AI Powered Platform to Identify Primary Prostate Cancer Patients with High Risk of Recurrence

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Background
Currently, there is no approved adjuvant therapy for primary prostate cancer (PCa). Long time to recurrence and a lack of a strong biomarker predicting recurrence after the first line of therapy is prohibitory to complete clinical trials within a short time frame for adjuvant therapy approval. Artificial intelligence (AI) offers a unique opportunity for extracting critical morphological features from PCa tissues as prognostic markers that have evaded human eyes [1-3]. We have built an AI-based platform to analyze H&E stained histological images of PCa. Our platform can accurately detect, grade and quantify PCa in patient tissue images [4,5]. Here, we show how this platform can identify morphometric features through unsupervised extraction that indicate biochemical recurrence within 3 years after radical prostatectomy (RP) with 84% accuracy. Our results highlight that our method is a better predictor of post surgical disease recurrence than any other marker in current clinical use.

Materials and Methods
Our dataset comprised of a cohort of 169 PCa patients who underwent RP. Whole slide H&E images (WSI) of their tissue sections were scanned at 40x magnification (Leica Aperio CS2). Corresponding pathologic parameters such as Gleason Score (Grade Group), tumor volume, TNM staging, margin status and post-treatment follow-up data were also collated. The samples were selected by an independent clinical data manager such that out of the 169 patients, ~50% patients recurred within 3 years of RP. Our platform technology involved two different deep CNN (Convolutional Neural Network) architectures. The platform first divided each WSI into multiple tiles. Each tile was analyzed using a CNN that graded the tile and generated a high dimensional vector to provide a mathematical equivalent of the morphology. The combination of high dimensional vectors across the WSI was then fed into a second CNN that generated a morphological score, which was combined with the clinical parameters to predict patient outcome. The platform accuracy on the dataset was established using industry standard (100 times 10-fold cross-validation).

Results

• The AI platform identifies high risk PCa patients early for tumor progression post RP (3-year PFS with 84% AUC) and can reduce cost and length of clinical trials necessary to develop adjuvant therapy.
• It also identifies previously unknown Regions Of Interest (ROI) on the H&E slide that are mapped to patient outcome – proteogenomic analysis of these AI-identified ROIs should lead to novel predictive biomarkers that drive disease progression.

Conclusions
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Figure 1. PathomIQ workflow
Figure 2. 84% AUC in predicting 3-year Progression Free Survival (PFS)

References

Disclosures
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