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Improved quantification of MRSI data using spatial constraints

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Introduction/Purpose: Magnetic Resonance Spectroscopic Imaging (MRSI) provides MR spectra from adjacent voxels aligned in a 2 or 3 D spatial grid. The spectra of these voxels are usually analyzed one by one, without exploiting their spatial context. We propose an improved metabolite quantification method, in which spatial information is included in the form of constraints on the nonlinear spectral parameters corresponding to neighboring voxels.
Methods: AQSES-MRSI is an extension of the time-domain quantification method AQSES [1]. We consider a signal $y_c(t)$ from a voxel c and a model $\hat{y}_c(t,\theta_c)$ as a weighted sum of metabolite signals with nonlinear corrections (i.e., damping corrections and frequency shifts), stacked in the parameter vector θ_c, which is considered to be dependent on the parameters θ_s of signals from surrounding voxels s. AQSES-MRSI starts by individually fitting each signal in the grid using nonlinear least squares [1]. Then several sweeps through the grid are performed until convergence, where each sweep changes the the nonlinear parameters starting values to the mean parameter values from the neighbors and further bounds the parameters' variability. The nonlinear least squares problem is modified by adding a penalty term, which encourages a spatially smooth parameter map:

$$\min_{\theta_c} \frac{1}{N}\sum_{t=t_0}^{t_{N-1}} \left| y_c(t) - \hat{y}_c(t,\theta_c) \right|^2 + \varepsilon \sum_{s \neq c} \beta_{cs} \left\| W(\theta_c - \theta_s) \right\|_2^2$$

Where
ε is a penalty parameter
β_{cs} is a neighborhood indicator (e.g., 1 if c and s are neighbors, 0 otherwise)
W is a weighting matrix.

Results: We showed in a previous simulation study [2] that by including prior knowledge in the form of spatial constraints, the accuracy of estimating metabolite concentrations improves up to 50%. Now we analyze the performance of AQSES-MRSI on *in vivo* MRSI and compare its results with the time domain quantification methods AQSES and QUEST [3] applied on individual voxels.
For all metabolites investigated in this study a substantial better contour of the tumor region is obtained with AQSES-MRSI, as can be seen from Figure 1, illustrating a patient with a meningioma (taken from the INTERPRET [4] dataset). In particular for the metabolites present at low tissue concentrations, such as myoinositol (Myo) and glucose (Glc), the proposed method provides a much less noisier spatial distribution than AQSES and QUEST.
Conclusion: Results suggest that taking into consideration simple spatial constraints on the nonlinear spectral parameters, while allowing total freedom to the metabolite weights, significantly improves metabolite estimates when quantifying MRSI data, which can be translated into easily interpretable metabolites maps.
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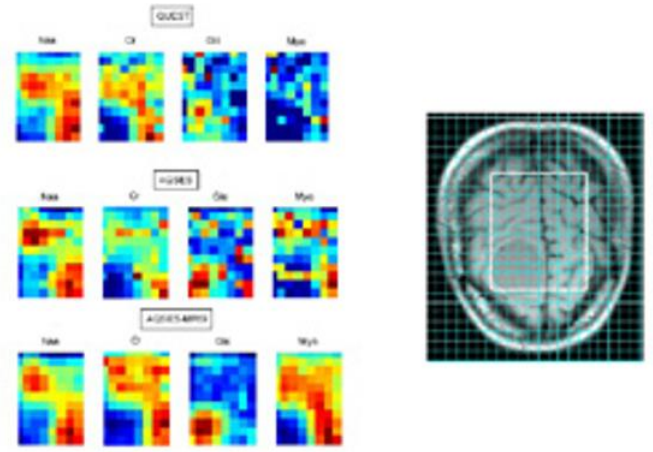


Figure 1: Metabolic maps obtained after applying QUEST, AQSES and AQSES-MRSI. The patient (from the INTERPRET database) is diagnosed with meningioma (lower left corner of the T2 weighted image). We observe a substantial difference in the weights of the corresponding metabolites in the tumor region compared to a region with normal tissue. Estimates of the metabolite weights obtained with AQSES-MRSI give well-contoured metabolic maps even for metabolites that are difficult to quantify with the conventional approaches.

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Spectroscopy with receive arrays: how to combine the signals

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Introduction: *In vivo* applications of MR spectroscopy are constrained by severe signal to noise ratio (SNR) limitations due to usually low concentrations of metabolites. Receive arrays increase SNR and cover a large volume [1]. Yet to maximise these benefits, it is important to combine the signals from each element intelligently. Using a Bayesian framework, we report a general purpose "pre-whitened singular value decomposition" (WSVD) algorithm that treats correlations in the noise from different elements explicitly and computes an optimal combined spectrum.
Subjects and Methods: The WSVD algorithm proceeds as follows. Noise is sampled from the ends of the spectra or from before the first RF pulse. The noise covariance matrix is computed. Using its Eigen decomposition, for each voxel, appropriate linear combinations of the spectra are taken to give "channel" spectra or FIDs $S_{i,k}$ which have independent normally distributed noise with standard deviation $\sqrt{½}$.
After this noise pre-whitening, the Bayesian "likelihood" is then (eq1) and the maximum likelihood spectra may be found using the singular value decomposition.
Data were acquired using 3T and 1.5T scanners (Siemens Trio and Avanto) with an 8-element ^{31}P array, a 12-element ^{1}H head array, and combinations of the Siemens TIM body matrix and spine array. Measurements were made on ^{31}P phantoms, and on the brain, liver and heart of normal volunteers using 2D, 3D CSI, STEAM and PRESS sequences. Combination of the data was performed both on the scanner hardware and in Matlab.
Results: Fig. 1 presents ^{31}P cardiac spectra acquired from the interventricular septum showing apodized spectra from each element, the results of the WSVD combination method and of Brown's widely used method [2]. The WSVD gives SNR ~60% greater than Brown's method. Similar results were obtained from ^{1}H and ^{31}P liver and ^{1}H brain spectra. Numerical simulations and ^{31}P phantom experiments quantify the power of this WSVD algorithm, which has high precision and minimal bias. It becomes more advantageous as the number of array elements increases.