

Haowen Zhou

PH.D. STUDENT · BIOINFORMATICS & SYSTEM BIOLOGY

☎ +1 443-527-7424 | ✉ haz115@ucsd.edu | 📄 haowen-zhou | 📖 Google Scholar

Education

University of California, San Diego

PH.D. BIOINFORMATICS & SYSTEMS BIOLOGY (BISB TRACK)

• Advisor: Dr. Neil C. Chi, MD, PhD

La Jolla, CA

Sep. 2024 - Present

Johns Hopkins University

MS BIOINFORMATICS

• GPA: 4.0/4.0
• Graduate RA in School of Public Health
• Advisor: Dr. Stephanie C. Hicks

Baltimore, MD

Aug. 2022 - Dec. 2023

Shanghai Jiaotong University

BS BIOSCIENCE

• Zhiyuan Honor Program (Admit the top 10% of freshmen)
• Thesis advisor: Dr. Xiao Wang and Dr. Jing Li

Shanghai, China

Sep. 2017 - Jun. 2021

Publications

PEER REVIEWED

* indicates co-first author / ✉ indicates correspondence author

Ren, J.* **Zhou, H.***, Zeng, H.*, Wang, CK., Huang, J., Qiu, X., Sui, X., Li, Q., Wu, X., Lin, Z., Lo, JA., Maher, K., He, Y., Tang, X., Lam, J., Chen, H., Li, B., Fisher, DE., Liu, J. & Wang, X. ✉ Spatiotemporally resolved transcriptomics reveals the subcellular RNA kinetic landscape. *Nat Methods* (2023). <https://doi.org/10.1038/s41592-023-01829-8>

Zeng, H.*, Huang, J.* **Zhou, H.***, Meilandt, W., Dejanovic, B., Zhou, Y., Bohlen, CJ., Lee, SH., Ren, L., Liu, A., Sheng, H., Liu, L., Sheng, M. ✉ & Wang, X. ✉ Integrative in situ mapping of single-cell transcriptional states and tissue histopathology in a mouse model of Alzheimer's disease. *Nat Neurosci* **26**, 430–446 (2023). <https://doi.org/10.1038/s41593-022-01251-x>

Zeng, H.*, Huang, J.*, Ren, J.*, Wang, CK., Tang, Z., **Zhou, H.**, Zhou, Y., Shi, H., Aditham, A., Sui, X., Chen, H., Lo, JA., Wang, X. ✉ Spatially resolved single-cell translomics at molecular resolution. *Science* **380**, eadd3067 (2023). <https://doi.org/10.1126/science.add3067>

He, Y.*, Tang, X.*, Huang, J., Ren, J., **Zhou, H.**, Chen, K., Liu, A., Shi, H., Lin, Z., Li, Q., Aditham, A., Ounadjela, J., Grody, El., Shu, J., Liu, J. ✉ & Wang, X. ✉ ClusterMap for multi-scale clustering analysis of spatial gene expression. *Nat Commun* **12**, 5909 (2021). <https://doi.org/10.1038/s41467-021-26044-x>

Li, Q.*, Lin, Z.*, Liu, R.*, Tang, X.*, Huang, J., He, Y., Sui, X., Tian, W., Shen, H., **Zhou, H.**, Sheng, H., Shi, H., Xiao, L., Wang, X. ✉ & Liu, J. ✉ Multimodal charting of molecular and functional cell states via *in situ* electro-seq. *Cell* **186** (9): 2002–17.e21. <https://doi.org/10.1016/j.cell.2023.03.023>

Chen, Z.*, Zhang, R.*, Fang, H., Zhang, YE., Bal, A., **Zhou, H.**, Rock, RR., Padilla-Coreano, N., Keyes, L., Zhu, H., Li, YL., Komiyama, T., Tye, KM. ✉ and Lu, C. ✉ AlphaTracker: A Multi-Animal Tracking and Behavioral Analysis Tool. *Frontiers in Behavioral Neuroscience* **17** (May): 1111908. <https://doi.org/10.3389/fnbeh.2023.1111908>

Kumar, A., Wang, J., Esterly, A., Radcliffe, C., **Zhou, H.**, Wyk, BV., Allore, HG., Tsang, S., Barakat, L., Mohanty, S., Zhao, H., Shaw, AC. & Zapata, HJ. ✉ Dectin-1 stimulation promotes a distinct inflammatory signature in the setting of HIV-infection and aging. *Aging (Albany NY)*. 2023 Aug 21;15(16):7866-7908. doi: 10.18632/aging.204927. Epub 2023 Aug 21. PMID: 37606991; PMCID: PMC10497004.

