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Data fusion of HR-MAS and in-vivo information with application in brain tumor recognition

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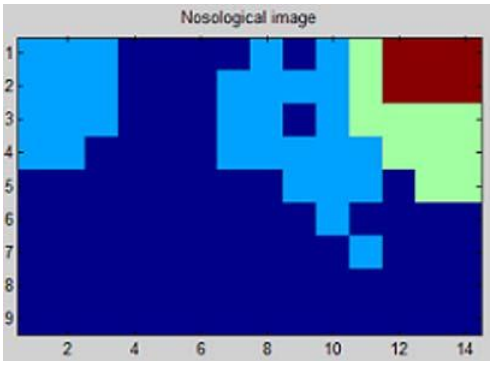
Purpose: The purpose of this study is to combine multimodal information coming from magnetic resonance imaging (MRI), magnetic resonance spectroscopic imaging (MRSI) and high resolution magic angle spinning (HR-MAS) in order to develop advanced pattern recognition methods able to help clinicians in diagnosing brain tumors.
Subjects and Methods: Recently, the use of multimodal information in diagnosis and tissue characterization of brain tumors has been shown to improve the performance of the classifiers. In particular, HR-MAS is seen as a promising complementary method, as it is very helpful for the assignment of well-resolved spectra of cellular metabolites [1] and, therefore, can strongly support in vivo MRSI by increasing its clinical value.
The pattern recognition technique used in this study is based on canonical correlation analysis (CCA) an accurate and efficient tissue segmentation technique that has recently been successfully applied to prostate and brain tumor recognition[2,3]. Here, the performance of CCA is further investigated by introducing HR-MAS information as prior knowledge. Specifically, we study the impact of using HR-MAS information in combination with in vivo MRI and MRSI information to detect and classify brain tumors.
Results: CCA is applied to each voxel and the tissue type giving rise to the largest canonical correlation coefficient is assigned to the voxel under investigation. The results are then exploited in order to construct nosologic images in which all the detected tissues are visualized.



Conclusions: We studied the possibility of combining multimodal information; we investigated which parameters influence our classification results and the impact of HR-MAS information in combination with *in vivo* information for brain tumor recognition. The model that performs best is the model that uses multimodal information coming from HR-MAS and MRI data.
Due to the fact that we have to manage the use of very different information/data, obtained with different measurement techniques, as well as the use of data coming from different clinical centers, a harmonization of all the input spaces is performed by extracting common characteristic features from all the different data types.
References:
1. Martinez-Bisbal M.C et al (2004) NMR in Biomedicine, Pages 191-205
2. De Vos M, Laudadio T et al., 200,. JMR 184:292-301
3. T. Laudadio et al (2005), Magn. Res. Med., 54, 1280-1284

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Automatic quantitative analysis of HRMAS 1D proton spectra from rat liver biopsies

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Introduction: ^{1}H NMR measurements by High Resolution Magic Angle Spinning (HR-MAS) is a non-destructive technique that permits to obtain biochemical information on intact tissues. In particular, this technique can be used to investigate cellular diseases from low grade fibrosis, cirrhosis to hepatocarcinoma of rat liver biopsies [1]. Liver metabolic profiles determined by HRMAS exhibit broad components from macromolecules and lipids which overlap with small molecules signals making their quantitative analysis challenging. The present work aims at retrieving information from an automatic Voigt lineshape parametrization of the 1D HRMAS spectra, especially of the lipid regions to characterize differences over time or in tissue type. Results were obtained on two different tissue samples from healthy and cirrhotic rat liver.
Method: Liver biopsies were obtained, immediately after animal killing, from control and carcinogen-treated [2] rats (Fischer-44), then freezed and stored at 193K until use. The samples were washed with D_2O. All NMR experiments were recorded at 11.7 T with a Bruker AVANCE Spectrometer equipped with a HR-MAS probe (rotor of 50µL). The samples were spun at 5kHz and the probe temperature was regulated at 293K. The 1D ^{1}H NMR spectra were acquired with an 8μs 90° pulse for three time points (0h, 4h, 10h) using sweep width of 5kHz, 16K data points, acquisition time of 1.64s, a 1.5s relaxation delay. A fully automatic time domain fitting scheme [3] based on the Voigt model function which is robust regarding the influences of the starting values and the model parameter bounds is used to quantify the broad resonances in 1D water presaturation ^{1}H spectra. The free parameters were the amplitude, frequency, and Gaussian/Lorentzian damping factors.
Results: In healthy rat liver tissue, Voigt lineshape estimations for the frequency region from 0.9-2.25ppm showed predominant Lorentzian contributions while in the cirrhotic sample the Gaussian contributions dominated, see Figures 1-2. Note that for the two samples, the choline-glucose frequency region (3-4ppm) demonstrated similar spectral resolution and shim quality. The contribution of the resonances (0.9-2.25ppm) did not change significantly over time (<3%) see Figure 3.
Discussion: This automatic method enables the quantitative analysis of lipid/macromolecules components in liver 1D HRMAS data. The lineshape estimates may reflect the tissue state and may help to assess the degree of fibrosis.
References: [1] B Martinez-Granados *et al*, NMR Biomed 2006; 19:90-100.