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Accelerated J-Resolved ^{1}H-MRSI with Limited and Sparse Sampling of (k, t_J)-Space

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Synopsis

J-resolved 1H-MRSI is a powerful tool for mapping brain molecules, especially those with large spectral overlaps (e.g., glutamate, glutamine and GABA), yet it requires very long data acquisition times. Building on work in accelerated subspace-based imaging, this work proposes an accelerated acquisition scheme with limited and sparse sampling of (k, t_J)-space, based on a physics-based spectral model and Cramer-Rao lower bound analysis. A model-based processing scheme is also proposed, which performs model-based reconstruction and spectral quantification directly from the measurement data. The proposed method has been evaluated with simulated and *in vivo* experiments which have yielded very encouraging results.

Introduction

Many challenges in conventional ^{1}H-MRSI stem from the fact that most of the detectable resonances lie in a small chemical shift range and the spectra of several key molecules (e.g., glutamate (Glu), glutamine (Gln) and γ-aminobutyric acid (GABA)) have significant overlaps with other brain metabolites (e.g., NAA, Cr, and Cho). J-resolved ^{1}H-MRSI addresses this issue by lifting the 1D NMR spectrum onto a two-dimensional space but is not practical due to the increased data acquisition time required to cover the high-dimensional (k, t_J)-space (t_J is TE time for J-coupling encoding). To address this problem, acceleration methods of J-resolved 1H MRSI[1-3] have been proposed. These methods were able to produce high-quality 2D spectra with 64, 20, and 6 J-encodings respectively. Building on these advances, this work further accelerates J-resolved 1H-MRSI with a limited and sparse sampling of (k, t_J)-space (3 J-encodings). The proposed sampling pattern is chosen based on a physics-based spectral model and Cramer-Rao lower bound (CRLB) analysis. A model-based processing scheme is also proposed, which performs spectral quantification directly from the (k, t_J)-space data. Simulation and *in vivo* experiments have been performed to evaluate the proposed method, which have produced very encouraging results.

Method

Data acquisition

In this work, data were acquired using semi-LASER localization, which is robust to B_1 inhomogeneity, combined with echo-planar spectroscopic imaging readouts (Fig.1 a). The water signal is only weakly suppressed, enabling the tracking and correction of field inhomogeneity, field variations, and eddy current effects. Data acquisition was further accelerated by limited and sparse sampling in (k, t_J)-space (Fig.1 b-e). The t_J dimension was highly undersampled, where the optimal selection of t_J was found by CRLB analysis. To this end, we calculated the CRLB of measurement GABA concentration with all possible t_J combinations (from 40 – 230 ms) and chose the one that lead to the minimal CRLB. In this work, we found the optimal t_J combination (t_J = 40, 90, and 110 ms). The scan FOV was 180x180 mm^2 with a slice thickness of 10 mm and excitation volume of 90x90x10 mm^3, leading to the in-plane resolution of 2.3x1.6 mm^2. Other parameters were: TR=1250 ms, total acquisition time = 3.43 mins.

Data processing

For the data acquired at the very first t_J value with high-resolution and high-SNR, nuisance signals can be effectively removed using a union-of-subspaces method[4]. For later t_J values, the limited k-space coverage and poor SNR makes nuisance removal rather challenging. We address this challenge by using generalized series model[5] to exploit the correlation between nuisance signals from different t_J acquisitions to remove nuisance signal in later t_J's. After nuisance signals removal, a physics-based spectral model is used to reconstruct the spatiospectral distribution of metabolites. The image function can be written as a partially separable (PS) function[6] to perform spectral quantification directly from the (k, t_J)-space data:

$$\rho(x, t_J, t_2) = \sum_{l=1}^{L} c_l(x) v_l(t_J, t_2),$$

where t_J is the TE time, t_2 is the chemical shift time, $\{c_l(x)\}$ are spatial coefficients, and $\{v_l(t_J, t_2)\}_{l=1}^{L}$ are the basis functions determined by quantum mechanical simulations and training data. The spatial coefficients are estimated from the solution to the following regularized least-squares problem

$$\hat{C} = \arg\min_{C} \|M\mathcal{F}B_0CV - d\|_2^2 + \lambda\|WD(CV)\|_2^2,$$

where M, $\mathcal{F}$, and B_0 are the sampling, Fourier encoding, and the field inhomogeneity operators, V is a row matrix of the basis functions, d is the vector of water removed k-space data, W is the edge weight matrix, D is the gradient operator, and λ is the regularization parameter. The B_0 map and edge weights in W are predetermined using the data from the first t_J encoding.

