WeiQin Zhao

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EDUCATION

The University of Hong Kong, Hong Kong SAR, China. *Ph.D.* 2021.09 – 2025.09 (Expected)

- Advised by Professor. Lequan Yu.

Beihang University, Beijing, China. *B.S. in Computer Science* 2017.09 – 2021.06

PUBLICATIONS

* indicates equal contributions

- **Weiqin Zhao**, Ziyu Guo, Yinshuang Fan, Yuming Jiang, Maximus Yeung, Lequan Yu. Aligning Knowledge Concepts to Whole Slide Images for Precise Histopathology Image Analysis. ***Nature npj Digital Medicine***.
- **Weiqin Zhao**, Shujun Wang, Maximus Yeung, Tianye Niu, Lequan Yu. MulGT: Multi-task Graph-Transformer with Task-aware Knowledge Injection and Domain Knowledge-driven Pooling for Whole Slide Image Analysis. *AAAI Conference on Artificial Intelligence (AAAI) 2023*.
- Yanyan Huang*, **Weiqin Zhao***, Shujun Wang, Yu Fu, Yuming Jiang, Lequan Yu. ConSlide: Asynchronous Hierarchical Interaction Transformer with Breakup-Reorganize Rehearsal for Continual Whole Slide Image Analysis. *International Conference on Computer Vision (ICCV) 2023*.
- Qinshuo Liu*, **Weiqin Zhao***, Yanwen Fang, Lequan Yu, Guodong Li. From Layers to States: A State Space Model Perspective to Deep Neural Network Layer Dynamics. *The Thirteenth International Conference on Learning Representations (ICLR 2025).*
- Ziyu Guo*, **Weiqin Zhao***, Shujun Wang, Lequan Yu. HIGT: Hierarchical Interaction Graph-Transformer for Whole Slide Image. *International Conference on Medical Image Computing and Computer Assisted Intervention (MICCAI) 2023.*
- Yanyan Huang, **Weiqin Zhao**, Yihang Chen, Yu Fu, Lequan Yu. Free Lunch in Pathology Foundation Model: Task-specific Model Adaptation with Concept-Guided Feature Enhancement. *The Thirty-Eighth Annual Conference on Neural Information Processing Systems (NeurIPS) 2024*.
- Yanyan Huang, **Weiqin Zhao**, Fu Yu, Lingting Zhu, Lequan Yu. Unleash the Power of State Space Model for Whole Slide Image with Local Aware Scanning and Importance Resampling. *IEEE Transactions on Medical Imaging*.
- Fuying Wang, Jiayi Xin, **Weiqin Zhao**, Yuming Jiang, Yeung, Maximus, Liangsheng Wang, Lequan Yu. TAD-Graph: Enhancing Whole Slide Image Analysis via Task-Aware Subgraph Disentanglement. *IEEE Transactions on Medical Imaging*.
- Yihang Chen, **Weiqin Zhao**, Lequan Yu. Transformer-based Multimodal Fusion for Survival Prediction by Integrating Whole Slide Images, Clinical, and Genomic Data. *IEEE International Symposium on Biomedical Imaging (ISBI) 2023*.
- Zhuo Liang*, **Weiqin Zhao***, Fuying Wang, Yuanhua Huang, Lequan Yu. ST-200K: A Large-scale Paired Dataset for Histology Imaging and Spatial Transcriptomics. *Machine Learning in Computational Biology (MLCB) 2024*.
- Zhaodong Chen*, **Weiqin Zhao***, Lei Deng, Yufei Ding, Qinghao Wen, Guoqi Li, Yuan Xie. Large-scale self-normalizing neural networks. *Journal of Automation and Intelligence*.
- Yihang Chen, **Weiqin Zhao**, Lequan Yu. Transformer-based Multimodal Fusion for Survival Prediction from Whole Slide Images. *Machine Learning in Computational Biology (MLCB) 2022*.
- Lei Li, Jiadong Wang, Rong Ding, **Weiqin Zhao**, Xuyang Wang, Su Huo. Aphasia Treatment Assistant System Based on Recommendation and Generation. *International Conference on Computer Research and Development (ICCRD) 2020*.
- Hao Peng, Lin Liu, Liya Ma, **Weiqin Zhao**, Hongyuan Ma, Long Yuntao. Approximate Error Estimation based Incremental Word Representation Learning. *Data Science and Pattern Recognition*.