PRE-PRINT

Zhou, H., Panwar, P., Guo, B., Hallinan, C., Ghazanfar, S. ✉ & Hicks, SC. ✉ “Spatial Mutual Nearest Neighbors for Spatial Transcriptomics Data.” bioRxiv. <https://doi.org/10.1101/2024.10.08.615307>.

Research Experience

Hicks Lab, Johns Hopkins Bloomberg School of Public Health

Baltimore, MD

ADVISOR: DR. STEPHANIE C. HICKS

Jun. 2023 - Aug. 2024

- ***Ongoing* Scalable Two-level Spatial Clustering for Integrative Analysis of Multi-sample SRT Data**

Developing a scalable method for integration and clustering large batch of spatially resolved transcriptomics data.

Wang Lab, Broad Institute of MIT and Harvard

Cambridge, MA

ADVISOR: DR. XIAO WANG

2020 - 2022, 2024

- **STARmap Plus: Advanced 3D Transcriptome Sequencing Analysis**

Applied time series and spatial analysis techniques to delve into the molecular and cellular changes underlying Alzheimer's disease. This research aims to enhance our comprehension of disease pathology and pinpoint potential therapeutic targets.

- **TEMPomap: Dissecting mRNA Dynamics at Sub-cellular Precision**

Formulated a model to elucidate the nuances of mRNA dynamics (e.g., synthesis, degradation) at sub-cellular resolution, leveraging in situ sequencing data.

- **ClusterMap: Multi-scale Analysis of Spatial Gene Expression**

Conducted benchmarking of ClusterMap against manual labeling and alternative algorithms. Engaged in collaboration with the Liu lab at Harvard SEAS.

- **In Situ Electro-sequencing in Three-dimensional Tissues**

Executed pseudo-time and differential expression analyses via Monocle3 and Seurat to identify genes that vary during the maturation process. Integrated Gene Set Enrichment Analysis with genes pinpointed by Electro-Seq. Collaborative effort with Liu lab.

Kay Tye Lab, Salk Institute / MIT BCS

Cambridge, MA

ADVISORS: DR. NANCY PADILLA

2020

- **A Web-based Multi-Animal Tracking and Behavioral Analysis Tool**

Developed the curate UI and cluster UI based on frameworks like Bootstrap and jQuery via JavaScript for the end-users to inspect and revise the tracking and clustering results visually.

Zhao Lab, Yale University

New Haven, CT

CO-ADVISORS: DR. HONGYU ZHAO & DR. ZAPATA HEIDI

Jul. 2019 - Sep. 2019

- **Transcriptomic Insights into Human Macrophages' Immune Response to HIV, Bacteria, and Fungi Infections**

Investigated gene expression differences in macrophages from HIV patients versus healthy individuals post bacterial/fungal infection, using DEseq and additional statistical tools. Introduced an innovative algorithm, tailored for scenarios with limited samples, relying on p-value computation. Further, probed the impact of differentially expressed genes on gene networks, utilizing WGCNA and gProfiler for analysis.

BioX Institute, Shanghai Jiao Tong University

Shanghai, China

SUPERVISORS: DR. LIN HE

2019

- iGEM (International Genetically Engineered Machine) 2019: "A Biological Storage Method with CRISPR and Off-target Detection in Gene Editing with LURE sequences"

Awards & Scholarships

2021 **Overseas Study Scholarship**, Zhiyuan College

2019 **Gold Medal Awarded & Best New Application Project Nominee (Top 5%)**, iGEM 2019
Overseas Study Scholarship, Zhiyuan College

2018 **Zhiyuan Sunshine Leader Scholarship**, Zhiyuan College

2017-2020 **Zhiyuan Honors Scholarships**, Zhiyuan College
Undergraduate Scholarships, Shanghai Jiao Tong Univ.

Proficiency

Coding **R, Python, Linux Shell, C++, Perl & MySQL**

Web **HTML, CSS, JavaScript & php**

Design **Adobe Illustrator, Photoshop, After Effects & Cinema 4D**