香港浸會大學理學院
HKBU Faculty of Science

DEPARTMENT OF COMPUTER SCIENCE

PhD Degree Oral Presentation

PhD Candidate:	Mr. YIN Chong
Date	16 August 2024 (Friday)
Time:	2:00 pm – 4:00 pm (35 mins presentation and 15 mins Q & A)
Venue:	ZOOM (Meeting ID: 934 9485 1320) (The password and direct link will only be provided to registrants)
Registration:	https://bit.ly/bucs-reg (Deadline: 12:00 nn, 15 August 2024)

Interpretable Liver Pathology Image Analysis with Limited Annotated Data

Abstract

Non-alcoholic fatty liver disease (NAFLD) is the most prevalent liver disease globally, with a high risk of severe complications, making it a public health priority to monitor its progression. Diagnosis involves quantitatively analyzing histological findings, including recognizing NAFLD Activity Score (NAS)-related components (ballooning degeneration, lobular inflammation, and steatosis) and staging fibrosis. Pathology image analysis is the gold standard for diagnosing NAFLD, providing visual cellular-level evidence. Deep learning excels in computer vision but faces challenges with histological images due to limited annotated medical data. The scarcity of annotated samples hinders deep learning techniques, and model interpretability is crucial in clinical practice, requiring more than simple image classification. This thesis proposes various interpretable pathology image analysis methods with limited annotated data.

Firstly, the sparsity of histological findings in gigapixel whole slide images (WSIs) poses a challenge for NAS-related component recognition and scoring. We propose extracting sparse and interpretable features to enhance the efficiency and interpretability of recognition and scoring of histological findings. Specifically, we encourage the model to focus on clinical interpretable features and enhance the recognition of NAS-related components. When quantifying the NAS-related components on WSIs, we introduce interpretable sampling to address sparsity in the spatial domain and incorporate low-rank decomposition to handle sparsity in the feature domain.

Then, to further tackle the small-scale dataset problems and enhance the recognition and scoring of NAS-related components, we investigate effective methods for adapting a large foundational model while also improving interpretability. Our proposed method, quantitative attribute-based prompting, is a novel approach designed specifically for liver pathology image analysis. It utilizes two quantitative attributes: K-function-based spatial attributes and histogram-based morphological attributes, which are intended for the quantitative assessment of tissue states. By utilizing quantitative attribute-based prompts, we can enhance the adaptation of a large foundation model for the analysis of NAS-related components and promote the generation of diverse pathology images.

Finally, to stage liver fibrosis in pathology images, it is crucial to analyze the spatial relationships between tissue structures in WSIs that indicate disease progression. We propose an explicit vessel-fiber modeling method for fibrosis staging from liver biopsy images. We convert two tissue structures related to diseases into graph-structured representations, with their micro-structures depicted as primal graphs and dual graphs. A primal-dual graph convolution module is designed to aid in learning the spatial relationships between tissue structures, enabling the joint exploration and interaction of their micro-structures.

***** ALL INTERESTED ARE WELCOME *****