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Short Communication

Prostate Cancer Recognition: Using the Random Forest Technique and Other Ml Techniques

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ABSTRACT

The exact etiology of prostate cancer is unknown. Prostate cells alter their DNA, which is how doctors know prostate cancer starts. The instructions that inform a cell what to do are encoded in its DNA. The adjustments instruct the cells to multiply and develop faster than usual. In the U.S., 98% of men with prostate cancer survive five years after diagnosis. The survival rate after ten years is similarly 98%. Prostate cancer is only detected in the prostate and adjacent organs in around 84% of cases. The local or regional level is what is being discussed here. Many men may pass away from other illnesses before prostate cancer becomes a serious concern because of its sluggish growth. However, many prostate cancers are more dangerous and may extend beyond the prostate gland because they are more aggressive. They were considering the importance of prostate cancer, in this article, using machine learning algorithms and features of sampled prostate tissues, 100 men, healthy and sick people were classified.

Keywords: Prostate cancer; Sluggish growth; Prostate tissues; Machine learning algorithms

DESCRIPTION

The second-leading cause of cancer-related mortality in males is Prostate Cancer (PCa) [1]. Even though prostate imaging and genetic testing have come a long way in recent years, PCa is still diagnosed by measuring the total serum prostate-specific antigen, using a digital rectal exam as a screening method, and using ultrasound-guided [2]. In the last 20 years, ultrasound-based elastography has developed into a fascinating technique for evaluating organ stiffness [3]. The analyses of Mitterberger and Junker have demonstrated that a 50% reduction in the number of biopsy cores using elastography offered the same prostate cancer detection rate as the conventional randomized TRUS-guided biopsy, leading to the development of elastographic targeted prostate biopsy as an alternative to traditional ultrasound-guided systematic biopsy in more recent years [4-7]. Deep learning algorithms were successfully applied in urology for the diagnosis of prostate cancer, the correlation of mp-MRI images with prostate biopsy results, and the prediction of the prognosis following robot-assisted radical prostatectomy, resulting in an average performance improvement of 30-80% in comparison to conventional diagnostic standards [8,9].

Research algorithms

Random forest: An ensemble learning method called Random Forest has been presented. One of the most reliable all-purpose learning algorithms is Radom Forest (RF). While just using a small number of computing resources, and Random Forest has been demonstrated to perform quite effectively RF significantly outperforms single-tree algorithms like CART in terms of performance. It is quick and has error rates equivalent to more time- and resource-consuming algorithms.

This method includes the prostate of 100 men was tested [10]. The prostate of some people had a benign gland, and some had a malignant prostate gland. The characteristics of diagnosis result, radius, texture, perimeter, area, smoothness, compactness, symmetry, and fractal dimension of the prostate glands of these 100 men were investigated. With the help of the Random Forest machine learning algorithm, healthy and sick people were identified. The 10-fold cross-validation approach [11,12] was utilized in the simulations, with 80 percent of the data taken into account for training, 10 percent for testing, and the remaining 10 percent for validation. The suggested Random Forest algorithm's hyperparameters were then adjusted. In Table 1, some tuned hyperparameters are presented (Table 1 and Figure 1).

Table 1: Hyper parameters of random forest for predicting prostate cancer.

Algorithm	Hyper parameters
Random forest	ccp_alpha=0, min_impurity_decrease=0, min_samples_leaf=1, min_samples_split=2

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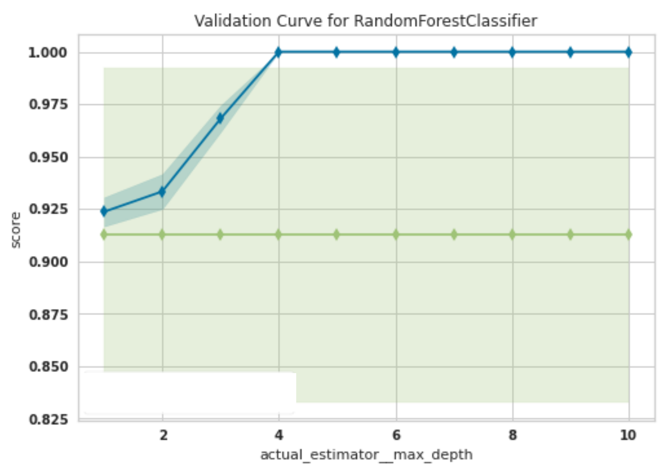

Figure 1: Validation curve for detecting prostate cancer with random forest. **Note:** (—◆—): Training score; (—◆—): Cross validation score.

The final results are shown in Figure 1 the Validation Curve for detecting prostate cancer. According to the shape of the accuracy of the training curve, it started from 0.925, and after the 4th stage of training, it reached 100 accuracies. The accuracy of the validation curve in all stages was about 91%. This showed that the proposed Random Forest algorithm detects sick and healthy people with a reasonable accuracy of 91%.

91% accuracy in diagnosing healthy and sick people by examining 100 healthy and ill people is an outstanding accuracy.

Evaluating the suggested random forest algorithm's performance in comparison to other algorithms

The Table 2 classification of prostate cancer using the proposed Random Forest algorithm and other techniques was discovered that the suggested Random Forest Classifier algorithm provided superior classification results for prostate cancer than other techniques by contrasting its output with that of different machine learning algorithms.

Table 2: The categorization of prostate cancer using the suggested random forest algorithm and other methods.

Model	Accuracy	AUC.	Recall	Prec.	F1	Kappa	MCC	Time (Sec)
Random forest classifier	0.9125	0.9467	0.943	0.93	0.933	0.807	0.822	0.447
Ada boost classifier	0.9	0.9133	0.923	0.933	0.921	0.782	0.805	0.071
K neighbors classifier	0.875	0.915	0.867	0.947	0.895	0.743	0.768	0.113
Light gradient boosting machine	0.8625	0.9333	0.903	0.897	0.889	0.703	0.731	0.022
Naive bayes	0.7875	0.9317	0.687	0.983	0.781	0.602	0.664	0.01
Dummy classifier	0.6375	0.5	1	0.638	0.778	0	0	0.009

CONCLUSION

This article examined the prostate tissues of 100 healthy and sick people. The proposed Random Forest Classifier algorithm examined healthy and ill people. 91% accuracy in identifying healthy and sick people by examining 100 healthy and ill people is an excellent accuracy. Also, comparing the results of the proposed Random Forest Classifier algorithm with other machine learning algorithm methods, the results of the proposed Random Forest Classifier method are very suitable, there were several methods.

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