Thao M. Dang

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Selected Publications

1. ..., **T. M. Dang**, ..., "Hyperbolic Gramian Volumes for Multimodal Alignment," CVPR, 2026
2. ..., **T. M. Dang**, ..., "Learning from Guidelines: Structured Prompt Optimization for Expert Annotation Tasks," AAAI, 2026
3. **T. M. Dang**, ..., "HAGE: Hierarchical Alignment Gene-Enhanced Pathology Representation Learning with Spatial Transcriptomics," MICCAI, 2025
4. ..., **T. M. Dang**, ..., "Text-Guided Multi-Instance Learning for Scoliosis Screening via Gait Video Analysis," MICCAI, 2025
5. **T. M. Dang**, ..., "Abnormality-aware Multimodal Learning for WSI Classification," Front. Med., 2025
6. ..., **T. M. Dang**, ..., "Visual-Language Contrastive Learning for Computational Pathology with Visual-Language Models," ISBI, 2025
7. **T. M. Dang**, ..., "MFMF: Multiple Foundation Model Fusion Networks for Whole Slide Image Classification," ACM BCB, 2024

Education

University of Texas at Arlington - Ph.D. (GPA: 4.0) — USA (2023 - Current)
Chonnam National University - Master (GPA: 3.89) — South Korea

Research Experience

Research Assistant at SMILE Lab — Aug 2023 – Current
University of Texas at Arlington — Supervisor: Dr. Junzhou Huang

- **AYCE** (Submitted ECCV'26): Engineered an alignment framework for unified RNA/ATAC/ADT representation learning across 300,000+ PBMC cells. Introduced a distributional SVD-based geometric loss to handle incomplete assay profiles, directly addressing real-world multi-omics mosaic integration. Achieved **41% MSE reduction** in cross-modality imputation, **69% higher** cell type prediction accuracy, and **17% improvement** in zero-shot label transfer to held-out patient cohorts.
- **HOMIE** (Submitted ECCV'26): Developed an omni-modal histopathology retrieval framework that transforms an MLLM into a pathology-specialized retrieval via a two-stage curriculum pipeline. Introduced the Pathology Composed Retrieval benchmark to evaluate compositional queries spanning cancer images, diagnostic text, and video. Achieved **34% higher R@1** on multi-image composed retrieval and SOTA zero-shot classification on 8 of 9 cancer tissue datasets.
- **HyperGRAM** (CVPR'26): Developed HyperGRAM, a hybrid hyperbolic-Euclidean Gramian volume framework resolving Euclidean volume collapse via exponential geometric capacity, with a learnable Lorentzian mixing parameter achieving **24x variance improvement**. Achieved SOTA zero-shot retrieval across four multimodal benchmarks; the Gramian SVD alignment principle was subsequently extended to multimodal single-cell genomics integration in the AYCE framework.
- **GDP** (AAAI'26): Developed a guideline-driven prompt optimization framework shifting LLM learning from data-intensive training to RAG-based structured reasoning via tree search decomposition, targeting clinical disease name recognition with minimal annotated examples. Introduced a CoT-aligned structured prompt capturing MeSH/OMIM normalization logic from biomedical guidelines, achieving 48.5% F1 on NCBI disease corpus and **6% higher F1** in clinical named entity recognition.
- **HAGE** (MICCAI'25): Developed a hierarchical alignment framework integrating co-expression embeddings into a model via cross-attention for spatially resolved gene expression prediction from pathology images. Introduced a molecular-morphological clustering strategy at local and global levels to overcome spatial transcriptomics data scarcity. Achieved **8% higher PCC, 18.1% lower MSE, and 38% lower MAE** on HER2+ cohort with improved downstream WSI-level classification.
- **TG-MILNet** (MICCAI'25): Developed a text-guided multi-instance learning framework for non-invasive scoliosis screening from gait videos, achieving **27% higher recall** on borderline cases and **19.1% accuracy improvement** over SOTA.
- **AAMM** (Front. Med'25): Developed a multi-instance learning framework integrating patch, cell, and text features from pathology foundation models, achieving **1.2% higher AUC** over SOTA for WSI-level cancer classification and subtyping.
- **MLLM4PUE** (ISBI'25): Developed a VLM-based contrastive pretraining framework for pathology vision-language alignment, achieving **+10% Recall@50** on cross-modal retrieval and **+7% accuracy** on zero-shot patch classification.
- **MFMF** (BCB'24): Developed a VAE-guided multimodal MIL framework fusing patch, cell, and text features from pathology foundation models via cascaded cross-attention, achieving **+14.6% AUC** for WSI-level classification and subtyping.
- **AstraZeneca's challenge** (2024): Applied SAM and ensemble learning to improve tumor segmentation, achieving **1st place** in round 1 and **top 3** in round 2 of the CoSolve Sprints challenge on 3D MRI mouse cancer segmentation.

Skills

Multimodal Representation Learning, Large Language Models, Retrieval Augmented Generation, Prompt Optimization, Whole Slide Images, Single-cell Multi-omics, Spatial Transcriptomics