Dramatic speedup in 1D-, 2D- and 3D-MRS scan times with linear algebraic modeling (SLAM)

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Introduction: Long scan time is a major problem for multi-voxel MRS and chemical shift imaging (CSI). While model-based MRS reconstruction methods, such as SLIM[1], GSLIM[2] and SLOOP[3] could reduce scan times in theory, their *in vivo* application remains very limited and focused on suppression of inter-compartment leakage[4,5] using entire CSI datasets. A significant speed advantage from these methods, has, to the best of our knowledge, not been realized *in vivo* or in humans, and it is unknown whether such speed-ups could be achieved with at least the same accuracy as CSI in practice. Here we propose localized spectroscopy with linear algebraic modeling (SLAM) to achieve dramatic speed-up advantages. We apply just a fraction of the CSI phase-encoding steps to acquire spectra from a set of C compartments that are selected from scout MRI. The signal-to-noise ratio (SNR) cost of truncating the data set is offset by using the highest SNR steps from central k-space. We demonstrate that SLAM yields essentially the same spectra as compartmentally averaged 1D, 2D and 3D CSI spectra, but 4-, 16- and 100-fold faster, respectively, at an SNR cost of at most ~50%.

Theory: The conventional CSI reconstruction can be cast as a linear vector equation: $S_{\mathrm{M\times N}} = \mathrm{PE}_{\mathrm{M\times M}} \times \rho_{\mathrm{M\times N}}$ {1}, where S is the known signal matrix, PE is the phase-encoding operator and ρ are the unknown spectra. For 1D CSI, PE is the Fourier Transform (FT) operator; for 2D CSI, PE is the Kronecker product[6] of double FT operators; for 3D CSI, PE is the Kronecker triple product of FT operators. M is the number of total phase-encoding steps, and N is the number of time-domain data points. In CSI, Eq. {1} is solved for M unknown spectra from M known signals. For SLAM, we define C (<<M) compartments with identical CSI spectra from MRI and reduce the number of unknowns in Eq. {1} from M to C by means of dimensional reduction. For this we introduce auxiliary matrix *b* containing the *a priori* spatial information from MRI to eliminate identical rows in the ρ matrix: $S_{\mathrm{M\times N}} = PE_{\mathrm{M\times M}} \times {b^{-1}}_{\mathrm{M\times M}} \times b_{\mathrm{M\times M}} \times \rho_{\mathrm{M\times N}}$, {2}. The elimination process retains one unique SLAM spectrum for each compartment such that the dimension of $(b_{M\times M} \times \rho_{M\times N})$ is reduced from M to C, for which a reduced number of acquisitions M' (C≤M'≤M) will suffice. In theory, each SLAM spectrum closely approximates the average of all the CSI spectra in each compartment.

Experiment: SLAM is implemented as follows: (i) Acquire MRI; (ii) Segment MRI into C compartments and overlay on the CSI grid; (iii) Apply M' central k-space phase encodes; and (iv) Reconstruct the spectra using SLAM. 1D-, 2D-, and 3D-SLAM experiments were done in a 3T Philips MRI system on the human heart (^{31}P), brain (^{1}H), and a phosphate phantom (^{31}P), respectively. The compartments were: chest, heart and background (1D); scalp, brain, lateral ventricle and background (2D); and H_3PO_4, H_3PO_2 disk phantoms plus background (3D). SLAM spectra were reconstructed with central 4 (1D), 7x7 (2D) and 2x4x2 (3D) phase-encodes, and compared with compartmental average CSI spectra obtained from the whole datasets with 16 (1D), 32x25 (2D), and 10x20x8 (3D) phase encodes. The heart study was ECG-gated (TR=15.7s); the brain study was lipid/water suppressed (TE/TR=0.144/3s); and the phantom study had TR=0.72s.

Results: Fig. 1 shows ^{31}P spectra for the same-sized chest (a) and heart (b) compartments reconstructed from 1D CSI (blue) and SLAM (red). Fig. 2 shows 2D SLAM and CSI spectra from the same brain (a) and lateral ventricle (b) volume. Fig. 3 shows H_3PO_2 (a) and H_3PO_4 (b) phantom spectra reconstructed from 3D CSI and SLAM. The speedup for the 1D, 2D and 3D SLAM compared with CSI are 4-, 16- and 100-fold, respectively: the SNR cost is 14%,<30% and 50%.

Conclusion: This new SLAM method applied in 1D, 2D and 3D yields spectra hardly distinguishable from the compartmental average spectra obtained from conventional CSI, while offering dramatic reductions in scan time not seen before.

References: [1] Hu X, et al. MRM 1988;8:314-322. [2] Liang ZP, et al. IEEE TMI 1991;10:132-137. [3] von Kienlin M, et al. JMR 1991;94:268-287. [4] Dong Z, et al. MRM 2006;55;1447-1453. [5] Loffler R, et al. JMR 1998;134:287-299. [6] Van Loan CF. J Comp Appl Math 2000;8:85-100.

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Fig. 1: 1D cardiac ^{31}P MRS (same volume, SLAM 4 times faster).

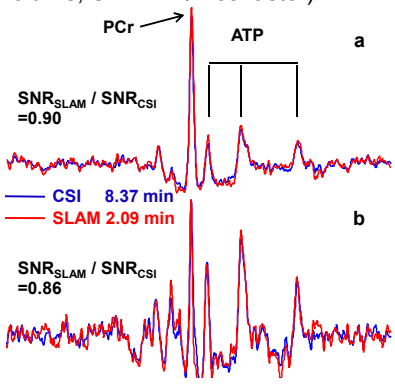

Fig. 2: 2D brain ^{1}H MRS (same volume, SLAM 16 times faster).

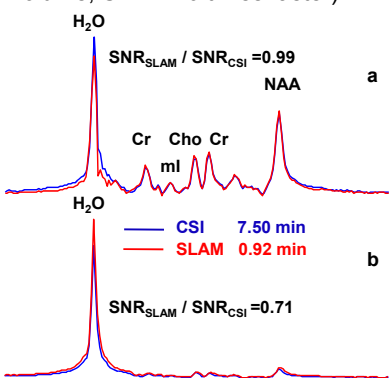

Fig. 3: 3D phantom ^{31}P MRS (same volume, SLAM 100 times faster).