

Education

Vanderbilt University

PHD IN COMPUTER SCIENCE

Nashville, TN, U.S

2021 - 2026

- Advisor: Dr. Maizie Zhou
- Dissertation: "Computational Methods for Learning, Evaluating, and Interpreting Spatial Organization in Transcriptomic Data"

Huazhong University of Science and Technology

MS IN COMPUTER SCIENCE

Wuhan, Hubei, China

2018 - 2021

- Thesis: Using Fourier Transform to Enhance Contour Feature in Aerial Image Object Detection

Huazhong University of Science and Technology

BS IN BIOINFORMATICS

Wuhan, Hubei, China

2014 - 2018

- Berkeley Biosciences Study Abroad, 2016 Fall, University of California, Berkeley

Experience

Postdoctoral Research Associate, Washington University School of Medicine in St. Louis

St. Louis, MO, US

ADVISOR: DR. GUANGHUA (ANDY) XIAO AND DR. YANG XIE

Aug. 2026 - Current

- Multi-omics foundation models.

NeuroAI Grad Research Intern, Cold Spring Harbor Laboratory

Cold Spring Harbor, NY, U.S.

ADVISOR: DR. FLORIN ALBEANU

May. 2025 - Oct. 2025

- Decoding glomerular odor space representations across ages using odor responses
- Image alignment of mouse olfactory bulbs

Publications

(†=co-first author; *=corresponding author)

- Wang, Q.†, **Yunfei Hu**.†, Zhu, Y., Peng, J., Chelliah, G., Sobanko, M., Sanchez, B., Ginty, D. D., Zhou, X. M., Meltzer, S. "Spatial transcriptomics reveals organizational properties of mouse spinal cord and alterations in neuropathic pain." *Proceedings of the National Academy of Sciences* (2026)
- Yuling Zhu†, **Yunfei Hu**†, Manfei Bella Xie†, Haoran Qin, Zuzanna J. Szul, Derek M. Young, Weiman Yuan, Qimeng Wang, Yichen Henry Liu, Shan Meltzer*, Xin Maizie Zhou*. "Benchmarking cell type annotation in spatial transcriptomics: resolving cellular hierarchies, biological fidelity, and dynamic cell states." *Nature Biomedical Engineering* (under revision) (2026)
- Liu, Y., Ma, K., Xu, H., Xu, K., **Yunfei Hu**, Lin, Z., Lin, J., Han, B., Li, S., Lin, Z., Zhou, X. M., Zhang, L. "Interpretable spatial multi-omics data integration and dimension reduction with SpaMV." *Nature Communications* (2026)
- Shen, W.*, **Yunfei Hu**, Liu, C., Lei, Y., Wong, H.-S., Wu, S.*, Zhou, X. M.* "CSsingle: a unified tool for robust decomposition of bulk and spatial transcriptomic data across diverse single-cell references." *Nucleic Acids Research* (2026)
- Potu, T.†, **Yunfei Hu**.†, Khan, R., Dharani, S., Ni, J., Zhang, L.*, Zhou, X. M.*, Mallory, X.* "SCGclust: single-cell graph clustering using graph autoencoders integrating SNVs and CNAs." *Mathematics* (2026)
- Z. Lin, H. Tong, **Y. Hu**, X. S. Gui, J. Shen, B. Lee, L. Zhang, D. Moyer, M. Zhou, X. M. Zhou*, K. Votanopoulos. "ResGAT: sample-efficient graph attention for appendiceal cancer subtypes whole slide image analysis." *MIDL* (2026)
- **Yunfei Hu**, Lin, Z., Xie, M., Yuan, W., Rao, M., Liu, Y. H., Shen, W., Zhang, L.*, Zhou, X. M.* "MaskGraphene: an advanced framework for interpretable joint representation for multi-slice, multi-condition spatial transcriptomics." *Genome Biology* (2025)
- **Yunfei Hu**.†, Wen, Z.†, Lin, Z., Qin, H., Yuan, W., Liu, Y. H., Klindt, D., Zhang, L., Carja, O., Zhou, X. M. "An Interpretable Framework for Decoding Transcriptomic Foundation Models." *Manuscript under review* (2025)
- Chen, Y., Xie, M., **Yunfei Hu**, Yuan, W., Sarkar, H., Li, B., Zhang, L., Zhou, X. M. "From features to slice: parameter-cloud modeling of spatial transcriptomics for simulation and 3D interpolatory augmentation." *Manuscript under review* (2025)
- Qin, H., **Yunfei Hu**, Zhu, Y., Baek, J., Yuan, W., Meltzer, S., Zhou, X. M. "BioLACE: unifying spatial geometry and marker priors for cohesive cell-type clustering in spatial transcriptomics." *Manuscript under review* (2025)
- Yuan, W.†, Luo, C.†, **Yunfei Hu**, Zhang, L., Wen, Z.-H., Liu, Y. H., Mallory, X.*, Zhou, X. M.* "CNVeil enables accurate and robust tumor subclone identification and copy number estimation from single-cell DNA sequencing data." *Preprint* (2025)
- **Yunfei Hu**, Xie, M., Li, Y., Rao, M., Shen, W., Luo, C., Qin, H., Baek, J., Zhou, X. M. "Benchmarking clustering, alignment, and integration methods for spatial transcriptomics." *Genome Biology* (2024)
- **Yunfei Hu**, Zhao, Y., Schunk, C. T., Ma, Y., Derr, T., Zhou, X. M. "ADEPT: Autoencoder with differentially expressed genes and imputation for robust spatial transcriptomics clustering." *iScience* (2023)

