

Accelerated Metabolic Imaging: Application of L1-SPIRiT to Hyperpolarized <sup>13</sup>C Parallel Imaging and Compressed Sensing MRSI

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**Introduction** Hyperpolarized <sup>13</sup>C MR is a powerful tool for studying metabolic processes *in vivo*. Combined with spectroscopic imaging techniques, this method enables monitoring of concentration and distribution of injected DNP pre-polarized <sup>13</sup>C substrates and downstream metabolic products. However, spatial coverage and resolution of such metabolic images are fundamentally limited by the rapid metabolism and T<sub>1</sub> relaxation, necessitating the development of fast data acquisition schemes. In this work, we investigated accelerating hyperpolarized <sup>13</sup>C spectroscopic imaging with L1-SPIRiT compressed sensing autocalibration parallel imaging [1]. An autocalibrating reconstruction method was chosen because, in hyperpolarized <sup>13</sup>C studies, acquiring accurate sensitivity maps through pre-scan is not possible. Here, a number of simulations were performed to quantitate the performance of SPIRiT on spectroscopic imaging data under various acceleration schemes.

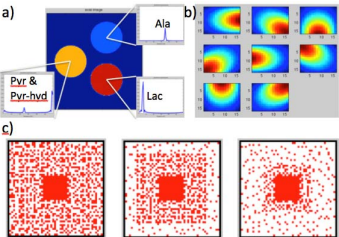
**Methods 1)** For initial investigation, a numerical phantom and coil sensitivity maps were simulated. We modeled data acquired with an 8-channel phased array receive coil and the MRSI pulse sequence described in [2]. k-space data of three circular phantoms were generated analytically using a Bessel function of the first kind and then smoothed with a 2D Hamming window to reduce the Gibbs ringing effect in the image domain. Each circle contains alanine (ala), lactate (lac), or a mixture of pyruvate (pyr) and pyruvate-hydrate (pyr-hyd). The time dimension of the data set was designed assuming a full echo acquisition, resulting in Lorentzian shaped spectra for each metabolite. k-space data (kx-ky-t) were Fourier transformed into the image domain (x-y-f), weighted by the coil sensitivity maps and then transformed back to k-space resulting in a matrix size of 64×64×59×8 (kx-ky-t-c). **2)** To evaluate the reconstructed image and noise performance, we tested both SPIRiT and traditional GRAPPA on a data set that was randomly under-sampled by a factor of 4 while keeping the center 16×16 in the kx-ky dimensions (overall factor of 3.4). Multiple image reconstructions were done over different kernel sizes (3×3, 5×5, 7×7 and 9×9). In the SPIRiT method, fully sampled data in the center part from all the time points (kf=1...59) were used to calibrate a single kernel and an iterative conjugate-gradient (CG) type optimization was used to solve the reconstruction problem. **3)** Hyperpolarized <sup>13</sup>C spectra are very sparse as there is virtually no background signal and peaks from metabolites are widely separated from one another at high fields (> 3T). Thus, enforcing sparsity in the reconstructed signal by L1-norm regularization could result in less noise amplification and possibly enable further acceleration in data acquisition. To demonstrate this capability, we prepared two other sets of randomly under-sampled data. One was under-sampled by a factor of 4.7 and the second with a factor of 6.4. Spectroscopic images were reconstructed using three algorithms: projection over convex set (POCS) SPIRiT, CG SPIRiT and L1 regularization SPIRiT. For this study, L1 penalty was enforced on the spectral dimension as simulated spectra itself were already sparse. Finally, all the results were compared using normalized root mean squared error (nRMSE) with the fully sampled reference image.

**Results 1)** Figure 1 shows the composition of the numerical phantom, coil sensitivity map and three random under-sampling patterns used in the simulation. **2)** In GRAPPA, larger kernels resulted in slightly better images at the cost of longer reconstruction time. However, GRAPPA tends to amplify noise in the pixels where other metabolites exist (Figure 2c), which can cause inaccurate metabolic mapping. For the CG SPIRiT reconstruction, the nRMSE value quickly reached its minimum around 12-14 iterations. Overall, SPIRiT showed less residual error over GRAPPA with better noise performance. This is because SPIRiT uses all the acquired data more efficiently compared to traditional GRAPPA method. **3)** Table 1 shows nRMSE values for different reconstruction done on various under-sampling schemes. All of the SPIRiT data shown used 12 iterations. The POCS method needed a few more number of iterations to reach the minimum nRMSE value compared to CG type algorithm. This data show that L1 regularization in SPIRiT can be used for highly accelerated data acquisitions with reliable quality in reconstructed image.

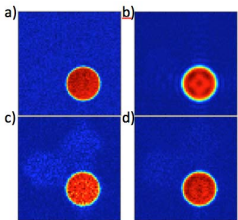
**Discussion** Accurate estimation of sensitivity map in hyperpolarized <sup>13</sup>C experiment is difficult. Thus autocalibrating reconstruction methods have advantages over explicit sensitivity-based reconstructions such as SENSE [3]. By exploiting both the coil sensitivity and signal sparsity in the spatial and spectral dimensions, higher acceleration in data acquisition compared to conventional spectroscopic imaging methods could be achieved. Here, we have shown that the application of SPIRiT on simulated hyperpolarized <sup>13</sup>C parallel imaging provided excellent noise performance and reduced artifacts in highly accelerated imaging schemes.

**References** [1] M. Lustig et al., Magn Reson Med 2010, 64:457-471. [2] S. Hu et al., Magn Reson Med 2010, 63:312-321. [3] A. Arjun et al., NMR Biomed 2009, 22:867-873.

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**Figure 1.** a) Numerical phantom with signal from four different metabolites. b) Coil sensitivity map of 8-channel phased array coils. c) Random under-sampling pattern used throughout the experiment. From left, a factor of 3.4, 4.7 and 6.4 under-sampling.



**Figure 2.** Lactate image of a) fully sampled data, b) randomly under-sampled data, c) GRAPPA reconstructed image and d) CG SPIRiT reconstructed image. Note the ringing in the under-sampled image. Both GRAPPA and SPIRiT used a [7,7] kernel window. SPIRiT shows better noise performance over GRAPPA.

	Factor of random under-sampling		
	3.4	4.7	6.4
GRAPPA	0.027	0.043	0.061
CG SPIRiT	0.021	0.027	0.035
POCS SPIRiT	0.026	0.033	0.042
L1 regularization SPIRiT	0.013	0.020	0.029

**Table 1.** nRMSE value for different factor of random under-sampling