Fast nosologic imaging of the brain

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Introduction

In this study we present a fast, automatic and accurate method that can be of great importance for brain tumour diagnosis. The presented method segments MRSI data, and labels the segments corresponding to the pathology of the tissue. The method is based on Canonical Correlation Analysis (CCA). The main advantage of this method is to integrate both spatial information and prior knowledge about the spectra of the considered tissues. Recently, CCA has been successfully applied to long echo-time prostate spectra [1]. Here, we adapt this method for short echo-time brain MRSI data processing. In order to obtain a reliable tissue segmentation and classification, we apply the method in two steps: one to label the tumour type, and one to show the heterogeneity of the tumour. We also demonstrate how the result can be improved by applying CCA on relevant features instead of spectra. Our studies demonstrate a high accuracy, robustness and efficiency.

Method

CCA is a multivariate generalisation of ordinary correlation analysis. 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. When processing MRSI data, X consists of the real spectra of the signals, measured in the considered voxel and in some surrounding voxels, and Y of the model tissue spectrum. By computing the canonical correlation coefficient for all possible tissue types (with different Y matrices), the voxel can be assigned to the tissue with the highest coefficient. Several spatial methods can be used [2]. We introduced a new spatial model, that gives at least as much importance to the voxel under investigation as to the surrounding voxels. In order to model the tissue spectrum, we use the PCA approach: we take as first component the mean of a database of validated spectra of one tissue type, and as second component the first principal component of the mean-subtracted database.

To show the heterogeneity of the tumour, we also constructed model spectra for all kinds of mixed tumour. However, CCA is not able to accurately distinguish these different mixed tissue types. Therefore, we apply the method in two steps. In the first step, we apply CCA with the model spectra of normal tissue, CSF and all pure tumour types in order to detect the type of tumour. In the second step, we use the model spectra of normal tissue, the detected tumour type and a mixed model to show the heterogeneity of the tissue.

Instead of using the measured real spectra of the signals, we can summarize the spectra into some features, like the quantified amplitudes of the 10 most important metabolites (Myo, pch, cr, gln, glu, Naa, ala, lac, lip1, lip2). We used AQSES [3] to quantify our spectra. The main advantage of this approach is that it provides the opportunity to add extra information, in our case image variables. We averaged out the (aligned) MRI pixels with 4 contrasts (T1, T2, proton density and Gd enhanced) over the MRSI voxel. Then we applied CCA on this set of features.

Results and conclusion

We optimized the proposed technique on simulated short echo-time brain MRSI data. CCA was always able to detect the correct tumour type in the first step. The simulations also showed a very high accuracy during the segmenting step (98%). The simulations clearly showed the advantage of using spatial information: CCA always segmented homogenous regions, while ordinary crosscorrelation sometimes wrongly detected 'spots'. The method is also very fast: processing a grid of 10x10 voxels takes only 2 seconds.

Comparing CCA on spectra and CCA on feature sets, we saw two improvements by using the last approach. Firstly, the ventricles are better segmented, which is due to the use of MRI information. Secondly, the method became more robust with respect to signals with a low signal to noise ratio.

The results are confirmed by several *in vivo* MRSI data. Fig. 1, 2 and 3 show respectively the results of a patient with a grade III glioma tumour, a meningioma tumour and a glioblastoma tumour. The MRI and MRSI data were acquired using a 2D STEAM H-MRSI sequence (TE=20ms) on a 1.5 T Siemens Vision whole body scanner, using a CP-head coil. Eddy current, phase and baseline correction and water removal were applied [4]. The figures show nicely segmented regions, and always the correct tumour type was convincingly detected! In the pictures, the blue and red color are always used for healthy tissue and CSF; yellow is used for tumour voxels of the type, detected in the first step, and green for the corresponding mixed type.

Based on all the results, we conclude that the proposed method for fast nosologic imaging of the brain is very accurate and robust!

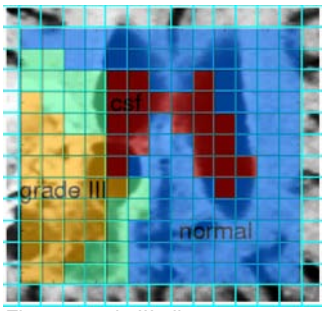

Fig1: a grade III glioma tumour

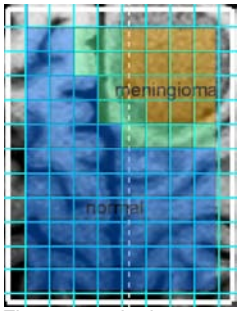

Fig 2: a meningioma tumour

Fig3: a glioblastoma tumour

References

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