

Haoyu Wang

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https://carlwhy-28.github.io

Education

University of Pittsburgh, School of Medicine

Ph.D. in Biomedical Informatics

Pittsburgh, PA

Aug 2025 - 2030

- Focus: Computational Biology, Machine Learning, Spatial Transcriptomics

University of Pittsburgh, School of Computing and Information

M.S. in Information Science

Pittsburgh, PA

Aug 2024 - May 2025

- Completed 30 of 36 credits (withdrew upon Ph.D. admission)

- Relevant Coursework: Data Mining, Machine Learning, Bioinformatics

Beijing Forestry University

B.E. in Computer Science and Technology

Beijing, China

Sep 2020 - Jun 2024

Professional Experience

University of Pittsburgh Medical Center, **Osmanbeyoglu Lab**

Computational Biology Intern

Pittsburgh, PA

Aug 2024 – Current

- Designed and implemented dual-graph attention neural networks (DGAT) for spatial multi-omics data integration, enabling accurate protein expression imputation from transcriptomic and spatial features
- Performed downstream pathway and transcription factor activity inference using statistical modeling and enrichment analysis to identify key regulatory signals in tumor microenvironments

Publications

Wang, H., Batz, C., Osmanbeyoglu, H.U. DGAT: A Dual-Graph Attention Network for Inferring Spatial Protein Landscapes from Transcriptomics. *bioRxiv* [Preprint], 2025 Jul 9. doi: 10.1101/2025.07.05.662121

Selected for oral presentation at ISMB 2025, poster at MLCB 2025. Under peer review at Nature Communications.

Research Experience

DGAT: Spatial Protein Landscapes Imputation from Transcriptomics

UPMC Research Project

Pittsburgh, PA

Sep 2024 – May 2025

- Developed a spatially-aware GAT-based model for protein imputation from mRNA and spatial data
- Improved protein-wise correlation by 5%–20% over prior methods in cross-sample predictions
- In spatial transcriptomic data lacking protein level but with pathological annotations, achieved 1%–3% Adjusted Rand Index gains in spatial domain clustering

Pancreatic Cancer Spatial Transcriptomics Analysis

UPMC Research Project

Pittsburgh, PA

Aug 2024 – Dec 2024

- Performed downstream analysis of pancreatic cancer Spatial Transcriptomics data, utilizing statistical models to infer transcription factor and pathway activities across patient groups
- Identification and visualization of significant patterns to uncover biological insights related to cancer progression

Driver Fatigue Detection Algorithm Based on Deep Learning

Graduation Project

Beijing, China

Mar 2024 – Jun 2024

- Realized the analysis of human fatigue states based on YOLOv8-pose and devised a multi-modal evaluation algorithm

Technical Skills

- **Programming Languages:** Proficient – Python, SQL; Intermediate – Java, C++, MATLAB, R; Basic – C
- **Machine Learning/AI:** PyTorch, TensorFlow, scikit-learn, GNNs, Computer Vision
- **Bioinformatics:** Spatial Transcriptomics, Single-cell Analysis, Genomics, Pathway Modeling
- **Tools & Platforms:** Linux (Ubuntu), Git, Jupyter, SLURM, VSCode