Computer Science
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Computational Image Processing and Deep Learning with Multi-Model Biomedical Image Data

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Abstract: With the rapid advance in medical imaging technology in recent decades, computational image analysis has become a popular research topic in the field of biomedical informatics. Images from various imaging acquisition platforms have been widely used for the early detection, diagnosis, and treatment response assessment in a large number of disease and cancer studies. Although computational methods present higher analysis efficiency and less variability than manual analyses, they require appropriate parameter settings to achieve optimal results. This can be demanding for medical researchers lacking relevant knowledge about computational method development. In the last decade, deep neural networks trained on large-scale labeled datasets have provided a promising and convenient end-to-end solution to biomedical image processing. However, the development of deep-learning tools for biomedical image analysis is often restrained by inadequate data with high-quality annotations in practice. By contrast, a large number of unlabeled biomedical images are generated by daily research and clinical activities. Thus, leveraging unlabeled images with semi-supervised or even unsupervised deep learning approaches has become a significant research direction in biomedical informatics analysis.

My primary doctoral research focuses on the field of medical image processing, utilizing computational methods to facilitate biomedical image analysis with limited supervision. I have explored two ways to achieve this primarily: (1) Optimizing the model of existing approaches for specific tasks and (2) Developing semi-supervised/unsupervised deep learning approaches. In my research, I mainly focus on image segmentation and object tracking, two common biomedical image analysis tasks. By experimenting with different types of images (e.g., fluorescence microscopy images and histopathology microscopy images) from various sources (e.g., bacteria, human liver biopsies, and retinal pigment epithelium tissues), my developed methods demonstrate their promising potential to support biomedical image analysis tasks.

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Monday, October 24, 2022, 3:00 pm
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