- Song, Q.[†], **Yunfei Hu**.[†], Ni, C., Yin, Z. “The hidden patient connections: predicting hormonal therapy medication discontinuation using hyper-graph neural networks on clinical communications.” *AMIA Summits on Translational Science Proceedings* (2023)
- **Yunfei Hu**, Yang, C., Zhang, L., Zhou, X. “Haplotyping-assisted diploid assembly and variant detection with linked reads.” *Methods in Molecular Biology* (2023)
- **Yunfei Hu**, Mangal, S., Zhang, L., Zhou, X. M. “Automated filtering of genome-wide large deletions through an ensemble deep learning framework.” *Methods* (2022)
- Li, S., Guo, Z., Ioffe, J. B., **Yunfei Hu**, Zhen, Y., Zhou, X. M. “Text mining of gene–phenotype associations reveals new phenotypic profiles of autism-associated genes.” *Scientific Reports* (2021)
- Zhao, Y., **Yunfei Hu**, Yuan, P., Jin, H. “Maximizing influence over streaming graphs with query sequence.” *Data Science and Engineering* (2021)

Presentations

(*=presenting author; †=mentored undergraduate)

- **Hu, Y.** “Investigating the Role of Sensory Activity in Somatosensory Circuit Assembly.” HHMI Science Meeting, Chevy Chase, MD (2026)
- **Hu, Y.** “Decoding the Olfactory Bulb Glomerular Map: Linking Odorants, Receptors, and Responses.” Poster session, Society for Neuroscience (SfN) Annual Meeting, San Diego, CA (2026)
- **Hu, Y.*** “MaskGraphene: An Advanced Framework for Interpretable Joint Representation for Multi-slice, Multi-condition Spatial Transcriptomics.” Poster session, Vanderbilt Symposium on AI, Spatial & Systems Biology, Nashville, TN (2025)
- **Hu, Y.*** “MaskGraphene: Advancing Joint Embedding, Clustering, and Batch Correction for Spatial Transcriptomics Using Graph-based Self-supervised Learning.” Oral presentation, 14th RECOMB Satellite Conference on Biological Sequence Analysis, Boston, MA (2024)
- **Hu, Y.*** “ADEPT: Autoencoder with Differentially Expressed Genes and Imputation for Robust Spatial Transcriptomics Clustering.” Oral presentation, 13th RECOMB Satellite Conference on Biological Sequence Analysis, Istanbul, Turkey (2023)
- **Hu, Y.*** “An Ensemble Deep Learning Framework to Refine Large Deletions in Linked-Reads.” Oral presentation, IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Remote (2021)

Honors & Awards

- 2025 **Edward Ferguson Jr. Graduate Award (for excellence in research)**, Vanderbilt University
- 2024 **VADD Travel Award**, Vanderbilt University
- 2024 **Graduate School Travel Grant**, Vanderbilt University
- 2023 **Graduate School Travel Grant**, Vanderbilt University
- 2021 **BIBM 2021 Travel Award**, BIBM, IEEE
- 2020 **Academic Excellence Scholarship**, Department of Computer Science, HUST
- 2019 **Academic Excellence Scholarship**, Department of Computer Science, HUST
- 2018 **Academic Excellence Scholarship**, Department of Computer Science, HUST
- 2016 **Scholarship for Academic Excellence (Undergrad)**, Department of Life Science and Technology, HUST

Teaching & Service

Dec, 2026	IEEE BIBM Workshop on algorithmic advances for spatial omics data analysis , Program Chair	Dallas, TX
Oct, 2026	MICCAI Workshop on Medical Imaging Analysis for Spatial Omics , Program Committee	Abu Dhabi, UAE
Mar, 2026	Pattern Recognition , Reviewer	
Mar, 2026	IEEE TKDE , Reviewer	
Dec, 2025	IEEE BIBM Workshop on algorithmic advances for spatial omics data analysis , Program Committee	Wuhan, China
Nov, 2025	Journal of Computational Biology , Reviewer	
Mar, 2024	Nature Communications , Reviewer	