Pattern and Model Based Analysis of Dynamic Contrast Enhanced Prostate MRI Data

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Purpose: To evaluate the performance of pattern based methods - independent component analysis (ICA) and principle component analysis (PCA) to analyze dynamic contrast enhanced (DCE) images of the prostate and compare to the performance of model based methods such as the three-time-points (3TP) analysis.

Introduction: High resolution contrast enhanced magnetic resonance imaging has been shown to be clinically useful for staging prostate cancer (1). The current strategies to differentiate between malignant and benign prostate tissues using DCE-MRI dataset include image subtraction and calculation of model based parameters. Naturally, recording images at high spatial and high temporal resolution, as well as high signal to noise ratio (SNR), and then analyzing them using an accurate physiological model and a robust non linear best fitting method are expected to produce the most reliable output results. However, in most clinical MRI examinations it is currently not possible to achieve these demands. In order to enhance our understanding and improve the interpretation of dynamic contrast enhanced images of the prostate we applied PCA and ICA methods on a selected DCE protocol performed on a 3T scanner that uses high spatial resolution on the expense of temporal resolution.

Methods: Whole histopathology preparation of the excised prostate gland was performed in 10 cases. The specimen was fixed in 10% buffered formaldehyde, embedded in paraffin, sectioned (3-4 mm thickness) consecutively in planes closely paralleling the MR images and stained with Hematoxylin-eosin. Areas of carcinoma were circumscribed by one pathologist with a black dotted line, unaware of the MRI results. The whole mount histopathology slices were correlated by visual inspection to the corresponding DCE-MR images.

Results: Whole histopathology slices were correlated by visual inspection to the corresponding DCE-MR images.

Fig 1: The results of PCA analysis for a representative slice in 12 patients. The plots show the three most significant eigen vectors (a-c) corresponding to the largest eigen values.

Fig 2: Correlation between whole mount histopathology (a), coefficient map for the 2nd eigen-vector produced by PCA (b) and the 3TP color map (c). Note that the bright orange area at (b) and the large red pattern at (c) match the blue dotted cancer foci at (a)