Prostate Lesion Segmentation Using a Deep Learning Ensemble

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Background:
With the recent rapid advancement in deep learning, prostate cancer detection in radiology using various convolutional neural network (CNN) architectures is an active area of research. In addition to anatomical information, multi-parametric MRI (mp-MRI) can provide metabolic, diffusion, and perfusion information of the prostate, which has the potential to improve the identification of clinically significant cancers. As the use of mp-MRI becomes more common in clinical practice, automatic lesion detection and localization as a part of the decision support system would help radiologists interpret images faster, more accurately, while reducing inter-observer variability.

We present a method that applies deep learning on prostate mp-MRI to identify possible prostate cancer lesions. We validate the accuracy of the proposed approach by comparing the distance between the identified the regions of interest (ROI) with respect to known clinically significant biopsy locations.

Methods:
Mp-MR images of 337 patients from the Cancer Imaging Archive data portal were used in the study. Prostate lesions that were PI-RADS 3 (v2) or higher were segmented by three different radiologists based on the examination of axial T2-weighted (T2W), apparent diffusion coefficient (ADC) map, and high b-value (BVAL) diffusion-weighted images. Segmentations provided by the most senior radiologist (genitourinary radiologist with 15 years of experience) were used as ground truth labels for algorithm training.

Two residual networks were trained using a patch-based approach: small patches (37.5mm x 37.5mm) and large patches (75mm x 75mm). The training and validation sets contained equal number of pathology patches (lesions) and non-pathology patches (healthy prostate tissue). Semantic segmentation was used to produce lesion probability maps. An adaptative threshold using random field theory was set to identify lesion boundaries in 3D. Accuracy was established by measuring the Euclidean distance between the known biopsy location (not available during training) and the identified lesion boundary (as predicted by the ensamble).

Results:
The network ensemble achieved an accuracy of 91.3% identifying clinically significant biopsy locations while controlling for false positives with a family-wise error of 10%.

Conclusions:
The deep learning ensemble presented in this paper has the potential to help radiologists reduce the time they spend on interpreting images, segmenting potential areas of prostate cancer, and reduce inter-observer variability.

Conflict of Interest:
Helen Xu, Alon Hazan, and Diego Cantor work at Ezra

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