Speeding up Dynamic Spiral Chemical Shift Imaging with Incoherent Sampling and Low-Rank Matrix Completion: Application in Hyperpolarized ^{13}C Metabolic Imaging

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Introduction: Hyperpolarization of ^{13}C-enriched substrates provides large SNR enhancements that make it possible to track metabolites and their products *in vivo*. However, the decay of polarization due to both relaxation and RF pulses creates a challenge, and it is advantageous to acquire images quickly using a minimum number of excitations. Spiral chemical shift imaging (spCSI) sequences are ideal for this situation, but their spectral bandwidth is limited by gradient strength and slew rate. The performance is reduced for ^{13}C compared with ^{1}H, as carbon's lower gyromagnetic ratio makes it necessary to acquire multiple spatial or spectral interleaves to fully sample the necessary k-space. On the other hand, advances in incoherent sampling and image reconstruction in MRI have provided ways to reduce the number of acquisitions by exploiting spatiotemporal correlations in time-resolved acquisitions[1,2]. In this work, we apply incoherent sampling and low-rank matrix completion-based reconstruction to dynamic spCSI imaging to achieve a significant increase in temporal and/or spatial resolution.

Methods: All measurements were performed with a clinical GE 750w 3T MR scanner (GE Healthcare, Waukesha, WI). A doubly tuned (^{1}H/^{13}C) quadrature coil (∅ = 80 mm, USA Instruments Inc., Aurora, OH) was used for both RF excitation and signal reception. Healthy male Wistar rats (251-343 g) were anesthetized with 1-3% isoflurane in ~1.5 L/min oxygen. The rats were injected in a tail vein with ~3 mL of [1-^{13}C]pyruvate (Pyr, ~80 or 125 mM), which was hyperpolarized to ~50% liquid state polarization via dynamic nuclear polarization using a SpinLab polarizer (GE Healthcare, Waukesha, WI).

We implemented a reconstruction algorithm based on low-rank matrix completion (LMRC) using iterative soft-thresholding of singular values to minimize the nuclear norm, i.e., the sum of singular values, subject to data consistency constraints as previously described[3,4]. This reconstruction scheme was applied to both retro- and prospectively undersampled data acquired after Pyr injection with 3D spCSI[5] (24 echoes, α_{exc} = 5.6°) using two parameter sets: (A) FOV = 80x80x60 mm^3, 16x16x12 matrix, 4 interleaves, SW=276 Hz; (B) FOV = 70x70x60 mm^3, 20x20x12 matrix, 8 interleaves, SW=280 Hz. Fully sampled data allowed temporal sampling at 6 and 12 second intervals, respectively. Undersampling by a factor of 2 was achieved by pseudo-randomly omitting spatial interleaves. Metabolic images of Pyr, lactate (Lac), and alanine (Ala) were calculated from their respective signals in absorption mode. LRMC reconstruction was compared to conventional reconstruction using 2D-NUFFT/1D-FFT.

Results and Discussion: Fig. 1a-c displays Pyr images from a single slice through the kidneys of a rat acquired with spCSI and reconstructed from a fully sampled and retroactively undersampled dataset. While the fully sampled data (a) produce clean images of metabolite concentrations, the undersampled data (b) display significant artifacts when processed with conventional reconstruction. The undersampled data reconstructed with LRMC (c) produce images closely matching the fully sampled images. LRMC removes the artifacts found in (b) and returns the signal/background ratio to ~1/√2 that of the fully sampled data (due to the two-fold reduction in total data points). Fig. 1d displays images of Pyr, Lac, and Ala from a single slice through the kidneys of a rat acquired with parameter set A, sampled with the full number of interleaves (left column), and acquired with parameter set B, but two-fold undersampled and reconstructed with LRMC (right column). Undersampling allows a higher spatial resolution to be achieved in the same amount of time as A (6 s) without deleterious effects on the measurement of dynamics (Fig. 1e). Fig. 1f displays a time course from data acquired with parameter set A, but two-fold undersampled and acquired every 3 seconds. In this case, undersampling provides higher temporal resolution of the dynamics.

