

Multi-protocol Prostate MRI Image Analysis: Image Segmentation, Registration, and Computer-aided Diagnosis

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Abstract: At the Laboratory for Computational Imaging and Bioinformatics (LCIB) at Rutgers University and in collaboration with clinical investigators at the University of Pennsylvania and Beth Israel Deaconess Medical Center we have been developing registration, segmentation and computer-aided diagnosis (CAD) tools for detection of prostate cancer (CaP) from multi-protocol MRI including MR Spectroscopy (MRS), T2-w, and dynamic contract enhanced (DCE) MRI. Below we briefly describe 4 related projects currently being pursued at LCIB.

A. Multi-modal Image Registration for Determining CaP Extent on MRI: Multi-modal registration of histology and MRI is critical for CAD evaluation of CaP [1]. Our registration technique termed Combined Feature-Ensemble Mutual Information (COFEMI) provides the ability to robustly register images from very different modalities, such as MRI and histology, as well as images that are affected by severe artifacts. COFEMI utilizes high-level texture feature representations of the images to incorporate additional information into the similarity measure and achieve robust and accurate alignment. In Figure 1 a prostate whole-mount histology image (Fig. 1(a)) is registered to a corresponding *in vivo* MRI image (Fig. 1(b)) using COFEMI followed by thin-plate splines non-linear image warping. The resulting histology image (Figure 1(c)) from which the ground truth for CaP extent is mapped directly on to the MRI (Figure1(d)).

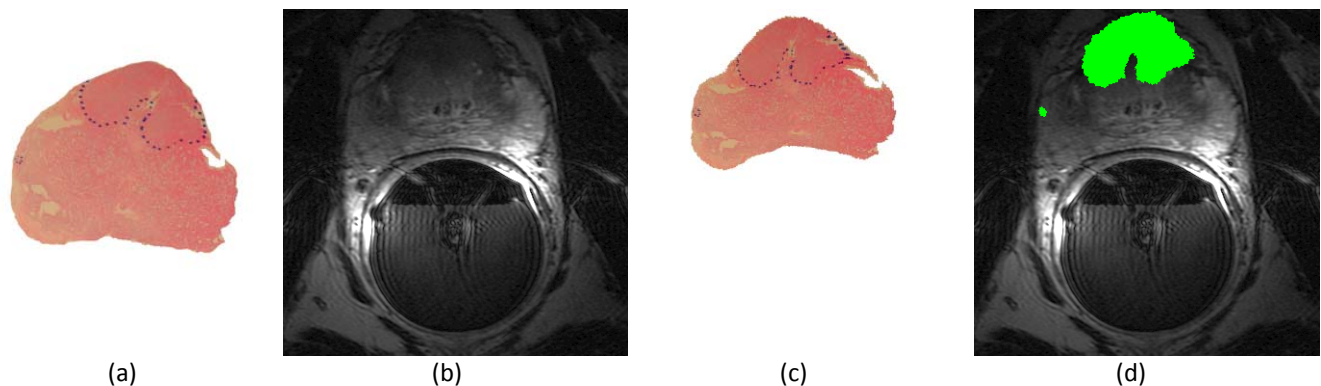
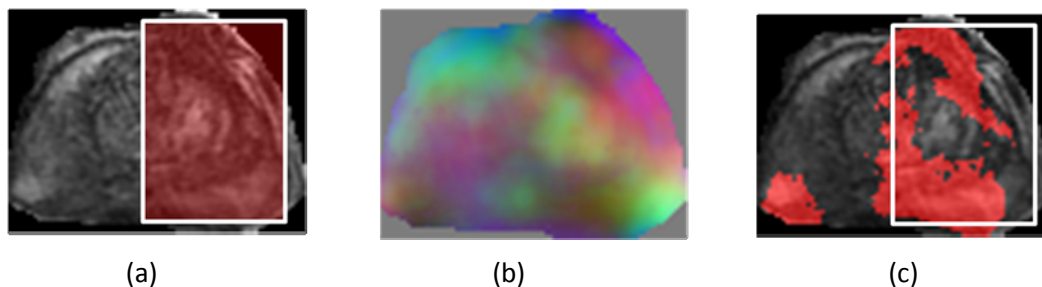


Figure 1: Registration of (a) whole mount histology to (b) *ex vivo* MRI using COFEMI and thin plate splines, results in (c) deformed histology that is in alignment with (b) MRI. The cancer ground truth for is then mapped from (c) to (d).

B. Computer-aided diagnosis of prostate cancer from high resolution T2-w and DCE MRI: Our current work in prostate cancer detection has focused on developing unsupervised techniques for *in vivo* endorectal T2-w and DCE MRI data via application of manifold learning and clustering techniques [2]. Having corrected the MRI data for image intensity artifacts, the T2-w MR (Figure 2(a)) imagery is characterized in terms of a large number of texture features, including 2nd order statistical (Haralick) and gradient (Gabor). The result of these operations is a high dimensional (400+) texture feature space. This data is then analyzed via manifold learning techniques such as Locally Linear Embedding and Graph Embedding, which project such high dimensional data into a lower dimensional subspace, while preserving object adjacencies. The data is then classified in the lower dimensional subspace via unsupervised consensus *k*-means clustering. We have found impressive results upon application of this methodology to T2-w and DCE-MRI data with sensitivity and specificity values of over 80% on over 30 1.5 Tesla and 3 Tesla *in vivo* MRI studies.



