

Removal of Nuisance Signals from Limited and Sparse 3D ¹H-MRSI Data of the Brain

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Target Audience: Researchers who are interested in high-resolution 3D ¹H-MRSI of the brain.

Purpose: In ¹H-MRSI of the brain, the signals from water and lipids are orders of magnitude stronger than the metabolite signals of interest and must be removed prior to any analysis. This work addresses the problem of removing these “nuisance” signals from 3D MRSI data that has sparse and limited coverage of (*k*, *t*)-space, a data acquisition strategy used in accelerated high-resolution MRSI [1]. More specifically, we extend the Union-of-Subspace (UoSS) method [2] to 3D MRSI where the slice direction has a small number (e.g., 16) of spatial encodings and is vulnerable to significant leakage of lipid signals from the subcutaneous region.

Methods: Compared with [2], a key novelty of this work lies in the way we handle 3D data sets with a small number of encodings along the slice direction. More specifically, we incorporate prior 3D spatial support constraints (readily available from high-resolution anatomical images) into the previously proposed UoSS model for the spatiotemporal signal

$$\rho(x, f) = w_W(x) \sum_{p=1}^{P_W} u_{W,p}(x) v_{W,p}(f) + w_L(x) \sum_{p=1}^{P_L} u_{L,p}(x) v_{L,p}(f) + w_M(x) \sum_{p=1}^{P_M} u_{M,p}(x) v_{M,p}(f),$$

where w_W, w_L, w_M are the respective spatial supports for the water, lipid, and metabolite signals, and $\{u_{W,p}\}_{p=1}^{P_W}, \{u_{L,p}\}_{p=1}^{P_L}, \{u_{M,p}\}_{p=1}^{P_M}$,

$\{v_{W,p}\}_{p=1}^{P_W}, \{v_{L,p}\}_{p=1}^{P_L}, \{v_{M,p}\}_{p=1}^{P_M}$ span the corresponding spatial and

spectral subspaces. This model enables us to enforce the boundary constraints in high-resolution without being subject to the limitation on the number of available spatial encodings (which is desirable especially along the slice-direction). To effectively exploit this property, our method removes the nuisance signals from the 3D data with both sparse and limited *k*-space coverage in three steps: (i) estimate the temporal subspaces from field inhomogeneity corrected data with limited *k*-space coverage but dense temporal sampling, (ii) estimate high-resolution spatial subspaces from the sparse but high-resolution data by solving a regularized least-squares problem and then subtracting the estimated water and lipid components from the data, (iii) remove the nuisance signals from the limited coverage data by solving another least-squares problem which combines the UoSS model with a generalized series model [3] utilizing the high-resolution estimates from step ii as the reference image. See [2] for more details on the formulation and algorithm.

We have tested our method on 3D *in vivo* ¹H-MRSI data acquired on a 3T Siemens TRIO scanner over a field of view of 240x240x72mm³. For the limited coverage data, we have 16x16x12 spatial encodings (12 for the slice direction) each with 256 spectral encodings acquired by a 3D EPSI sequence. The sparsely sampled data was obtained using another 3D EPSI sequence with elliptical sampling in the phase and slice directions. 80x80x24 spatial encodings each with 128 spectral encodings were acquired. WET water suppression [4] and outer-volume-suppression [5] bands were used to reduce the amount of water and fat contributions in the data prior to removal. A 3D anatomical image was acquired and automatically segmented using a 3D segmentation algorithm [6] to extract the support information for the water, lipids, and metabolites. Field maps were also obtained for field inhomogeneity correction. As described above, the reconstruction of the water and lipid signals was performed on a high-resolution grid (110x110x32).

Results: A set of representative experimental results is shown in Fig. 1, which depicts the spectral integrals of the central slices from the limited and sparse data sets before and after nuisance signal removal. Estimated spectra (original, estimated water and fat, and residual) are also shown for each of the data sets with locations indicated by the red squares. The method accurately estimated the water and lipid signals in both data sets and successfully removed their contributions from the data while preserving the metabolic signals of interest.

Conclusions: The Union-of-Subspace method can successfully remove water and lipid signals from 3D ¹H-MRSI data of the brain, with both sparse and limited (*k*, *t*)-space coverage. The method is particularly useful and desirable for accelerated high-resolution 3D ¹H-MRSI of the brain using sparse sampling.

References: [1] F. Lam and Z.-P. Liang, *MRM*, 71:1349-1357, 2014. [2] C. Ma, *et al.*, “Removal of Nuisance Signals from Limited and Sparse ¹H MRSI Data Using a Union-of-Subspace Model.” *MRM*, under rev. [3] Z.-P. Liang and P.C. Lauterbur, *IEEE-TMI*, 13:677-686, 1994. [4] R.J. Ogg, *et al.*, *JMR Series B*, 104:1-10, 1994. [5] J.H. Duyn, *et al.*, *Radiology*, 188:277-282, 1993. [6] K. J. Friston, *Eds.*, “Statistical parametric mapping: the analysis of functional brain images.” Amsterdam, Elsevier/Academic Press. 2007.

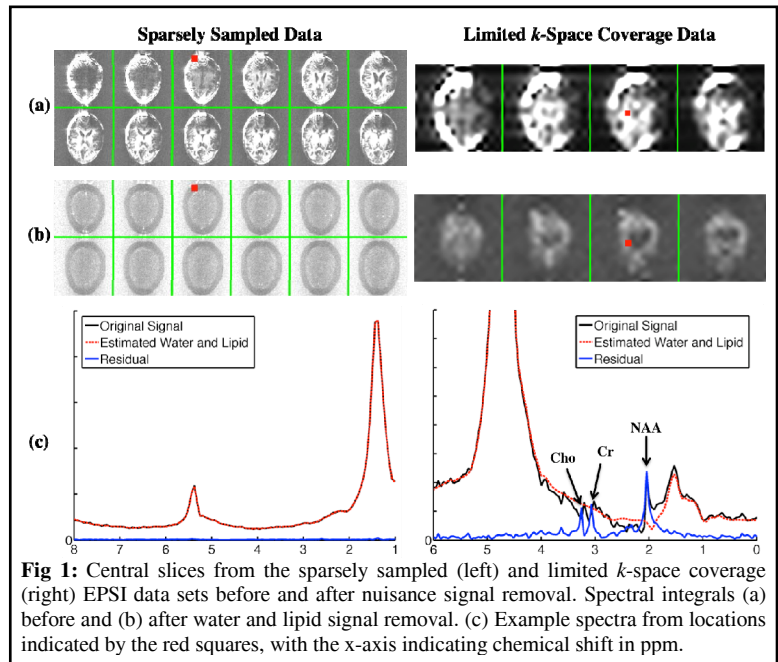


Fig 1: Central slices from the sparsely sampled (left) and limited *k*-space coverage (right) EPSI data sets before and after nuisance signal removal. Spectral integrals (a) before and (b) after water and lipid signal removal. (c) Example spectra from locations indicated by the red squares, with the x-axis indicating chemical shift in ppm.