Towards Short-TE MR Spectroscopic Imaging: Spectral Decomposition and Removal of Baseline Signals

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***Abstract*— Using short echo times (TE) for magnetic resonance spectroscopy imaging (MRSI) is a promising method to enhance signal-to-noise ratio, especially for metabolites with very short T_2 values. However, short-TE MRSI data often contain significant nuisance signals (e.g., baseline signals), which render spectral quantification difficult. This paper presents a novel method to address this problem using the temporal separability of MRSI data.**

I. INTRODUCTION

A long-standing problem with high-resolution MRSI is very low signal-to-noise ratio (SNR). Short-TE acquisitions provide a promising method to enhance SNR especially for metabolites with very short T_2 values. However, practical utility of short-TE MRSI has been limited because of strong nuisance signals (e.g., baseline signals).

This paper presents a novel method to address this issue. The proposed method is based on the observation that the baseline signals become negligible a few milliseconds after TE, and short-T_2 metabolite signals also decay quickly in a short-TE acquisition. Taking advantage of this temporal separability, we decompose the short-TE signal into three components, each of which only contains signals from long-T_2 metabolites, short-T_2 metabolites and baselines, respectively. Removal of the baseline signals is then straightforward, resulting in a much easier quantification problem.

II. METHOD

MRSI data can be expressed as

$$d(t) = \sum_{n=1}^{N} c_n e^{-\frac{t}{T_{2,n}}} e^{-i2\pi f_n (t-T_E)} g(t-T_E) + \xi(t), \quad (1)$$

where $\xi(t)$ represents the measurement noise and $g(\cdot)$ is the signal decay caused by field inhomogeneity, which can be modeled using the conventional exponentially decay model or directly derived from a known field map.

Suppose two datasets are acquired, i.e., a short-TE data $\boldsymbol{d}_S$ and a long-TE data $\boldsymbol{d}_L$. As shown in the insert of Fig. 1, we also construct $\boldsymbol{d}_S^{(1)}$ and $\boldsymbol{d}_S^{(2)}$ such that $\boldsymbol{d}_S^{(1)}$ only contains long-T_2 metabolite signals, while $\boldsymbol{d}_S^{(2)}$ contains all the metabolite signals but baseline signals.

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To perform signal decomposition, we first solve the following nonlinear least-squares problem using the variable projection method [2] to obtain an estimation of the long-T_2 metabolite signals:

$$\min_{\boldsymbol{\alpha}_L, \boldsymbol{c}_L} \left\| \begin{bmatrix} \boldsymbol{d}_S^{(1)} \\ \boldsymbol{d}_L \end{bmatrix} - \begin{bmatrix} \boldsymbol{\Phi}_S^{(1)}(\boldsymbol{\alpha}_L) \\ \boldsymbol{\Phi}_L(\boldsymbol{\alpha}_L) \end{bmatrix} \boldsymbol{c}_L \right\|_2, \quad (2)$$

where $\boldsymbol{\alpha}_L$ and $\boldsymbol{c}_L$ are the nonlinear and linear parameters in Eq. (1) of the long-T_2 metabolite signals. The estimated long-T_2 metabolite signals are then subtracted from $\boldsymbol{d}_S^{(2)}$ and the short-T_2 metabolite signals can be estimated from the residual of $\boldsymbol{d}_S^{(2)}$ using HSVD [1]. Finally, the estimated long-T_2 and short-T_2 metabolite signals are subtracted from $\boldsymbol{d}_S$, and the baseline signal is determined by fitting the residual of $\boldsymbol{d}_S$ with spline functions.

III. RESULTS

Figure 1 shows a representative set of results from applying the proposed method to an in vivo MRSI data set of the brain acquired with 30 ms and 135 ms TE. As can be seen, the residual signal after decomposition (Fig. 1c) is at the noise level, indicating a successful signal decomposition.

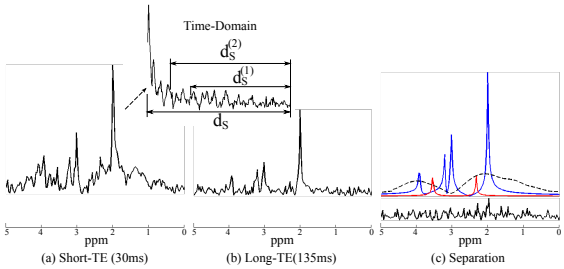

Fig. 1. **a**: The spectrum of $\boldsymbol{d}_S$; **b**: The spectrum of $\boldsymbol{d}_L$; **c**: Signal decomposition results, where the blue/red line represents the long-T_2/short-T_2 metabolites, the black dashed line the baseline signal, and the black solid line the residual.

IV. CONCLUSION

A novel method has been proposed for processing short-TE MRSI data, which may improve the practical utility of short-TE MRSI experiments.

REFERENCES

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