

Undersampled MRSI k-space for spectra with limited support

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Introduction. A major drawback in application of magnetic resonance spectroscopic imaging (MRSI) is the long acquisition time required to gather necessary data to achieve satisfactory resolution. When the chemical shift spectrum is inherently sparse, i.e. with a limited support, it is possible to reconstruct this spectrum from a subset of the k-space samples, thus reducing the number of phase encoding steps and subsequently reducing acquisition time. In this case, our approach outperforms compressed sensing using L1-minimization.

Theory. In conventional two dimensional MRSI we can represent both the complete k-space samples, and the unknown spectrum, of all the voxels simultaneously, in column ordered vectors \mathbf{y} , \mathbf{x} , respectively. Then the mapping from the unknown spectrum to the k-space measurements (in the noise free case) can be expressed as $\mathbf{y}=\mathbf{F}\mathbf{x}$ (1) where $\mathbf{F}=\mathbf{F}_t^* \otimes \mathbf{F}_y \otimes \mathbf{F}_x$, $\mathbf{F} \in \mathbb{C}^{n \times n}$, and \mathbf{F}_x , \mathbf{F}_y , \mathbf{F}_t are the one dimensional unitary Fourier transform matrix related to directions k_x , k_y and t . When the spectrum is inherently sparse, (e.g. some in vivo / in vitro acquisitions, hyperpolarized spectroscopy [1]), we can deduce its support from quantum mechanics based simulations or directly from a single voxel acquisition over the whole volume of interest. Let \mathbf{x}_s be the restriction of \mathbf{x} to the coefficients of the support of cardinality s , then from (1) we can derive that $\mathbf{y}=\mathbf{F}_s \mathbf{x}_s$ (2) where \mathbf{F}_s is a full rank $n \times s$ matrix formed by selecting the columns of \mathbf{F} having the same indices as the coefficients in the support. Eq. (2) is an over determined system of linear equations. Undersampling the k-space is equivalent to selecting a limited set of m measurements with $s < m < n$. This corresponds to extracting from \mathbf{F}_s , a matrix \mathbf{A} of size $m \times s$, by selecting the m rows which correspond to the acquired \mathbf{y}_m form \mathbf{y} . The undersampled acquisition can then be expressed as $\mathbf{y}_m=\mathbf{A} \mathbf{x}_s$ (3) where \mathbf{y}_m is the restriction of \mathbf{y} to its m acquired measurements. Let $\mathbf{A}^\dagger=(\mathbf{A}^T \mathbf{A})^{-1} \mathbf{A}^T$ (4), then the least squares estimate of the coefficients of the spectrum is given by: $\mathbf{x}_{ls}=\mathbf{A}^\dagger \mathbf{y}_m$ (5). Following our hypothesis in the noise free case, and incorporating (3) into (5) results in the exact spectrum:

$\mathbf{x}_{ls}=\mathbf{A}^\dagger \mathbf{y}_m=\mathbf{x}_s$. In a real life noisy setup we get $\mathbf{x}_{ls}=\mathbf{x}_s+\mathbf{A}^\dagger \mathbf{w}$ where \mathbf{w} represent the noise term on the acquired measurements.

Material and Method. MRSI k-space simulations (16x16 matrix and 1024 data points) were generated in Matlab by assigning in each of three spatially distributed ellipsoids a metabolite signal simulated with the GAMMA library. For in vitro data, a standard two-dimensional CSI spin-echo sequence was performed on a solution containing 11 metabolites, using a 4.7 T Bruker Avance (Bruker BioSpin Corp.), and with the following parameters: TR/TE = 1500/144 ms, 20x20x2 mm3 FOV, 16x16 in-plane CSI matrix, 4096 data-points, bandwidth of 6 kHz, acquisition time = 40 min. In-vivo experiment was conducted on a Swiss mouse in a 7T scanner (Bruker Biospin). K-space-weighted spin echo CSI sequence was used (TR/TE = 2500/6.5 ms, 20x20x2 mm3 FOV, 16x16 in-plane CSI matrix, 1024 data-points, bandwidth 4 kHz, acquisition time 40 min. These set up are for complete k-space acquisitions.

Comparative study. We have compared our approach to the recently introduced method of Compressed sensing (CS), an emerging signal processing framework for efficient acquisition and recovery of sparse or compressible signals [2]. CS reconstructions were performed using Sparco toolbox [3]. CS random undersampling was performed in the k_x, k_y directions using a bivariate normal distribution centered at the middle of the k-space with an adequate diagonal covariance matrix. In contrast the subsampling for our method is deterministic and centered at the middle of the k-space. The two methods were assessed in terms of SNR of the reconstructed CSI and quality of the data for subsequent quantification was addressed.