WORKING PAPERS

* indicates equal contributions

- **Weiqin Zhao**, Zhuo Liang, Xianjie Huang, Yuanhua Huang, Lequan Yu. Hist2Cell: Deciphering Fine-grained Cellular Architectures from Histology Images. ***Under Revision of Cell Genomics.***

- Zhuo Liang*, **Weiqin Zhao***, Fuying Wang, Yuanhua Huang, Lequan Yu. BRIDGE: A Cross-organ Foundation Model for Bridging Histology Imaging and Spatial Transcriptomics. *Submitted to Nature Communications.*
- Yanyan Huang, **Weiqin Zhao**, Yihang Chen, Yu Fu, Yuming Jiang, Li Liang, Shujun Wang, Lequan Yu.. Knowledge-Guided Adaptation of Pathology Foundation Models Improves Cross-domain Generalization and Demographic Fairness. *Submitted to Nature Computational Science.*
- Yu Liting, Ma tao, Weiqin Zhao, Zhuo Liang, Lequan Yu. MOSTalign: Morphology Images-Guided Spatial Transcriptomics Alignment through Image-Gene Graph Optimal Transport. *Submitted to MICCAI 2025.*
- Peixiang Huang, Yanyan Huang, Weiqin Zhao, Junjun He, Lequan Yu. HyperPath: Learning Hierarchical Representations in Hyperbolic Space for Whole-Slide Image Classification. *Submitted to MICCAI 2025.*
- Tao Ma, Lingting Zhu, **Weiqin Zhao**, Lequan Yu. ST-Diffusion: A Unified Conditional Framework for Diffusion-based Spatial Transcriptomics Data Generation and Enhancement. *Working Paper.*
- Qinshuo Liu, Yanwen Fang, Peng-Tao Jiang, **Weiqin Zhao**, Guodong Li. DGCformer: Deep Graph Clustering Transformer for Multivariate Time Series Forecasting. *Working Paper*.

PROFESSIONAL ACTIVITIES

Conference Reviews:

- The Thirteenth International Conference on Learning Representations (ICLR 2025)
- International Conference on Computer Vision (ICCV 2025)
- IEEE Conference on Computer Vision and Pattern Recognition (CVPR 2024, 2025)
- IEEE International Symposium on Biomedical Imaging (ISBI 2025)
- Machine Learning in Computational Biology (MLCB 2024, 2023)
- Computer Vision for Automated Medical Diagnosis (CVAMD 2023)
- Women in Medical Image Understanding and Analysis (WiMIUA 2022)

Journal Reviews:

- IEEE Transactions on Medical Imaging (IEEE TMI)
- Journal of Healthcare Informatics Research (JHIR)
- Scientific Reports
- Signal, Image and Video Processing

SELECTED AWARDS

- Excellent research award at Department of Statistics & Actuarial Science, HKU in 2022.
- AAAI Conference on Artificial Intelligence (AAAI) 2023 student scholarship.
- Annual outstanding student leader of Beihang University in 2019.
- Annual excellent students of Beihang University in 2017 and 2018.
- Third prize for band C in 2018 National English Competition for Chinese College Students.

TEACHING EXPERIENCES

• STAT8307 Natural language processing and text analytics	2025Spring, 2023 Spring, HKU
• STAT3612 Statistical machine learning	2024 Fall, 2023 Fall, 2022 Fall, HKU
• STAT8017 Data mining techniques	2022 Spring, HKU
• STAT2601 Probability and statistics	2024 Spring, HKU

SELECTED RESEARCH EXPERIENCES

Fine-grained Cell Architecture Detection from Whole Slide Image, HKU, *Ph.D. Candidate*

- Developed a one-stage prediction model for identifying spatial transcription-related fine-grained cell types from histology images, enhancing cost-efficient analysis for cancer studies and clinical applications.
- Designed a novel Graph-Transformer architecture that captures both local and distant tissue correlations, employing a subgraph sampling strategy during training to maintain data diversity.
- Achieved accurate cell-type identification and colocalization on external datasets, validating existing biological findings using cost-effective histology images.
- Enabled large-scale fine-grained cellular analysis on public histology cohorts, producing significant consensus findings for clinical applications that were previously unattainable.

