EXPLOITING SPATIAL INFORMATION FOR ESTIMATING METABOLITE CONCENTRATION IN MRSI

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INTRODUCTION

Magnetic Resonance Spectroscopic Imaging (MRSI) is a noninvasive monitoring technique that provides significant biochemical information on the molecules of the organism under investigation. Metabolite quantification of MRSI data needs to be accurate to help in brain tumor diagnosis. The quantities of interest are the metabolite concentrations, which can be computed from the weighting coefficients (amplitudes) of the linearly combined *in vitro* profiles. In this study we propose a new quantification method for MRSI data, which exploits spatial prior knowledge. Previous studies showed that the exploitation of spatial context led to significantly better results for quantification, see [1].

METHOD

During an MRSI acquisition, MR spectra are measured in a grid of voxels. The signal from each voxel is quantified using information coming from the spectral parameters (frequency shifts, damping corrections, phase shifts, etc) of the surrounding voxels. This new approach is implemented as a new version of AQSES (Accurate Quantification of Short-echo Time Magnetic Resonance Spectroscopic Signals) [2], which fits the whole *complex* signal in the *time-domain*. AQSES is already proved to be a robust quantification method. Our assumption is that adjacent voxels should have signals with similar spectral parameters. If we consider a center voxel and its corresponding nonlinear parameters, than the signals of the surrounding voxels are characterized by the nonlinear parameters θ_s, with *s = 1…S*. The parameter vector θ_c should depend on the parameter vectors θ_s. The number of parameters is assumed to be the same for all voxels. In order to take into account the dependence between the parameters of the center voxel θ_c and those of the surrounding voxels θ_s, the nonlinear least squares problem becomes: $\min_{\theta_c} \frac{1}{N}\sum_{t=t_0}^{t_{N-1}} \left| y_c(t) - \hat{y}_c(t,\theta_c) \right|^2 + \sigma^2 \sum_{\theta_c \neq \theta_s} \beta_{cs} \left\| W(\theta_c - \theta_s) \right\|_2^2$

where $y_c(t)$ is the time-domain signal of the center voxel. $\hat{y}_c$ is the estimated signal characterized by the parameters θ_c, σ^2 is the variance of the noise, β_{cs} is a weighting scalar which gives the influence of the parameters θ_s on the parameters θ_c. The (diagonal) matrix *W* provides possibility different weightings for each nonlinear parameter. Several sweeps through all voxels are performed until convergence.

RESULTS

We analyzed the performance of our method, by computing the relative root mean square error (RRMSE) on a set of 10 simulated MRSI images of a 6x6 grid of voxels, considering different levels of signal to noise ratios (SNR). We compared the results with the performance of the initial version of AQSES, see Table1. Results on in vivo MRSI from a patient with glioblastoma are shown in Figure1.

CONCLUSIONS

A new automated method for quantification of MRSI data, able to deal with spatial information, is proposed. This yields more accurate spectral parameter estimation then the one obtained with a single voxel quantification method such as AQSES.

REFERENCES

[1] Kelm B.M., Evaluation of Vector-Valued Clinical Image Data Using Probabilistic Graphical Models: Quantification and Pattern Recognition, Phd thesis

[2] Poullet J-B., Sima D.M. et al., NMR in Biomedicine, vol. 20, no. 5, Aug. 2007, pp. 493-504.

SNR	10	20	30	40	50
RRMSE AQSES	1,84	1,2	0,48	0,38	0,12
RRMSE AQSES-MRSI	1,06	0,7	0,42	0,19	0,03

Table1: Mean of the RRMSE amplitudes values computed for the 10 simulated MRSI images of a 6x6 grid of voxels, considering different levels of SNR. In the new approach, AQSES-MRSI, a 50% improvement in terms of accuracy is obtained.

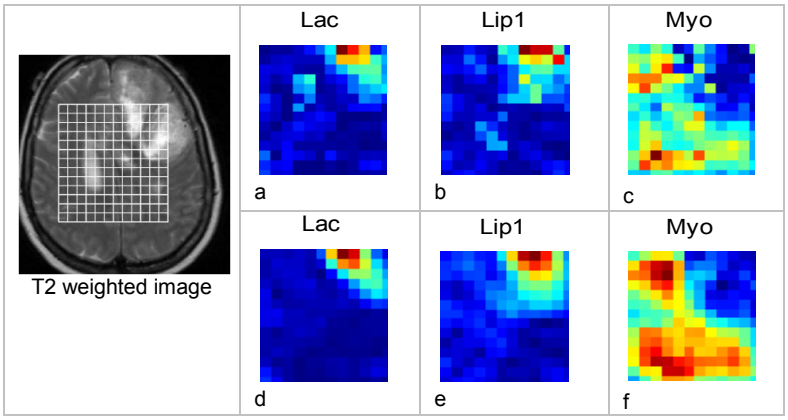


Figure1: Metabolic maps obtained after applying AQSES (Figure1 a-c) compared with the maps obtained with new version of the method (Figure1 d-f). The patient (I1285 from the INTERPRET database) is diagnosed with glioblastoma (upper right corner of the T2 weighted image). We observe in the tumor region a substantial difference in weight of the corresponding metabolites compared to a region with normal tissue (Figure1 a-f). Better estimates of the metabolites weights are obtained with the new version of AQSES.