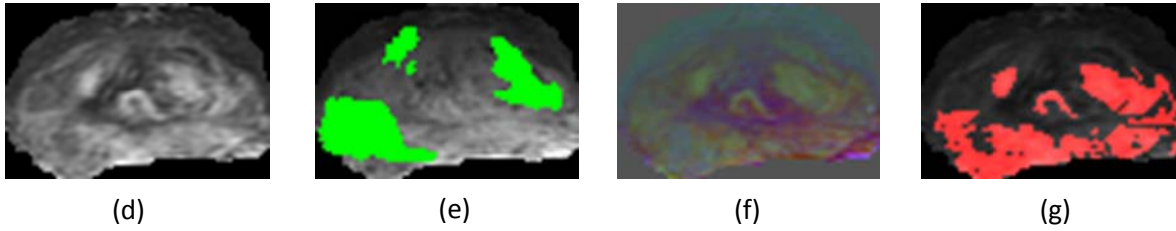


Figure 2. (a) Original T2-w MR image with potential region of cancer overlaid in red. (b) Result of visualizing lower dimensional subspace onto this image. Regions with similar colors are adjacent in the subspace (c) Final CAD result (via unsupervised classification) corresponding to CaP shown in red. Note the correspondence to the surrogate ground truth (outlined in white). (d) Sample DCE-MRI slice from time point 4 (e) Ground truth estimate of cancer mapped onto the slice via registration (f) Result of visualizing lower dimensional embedding onto the slice (g) Final result of unsupervised classification best corresponding to cancer shown in red. Note the correspondence to the ground truth in (e).

C. Computer-aided diagnosis of prostate cancer from Magnetic Resonance Spectroscopy: Our work in CAD for MRS for CaP detection employs the use of non-linear dimensionality reduction (NLDR) methods to transform high dimensional spectral data to an alternate lower dimensional space [3]. Classification of each MR spectra is obtained via unsupervised k -means clustering which clusters low dimensional representations of MR spectra (obtained from NLDR) into distinct classes based on spectral adjacency in reduced dimensional space. We have obtained high detection accuracy of close to 87% using our novel integrated NLDR-clustering scheme compared to the current state of art MRS analysis techniques like peak detection, z-score and principal component analysis (PCA) (Figure 3). To qualitative validate the clustering results obtained from our scheme; we perform Independent Component Analysis (ICA) on each cluster where each independent component (IC) is compared to a typical CaP, benign signature (Figure 3(e)-(g)). Figures 3(e)-(g) show that the IC obtained from the cluster identified as CaP via our scheme (3(f)) corresponds resembles typical CaP MR spectra (3(e)) compared to the IC obtained via PCA (3(g)).

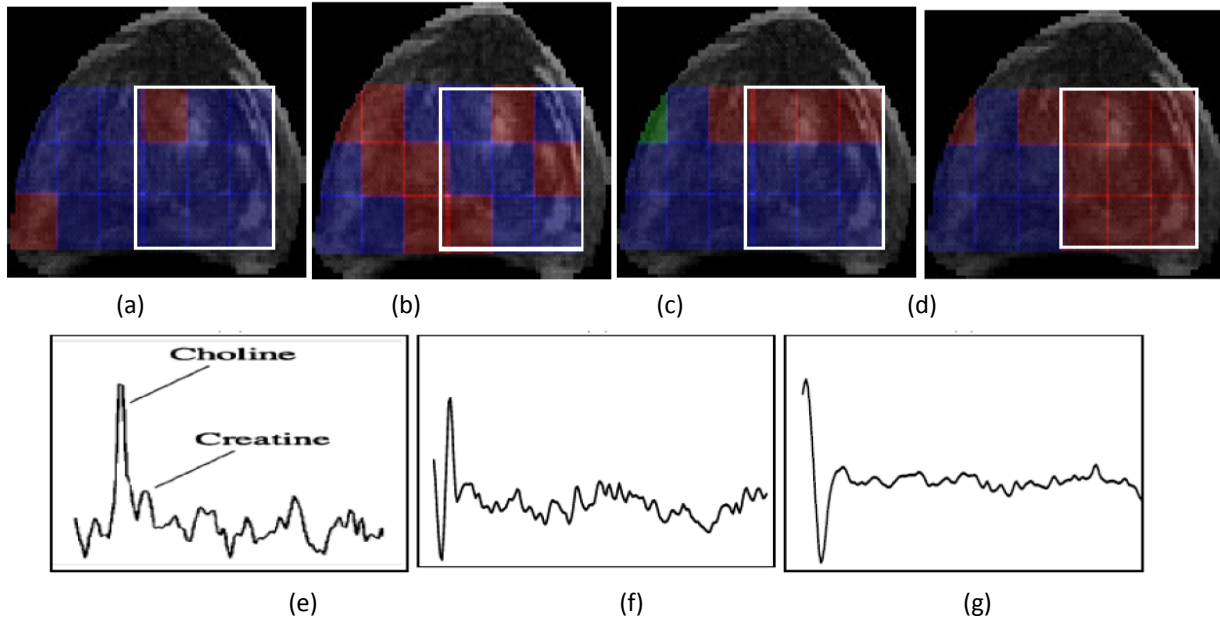


Figure 3: Clustering results using popular MRS analysis schemes (a) peak detection, (b) z-score and (c) PCA compared to (d) our NLDR scheme. The white box superposed on the T2 corresponds to the ground truth region. In each image the red cluster corresponds to the locations identified as cancer by each of the methods (blue voxels being those identified by the method as benign). (g) shows a typical Cancer MR spectra, (h) shows the IC obtained from clusters identified as cancer by our method, (g) shows the corresponding IC obtained via PCA as DR method. Note the high correlation of (e) and (f) compared to (g).

References

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