Conclusion: The presented data demonstrate that LRMC reconstruction in combination with incoherent undersampling permits substantial reduction in minimum acquisition time of dynamic spCSI without significantly compromising image quality. The increased imaging speed can be leveraged to increase temporal and/or spatial resolution in hyperpolarized ^{13}C metabolic imaging. The approach is particularly useful when translating this methodology to the clinic as larger FOVs/matrix sizes are required.

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References: [1] S. G. Lingala et al., IEEE T-MI, 2011, 30:1042. [2] B. Zhao et al., IEEE T-MI, 2012, 31:1809. [3] E.J. Candes and B. Recht, Found Comput Math, 2009, 9:717. [4] R. Otazo et al., MRM 2014, 10.1002/mrm.25240. [5] S. Josan et al., NMR Biomed 2012, 25:993.

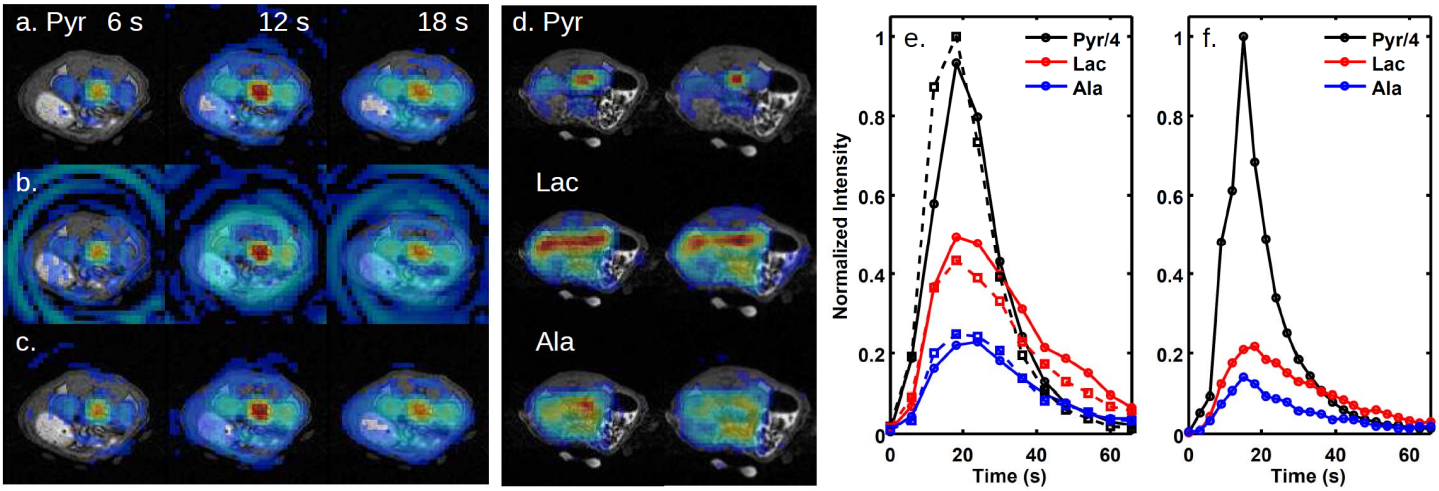

Fig. 1: (a-c) Pyruvate maps superimposed onto a proton MRI at 3 of 12 time points: a. Fully sampled data. b. Two-fold randomly undersampled data using conventional reconstruction. c. Two-fold randomly undersampled data reconstructed with LRMC. The images are displayed as √intensity to reduce the dynamic range. (d) Metabolite maps superimposed onto a proton MRI. Left column: fully sampled, 4 interleaves. Right column: two-fold undersampled from 8 interleaves. (e) Corresponding metabolite intensity within a kidney measured from fully sampled data (solid line) and undersampled data (dashed line). (f) Metabolite intensity within a kidney measured from an undersampled dataset randomly acquiring 2 of 4 interleaves.