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 highly prevalent and heterogeneous disease characterized by a wide range of tumor characteristics, resulting in varying clinical outcomes [1]. Non-muscle invasive bladder cancer (NMIBC), which includes stages Ta, Tis, and T1, typically have a lower risk of recurrence. This type of cancer is usually managed with intravesical therapies and transurethral resection of bladder tumor (TURBT) [2]. In contrast, muscle invasive bladder cancer (MIBC), consisting of stages T2 to T4, has a higher likelihood of metastasis and requires radical cystectomy along with chemotherapy [3]. Tumors classified as low-grade grow at a gradual pace and need prompt endoscopic intervention and supervision. They infrequently present a major threat to patients. On the other hand, high-grade tumors possess a significant likelihood of malignancy and are linked to substantial advancement and higher cancer mortality rates. Therefore, the most appropriate treatment options depend on the stage and grade of the cancer [4].

Various conventional machine learning and deep learning techniques have been deployed to identify and classify bladder cancer using medical imaging. The following two studies utilized traditional machine learning methods. In the first paper [5], as part of feature engineering, intensity properties and texture properties from Local Binary Patterns (LBP) and Grey Level Co-occurrence Matrix (GLCM) were extracted. Classification was conducted using a Support Vector Machine (SVM) and involved preoperative T2-weighted MRI scans from 65 consecutive patients undergoing radical cystectomy. The algorithm achieved a sensitivity of 74.2%, a specificity of 82.4%, an accuracy of 78.5%, and an AUC of 80.6% at the patient level. In the second paper [6] the authors introduced an algorithm based on texture analysis, specifically using the cooccurrence matrix and 2-D Fourier transform to differentiate between cancerous and noncancerous tissue in OCT images. The algorithm used decision tree for classification and was tested on a set of 182 OCT images from 21 patients and achieved a sensitivity of 92% and specificity of 62% in classifying tissue as cancerous or noncancerous.

The following two papers employed deep learning methods for bladder cancer classification. The first paper [7] presented a deep learning convolutional neural network (DL-CNN) designed to differentiate between muscle-invasive bladder cancer (MIBC) and non-muscle invasive bladder cancer (NMIBC) using contrast-enhanced CT scans. The authors trained a small DL-CNN from scratch and evaluated eight additional DL-CNNs that had been pre-trained on the ImageNet dataset. The study utilized a total of 1,200 cross-sectional CT images from 369 bladder cancer patients undergoing radical cystectomy. Among the eight DL-CNNs assessed, the VGG16 model achieved the highest area under the receiver operating characteristic curve (AUROC) at 0.997 in the testing dataset. In the second paper referenced [8], the authors investigated the development of a deep learning convolutional neural network (DL-CNN) designed to assist clinicians in staging bladder cancer using computed tomography urography (CTU). The model was trained on a dataset consisting of 84 bladder cancer cases from 76 patients, and it was subsequently tested on an independent dataset of 90 bladder cancer cases from 86 patients. The DL-CNN achieved a classification accuracy of 91% on the independent test set.

In the paper referenced as [9], the authors utilized a pre-trained ResNet-18 model with 71 layers for feature extraction. They implemented five different machine learning classifiers: k-nearest neighbor (KNN), support vector machine (SVM), linear discriminant analysis (LDA), decision tree (DT), and naive Bayes (NB). These classifiers were applied to three distinct classification tasks: (1) distinguishing between bladder cancer tissue and normal tissue, (2) differentiating muscle-invasive bladder cancer (MIBC) from non-muscle-invasive bladder cancer (NMIBC), and (3) detecting post-treatment changes (PTC) in comparison to MIBC. The model achieved a high F1-score across all these tasks.

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. To address this gap, our project employs various methods for feature extraction, including texture analysis, feature descriptors, frequency-based analysis, and pre-trained models to analyse cancerous and non-cancerous regions of interest (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.

References

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