Learning cancer grade in an automated manner

Abstract:

Owing to the molecular heterogeneity of bladder cancers in general, and urothelial carcinoma in particular, it often manifests differently in different patients based on the underlying genetic mutations. And this manifestation is often variable across stages and grades of the disease. The treatment strategies for early-stage tumors are often very different from late-stage ones; likewise, those of metastasized growths are different from localized ones. Muscle invasive tumors often require chemotherapy, whereas for non-muscle invasive ones the preferred course of treatment is surgical intervention, specifically resection. In this project, we employ a genetic algorithm-based approach to synthetically mimic tumor regions of interest from healthy tissue segments, in the process learning characteristic features pertinent with specific stages as they manifest on the CT scans. The proposed method detects cancer stage from images based on cancer and healthy segments. The results are <describe results>.

Introduction:

Bladder cancer is a is a highly prevalent and heterogeneous disease, exhibiting a diverse range of tumor traits and leading to different clinical results.

Identifying the cancer stage accurately from medical imaging is crucial for determining the appropriate course of treatment. However, current imaging-based diagnostic techniques face challenges in distinguishing between subtle tissue variations that correspond to different cancer stages and in further identifying the grade. Addressing this gap, our project employs various methods for feature extraction, including texture analysis, feature descriptors, frequency-based analysis, and pre-trained models, to analyze cancerous and non-cancerous ROIs from 100 bladder cancer CT scans. Subsequently, we apply a genetic algorithm to features derived from non-cancerous tissue, creating synthetic ROIs that mimic cancerous patterns. By analysing and comparing these synthetic cancerous ROIs with actual cancerous regions, we extract meaningful differences that reflect the underlying pathology. Finally, we investigate the relationship between these differences and cancer staging using a combination of traditional machine learning and advanced deep learning techniques.