Exploration of BOLD-MRI in Prostate Cancer using Principal Component Analysis

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**Background:** Dynamic contrast enhanced MRI (DCE-MRI) has become the standard for assessing prostate cancer microvascular environment. However, Blood oxygen level dependent (BOLD) signal assessment has also shown sensitivity to the microvascular environment of tissues. Typical methods of assessment, common in DCE-MRI, such as visual examinations or pharmacokinetic models are difficult with BOLD due to the myriad of factors which affect BOLD signal [1]. As such, most BOLD imaging methods for assessing cancer have resorted to approaches that externally modulate the signal (e.g. carbogen breathing [2]). These approaches typically rely on changes in oxygenation rates before and after inhalation to locate tumors. Alternatively, fractal dimension (FD) mapping, has recently shown promise for assessing intrinsic BOLD signal [3], suggesting data driven approaches may be of use without external perturbation.

Principal component analysis (PCA) is a data driven method, which has been used previously to assess DCE-MRI [4]. PCA decomposes a large number of correlated variables into uncorrelated variables. The vectors that define the new space are called the principal components, and are defined such that the first principal component accounts for the largest variance in the variable space. Subsequent components define the next most variance, while uncorrelated to previous components, until the entire original space is defined. Since the method is data driven, it offers a possible means of exploring the BOLD signal differences between tumor and normal tissues. Here BOLD-MRI of prostate cancer subjects was analyzed using PCA in attempt to differentiate tumor regions from normal tissue.

**Materials and Methods:** In a study approved by our local research ethics board, BOLD-MRI (TE=35ms, TR=250ms, slice thickness=6mm, \(s=70^\circ\), 112x112 matrix, FOV=18mm x 18mm, 2400 temporal samples, 3 slices) scans were performed on five (age 60.8\pm7.6) prostate cancer patients in addition to the clinically prescribed anatomical and DCE_MRI scans. The scans were performed using a Philips 3T Achieva and 8 channel cardiac phased array coil. All had radical prostatectomy as part of their routine treatment and whole mount specimens were compared retrospectively to BOLD scans analyzed using PCA.

For each subject, BOLD data was manually segmented and a mask created to remove the surrounding tissue. The 4D BOLD dataset was unfolded along the spatial dimensions to produce a 2D matrix, such that the columns of the matrix consisted of the time points and the rows were formed from different pixels within the prostate images. The first time point was used as a mask and subtracted from the remaining points. The data was mean centered along the columns to remove any drift associated with a prolonged scan. PCA was used to decompose the matrix into the principal components and the resulting scores for each principal component. The scores are the result of projecting a given pixel onto a calculated principal component. Bootstrapping was used to remove excess components and score values for the remaining principal components were unfolded to produce score value images. The images were compared to prostate whole mounts using visual inspection.

**Results and Discussion:** The bootstrapping produced between 3 and 9 statistically significant components. For all five subjects, the score maps from the most significant component was noise, most likely a result movement during the scan (Fig. 1). For two of the subjects, the score maps for the second and third component distinctly indicated the tumor regions (Fig. 2), when compared to whole mount resections (Fig. 3). For these two subjects, the DCE-MRI indicated similar location and extent for tumor as the 2\(^{nd}\) and 3\(^{rd}\) score maps combined. For the other three subjects, no statistically significant components showed any visible similarities to the whole mount resections. Examination of the second and third principal components from the two correlated subjects showed that the components had small sinusoidal patterns with frequencies in the cardiac range.

**References:**


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Fig. 1: The 1\(^{st}\) score map from a representative subject that showed differentiation between normal and tumor

Fig. 2: 2\(^{nd}\) score map from a representative subject that showed differentiation between normal and tumor

Fig. 3: Whole mount resection of same subject as Fig. 1 & 2, with tumor region indicated.