Results. Fig.1 displays our results for simulated and in-vitro reconstructions. Compared to a CS reconstruction, we succeeded to have further reduction of acquired k-space samples, and maintain largely better SNR. Another impressive advantage is the reduction of the reconstruction time; while it varies for the CS reconstructions from 40' to more than 1h (depending on the use of sparsifying transform), it takes less than 1 minute to obtain our results on a standard personal computer. Fig2 shows mouse brain spectrum reconstructed using the proposed approach and quantified by the QUEST method[4].

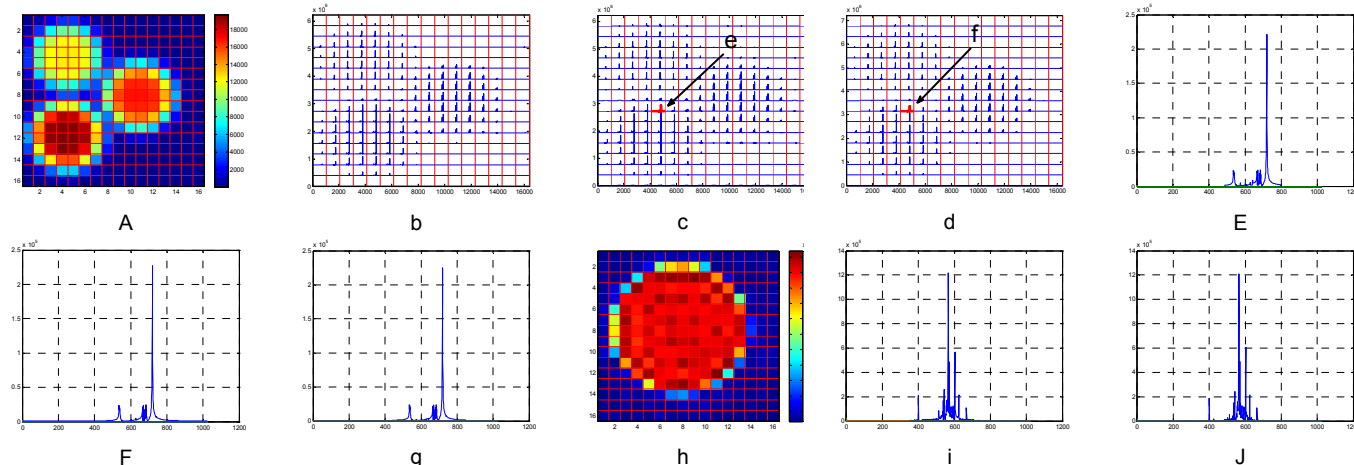


Fig. 1: (a) Simulated phantom. Spectrum reconstruction: (b) from complete k-space (c) from 30 % of k-space samples using our method (d) from 40 % of k-space samples using L1-minimisation (CS) (e) at voxel 9,5 (arrow e in(c)) with our method, SNR= 19.0 dB (f) at voxel 9,5 (arrow f in(d)) with CS, SNR= 16.4 dB (g) at voxel 9,5 with our method and 40% of k-space samples, SNR=23.0 dB (h) image of 11 in vitro metabolites. Spectrum reconstruction (i) from 30 % of k-space samples at voxel 9,5 with our method SNR= 18.7 dB (j) from 40 % of k-space samples at voxel 9,5 with CS, SNR= 15.9 dB.

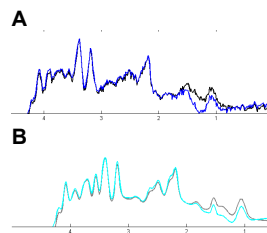


Fig2: Overlay of A) a spectrum acquired at 7T located in the middle of the mouse brain and obtained from a full k-space sampling (black) and spectrum reconstructed from 50% of the k space samples using the proposed approach (blue). B) of their corresponding QUEST estimates respectively in gray and cyan. Here only the frequencies between 0 ppm and 5 ppm were used in the reconstruction computation. Except for the lipid region, quantitative results are in agreement.

References: [1] S. Hu, et al. "Compressed Sensing for Resolution Enhancement of Hyperpolarized 13C Flyback 3D-MRSI" J. M. R., 2008;192(2), pp. 258-264 [2] D. Donoho, "For most large underdetermined systems of linear equations the minimal ℓ_1 -norm solution is also the sparsest solution," Comm. Pure and Applied Math., vol. 59, no. 6, pp. 797–829, 2006 [3] E. van den Berg, et al., "Sparco: A testing framework for sparse reconstruction," Tech.Rep. No TR-2007-20, Univ. of British Columbia, 2007 <http://www.cs.ubc.ca/labs/sci/sparco/> [4] Ratiney, H et al, "Time-domain semi-parametric estimation based on a metabolite basis set", NMR Biomed. 2005 Feb;18(1):1-13