Precise WSI Analysis with Aligned Human Expert Knowledge, HKU, *Ph.D. Candidate*

- Developed a knowledge concept-based framework for precise Whole Slide Imaging (WSI) analysis by integrating human expert knowledge with data-driven concepts.
- Employed Large Language Models (LLMs) to derive reliable human expert knowledge from medical literature and align it with histology images using a pathology vision-language model.
- Introduced key components such as learnable data-driven concepts to complement human expertise, and a two-stage aggregation paradigm that efficiently processes gigapixel WSIs and transfers concept knowledge into histopathology images.
- Enhanced automated diagnostic precision in classifying various cancer subtypes, including lung cancer subtypes, breast cancer HER2 status, and immunotherapy-sensitive subtypes of gastric cancer.

Multi-task Learning for Whole Slide Image Analysis, HKU, *Ph.D. Candidate*

- Devised a novel multi-task Graph-Transformer for slide-level WSI analysis, benefiting from learning both the commonalities and differences of multiple tasks.
- Designed a novel Task-aware Knowledge Injection module to transfer the task-shared feature into task-specific feature spaces via the cross-attention mechanism with the latent tokens that contain task-specific knowledge.
- Designed a novel Domain Knowledge-driven Graph Pooling module to represent the information of the whole graph more properly for different tasks, importing the prior knowledge from pathologists, facilitating the prediction process, and reducing the computation cost.
- Outperformed single-task counterparts and the state-of-the-art methods.

Hierarchical Interaction Graph-Transformer for Whole Slide Image Analysis, HKU, *Ph.D. Candidate*

- Developed a novel Hierarchical Interaction Graph-Transformer (HIGT) for analyzing Whole Slide Images (WSIs), effectively capturing both local and global correlations within WSI pyramids.
- Designed a Bidirectional Interaction module to facilitate communication between different resolution levels, enhancing multi-resolution information integration for accurate slide-level predictions.
- Implemented efficient pooling and separable self-attention mechanisms to reduce computational and memory costs while maintaining high performance.
- Achieved state-of-the-art results on kidney and esophageal carcinoma datasets, surpassing existing hierarchical and non-hierarchical methods in tumor subtyping and staging tasks.

Continual Whole Slide Image Analysis with ConSlide, HKU, *Ph.D. Candidate*

- Developed ConSlide, the first continual learning framework for Whole Slide Image (WSI) analysis, addressing the challenges of enormous image size and hierarchical structure with progressive model updating on sequential datasets.
- Designed a Hierarchical Interaction Transformer (HIT) to model and utilize the hierarchical structural knowledge of WSIs, achieving accurate slide-level predictions.
- Implemented a novel Breakup-Reorganize (BuRo) rehearsal method to efficiently manage WSI data replay, enhancing knowledge retention and minimizing catastrophic forgetting.
- Outperformed state-of-the-art methods on four public WSI datasets, demonstrating superior performance in balancing overall accuracy and knowledge preservation across continual learning tasks.

State Space Model for Neural Network Layer Interaction, HKU, *Ph.D. Candidate*

- Proposed a novel approach to layer aggregation in deep neural networks by treating layer outputs as states of a continuous process and leveraging State Space Models (SSM) for efficient aggregation in very deep networks.
- Introduced Selective State Space Models (S6) to design the Selective State Space Model Layer Aggregation (S6LA), a new module that integrates traditional CNN or transformer architectures within a sequential framework.
- Enhanced the representational power of state-of-the-art vision networks, improving performance on image classification and detection tasks.
- Demonstrated through extensive experiments that S6LA significantly improves the performance of deep neural networks, showcasing the potential of integrating SSMs with modern deep learning techniques.

