Efficient 2D MRI Relaxometry via Compressed Sensing

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Target Audience: Clinicians and basic scientists who are interested in quantitative relaxometry, multi-dimensional relaxometry, compressed sensing, and noise floor correction.

Introduction: In recent years, important developments in and novel applications of multi-dimensional MR relaxation spectral methods have enabled the characterization of microstructure-related water dynamics in biological tissue.[1-3] Compared to the conventional 1D relaxation spectrum, more information can be obtained from the 2D relaxation spectrum, such as distinguishing between distinct compartments that are masked in the 1D spectra, measuring correlations between different relaxation parameters, characterizing proton exchange dynamics among compartments, etc. However, the amount of MR relaxation data and scan time currently required to reconstruct 2D-relaxation spectra makes this infeasible and impractical for most preclinical and clinical applications. Here we present a new MR pipeline that incorporates compressed sensing (CS) as a means to vastly reduce the amount of relaxation data needed for material and tissue characterization without compromising data quality using a recently published processing framework.[4] This method is validated using both synthetic and experimental MR data acquired in a well-characterized urea/water phantom and in a fixed porcine spinal cord.

Experiments: T_1-T_2 and T_2-T_2 relaxometry NMR were performed on a 7M urea-water phantom with an urea/water proton ratio of 20/80% using inversion-recovery (IR) filtered Carr–Purcell–Meiboom–Gill (CPMG) and relaxation exchange spectroscopy (REXSY). The latter consists of two CPMG pulse trains separated by a mixing time during which the magnetization is stored back along the longitudinal axis. T_1-T_2 MRI of the fixed porcine spinal cord was performed by an IR-preparation multiple spin echo (ME) sequence. All data were acquired on a 7T Bruker vertical-bore microimaging MR scanner.

Data Analysis: To remove the bias caused by Rician noise in the IR-ME MRI data, the noisy ME MRI magnitude data were first pre-processed by a framework previously proposed and validated to transform Rician distributed magnitude data to Gaussian-distributed data.[5,6] After processing the raw data, random samples were obtained with different acceleration factors, R (where $1/R$ is the fraction of the full data). Sub-samples were then reconstructed using CS and conventional reconstruction. 2D relaxation spectra from each sub-sample were then compared to the result obtained from the complete data set in the experiments or the ground truth in the simulations

Results:

(1) T_2-T_2 relaxometry NMR of urea/water phantom.

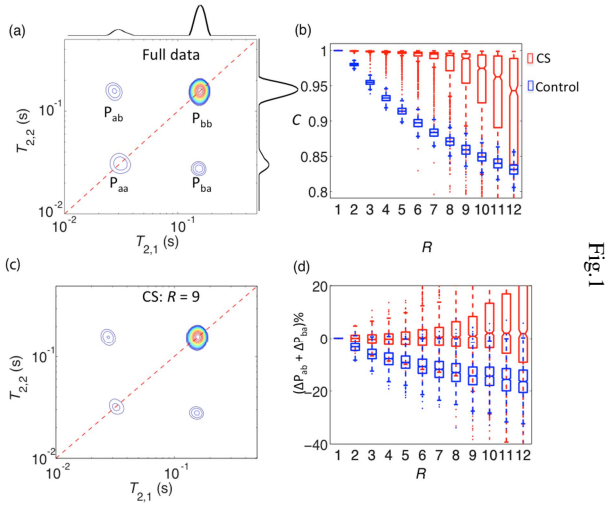

Fig. 1

(2) T_1-T_2 relaxometry MRI of the fixed porcine spinal cord

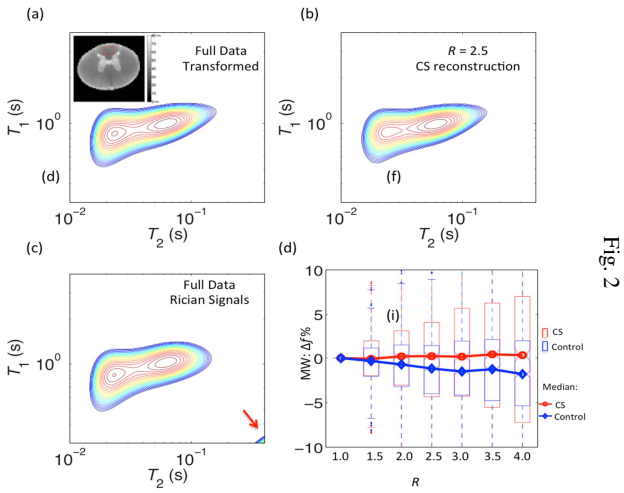

Fig. 2

At mixing time τ_m = 1000 ms, the total relative volume fraction of the off-diagonal peaks (P_{ab} and P_{ba}) is 15.1%, where the relative volume fractions of the non-exchanging urea and water peaks are 11.3% and 73.6% respectively (Fig. 1a). At $R \leq 9$, the correlation coefficients (C) between the CS reconstructed T_2-T_2 spectra and the one from ground truth data can be maintained as high as ≥ 0.989, which begins to fall quickly at $R \geq 10$ (Fig. 1b). In the control, the relative fraction of the off-diagonal peaks, $P_{ab} + P_{ba}$ is underestimated and the water peak P_{bb}, is overestimated by as much as 14.5% and 1.8% respectively at R = 9 (Fig. 1d). CS reconstruction successfully corrects these biases back to 1.1% (overestimation) and 0.36% (overestimation) though with slightly larger variance. Except for the precise reconstruction of each peak's relative fraction, the other relaxation parameters are also more accurate. For example, the geometric mean (gm)T_2 of the peak P_{ab} is underestimated by 8.2% and 3.1% at the first and second dimension in the control case at R = 9, while biases in the CS reconstruction are only 1.6% and 0.24% overestimation in these peaks.

References: 1. English A.E. et. al., *MRM*, 1991; 2. Saab G. et. al., *MRM*, 2001; 3. Dortch R. D. et. al., *MRM*, 2010; 4. Cloninger A. *SIIMS*, 2014; 5. Bai R. et. al., *JMR*, 2014; 6. Koay C. G. *JMR*, 2009.

Two broad peaks are observed in the T_1-T_2 spectra from the full data (pre-processed) with the myelin water (MW): f = 46.1%, gmT_2 = 23.8 ms and gmT_1 = 837 ms; and the intracellular/extracellular water (IEW): f = 53.9%, gmT_2 = 62.3 ms and gmT_1 = 993 ms. The noisy Rician signal introduces spurious peaks in the long T_2 regime (red arrow in Fig. 2) but the signal transformation scheme we use successfully corrects this artifact. CS performs adequately at R = 2.5, where the correlation coefficient is 0.97 and the contrast between the two peaks is preserved (93% for the CS, 93% for the full data and a single peak in the control). At R = 4.0, the two peaks are still visible although the correlation coefficient (0.91) is lower than the control (0.93) now. Interestingly, the CS reconstruction captures the MW relative fraction (bias $\leq$ 0.41%), where the underestimation can be as large as 1.8% in the control at $R \leq$ 4.0.

Discussions and Conclusions: A new MR pipeline designed to vastly reduce the amount of 2D relaxation spectra data via compressed sensing is proposed and demonstrated to preserve data quality. Except for the global correlations, the CS reconstruction yields spectra of comparable quality as assessed using local contrast between peaks, peaks amplitudes, relaxation parameters, etc. bringing the imaging of this important type of contrast closer to being realized in preclinical and clinical applications.