Qifeng Zhou

Arlington, TX | qfchou@gmail.com | Website | Linkedin

Education

University of Texas at Arlington, *Ph.D. student in Computer Science (GPA 4.0/4.0)* Sept. 2022 – Now
- Supervisor: Dr. Junzhou Huang

Zhejiang University, *BS in Chu Kochen Honors College (Rank Top5%)* Sept. 2018 – June 2022

Publications

[1] **Qifeng Zhou**, Thao M Dang, Yuzhi Guo, Hehuan Ma, Wenliang Zhong, Saiyang Na, Jean Gao, and Junzhou Huang, "Contrastive Pretraining for Computational Pathology With Visual Language Models", **ISBI 2025**.
[2] **Qifeng Zhou**, Wenliang Zhong, Yuzhi Guo, Michael Xiao, Hehuan Ma, and Junzhou Huang, "PathM3: A Multimodal Multi-Task Multiple Instance Learning Framework for Whole Slide Image Classification and Captioning", **MICCAI 2024**.
[3] **Qifeng Zhou**, Thao M Dang, Wenliang Zhong, Yuzhi Guo, Hehuan Ma, Saiyang Na, Haiqing Li, Junzhou Huang, "MLLM4PUE: Toward Universal Embeddings in Digital Pathology through Multimodal LLMs".
[4] Thao Dang, Haiqing Li, Yuzhi Guo, Hehuan Ma, Feng Jiang, Yuwei Miao, **Qifeng Zhou**, Jean Gao and Junzhou Huang, "HAGE: Hierarchical Alignment Gene-Enhanced Pathology Representation Learning with Spatial Transcriptomics", **MICCAI 2025**.
[5] Thao M. Dang, Yuzhi Guo, Hehuan Ma, **Qifeng Zhou**, Saiyang Na, Jean Gao, and Junzhou Huang, "MFMF: Multiple Foundation Model Fusion Networks for Whole Slide Image Classification", **ACM BCB 2024**.

Experiments

Digital Pathology Intern | Genmab | Princeton, NJ Jun. 2025 - Aug. 2025
- Engineered an end-to-end multi-modal deep learning framework using **cross-attention** to fuse Whole Slide Images (WSI), omics, and clinical data for patient survival analysis in oncology.
- Developed a novel deep learning pipeline for non-invasive prediction of **Folate Receptor Alpha** expression from H&E pathology images, creating a scalable method for computational biomarker discovery.
- Managed model development and large-scale data processing in a GPU-enabled cloud environment (AWS, Databricks) utilizing Python and PyTorch.

Research Projects

MLLM-based foundation model for pathology vision-language data Sept. 2024 - Feb. 2025
- Built a foundation model based on LLaVA, surpassing SOTA methods (including **CONCH, MUSK**) in **10 datasets**.
- Employed prompts to guide the MLLM for representation learning and used LoRA to fine-tune MLLM with pathology image-text pairs.
- Published a research paper to **ISBI 2025**.

Spatial Transcriptomics data guided pathology image representation learning Dec. 2024 - Feb. 2025
- Proposed a framework integrating Spatial Transcriptomics into the pathology image encoder via cross-attention, outperforming SOTA methods in **6 datasets across 3 different tasks**.
- Introduced a hierarchical clustering strategy to align image-gene pairs, leading to a publication at **MICCAI 2025**.

Multimodal foundation model integrating for WSI classification Apr. 2024 - July 2024
- Developed a framework integrating image, cell, and text foundational models to enhance WSI classification, improving **AUC score to 98.15** in TCGA and Camelyon16 dataset.
- Introduced a three-step cross-attention module to integrate multimodal features and an abnormality-aware module based on auto-encoders to identify abnormal instances.
- Published a research paper to ACM BCB 2024 and a research paper to Frontiers in Medicine.

Multi-instance image-text learning for WSI classification and captioning Nov. 2023 - Feb. 2024
- Developed a multimodal, multi-task MIL framework for WSI classification and captioning, improving **5% accuracy and 0.2 BLEU scores** over SOTA methods.
- Developed a correlation module to reduce redundancy and a query-based transformer to align WSIs with texts, resulting in a publication at **MICCAI 2024**.

Technologies

Python, C/C++, Pytorch, Scikit-learn, OpenCV, Scikit-Image, Hugging Face, Git, Shell, DDP, Openslide, LLM, MLLM