Prostate Cancer Probability Estimation Based on DCE-DTI Features and Support Vector Machine Classification

M. Moradi[1], S. E. Salcudean[1], S. D. Chang[2], E. C. Jones[3], S. L. Goldenberg[4,5], and P. Kozlowski[2,6]

[1]Electrical and Computer Engineering, University of British Columbia, Vancouver, BC, Canada, [2]Radiology, University of British Columbia, [3]Pathology and Laboratory Medicine, University of British Columbia, [4]Urologic Sciences, University of British Columbia, [5]Vancouver Prostate Centre, University of British Columbia, [6]MRI Research Centre, University of British Columbia, Vancouver, Canada

Introduction: Prostate cancer is the most common noncutaneous malignancy among men. The clinical routine for diagnosis is biopsy under ultrasound guidance. However, as a result of the multi-focal nature of the disease, clinically significant cases of cancer can be missed, resulting in repeated biopsies. We have previously shown that Diffusion Tensor Imaging (DTI) and Dynamic Contrast Enhanced (DCE) MRI provide a high degree of sensitivity in detecting prostate cancer [1,2]. In this study we present a framework of classification using multi-parametric MRI feature vectors and Support Vector Machines (SVMs) to detect prostate cancer and to create cancer probability maps that highlight areas of tissue with high risk of cancer. The correlation of this probability with Gleason Grade is also studied.

Data: Twenty nine men with a high clinical suspicion for prostate adenocarcinoma were included in this study. All MRI exams were carried out on a 3T Philips Achieva MRI scanner. Twelve axial slices (4 mm, no gap) across the prostate gland were acquired for both DTI and DCE MRI data with FOV of 24 cm. The DTI data were processed off-line to generate maps of Apparent Diffusion Coefficient (ADC) and Fractional Anisotropy (FA) [2]. Three DCE-based pharmacokinetic parameters, namely volume transfer constant K^{trans}, fractional volume of the extra-vascular extra-cellular space v_e, and fractional plasma volume v_p, were calculated by fitting the Gd concentration vs. time curves to the extended Kety model [3]. After imaging, from 8 to 12 needle biopsies were collected from each subject depending on the size of the prostate. The dataset included a total of 240 negative biopsy cores and 29 positive biopsy cores. The histology was interpreted with assignment of the Gleason score by a number of different anatomic pathologists who practice general and subspecialty uropathology

Classification and mapping method: Each biopsy core in the dataset was represented by a feature vector consisting of the average values of the five DCE-DTI features ($\boldsymbol{X} = [K^{trans}, v_e, v_p, ADC, FA]$) in its corresponding area in the MRI data. Following [2], for negative biopsies, this corresponding area was set to be the entire biopsy target volume (e.g. mid-left-lateral), while for positive cores, this area was determined from a combination of manual segmentation and thresholding based on biopsy (see [2] for details). SVM classification with radial basis kernel function [4] was used to separate the data into "normal" and "cancer" classes based on these feature vectors. The parameters of the SVM kernel function were chosen in a grid-based search [5,6]. The training-testing validation was performed in leave-one-patient-out manner. For each patient, we trained the SVM based on biopsy cores from all other patients and tested it on the cores from the patient in question. To acquire post-classification cancer probabilities ($P_c = P(cancer|\boldsymbol{X})$), the extension of the SVM training proposed by Platt [7] was used. The P_c value acquired for each biopsy core was used as a decision threshold for cancer detection. The Receiver Operating Characteristic (ROC) curve was obtained by setting this detection threshold to values in the range of [0,1]. Given $\boldsymbol{X}$ for all pixels in one MRI slice, cancer probability maps were created by calculating and plotting the values of P_c - using the SVM trained on data from all other subjects - for the entire prostate region in the slice.

Results and discussion: The ROC curves were obtained separately for DCE features $\boldsymbol{X_{DCE}} = [K^{trans}, v_e, v_p]$, for DTI features $\boldsymbol{X_{DTI}} = [ADC, FA]$, and for the combined feature vector $\boldsymbol{X} = [K^{trans}, v_e, v_p, ADC, FA]$ resulting in area under ROC curve (AUC) values of 0.867, 0.919 and 0.956 respectively (Fig.1). The combined feature vector resulted in higher AUC than DCE (p=0.002) and DTI (p=0.01). With the combined feature vector, at the decision threshold of $P_c = 0.5$, three of the 29 tumors were misclassified while a specificity of 91% was obtained. At the decision threshold of $P_c = 0.7$, only one tumor was misclassified, while a high specificity of 87% was maintained. We also noted a correlation between the P_c value and the Gleason grade of the tumors. The average P_c value was 0.555 for tumors of grade 3+3 (number of tumors=7), 0.778 for tumors of grade 3+4 and 4+3 (n=19), and 0.963 for grade 4+5 (n = 3). The increase in P_c values was significant from Grade 6 to 7 (p=0.01). The small number of tumors in grade 4+5 did not warrant an analysis of statistical significance. None of the 4+5 tumors were misclassified in any of the experiments. The T2W image and the cancer probability map obtained for the mid slice MRI data of a patient with positive biopsy cores in the mid-left-lateral and mid-left-medial regions of the prostate are illustrated in Fig. 2.

Conclusions: Our result is in agreement with the previous work that shows the diagnostic power of combined DTI and DCE MRI [2]. The developed SVM-based probabilistic approach to cancer detection provides a high level of sensitivity while maintaining high specificity. The observed increase in cancer probability with increasing Gleason grade is promising. This suggests that multi-class SVM-based classification is a potential tool for non-invasive grading, given a sufficiently large dataset to enable training on tumors of different grades.

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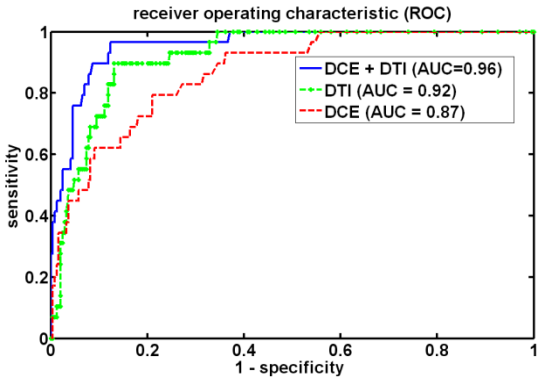

Figure 1- ROC curves, for different groups of features acquired by changing the decision threshold, P_c, from 0 to 1.

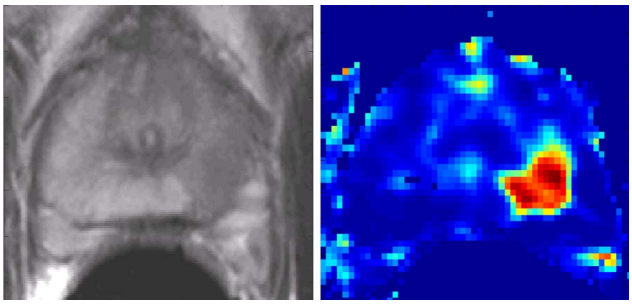

Figure 2 – Left: T2W image of mid region of a patient with biopsy confirmed cancer in mid-left region. Right: The SVM-based cancer probability map, with hot colors corresponding to higher P_c. The tumor is distinguished.