High-Resolution ^{1}H-MRSI of the Brain using Short-TE SPICE

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Target audience: Scientists and clinicians interested in high-resolution ^{1}H-MRSI of the brain.

Purpose: SPICE (SPectroscopic Imaging by exploiting spatiospectral CorrElation)[1] is emerging as a powerful tool for high-resolution spectroscopic imaging of the brain. As voxel size is getting smaller at higher resolution, further improvement of signal-to-noise ratio (SNR) becomes essential, especially with sparse sampling in (k,t)-space. Compared to long TE acquisitions, short-TE acquisitions (TE ≤ 30ms) can significantly enhance SNR by minimizing the signal loss due to T_2 relaxation[2]. It also better detects metabolites of the brain with coupled spin systems, such as mI, Glu and Gln. This work presents a novel data acquisition and processing method to enable short-TE SPICE for high-resolution ^{1}H-MRSI of the brain. The key issues addressed include the removal of the overwhelming nuisance signals (water and lipid signals) and the increased baseline signals at short TE from the sparsely sampled (k, t)-space data. In vivo experimental results show that short-TE SPICE is feasible and the proposed data acquisition and processing method can achieve 2mm in-plane resolution in good SNR with a TE of 20ms in a 30min scan, which is significantly better than the traditional long-TE methods.

Methods: The underlying spatiospectral signal ρ of a short-TE MRSI experiment consists of water (ρ_{W}), lipid (ρ_{L}), baseline (ρ_{B}), and metabolite (ρ_{M}) signals. Each of these signal components can be represented as a PS function[1,3,4]: $\rho = \rho_{\mathrm{W}} + \rho_{\mathrm{L}} + \rho_{\mathrm{B}} + \rho_{\mathrm{M}}$, where $\rho_{\mathrm{W}} = \sum_{p=1}^{P_{\mathrm{W}}} u_{\mathrm{W}}^{p}(\boldsymbol{x})\, v_{\mathrm{W}}^{p}(t)$, $\rho_{\mathrm{L}} = \sum_{p=1}^{P_{\mathrm{L}}} u_{\mathrm{L}}^{p}(\boldsymbol{x})\, v_{\mathrm{L}}^{p}(t)$, $\rho_{\mathrm{B}} = \sum_{p=1}^{P_{\mathrm{B}}} u_{\mathrm{B}}^{p}(\boldsymbol{x})\, v_{\mathrm{B}}^{p}(t)$, and $\rho_{\mathrm{M}} = \sum_{p=1}^{P_{\mathrm{M}}} u_{\mathrm{M}}^{p}(\boldsymbol{x})\, v_{\mathrm{M}}^{p}(t)$. This PS model exploits the fact that each signal component resides in a very low-dimensional subspace (e.g., ρ_{W} in a subspace spanned by a set of temporal basis $\{v_{\mathrm{W}}^{p}(t)\}$ with spatial coefficients $\{u_{\mathrm{W}}^{p}(\boldsymbol{x})\}$) and enables special data acquisition and processing schemes to estimate these signal components from sparse (k,t)-space data. As in SPICE, two datasets are acquired: a dataset (called $\mathbf{D_1}$) covering limited k-space but at a high temporal rate (for determining the temporal bases) and a dataset (called $\mathbf{D_2}$) covering extended k-space but with limited temporal sampling (for determining the spatial coefficients).

We first remove the dominating nuisance signals from $\mathbf{D_1}$ and $\mathbf{D_2}$. The field inhomogeneity effects in $\mathbf{D_1}$ data are corrected using a measured field map[1]. The water signal in the field inhomogeneity corrected $\mathbf{D_1}$ data can be separated based on its spectral support (e.g., using the HSVD method[5]), while the lipid signal can be separated based on its spatial support. SVD is used to estimate the temporal bases from the separated water and lipid signals. The spatial coefficients of the water and lipid signals are estimated by fitting the $\mathbf{D_2}$ data, while incorporating the spatial support of the lipid signal for better estimation. The nuisance signals in $\mathbf{D_1}$ (limited k-space data) and $\mathbf{D_2}$ (sparse (k,t)-space data) are then removed using the estimated high-resolution water and lipid signals.

