Automatic 31P MRS Quantification in the human brain based on OASIS-HSVD Algorithm

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Introduction

A major difficulty in MRS data processing is attempting to separate the target chemical compound signals from a distorted baseline in data with a great deal of noise. In this work, we propose a new post-processing scheme based on the Optimal Adaptive Separation of Interference Signal Hankel Singular Value Decomposition (OASIS-HSVD) algorithm for a consistent and automatic quantification of multidimensional human brain ^{31}P MRS data.

Methods

One of the difficulties associated with ^{31}P MRS data quantification is the separation of the broad distorted baseline. It is our hypothesis that, using the Lorentzian model [1], interested MR peaks and the distorted baseline can be represented by different signal subspaces spanned by a limited number of signal basis (i.e. signal pole) [2]. With the help of prior knowledge such as T_2 relaxation time and chemical shift values, we can optimize this separation process by an adaptive minimization of imperfect signals described below:

1. Acquisition of the prior knowledge: For multi-voxel (e.g. 3D) MRS experiments, the averaged spectra can yield a good estimate of resonance frequencies and damping factors. The prior knowledge signal poles, *estzk*, representing the interested or target compounds can be estimated when using HSVD [1].

2. Baseline separation and interference signal identification: For spectrum at each voxel, the ratio of singular values can estimate the number of total poles (representative of both the signal and the baseline) according to a statistical analysis [3]. Then, the separation of the *estzk* subspace from the baseline can be performed using the orthogonal matrix triangularization (a.k.a. QR decomposition) method, which yields an estimated target signal and the residuals. The residuals, theoretically, contain only baselines and noises. However, the imperfect *estzk* (i.e. the disagreement between *estzk* and "true values") can cause small peaks near some signal poles in the residuals. This imperfection can further be supported by the phase difference between the estimated target signal poles and the prior knowledge [2]. We termed these small peaks interference signals.

3. Prior knowledge optimization: After adding or "compensating" the interference signals to the estimated target signals, a HSVD decomposition can be used to yield a new set of prior knowledge poles (*estzk**) for subsequent iterations. These processes will repeat until interference poles are minimal. The final residual signal contains only the baseline and the noise; and the final target signal contains only the interested chemical compounds' peaks.

Results

A Monte Carlo experiment with 1000 simulated spectra for different noise levels was performed to compare 3 automatic methods: HSVD [1], HTLS-PK [2] and this algorithm, OASIS-HSVD. The parameters used for simulated data and SNR levels were based on typical *in vivo* ^{31}P data from 4T, including broad baseline components. The frequency and amplitude estimation relative root mean square errors (RRMSE) and Cramer-Rao Bound (CRB) [1] for the γ-ATP signal's quantification result are shown in Figure 1. It demonstrated that OASIS-HSVD outperformed both HSVD and HTLK-PK for frequency and amplitude estimations. Similar results also held true for other resonances.

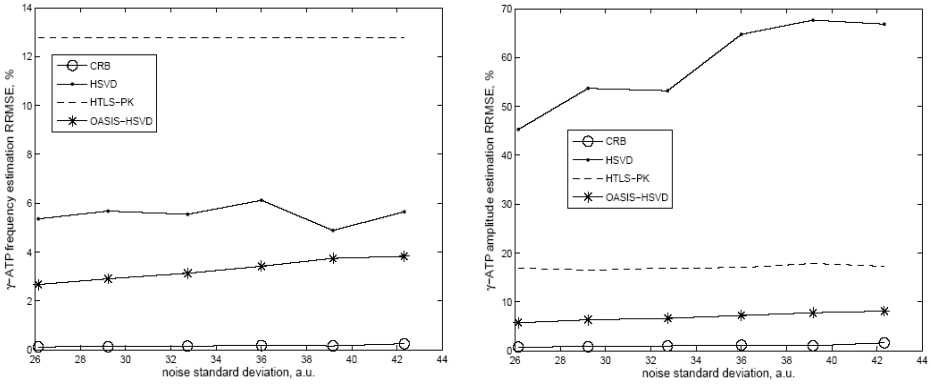

Fig 1 γ-ATP frequency and amplitude CRB and RRMSE for Monte Carlo study on estimation accuracy of HSVD, HTLS-PK and OASIS-HSVD. a.u.: arbitrary units.

A typical example of a 4T *in vivo* ^{31}P MRS with moderate baseline distortion is shown in Figure 2. This spectrum was acquired from the anterior cingulated region (a 12 cc volume) of a healthy subject. Ten Hz exponential digital filtering was applied to reduce noise. Note that the baseline is accurately identified, and the target signal together with the baseline agreed well with the original signal.

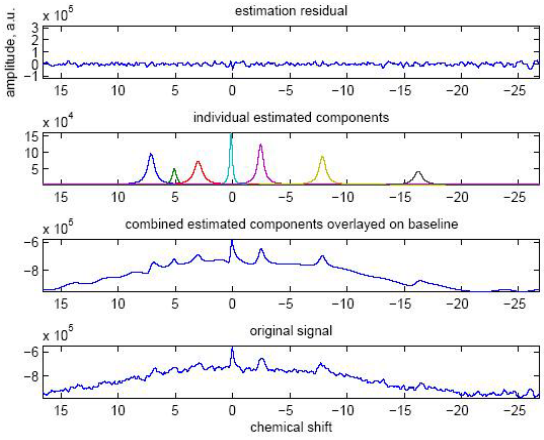

Fig 2 *in vivo* data estimation result

Conclusions and Discussions

The OASIS-HSVD method was developed and tested with the Monte Carlo studies and in vivo data for automatic baseline separation and signal quantification for *in vivo* ^{31}P MRS data. Because this method doesn't discard any sample data, theoretically, it can maximally preserve the interested signal during the parameter estimation. Further improvement will be focused on the robustness and speed of this algorithm.

Reference

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