Ultra-High Resolution 3D ^{1}H-MRSI of the Brain: Subspace-Based Data Acquisitions and Processing

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Target Audience: Those who are interested in high-resolution MR spectroscopic imaging (MRSI).

Purpose: We propose a new data acquisition and processing method to enable ultra-high resolution (on the order of mm) 3D MRSI of the brain based on the recently proposed subspace imaging framework, known as SPICE[1]. SPICE exploits the unique property of high-dimensional spectroscopic signals being in a low-dimensional subspace to achieve fast high-resolution MRSI with good SNR[1-4]. SPICE has two significant advantages over existing methods to accelerate MRSI: a) SNR: conventional fast-scan sequences (often combined with parallel imaging) sacrifice SNR for speed (which typically renders ultra-high resolution infeasible because of limited SNR), and b) speed: compressed sensing based sparse sampling methods require high SNR data for joint subspace pursuit and missing data recovery; while such an approach is useful for hyperpolarized ^{13}C MRSI[5], it offers limited accelerations for regular MRSI experiments. This work is focused on 3D ^{1}H-MRSI of the brain. We will present a new data acquisition and processing method for SPICE to provide an unprecedented combination of speed, resolution and SNR. In particular, for in vivo experiments on a 3T scanner, we are able to produce spatial distributions of ^{1}H metabolites with approximately 3mm isotropic resolution, which is an order of magnitude improvement over the existing MRSI methods[6-8] while achieving very good SNR. We hope to report, share, and discuss this exciting advance with our MR colleagues at the ISMRM meeting.

Methods: **(I) Acquisition:** Based on the subspace model, two complementary data sets, $\mathbf{D}_1$ (with fully encoded spectral information and high SNR) and $\mathbf{D}_2$ (with fully encoded spatial information), are collected for subspace determination and image reconstruction. For 2D SPICE, we implemented this strategy using a hybrid CSI/EPSI sequence[4]. However, this scheme is still too slow to provide the desired number of spatiospectral encodings for high-resolution 3D MRSI in a reasonable time frame (e.g., ~20min). To address this issue, we propose a new sequence that performs a hybrid of slow EPSI scans (to acquire $\mathbf{D}_1$) and rapid EPSI-like scans (to get $\mathbf{D}_2$). During the slow EPSI scans, we encode one spatial and the entire spectral dimensions in one TR and phase encode the other two spatial dimensions in different TRs, as in [7,8]. The echospacing between gradient pairs satisfies spectral Nyquist in order to fully capture the spectral information. For SNR considerations, we only cover a central portion of k-space in the slow EPSI scans, thus this acquisition can be done very quickly. During the rapid EPSI scans, we simultaneously encode two spatial dimensions (to achieve the desired spatial resolution and acquisition speed) as well as a small number of spectral encodings in each TR. The third spatial dimension is phase encoded, and echo shifts are used to obtain additional spectral encodings. This special spatiospectral encoding strategy is enabled by the subspace model. Specifically, given the subspace structure estimated from $\mathbf{D}_1$ (fully specifying the spectral dimension), only a limited number of spectral encodings is needed in $\mathbf{D}_2$. This allows us to use the FID period to encode as much spatial information as possible, significantly shortening the time for obtaining the number of spatial encodings needed for ultra-high resolution 3D MRSI. The resulting sampling trajectories therefore sparsely sample the (k,t)-space, as illustrated in Fig. 1.

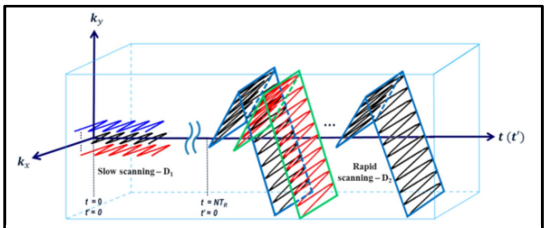

Fig. 1: An illustration of the proposed (k,t)-space trajectories. The encoding along $\mathbf{k}_y$ for $\mathbf{D}_2$ was done by blip gradients which can be reversed every other TR, leading to a center-out pattern (along $\mathbf{k}_y$) for better SNR efficiency.

