

The application of artificial intelligence for enhanced diagnosis of prostate cancer using biopsy evidence that are substantiated by genetic markers

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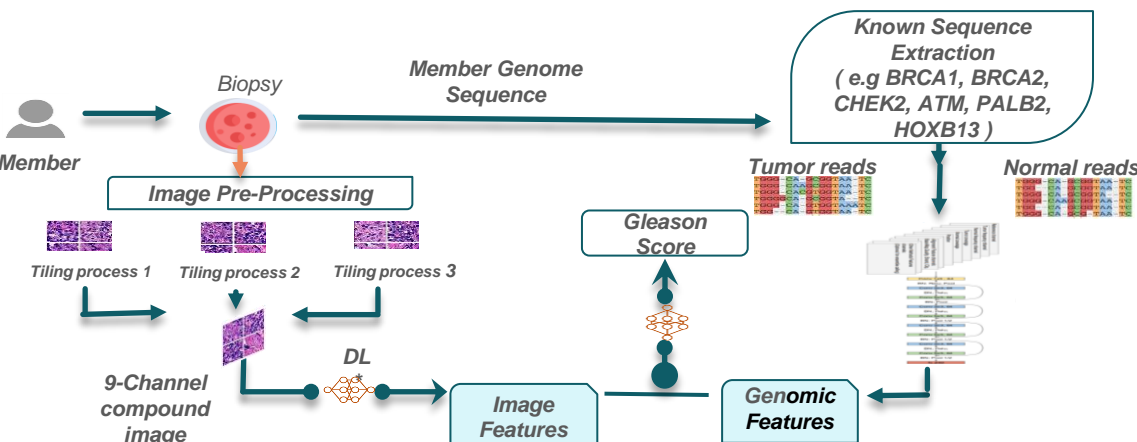
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Introduction

- Although the most prevalent approach for the diagnosis of prostate cancer is by examining the biopsy images, the presence of substantial variability in biopsy analysis often leads to delays in optimized treatment. The recent advancements in the genomic domain, with coding and non-coding genes as biomarkers along with sequencing data using artificial intelligence (AI), have led to improved decision making and better clinical management.
- In this study, we propose a hybrid approach that combines the state-of-the-art technologies for image processing and genomic features for an effective detection of Gleason score in the field of prostate carcinogenesis.

Method

- Apart from deep learning architecture, tiling method in image processing plays a significant role in Gleason detection. Since each tiling mechanism captures slightly varied information, it can lead to deviation in the final output, especially in the boundary cases. For our analysis, we have used a 9-channel compound image tiling process from three different tiling mechanisms.
- To determine the somatic mutations in genes that fit our framework, NeuSomatic method was used for its standalone accuracy and convoluted architecture. The image model and the genomic model were separately trained and combined to complement the final Gleason score.



Results

- The quadratic Kappa coefficient for standard tiling procedure was 0.76, while the two tiling procedures that was designed in our approach was found to have a Kappa coefficient of 0.65 and 0.71, respectively.
- A combined image was created using all three tiling processes which involved larger data volume and hence better reproducibility of results.
- In addition, the time required for model training was reduced by almost a third. This combination of genomic and image features was a better fit for downstream framework.

Tiling Process	Scoring (Quadratic kappa)
Process 1	0.76
Process 2	0.65
Process 3	0.71

The Kappa coefficient is a chance-adjusted index of agreement. In machine learning it can be used to quantify the amount of agreement between an algorithm's predictions and some trusted labels of the same objects.

Conclusion

New advances in genomic analyses coupled by deep learning techniques can provide improved prognosis and personalized management in prostate cancer.