Unsupervised tissue segmentation of MRSI data using Canonical Correlation Analysis

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Introduction

In this study we present an accurate and efficient tissue segmentation technique based on Canonical Correlation Analysis (CCA), a statistical method able to simultaneously exploit the temporal and spatial information characterizing the MRSI data. Recently, CCA has been successfully applied to other types of biomedical data, such as functional MRI (fMRI) [1] and electroencephalogram (EEG) data. Here, we adapt this method for MRSI data processing in order to retrieve in an accurate and efficient way the possible different tissue types that characterize the organ under investigation. The potential and limitations of the new technique have been investigated by using simulated as well as *in vivo* prostate MRSI data, and our studies demonstrate a high accuracy, robustness and efficiency.

Method

CCA quantifies the relationship between two sets of variables by means of correlation coefficients. More precisely, given two zero mean multivariate random vectors $X=[x_1,\ldots,x_m]^T$ and $Y=[y_1,\ldots,y_n]^T$, two new scalar variables x' and y' are obtained as linear combinations of the components of X and Y, respectively. CCA computes the linear combination coefficients so that the correlation between the new variables x' and y' is maximum. The obtained maximum correlation values are afterwards exploited in order to construct correlation maps in which the detected tissue regions are visualized.
When processing MRSI data, X consists of the magnitude spectrum of the measured signal and Y of the model tissue spectrum. In order to exploit the spatial information of the measured signals, we can consider as components of the vector X the spectrum contained in the voxel under investigation as well as the spectra contained in the neighbor voxels. Several spatial models can be adopted to choose the neighbor voxels such as the symmetric 3x3 model, as used in our studies [1]. In order to model the tissue spectrum, we use the Taylor approach in which we consider as basis functions the known model spectrum and its first order derivative, in order to take into account frequency variations which might characterize the MRSI data. Amplitude and damping variations can be taken into account as well by adopting a PCA subspace model [1].

Results and conclusion

We applied the proposed technique to simulated as well as *in vivo* prostate MRSI data. Fig.1 (left) shows the known model spectra we use for aggressive tumor, tumor, mixed and normal tissues, respectively. They contain different contributions of Choline, Creatine and Citrate since it is known that tumor regions yield higher levels of Choline and reduced levels of Citrate compared to healthy regions. We perturbed the model spectra by adding white Gaussian noise and inserted them in four different regions of a 42x42 grid of voxels. Fig.1 (right) shows the noisy spectra and Fig.2 shows the detected regions (red color). The detected regions show a high level of correlation with the original regions (see corrcoef value). Concerning the *in vivo* studies, CSI data were measured in a healthy volunteer. They were acquired on a 1.5T Siemens scanner operating at 63.61MHz, with echo time of 120ms. Only 10x14 voxels from one 16x16 slice (FOV=80mmx80mm), within the PRESS box region, were selected and their spectra were processed by applying CCA after water and lipid removal. Fig.3 shows the tissue detection results: CCA is able to provide a map in which the spatial location of the different tissues is visualized. In this particular example, only normal tissue is detected since the given spectra are mostly characterized by the presence of high levels of Citrate. Finally, Fig.4 shows the spectrum obtained as average of the spectra contained in the detected voxels and also the model normal tissue spectrum. They show a high level of correlation (correlation coefficient equal to 0.87). The required computational time is around 0.63s. Accuracy, robustness and efficiency of the proposed technique are supported by the results of our simulation studies, including tests on signals with a low Signal to Noise Ratio.

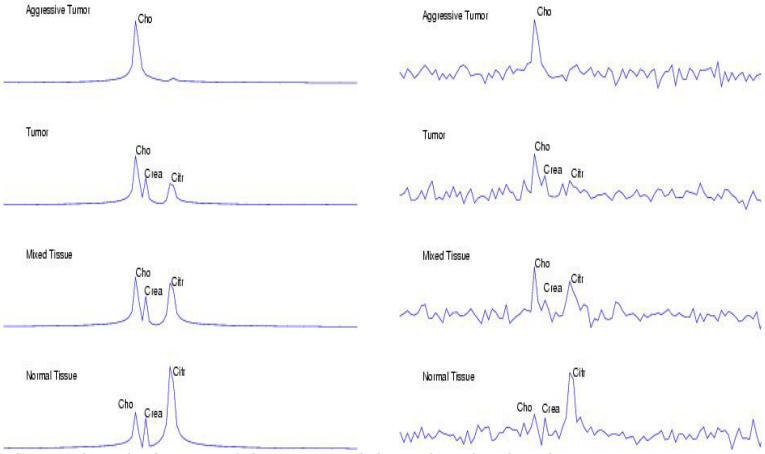

Fig.1 Left: noiseless model spectra. Right: noisy simulated spectra.

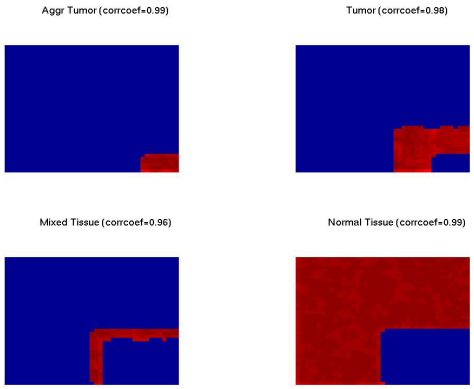

Fig.2 Detected regions by CCA for 4 simulated prostate tissues.

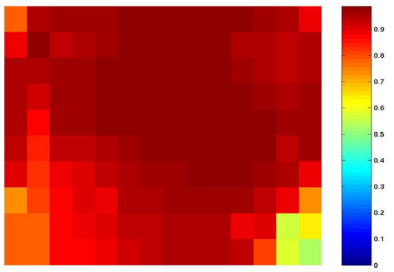

Fig.3 Extracted normal tissue region for *in vivo* prostate MRSI data.

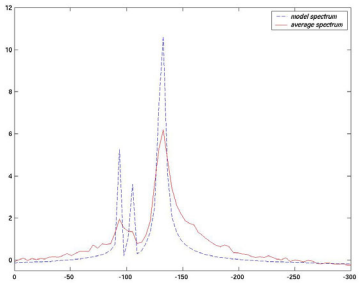

Fig.4 Model and average spectra for normal tissue.

References [1] Friman O., PhD thesis, Dept. of Biom. Engin., Linköpings Universiteit, Sweden, 2003.