# Joint Estimation of Spectral Parameters from MR Spectroscopic Imaging Data

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**Targeted Audience:** Researchers who are interested in MR spectral quantitation and signal processing.

**Purpose:**

Spectral quantitation is a key problem in MR spectroscopic imaging (MRSI), and a large body of work has been done to develop robust solutions for practical MRSI applications[1]. Existing methods have effectively exploited the prior knowledge about the spectral structures of metabolites by incorporating known spectral basis into spectral quantitation[2-8], which has significantly improved spectral estimates over classical spectral integration methods. However, very limited work has been done to exploit the spatial characteristics of metabolite distributions (e.g., smoothness or transform sparsity). As a result, state-of-the-art methods (e.g., the popular VARPRO[2], LCModel[4], and QUEST[7] method) perform spectral quantitation of MRSI data voxel by voxel independently and the estimated spectral parameters (e.g., metabolite concentrations) often have large variations, especially for MRSI data with low signal-to-noise ratio (SNR), as is often the case in practice. This work addresses this problem by jointly estimating the concentration map of each metabolite over all the voxels of interest, incorporating spatial regularization. An alternating minimization method of multiplier (ADMM) algorithm is applied to solve the constrained optimization problem. Experimental results show that the proposed method produced significantly improved estimates of spectral parameters over state-of-the-art methods.

**Methods:**

MRSI signals s(x, t) can be expressed as:, $s(x,t) = \sum_n a_n(x) e^{-t/T_{2,n}^*(x) - i2\pi\Delta f_n(x)} \varphi_n(t)$, where the $\varphi_n(\cdot)$ are spectral basis functions obtained from experimental data and/or using quantum simulation. Given a sequence of measurements $\mathbf{d} = [\mathbf{d}(x_1), \mathbf{d}(x_2),\ldots, \mathbf{d}(x_M)]$, where $\mathbf{d}(x_m)$ denotes the localized signal at voxel $x_m$ corrupted by additive Gaussian noise, the goal is to estimate the unknown spectral parameters, especially $a_n(x_m)$, the concentration map of each metabolite. The problem is challenging because of model nonlinearity and low SNR. Instead of solving this problem voxel by voxel, we estimate the spectral parameters jointly by imposing a spatial regularization:

$$(\hat{\boldsymbol{a}}, \hat{\boldsymbol{\theta}}) = \arg\min_{\boldsymbol{a},\boldsymbol{\theta}} \beta \|\boldsymbol{d} - \boldsymbol{K}(\boldsymbol{\theta})\boldsymbol{a}\|_2^2 + \mathrm{R}(\boldsymbol{a}),$$

where $\boldsymbol{\theta}$ denotes all the nonlinear parameters (i.e., $T_2^*$ and $\Delta$f's) of the signal model. Here $\mathrm{R}(\boldsymbol{a})$ can be used to incorporate any useful spatial prior, such as smoothness, anatomical structure, and transform sparsity. In this work, $\mathrm{R}(\boldsymbol{a})$ is chosen to be the 2nd order total generalized variation[9] (TGV). The optimization problem is solved using the ADMM algorithm[10].

**Results:**

We have evaluated the performance of the proposed method in comparison with VARPRO, which is a standard method used in practice. VARPRO performs spectral quantitation voxel-by-voxel, where a set of spectral basis is incorporated as prior information, as is done in other state-of-the-art frequency-domain methods (LCModel[4], etc.) and time-domain methods (QUEST[7], AQSES[8] etc.). The dataset was acquired in vivo at $B_0$=3T with an echo-time $T_E$=30ms using an echo-planar spectroscopic imaging (EPSI) sequence.

Figure 1 shows a set of representative results of NAA and creatine maps to illustrate the effectiveness of the proposed method. The estimated metabolite concentrations by VARPRO showed large spatial variations, including "spikes" at some locations. The proposed method significantly reduced the estimation variance of VARPRO, as expected. The performance improvement of the proposed method over existing methods observed from the experimental data was consistent with our simulation results (which is not included here due to space limitation).

Another approach to apply spatial regulation is to denoise the VARPRO estimates by enforcing the spatial smoothness constraint (VARPRO+Denoising). Such an approach can help reduce the noise, but it also introduces some blurring artifacts, and the estimates may also be biased due to non-Gaussianarity of the noise in the VARPRO results (see the results in Fig. 2). The proposed method overcomes such a problem by incorporating the spatial constraint directly into the quantitation process and produced better quantitation results (Fig. 2). Furthermore, the performance of the proposed joint estimation can be characterized using, for example, the constrained Cramér-Rao Bound[11], which is very desirable for practical application.

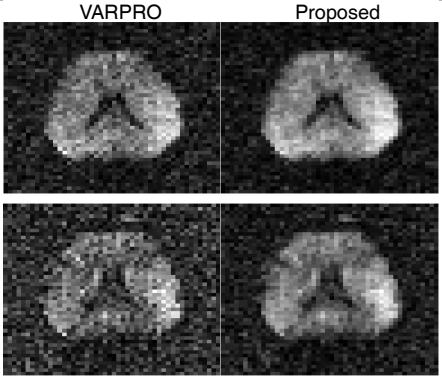


Fig. 1. A representative result of the quantitation of in vivo MRSI data at 3T. Two metabolites, NAA and creatine, are presented in each row. And the two columns correspond to the methods of VARPRO, and the proposed, respectively. It can be seen that the proposed method improved the results significantly.

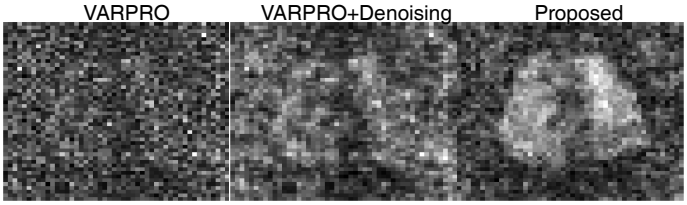


Fig. 2. Spectral quantitation of metabolite Glx (glutamate/glutamine) using VARPRO (left), denoising of VARPRO (middle) and the proposed method (right) to is presented, respectively.

**Conclusion:**

We have presented a new method for spectral quantitation of MRSI data. The proposed method jointly estimates the metabolite concentrations for all spatial locations, while enforcing the transform sparsity of the metabolite concentration maps, and has produced significantly improved estimation results. The method should prove useful for spectral quantitation in various MRSI studies.

**Reference:**

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