

# Direct Estimation of Hyperpolarized Metabolites with IDEAL Spiral CSI

Jeremy Gordon<sup>1</sup>, Sean B. Fain<sup>1,2</sup>, and Kevin Johnson<sup>1</sup>

<sup>1</sup>Medical Physics, University of Wisconsin-Madison, Madison, WI, United States, <sup>2</sup>Radiology, University of Wisconsin-Madison, Madison, WI, United States

**INTRODUCTION:** Hyperpolarization can dramatically improve the signal from metabolic tracers, such as <sup>13</sup>C labeled molecules; however, the transient polarization must be used efficiently. Highly efficient acquisition trajectories, such as spirals, are well-suited to maximize utilization of hyperpolarization. Unfortunately, gains in efficiency are limited by off-resonance blurring, forcing the use of inefficient, short readout duration spirals for imaging [1]. Several techniques have been developed to mitigate off-resonance artifacts, including k-space IDEAL [2] and minimum-norm IDEAL [5], but these require simplifying approximations to enable processing. In this work, we develop a least squares technique for <sup>13</sup>C spectroscopic imaging that includes prior information from <sup>1</sup>H images to directly solve for chemically shifted species from raw data, using a derived method we call “Direct” IDEAL.

**THEORY:** Signal from <sup>13</sup>C can be modeled as the Fourier transform of N chemically shifted species:

$$s(\psi, \rho, t) = \int e^{-i\vec{k}\cdot\vec{r}} e^{i\psi(r)t} \sum_{i=0}^N \rho_i e^{i\Delta\omega_i t}$$

where  $\rho_i$  is the signal intensity from the  $i$ th species and  $\psi(r)$  is the field map at position  $r$ . Without the confounding field-map term, this is a linear problem. We propose to utilize separately acquired <sup>1</sup>H data to provide a known field map and region of support. With these known values, <sup>13</sup>C images can be estimated by minimizing the difference  $\|s(\rho, t) - d\|_2^2$  between the signal model and the data  $d$  using a least squares approach. As with other least squares approaches, accelerated imaging schemes such as parallel imaging or compressed sensing [3] are easily incorporated by modifications to the signal model.

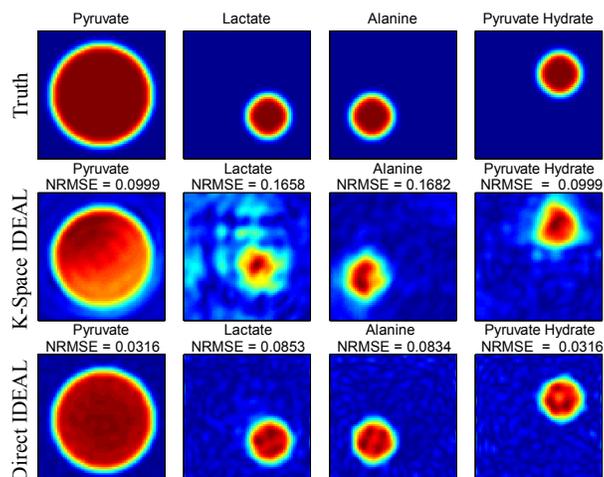
**METHODS:** Direct IDEAL was implemented in MATLAB (R2009b, The MathWorks, Natick, MA). Field maps were incorporated into signal equations using time-segmentation [4] and images were solved utilizing conjugate gradient minimization. Spiral <sup>13</sup>C sampling (single shot, 4 echoes/shot) was simulated for pyruvate and downstream metabolites with chemical shift frequency separations expected at 4.7T. SNR and metabolite ratios were calculated for Direct IDEAL and compared to k-space IDEAL. Normalized root-mean square error (NRMSE) between the digital phantom and reconstructed images was measured to assess reconstruction accuracy. Experimentally, <sup>1</sup>H data was collected with a spiral sequence on a 3T system (GE Healthcare, Waukesha WI) to assess the efficacy of the reconstruction algorithm. Images were collected from a <sup>1</sup>H phantom (DMSO, Si Oil, H<sub>2</sub>O) constructed to mimic the frequency separation of <sup>13</sup>C metabolites. Field maps were derived from a high BW Cartesian IDEAL acquisition and utilized in the spiral reconstruction. Additionally, data was retrospectively undersampled and reconstructed with compressed-sensing (CS) Direct-IDEAL. NRMSE and SNR measurements on the reconstructed datasets were used to quantify reconstruction accuracy and noise performance.

