Automatic Tumor Grade Classification From MRI

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I. Introduction

Prostate cancer (PCa) is one of the most common types of cancer in men, and manifests in the form of malignant growths on the prostate gland. One of the main ways doctors evaluate the severity of the cancer is using the Gleason grading system. The Gleason grade is a number from 1 to 5, with 1 being the most pathologically similar to healthy tissue, and 5 being the most aggressive growths. It is determined by examining the largest and second largest areas of the tumor and assigning them scores from 1 to 5, though 1 and 2 are rarely used. The grade is then determined by the following:

Scores	Grade
3+3	1
3+4	2
4+3	3
4+4	4
4+5, 5+4, 5+5	5

Gleason scores are traditionally determined through a transrectal ultrasound biopsy, where a doctor uses a needle to extract tissue samples from the patient's prostate. The doctor then scores the samples based on how well-formed the tissues are, by looking for small uniform glands and irregular masses of neoplastic cancer cells [1].

II. Existing Works

The process of determining a Gleason score through the analysis of live tissue samples by an experienced physician has its merits. However, the manual aspects of the process also make it highly subjective and time-consuming and consequently, difficult to standardize and test for errors. Therefore, a number of research efforts have been directed toward finding automated, software based solutions to prostate cancer detection that are faster, more scalable, and less prone to error than human processing methods.

Currently, research approaches that apply machine learning methods on multiparametric magnetic resonance imaging (MPMRI) images have shown great success. MPMRI is a composite imaging technique that utilizes two or more parameters to highlight differences between healthy and unhealthy tissue. The four parameters often used for prostate cancer detection are T2-weighted imaging (T2WI), diffusion-weighted imaging (DWI), MR spectroscopy, and dynamic contrast-enhanced (DCE) MRI [2]. Given a data set of these segmented MPMRI images, machine learning techniques are applied to determine the presence of cancerous regions. The performance of different ML models can be evaluated and scored using the receiver operating characteristic area under the curve (AUC) which measures the ability of a test to correctly identify those with and without the disease. Scores closer to 1.00 indicate high performing algorithms [3].

Traditional ML image recognition methods utilize image features such as texture, shape, pixel density, and gradient to classify images. The most robust and generizable supervised learning model currently used for PCa image classification involves support vector machines (SVMs) with recent studies exhibiting AUC scores ranging from 0.83 to 0.97 [4]. Decision tree models making use of random forest classification have also shown similar success with AUC scores ranging from 0.79 to 0.92 [5]. Moreover, other promising machine learning approaches involve artificial neural networks (ANNs) and k-nearest neighbors (k-NN) classification. One key limitation in the aforementioned image recognition algorithms is that they depend on thorough feature extraction, a step which does not always yield a sufficient data set. Thus, research efforts attempt to resolve this by exploring deep learning models - models which learn adaptive image features and perform image classification at the same time. Recent studies show that deep learning performed with deep convolutional neural networks resulted in AUC scores ranging from 0.84 to 0.92 [6].

III. Proposal

For this project, we want to test the possibility of a non-invasive and automatic method of classifying prostate cancers using MRIs of prostate tissue. We will apply various machine learning techniques on a single data set in order to evaluate which method or combination of methods results in the most accurate diagnoses when used alongside MPMRI. Our goal will be to achieve AUC scores at or above previous works, as well as gain insight to how we can extract additional accuracy by tuning our selected model to the given data set.

References

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