(II) Reconstruction: Given $\mathbf{D}_1$ and $\mathbf{D}_2$, we propose the following reconstruction method. First, we estimate a temporal subspace $\boldsymbol{\Phi}$ from $\mathbf{D}_1$. To this end, the B_0 inhomogeneity has to be corrected, which is done by performing a regularized reconstruction as $\hat{\boldsymbol{\rho}} = \arg\min_{\boldsymbol{\rho}} \|\mathbf{d}_1 - \boldsymbol{F}_T\{\mathbf{B} \odot \boldsymbol{\rho}\}\|_2^2 + \lambda_\rho \|\boldsymbol{\rho}\|_*$, where $\mathbf{d}_1$ contains data from $\mathbf{D}_1$, $\boldsymbol{F}_T$ is a truncated Fourier encoding operator, $\mathbf{B}$ models the B_0 effects[1] and $\|\cdot\|_*$ denotes the nuclear-norm penalty that encourages low-rankness of the reconstruction[9]. The field corrected $\hat{\boldsymbol{\rho}}$ (a spatiotemporal reconstruction) is then used to estimate $\boldsymbol{\Phi}$ using an SVD analysis. Second**,** we estimate a set of spatial coefficients by solving $\hat{\mathbf{C}} = \arg\min_{\mathbf{C}} \|\mathbf{d}_2 - \boldsymbol{F}_\Omega\{\mathbf{B} \odot \mathbf{C}\boldsymbol{\Phi}\}\|_2^2 + \lambda_C \|\mathbf{D}\mathbf{C}\boldsymbol{\Phi}\|_1$, where $\mathbf{d}_2$ contains data from $\mathbf{D}_2$, $\boldsymbol{F}_\Omega$ is a sparsely sampled Fourier encoding operator and $\mathbf{D}$ is a finite difference operator for the spatial total-variation regularization. The final reconstruction was then constructed as $\hat{\mathbf{C}}\boldsymbol{\Phi}$.

Results: Data were acquired from a customized brain metabolite phantom (containing vials with various diameters and lengths filled with solutions of NAA, creatine, choline and myo-inositol at physiologically relevant concentrations) and healthy volunteers (IRB approved). All experiments were conducted on a 3T Siemens Trio using the proposed sequence. WET water suppression[10] and PRESS excitation were incorporated. For in vivo studies, 8 lipid suppression bands were used. Auxiliary data including ΔB_0 maps and water/fat images were also collected for B_0 inhomogeneity correction and subspace-based nuisance signal removal[11]. The echo times for both the phantom and in vivo experiments were 30ms. Fig. 2 shows some representative phantom results from an approximately 20min SPICE acquisition, with an encoding matrix size of 80x80x20 ($\mathbf{k}_x$-$\mathbf{k}_y$-$\mathbf{k}_z$) over a FOV of 240x240x80mm^3. As can be seen, the proposed 3D SPICE achieved very high resolution, resolving the smallest vials as opposed to the significantly blurred NAA maps from an equivalent-time low-resolution 3D scan, with very high SNR. Fig. 3 shows some representative in vivo results from an approximately 30min SPICE acquisition, with a matrix size of 80x80x24 over a FOV of 240x240x72mm^3. As can be seen, the SPICE reconstructions show excellent resolution and SNR. To our knowledge, these are the highest resolution ^{1}H metabolite maps ever obtained from the brain.

Conclusion: We have presented a new data acquisition and processing method for ultra-high resolution 3D ^{1}H-MRSI of the brain. Very exciting experimental results have been obtained, demonstrating an unprecedented capability of the proposed method.

Reference: [1] Lam et. al., MRM, 2014. [2] Nguyen et. al., IEEE-TBME, 2013. [3] Liang, ISBI, 2007. [4] Lam et. al., IEEE-EMBC, 2014. [5] Hu et. al., JMR, 2008. [6] Posse et. al., JMRI, 2013. [7] Posse et. al., MRM, 1995. [8] Maudsley et. al., MRM, 2009. [9] Recht et. al., SIAM Rev., 2010. [10] Ogg et. al., JMR, 1994. [11] Ma et. al., ISMRM, 2014.

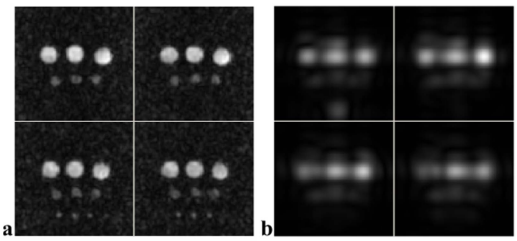

Fig. 2: NAA maps (4 different slices from the phantom) obtained by 3D SPICE (**a**) and an equivalent-time low-res 3D scan (**b**).

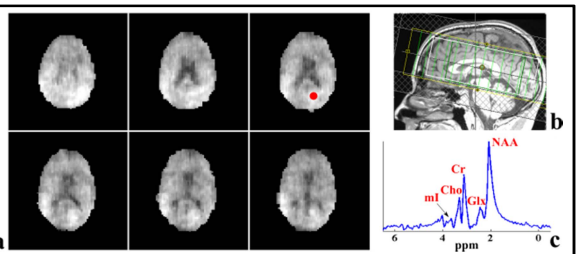

Fig. 3: Results from a healthy human brain: (**a**) NAA maps for 6 different slices from the brain coverage illustrated in (**b**). A representative spectrum from the voxel indicated by the red dot is shown in (c).