Results and Discussion

Simulation results (Fig. 2) show that the proposed reconstruction and quantification method can produce accurate reconstruction from sparse and limited data. *In vivo* data were acquired from a healthy volunteer (with IRB approval) on a 3 T Siemens Prisma scanner using a commercial 20-channel head and neck coil, with the parameters described in the data acquisition scheme. We obtained very encouraging *in vivo* experimental results (Fig.3., Fig.4.) with the proposed

method using only 3 J-encodings (3.43 mins). This highly sparse acquisition method is enabled by the subspace model[7]. Since we have high-quality physics-based subspace structure, only a few spectral samplings in t_J and t_2 are needed.

Conclusion

A new method is proposed to accelerate J-resolved ^{1}H-MRSI with limited and sparse sampling of (k, t_J)-space, which is enabled by subspace modeling and prior spectral knowledge derived from quantum mechanics simulation. Experimental results show high-quality 2D spectra can be reconstructed using as few as 3 J-encodings (3.43 mins). Our method may enable J-resolved 1H-MRSI for simultaneous mapping of brain neurotransmitters such as glutamate and GABA in clinical applications.

Acknowledgements

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References

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Figures

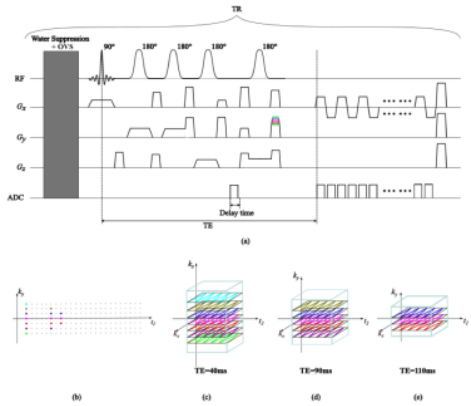

Fig. 1 The J-resolved semi-LASER sequence diagram is shown in (a). The delay time controls the J-coupling encoding, t_J. (b-e) depict the proposed sparse sampling strategy which is enabled by the partially separable model.

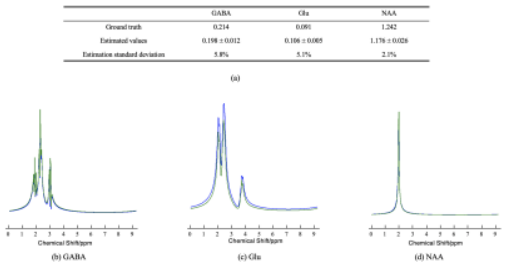

Fig. 2. Simulation results demonstrating the proposed method's ability to produce accurate reconstructions from sparsely sampled, noisy data. (a) shows the ground truth, estimated values, and estimation standard deviation. (b)-(d) show 1D spectra for GABA, Glu, and NAA from one of the 40 realizations. The spectra from the ground truth and reconstruction are shown in green and blue, respectively.

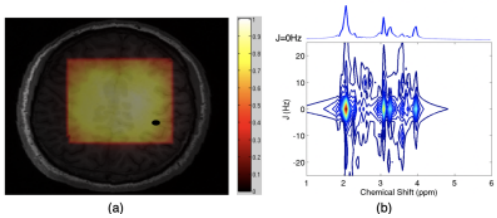

Fig. 3. In vivo results using the proposed method. (a) Shows the metabolite signal energy map estimated at 2.3 mm x 1.6 mm x10 mm nominal resolution, and (b) shows a representative localized 2D spectra from the position indicated by the black dot.

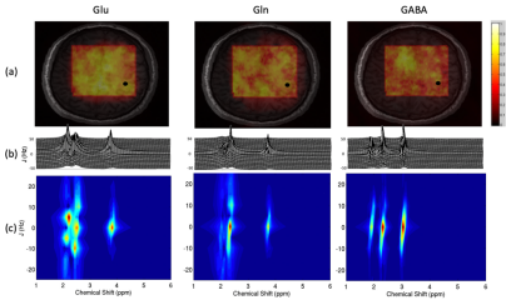

Fig. 4. In vivo results using the proposed method, (a) Glu, Gln, and GABA map (norm to 0-1individually, 2.3 mm x 1.6 mm x10 mm nominal resolution), (b), (c) Representative 2D spectra of black dot position.