Multimodal Fusion for Survival Prediction, HKU, *Ph.D. Candidate*

- Developed a novel transformer-based multimodal fusion framework that integrates Whole Slide Images (WSIs), clinical data, and genomic data to predict patient survival, overcoming the challenges of gigapixel WSI analysis.

- Utilized a graph-based approach to model WSIs as graphs, where patches are treated as nodes, and employed Graph Convolutional Networks (GCNs) to capture spatial information for better feature aggregation.
- Implemented TabNet for effective encoding of clinical and genomic data, and combined these features with WSI embeddings using a transformer architecture to improve survival prediction accuracy.
- Demonstrated superior performance over traditional methods on two public datasets from The Cancer Genome Atlas (TCGA), achieving significant improvements in survival prediction and risk stratification.

Task-specific Model Adaptation with Concept-Guided Feature Enhancement, HKU, *Ph.D. Candidate*
- Developed a novel Concept Anchor-guided Task-specific Feature Enhancement (CATE) framework to enhance pathology foundation models, enabling more effective and discriminative feature extraction for specific downstream tasks in Whole Slide Image (WSI) analysis.
- Designed the Concept-guided Information Bottleneck (CIB) module to calibrate generic image features by maximizing task-relevant information while minimizing superfluous details, improving task-specific adaptation.
- Implemented the Concept-Feature Interference (CFI) module to generate discriminative features by leveraging the similarities between calibrated features and task-specific concept anchors.
- Significantly improved the performance and generalizability of Multiple Instance Learning (MIL) models on public WSI datasets, demonstrating enhanced accuracy and robustness across various cancer subtyping tasks.

State Space Model for Whole Slide Image Analysis, HKU, *Ph.D. Candidate*
- Developed the Pathology Mamba (PAM) framework, a novel approach utilizing State Space Models (SSM) for efficient and accurate Whole Slide Image (WSI) analysis, overcoming challenges related to the gigapixel size of WSIs.
- Designed a Bi-directional Mamba Encoder (BiME) to model the sequential and hierarchical information within WSIs, integrating local-aware scanning to enhance local and global feature extraction.
- Implemented a Test-time Importance Resampling (TIR) module to align feature distributions between training and testing phases, significantly improving model prediction stability and accuracy.
- Demonstrated superior performance over state-of-the-art methods on nine WSI datasets for cancer subtyping and survival prediction tasks, setting new benchmarks for WSI analysis.

Bi-modal Representation for Histology Imaging Decoding Gene Expression, HKU, *Ph.D. Candidate*
- Developed BRIDGE, a multi-organ bi-modal foundation model, to predict gene expression patterns from histology images, combining the strengths of Whole Slide Images (WSIs) and Spatial Transcriptomics (ST) to overcome the limitations of single-modality approaches.
- Constructed the BIG-600K dataset, a large-scale bi-modal resource comprising histology imaging and gene expression data across 13 human organs, significantly enhancing the model's ability to generalize across diverse tissues.
- Implemented novel pretraining strategies on BIG-600K, enabling BRIDGE to perform zero-shot gene expression prediction across ten organs, achieving high accuracy in downstream tasks such as cell clustering and survival analysis.
- Demonstrated BRIDGE's superior performance in integrating WSIs and ST data, setting new benchmarks for bi-modal models in pathology and advancing the field of spatial gene expression analysis.

Task-Aware Subgraph Disentanglement for Whole Slide Image Analysis, HKU, *Ph.D. Candidate*
- Proposed a Pathological Interpretable Graph-based Model (PI-Graph) for WSI analysis, enabling the extraction of task-relevant contextual features for cancer diagnosis and prognosis.
- Introduced a novel disentanglement mechanism that separates WSI graphs into task-relevant and task-irrelevant subgraphs, improving interpretability and blocking spurious correlations.
- Demonstrated superior predictive performance on three TCGA benchmark datasets (TCGA-ESCA, TCGA-RCC, and TCGA-BLCA) for survival prediction and tumor staging tasks.