Mapping Prostate Cancer on Multi-Parametric Magnetic Resonance Imaging using Machine Learning

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Introduction: Prostate cancer (PCa) is one of the most prevalent non-cutaneous cancers among men. Diagnosis depends on a trans-rectal ultrasound (TRUS)-guided biopsy to estimate the stage and aggressiveness. The accuracy of this estimate is confounded by a high false negative rate due to the invisibility of PCa foci on TRUS and consequent use of a universal sextant needle targeting scheme for all patients. Multi-parametric magnetic resonance imaging (mpMRI) maps the prostate in 3D, but interpretation by the human expert is challenging due to the complex, multi-dimensional nature of the signals. Our development of novel texture analysis and machine learning techniques for heterogeneous, multi-dimensional signals will close a gap in knowledge regarding the complex relationship between mpMRI signals and PCa status.

Hypothesis: A computer-assisted diagnosis (CAD) system will accurately characterize malignant vs. benign tissue at all intraprostatic loci on mpMRI, validated using accurately co-registered whole-mount digitized histology [1].

Materials and Methods: Using a prostatectomy cohort of 22 patients with T2-weighted and ADC maps derived from diffusion weighted imaging, we generated mpMRI texture maps characterizing subtle spatial intensity patterns potentially reflective of PCa presence. A grid of square 4.11 mm \times 4.11 mm regions of interest (ROIs) were defined throughout the entire interior of each prostate on each mpMRI slice corresponding to a co-registered histology image. A reference standard label of malignant or benign was established for each ROI according to histology. To maximize the number of malignant ROIs available for training and testing, the grid position was optimized for each lesion. Malignant ROI duplication was performed to balance the two classes to avoid classifier training bias. 22 first and 33 second order texture features were extracted from each ROI for both the T2-weighted images and ADC maps. Support-vector machine (SVM) and k-nearest neighbours (KNN) classifiers were implemented to classify malignant vs. healthy ROIs. Forward feature selection was used to select the 3 most discriminative features. Area under the receiver operating characteristic curve (AUC), false positive rates and false negative rates were used to assess the models during 4-fold cross validation.

Results: In classification of malignant vs. healthy tissue in the peripheral zone, we found an AUC of 0.86 (0.18 false-positive rate (FPR), 0.28 false-negative rate (FNR)) for an SVM and 0.77 (0.03 FPR, 0.61 FNR) for KNN (n=1724). In characterization of malignant from healthy tissue in the central gland we were able to achieve an AUC of 0.83 (0.23 FPR, 0.41 FNR) for an SVM and 0.78 (0.01 FPR, 0.55 FNR) for KNN (n=1860).

Discussion and Summary: We developed a CAD system for characterization of benign vs. malignant tissue throughout the entire peripheral zone and central gland. Due to cancerous tissue primarily residing in the peripheral zone, our central gland cancerous samples were limited but this will be addressed via the incorporation of data from additional patients accrued into our trial. Once fully validated, the system may improve the radiologist’s lesion characterization.
performance and may have the potential not only to improve treatment selection for PCa patients but also to optimize focally-targeted treatments by revealing the locations of all threatening foci.