A Subspace Approach to High-Resolution Spectroscopic Imaging: In Vivo Experimental Results

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Introduction: A new approach to high-resolution MR spectroscopic imaging (MRSI), called SPICE (SPectroscopic Imaging by exploiting spatiospectral CorrElation) has recently been proposed. This approach is characterized by the use of a subspace model for both data acquisition and reconstruction of the spatiospectral function. More specifically, SPICE models the spatiospectral function as $\rho(\mathbf{r}, t) = \sum_{l=1}^{L} c_l(\mathbf{r}) \phi_l(t)^l$, where $\{\varphi_l(t)\}_{l=1}^{L}$ or $\{\phi_l(t)\}_{l=1}^{L}$ represent spectral/temporal basis functions, $\{c_l(\mathbf{r})\}_{l=1}^{L}$ are the corresponding spatial coefficients, and L is the model order. With this model, SPICE employs a hybrid (k,t)-space sampling strategy to acquire two MRSI data sets: (i) D_1 with limited k-space coverage but high temporal resolution and (ii) D_2 with high-resolution k-space coverage but flexible temporal sampling. Usually, a companion anatomical scan is also performed to obtain a map of B_0 field inhomogeneity (plus a water map and a fat map for 1H MRSI experiments). A low-rank model-based reconstruction algorithm is used to estimate $\{\phi_l(t)\}$ (the temporal subspace) from D_1 , followed by estimating $\{c_l(\mathbf{r})\}$ from D_2 with the capability to incorporate field-inhomogeneity correction and additional prior information. In this work, we will present experimental results from both rat and human brains to demonstrate the unprecedented capability of SPICE for in vivo high-resolution MRSI. In summary, SPICE obtained spatiospectral reconstructions with 0.5mm in-plane resolution from a rat brain in 34 minutes and 2.5mm in-plane resolution from a human brain in 12 minutes, both with good signal-to-noise ratio (SNR).

Methods: Rat experiment: The proposed SPICE acquisition has been implemented on a 7T animal scanner (Bruker BioSpec AV3) with a single channel receiver surface coil using a hybrid CSI/EPSI sequence. CSI data were acquired using a modified spin-echo CSI sequence^{2,3}, with 5000Hz readout bandwidth (BW) and 1024 FID points. EPSI data were acquired using a modified spin-echo EPSI sequence⁴ with 250kHz readout BW and 512 FID points. VAPOR water suppression⁵ and 5 outer-volume suppression slices were used for both sequences. Human experiment: The same hybrid CSI/EPSI acquisition has also been implemented on a 3T human scanner (Siemens Trio) with a 12-channel receiver headcoil. CSI data were acquired using a modified spin-echo CSI sequence, with 2000Hz readout BW and 512 FID points. EPSI data were acquired using a customized EPSI sequence with 167kHz readout BW and 256 FID points. WET water suppression⁶, PRESS selective excitation and 8 outer-volume suppression slices were used for both sequences. For both rat and human experiments, a multi-point Dixon acquisition was used to obtain a fat mask for lipid signal removal and a field map for field-inhomogeneity correction. A high-resolution T2-weighted image was also acquired to extract edge weights for reconstruction. Data processing: (a) Remove residual water signals using HSVD⁷ and lipid signals using the method in [8] from both the CSI and

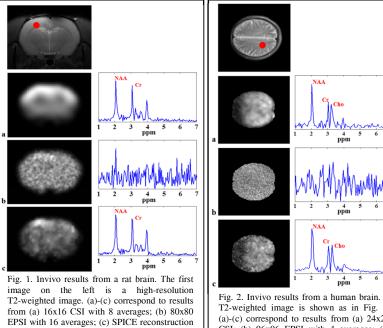


Fig. 2. Invivo results from a human brain. A T2-weighted image. (a)-(c) correspond to results from (a) 16x16 CSI with 8 averages; (b) 80x80 EPSI with 16 averages; (c) SPICE reconstruction with 10x10 CSI averaged 8 times and 80x80 EPSI averaged 16 times. Left column: NAA distributions from peak integration (zoomed-in segmented brain-only region); Right column: representative spectra from a voxel (red dot).

EPSI data; (b) Correct the field-inhomogeneity effects in the CSI data (D_1) using the method in [9]; (c) Estimate { $\phi_l(t)$ } from the corrected data in D_1 ; (d) Estimate { $c_l(\mathbf{r})$ } from D_2 with field inhomogeneity correction and regularization (total variation for the rat data and weighted- l_2 for the human data).

Results: Figure 1 shows a set of representative results from a rat brain data set. Three acquisition schemes are compared: (i) a 16x16 CSI with 8 averages; (ii) an 80x80 EPSI with 16 averages; (iii) a SPICE acquisition with 10x10 CSI encodings averaged 8 times in D_1 and 80x80 EPSI averaged 16 times in D_2 . The rest of the imaging parameters were: FOV = 40x40mm², slice thickness = 2.5mm and TR/TE = 1000/80ms. As can be seen, CSI reconstruction has high SNR spectrum but poor spatial resolution. SPICE, with approximately the same acquisition time (~34min), obtained much higher resolution (revealing very interesting spatial heterogeneity) with similar SNR. On the other hand, the high-resolution EPSI reconstruction has unacceptably low SNR. Figure 2 shows a set of representative results from a human brain data set. Similar to the animal data, we compare three methods: (i) a 24x24 CSI; (ii) a 96x96 EPSI with 4 averages; (iii) SPICE with 12x12 CSI in D_1 and 96x96 EPSI averaged twice in D_2 . The rest of the imaging parameters were: FOV = 240x240mm², volume of excitation = $135x145x15mm^3$ and TR/TE = 1200/130ms. All three acquisitions took approximately the same time (~12min). As can be seen, SPICE produced reconstructions with similar spectral quality to CSI but much higher spatial resolution. EPSI reconstruction has significantly low SNR.

Conclusion: In vivo results from rat and human brains have been obtained to evaluate the capability of SPICE for high-resolution MRSI with comparison to CSI and EPSI. Our results demonstrate that in similar acquisition time, SPICE can obtain much higher spatial resolution than CSI, and significant gain in SNR compared to high-resolution EPSI. SPICE may provide a new, effective tool for high-resolution metabolic imaging.

References: [1] Liang, IEEE-ISBI, 2007. [2] Brown et. al., PNAS, 1982. [3] Pohmann et. al., JMR, 1997. [4] Posse et. al., MRM, 1995. [5] Tkac et. al., MRM, 1999. [6] Ogg et. al., JMR, 1994. [7] Barkhuysen et. al., JMR, 1987. [8] Ma et. al., ISMRM, 2013. [9] Peng et. al., IEEE-EMBC, 2010.