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Computer Assisted Prostate Cancer Diagnosis - Literature Review

Introduction

Prostate cancer (PCa) is the third leading cause of cancer death in America. However, current diagnostic practices such as digital rectal examination (DRE), prostate-specific antigen (PSA), and transrectal ultrasound (TRUS) underestimate the severity of the cancer in 30% of patients[1]. The low sensitivity and suboptimal accuracy of traditional PCa classification techniques has lead to a popularity increase in multiparametric magnetic resonance imaging (MPMRI)[2]. MPMRI is a composite imaging technique consisting of capturing T2-weighted imaging (T2WI), diffusion-weighted imaging (DWI), and apparent diffusion coefficient (ADC) or dynamic-contrast enhanced (DCE) MRI[1,2,3]. However, diagnostic accuracy is still largely dependent on the skill of the radiologist and is a time consuming task. In response to these issues, researchers have developed several methods that incorporate machine learning (ML) to assist in PCa classification and diagnosis.

Current Research

Current research uses supervised learning machine learning (ML) technologies on preprocessed, segmented MPMRI images with cancerous regions registered by experts and confirmed with ground truths determined by professional pathologists[2]. Performance of ML techniques is measured with K-fold cross validation scores based on a receiver operating characteristic (ROC) area-under-curve (AUC) metric[2]. AUC scores measure the propensity of an ML algorithm to predict true positives vs. false positives; due to the small (< 100 case) data set size used in many SVM PCa detection studies, the size of each fold's testing set during cross validation is unity. High AUC scores indicate accurate algorithms.

Kernel-based ML methods such as support vector machines (SVM) are the most popular for PCa classification due to their extreme generalizability[2]. Modifications to traditional SVM margin maximization techniques[4] including probability weighting (p-SVM)[5], cost-sensitivity[6], Fisher linear discriminant analysis[7], fuzzy *c*-means[8], and genetic algorithm-based hyperparameter maximization[9] generally improve AUC scores. The AUC of SVM MPMRI applications range from 0.83-0.96, with the majority of AUC scores[2] below 0.90, which suggests there is still considerable room for improvement[2,10,11].

In recent years, several groups[8,12,13,14,15] have found high AUC scores using ML technologies other than SVM derivatives. Random forest classification studies have shown AUC as high as 0.923 but with widely variant dataset sizes, ranging between 12 and 347 patients[12,13,15]. K-nearest neighbors classification[16] and convolutional deep-learning networks trained in 3D space also appear promising (AUC 0.84)[14].

Project Direction

While previous studies have examined the effect of isolated ML algorithms on different datasets for PCa identification or Gleason scale classification, researchers have yet to compare multiple ML technologies on a single, consistent dataset. In this project, we will compare various optimized ML techniques (e.g., random forest, deep learning, SVM) on a single dataset to study the most effective ML techniques for combination with MPMRI.

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