Accelerated Echo-Planar Correlated Spectroscopic Imaging in the Human Calf Muscle using Compressed Sensing

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Introduction – Localized Correlated Spectroscopy (L-COSY) has previously been shown to be a powerful tool in the study of lipid metabolism in human muscle [1]. Recently, a novel four-dimensional (4D, 2 spectral and 2 spatial) Echo-Planar based Correlated Spectroscopic Imaging (EP-COSI) technique was introduced that allows for the multi-voxel collection of L-COSY spectra in a single experiment [2]. Despite the improved acquisition speed from the echo-planar spectroscopic imaging (EPSI) readout, which simultaneously acquires 1 spatial and 1 spectral dimension (k_x and t_2), the minimum required scan times can still be considerably long due to the need to individually increment the remaining 1 spectral and 1 spatial dimensions (k_y and t_1), requiring on the order of 20 minutes. We show that the application of Compressed Sensing (CS) [3] can be used to accelerate the collection of the incremented dimensions in the EP-COSI sequence by reconstructing non-uniformly under-sampled datasets with only 33% of the original data. We show that the under-sampled datasets can successfully be reconstructed, preserving the important metabolic information present in the human calf muscles such as the detection and separation of both extra- and intra-myocellular lipids (EMCLs and IMCLs).

Methods – CS was simulated using fully sampled EP-COSI datasets acquired from the calf muscles of healthy (n=2) and diabetic volunteers (n=6). As the k_x and t_2 dimensions are sampled together by the echo-planar readout, the under-sampling was simulated in the remaining $k_y t_1$ plane. Non-uniform under-sampling was imposed by deleting data points according to a probability-weighted sampling mask as shown in Fig. 1a. The data was reconstructed using the Split Bregman method for l_1 regularized problems [4] which solves the unconstrained optimization problem

$$\min_m \|\nabla m\|_1 + \lambda \|F_u m - y\|_2 \qquad (1)$$

where ∇ is the gradient operator, m is the reconstructed data, $||x||_n$ is the l_n norm, λ is a regularization parameter, F_u is the under-sampled Fourier transform, and y is the under-sampled data. Equation 1 removes the artifacts due to the non-uniform under-sampling by minimizing the total variation (TV) while maintaining fidelity with the sampled measurements. For this study, only 33% of the original data was used in the reconstruction.

Results – Select spectra of the tibialis anterior muscle from a healthy and diabetic volunteer can be seen in Figs. 1b and 1c respectively. The splitting of the labeled creatine (Cr) diagonal peak at (3.9,3.9) confirms the muscle location, as the structure of the tibialis anterior muscle is known to exhibit residual dipolar couplings [2,5]. As can be seen in Fig. 1b, only cross peaks from the EMCLs (F_2 = 5.55ppm) are detectable, characteristic of healthy metabolism. Figure 1c shows the buildup of cross peaks from IMCLs (F_2 = 5.35ppm), indicative of abnormal lipid metabolism, as is characteristic in patients with diabetes. The EMCL and cross peaks from the olefinic protons are seen to be nicely resolved compared to the methylene and methyl protons (1.4ppm and 0.9 ppm respectively).

Discussion – Despite only using 33% of the original data, both reconstructed data sets show the expected metabolic features characteristic of both healthy and diabetic calf muscles. The EMCL and IMCL cross peaks from the olefinic protons are nicely resolved compared to the methylene and methyl which are typically used for EMCL/IMCL quantitation in 1D studies. The overall quality and resolution of the reconstructed spectra is comparable to the fully sampled dataset (not shown), indicating a successful implementation of CS in reconstructing the incremented spatial and spectral dimensions in the EP-COSI sequence.

Conclusion – We have shown that CS can successfully be applied to the EP-COSI sequence in the human calf, providing an acceleration factor of at least 3x. Such a reduction in scan time has the potential to reduce multi-dimensional spectroscopic imaging scan times well below the coveted 10-minute mark, bringing it closer to becoming a clinical reality.

References – [1] Velan *et al*. J. Magn. Reson. Imag. **25** 192-199 (2007). [2] Lipnick *et al*. Magn. Reson. Med. **64**, 947-956 (2010). [3] Donoho. IEEE Trans Info Theory. **52**, 1289-1306 (2006). [4] Goldstein *et al.* SIAM J. Imaging Sci. **2**, 323-343 (2009). [5] Kreis *et al*. J Magn Reson. SerB. 113, 103-118 (1996).

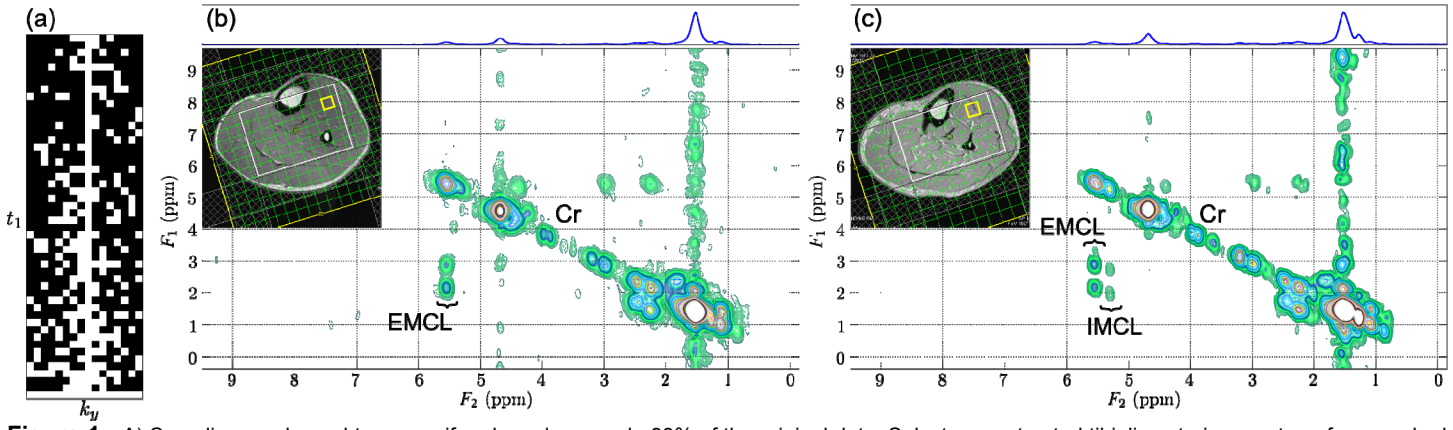

Figure 1 - A) Sampling mask used to non-uniformly under-sample 33% of the original data. Select reconstructed tibialis anterior spectrum from marked by the yellow box in the localized image taken from a B) healthy volunteer and a C) diabetic volunteer. The spectra are summed along the F_1 dimension to show the respective 1D spectrum.