We then estimate the metabolite and baseline signals from the nuisance signal removed $\mathbf{D_1}$ and $\mathbf{D_2}$ data. The metabolite and baseline signals in the nuisance signal removed $\mathbf{D_1}$ data can be separated from each other in the time domain: the baseline signal becomes negligible a few milliseconds after TE and can be modeled as smooth functions in the frequency domain[6,7]. The temporal bases for the metabolite and baseline signals are then estimated from the separated signals; and the spatial coefficients for both components are jointly determined by fitting the nuisance signal removed $\mathbf{D_2}$ data with a total variation penalty to promote sparsity of the reconstructed metabolite signals in the spatial domain and an ℓ_2-norm penalty to promote smoothness of the reconstructed baseline signals in the frequency domain.

Results and Discussion: MRSI datas were collected from a healthy volunteer on a 3.0T Siemens scanner with IRB approval. The $\mathbf{D_1}$ dataset was collected using a CSI sequence with 20ms TE, 10mm slice thickness, and 12x12 spatial encodings. WET[8] pulses and outer-volume-bands were used to suppress water and lipid signals. The $\mathbf{D_2}$ dataset was collected using an EPSI sequence with 110x110 spatial encodings (2mm nominal in-plane resolution), bipolar acquisition, 8 averages and 2.66ms echo spacing. The total acquisition time was about 30min. The same experiment was repeated at 130ms TE.

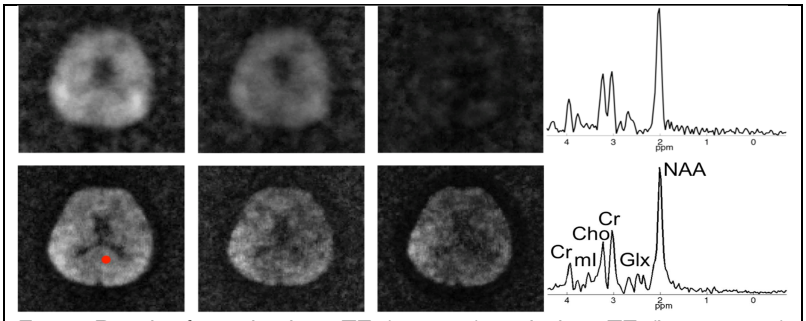

Fig 1. Results from the long-TE (top row) and short-TE (bottom row) experiments. The first to the third columns show the concentration maps of NAA, Cr and Glx (Glu+Gln) at 2mm in-plane resolution; and the forth column shows representative spectra.

Figure 1 shows the results from the long-TE and short-TE experiments. Metabolite concentration maps and representative spectra from both experiments show almost no lipid signals. This is significant, as removing the strong lipid signals at short-TE is difficult even with lipid suppression, and the problem is even more challenging with sparse (k,t)-space data. The results from the short-TE experiment show better SNR than the long-TE experiment as expected. Notably, the ventricle structures of the brain can be more clearly seen in the NAA map at short-TE (the first column); and the noise floor of the short-TE spectrum (around 0 ppm) is lower than the long-TE spectrum. The short-T_2 metabolites were better detected at short TE as shown in the concentration maps of Glx (Glu+Gln, the third column) and the representative spectra. Also note that the short-TE spectrum is almost free of baseline signals.

Conclusion: We have presented a novel data acquisition and processing scheme for subspace-based high-resolution short-TE ^{1}H-MRSI of the brain. Experimental results show that the proposed method can obtain MRSI images at 2mm in-plane resolution in good SNR in a 30min scan. The proposed method should prove useful for high-resolution metabolic imaging of the brain.

References: 1. Lam et al., MRM 2014;71:1349-1357. 2. Mlynarik et al., MRM 2006;56:965-970. 3. Ma et al., ISMRM 2014:2887. 4. Liang, IEEE-ISBI 2007:988-991. 5. Barkhuysen et al., JMR 1987;73:553-557. 6. Ratiney et al. MAGMA 2004;16:284-296. 7, Ning et al. IEEE-EMBC 2014. 8. Ogg et al., JMR 1994;104:1-10.