Using deep learning to detect patients at risk for prostate cancer despite benign biopsies

Boing Liu[1], Yinxi Wang[1], Philippe Weitz[1],Johan Lindberg[1], Lars Egevad[2], Henrik Grönberg[1],Martin Eklund[1], Mattias Rantalainen[1]

1. Department of Medical Epidemiology and Biostatistics, Karolinska Institutet; 2. Department of Oncology-Pathology, Karolinska Institutet

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Conclusions The developed deep learning model has the ability to detect men with risk of missed prostate cancer (PCa) due to under-sampling of the prostate. The proposed model has the potential to reduce false negatives in routine systematic prostate biopsies and to indicate men that could benefit from re-biopsies.

Introduction

Transrectal ultrasound guided systematic biopsies of the prostate is a routine procedure to establish a PCa diagnosis. However, the 10-12 prostate core biopsies only provide sampling of a relatively small volume of the prostate, and tumour lesions in regions between biopsy cores can be missed, leading to a well-known low sensitivity to detect presence of clinically relevant cancer.

Aim

We aim to develop and validate a deep convolutional neural network to distinguish between morphological patterns in benign prostate biopsy whole slide images from men with and without established PCa.

Results

Area under the receiver operating characteristic curve (ROC-AUC) (Fig 1a)

- Tile level: 0.701 (bootstrap 95% CI: 0.700 - 0.703)
- Biopsy level: 0.727 (bootstrap 95% CI: 0.708 - 0.745)
- Patient level: 0.738 (bootstrap 95% CI: 0.682 - 0.796)

Results (cont.)

- At specificity of 0.90, the sensitivity is 0.348 (Fig 1b)
- 2-D UMAP projection of learned feature vector separated benign tiles from men with or with PCa diagnosis (Fig 2)

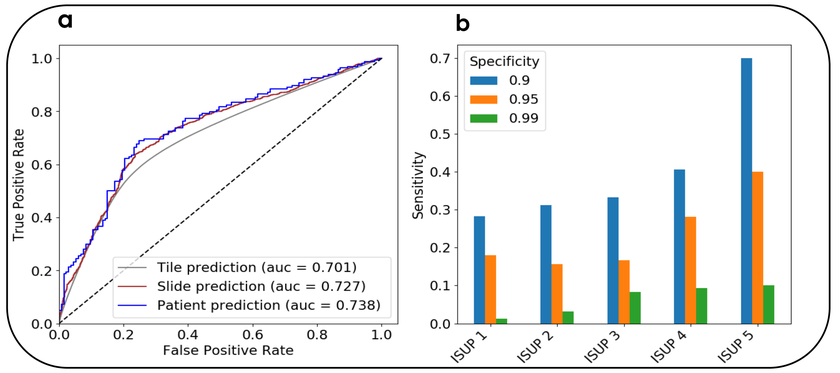

Fig 1. Prediction performance a) ROC curves and associated AUC estimates in the held-out test set for prediction of PCa versus benign diagnosis on tile, slide, and patient level; b) corresponding sensitivity by ISUP groups at various specificity levels. ISUP: International Society of Urological Pathology

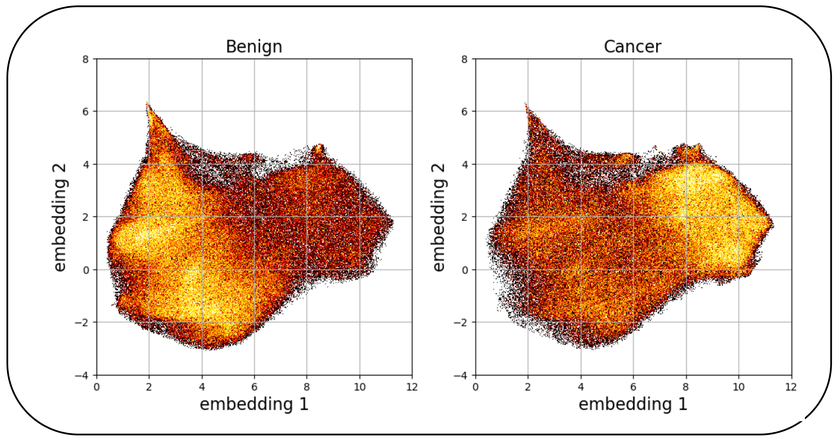

Fig 2. Model interpretation using UMAP UMAP projection of benign tiles from benign men (left) and benign tiles from PCa patients (right). The two-dimensional plots are reduced from 512-dimensional feature vector from the last fully connected layer

Methods

- 15,231 H&E **benign** prostate biopsy whole slide images (WSIs) from 1,605 men in two groups: men without a PCa diagnosis and men with established PCa diagnoses
- 80% (1,267 men) training data used for model optimization and 20% (316 men) held-out testing data used to evaluate model performance
- An ensemble of 10 deep convolutional neural networks was optimised for classification of biopsies from men with and without PCa (Fig 3)
- Hyperparameter tuning and model selection were performed by cross-validation

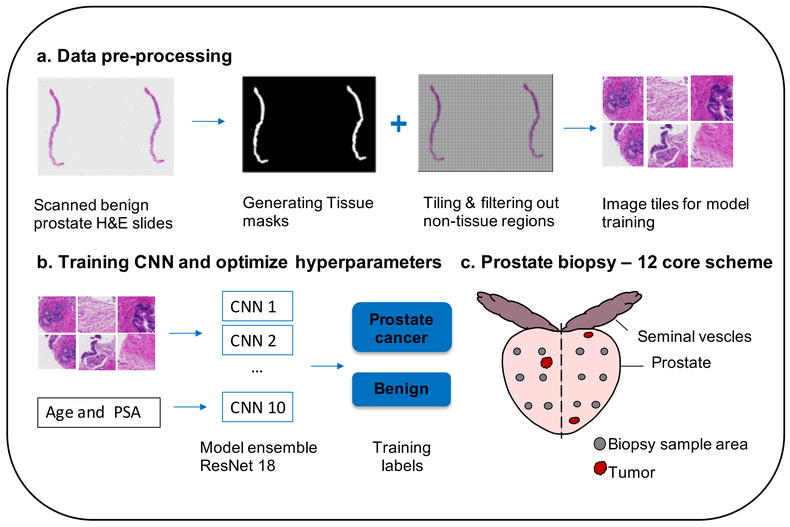

Fig 3. Overview of model development for detecting PCa patients from benign prostate core biopsies. a) Pre-processing of WSIs. b) schematic overview of the image classification by a deep CNN ensemble. c) systematic prostate biopsy 12-core scheme. CNN: convolutional neural network

Bojing Liu
E-mail: bojing.liu@.ki.se
Dept. of Medical Epidemiology and Biostatistics, **Karolinska Institutet**
SE-171 77, Stockholm, Sweden

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