, Z., Luo, S., Zeng, H., **Huang, J.**, Sui, X., Wu, M., ... & Wang, X. Search and match across spatial omics samples at single-cell resolution. Nature Methods 2024
7. Ren, J., Zhou, H., Zeng, H., Wang, C.K., **Huang, J.**, Qiu, X., Sui, X., ... & Wang, X. Spatiotemporally resolved transcriptomics reveals the subcellular RNA kinetic landscape. Nature Methods 2023

SKILLS

- **Programming Languages:** Python, Matlab, R, Shell, HTML, JavaScript
- **Tools:** PyTorch, smolagents, LlamaIndex, LangGraph, HuggingFace, Scanpy, Seurat, Sklearn, scikit-image, Fiji/ImageJ, CellProfiler, Matplotlib, Vega-lite, Altair, plotly, snakemake, nextflow, Git, Docker, SLURM