Automatic classification of benign and malignant prostate lesions in VERDICT DW-MRI using convolutional encoder-decoder architectures

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Introduction With the increasing availability of medical imaging data many studies exploit convolutional neural networks (CNNs) to improve the diagnostic clinical pathways for many pathologies. This study focuses on prostate cancer characterization in VERDICT (Vascular, Extracellular and Restricted Diffusion for Cytometry in Tumors) diffusion-weighted (DW)-magnetic resonance imaging (MRI), which is a non-invasive microstructural imaging technique that comprises an optimized acquisition protocol and a computational model to map histological indices in vivo[1,2]. Specifically, we investigate the potential of model-free PCa characterization on raw VERDICT DW-MRI data using CNNs.

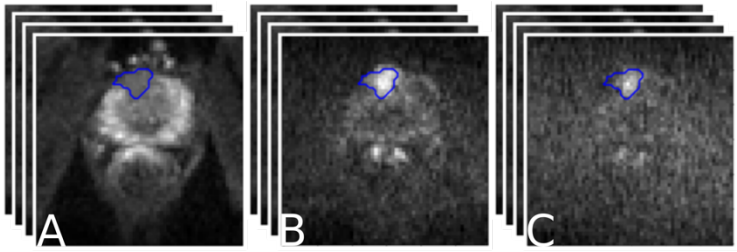

Fig. 1 Cancerous regions are seen as a focus of high signal intensity on DW-MRI of b = 2000, 3000 s/mm^2 (B, C) and as a focus of low signal intensity on b = 90 s/mm^2.

Materials We use VERDICT DW-MRI data from 103 patients. VERDICT DW-MRI (Fig. 1) were acquired with pulsed-gradient spin-echo sequence (PGSE) using an optimized imaging protocol for VERDICT prostate characterization with 5 b-values (90-3000 s/mm^2) in 3 orthogonal directions, on a 3T scanner (Achieva, Philips Healthcare, NL) [3]. Also, images with b = 0 s/mm^2 were acquired before each b-value acquisition. A dedicated radiologist contoured malignant and benign lesions on the registered VERDICT DW-MRI using multi-parametric (mp)-MRI for guidance.

Methods We perform pixel-wise classification on predefined regions of interest (ROIs) on DW-MRI data using two different convolutional encoder-decoder architectures. We consider two different classes (malignant, benign/normal) and train the networks using weighed pixel-wise cross-entropy loss. The first CNN (MRI-UNet) is based on the U-Net architecture[4] and is represented as C_{64}-P-C_{128}-P-C_{256}-P-C_{256}-TC_{256}-TC_{128}-TC_{64}-TC_{2}, where P is a max-pooling layer and TC_K is a transposed convolutional layer with K 2x2 filters. The encoder module of the second network (MRI-ResNet) is similar to the ResNet-18[5]. The MRI-ResNet has the following form: C_{64}-C_{64}-C_{64}-C_{128}-C_{128}-C_{128}-C_{128}-BU-C_{128}-C_{64}-BU-C_{64}-C_{64}-BU-C_{64}-C_{2}, where BU is a bilinear upsampling operation with a scale factor of 2. We implement both networks using Pytorch. We employ a 10-fold cross validation (CV) approach to train and test the networks and repeat each 10-fold CV 5 times. We train the networks for 200 epochs and select the model which has the smallest loss on a validation set (20% of the training set). We use stochastic gradient descent (SGD) with a mini-batch size of 32, a constant learning rate of 1e-5, a momentum of 0.9 and a weight decay of 1e-3.

Results and Discussion We perform two different experiments and present the results (Fig. 2). In the first experiment, we train the networks on predefined malignant and benign/normal ROIs and ignore the rest of the pixels. In the second experiment we increase the number of negative labelled ROIs by randomly selecting normal/background regions. In both experiments, we evaluate the performance of the networks i) in classifying pixels only in predefined malignant and benign/normal ROIs and ii) in classifying malignant pixels in the entire image. The results show that raw VERDICT DW-MRI data combined with CNNs can achieve high classification performance.

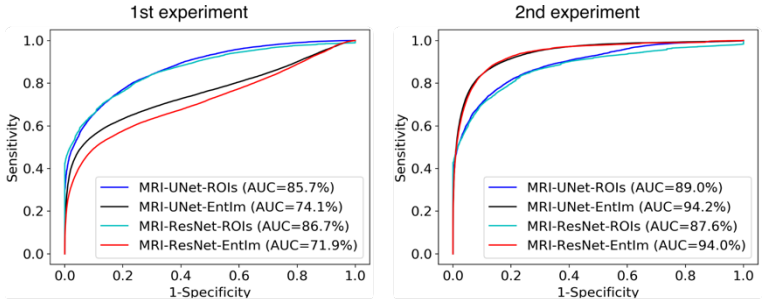

Fig. 2 ROC curves of MRI-UNet and MRI-ResNet when evaluation is performed on i) predefined malignant and benign ROIs and ii) the entire image (EntIm).

1]Panagiotaki et al., Cancer Res. 2] Panagiotaki et al., Invest. Radiol. 3] Panagiotaki et al., ISMRM. 4] Ronneberger et al., MICCAI. 5] He et al., CVPR.