**RESULTS & DISCUSSION:** Simulations of k-space IDEAL and Direct IDEAL can be seen in Fig. 1. In the presence of noise and field inhomogeneities, Direct IDEAL has similar noise performance with superior B<sub>0</sub> demodulation. Quantitatively, the NRMSE is significantly lower for Direct IDEAL, indicating a higher degree of accuracy in the reconstruction. SNR and metabolite ratios from 50 noise realizations can be seen in Fig. 2. While the two reconstruction methods yield similar SNRs, metabolite ratios reconstructed with k-space IDEAL deviate significantly from the truth. Comparatively, Direct IDEAL metabolite ratios conform closely to the true values, which is essential for accurate metabolite maps and quantitative modeling. In Fig. 3, <sup>1</sup>H data acquired with a spiral sequence and reconstructed with either Direct IDEAL or a dataset retrospectively accelerated by a factor of 4 and reconstructed with CS Direct-IDEAL are compared using NRMSE to a fully sampled Cartesian acquisition. Both Direct IDEAL and the 4X undersampled reconstruction agree well with the fully sampled Cartesian dataset. The undersampled acquisition still provides comparable SNR and low NRMSE, even with 75% of the data retrospectively removed.

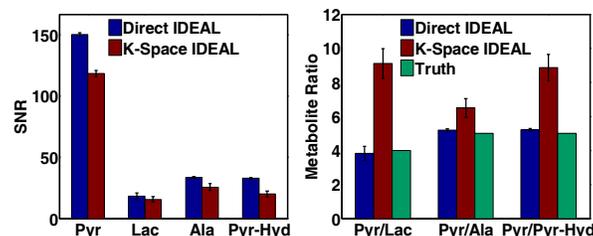
**CONCLUSION:** Direct IDEAL utilizes an iterative, least-squares approach to directly solve for chemically shifted species by constraining with an independently measured field map. Images of <sup>13</sup>C metabolites can be reconstructed directly with conjugate gradient minimization, enabling longer readout duration spirals that more efficiently utilize the hyperpolarized signal. NMRSE and SNR measurements on a digital phantom indicate that Direct IDEAL is both accurate with improved noise performance over k-space IDEAL. Furthermore, <sup>1</sup>H spiral images equivalent to an acceleration factor of 4 with CS compare well with fully sampled images, indicating compatibility with accelerated acquisition methods.

**References:** [1] Mayer et al., MRM 2011. [2] Brodsky et al., MRM 2008. [3] Schulte et al., ISMRM 2011. [4] Sutton et al., IEEE TMI 2003. [5] Weisinger et al., ISMRM 2010.

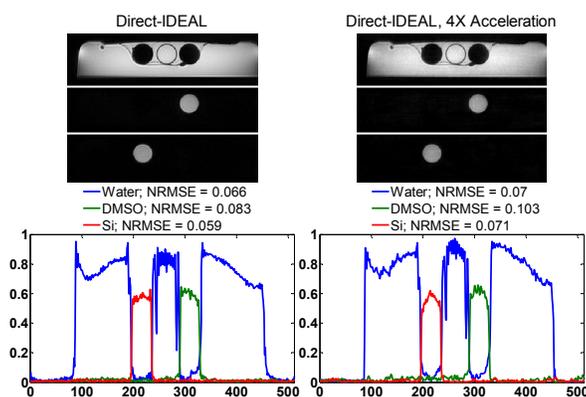
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**Figure 1.** Comparison of a digital metabolite phantom (top) to metabolite images reconstructed with k-space IDEAL (middle) and Direct IDEAL (bottom). Simulations were in the presence of B<sub>0</sub> inhomogeneities (50 Hz) and 1% noise in k-space. Note the better NRMSE and robustness to B<sub>0</sub> inhomogeneities for the proposed Direct IDEAL.



**Figure 2.** SNR (left) and metabolite ratios (right) for k-space IDEAL and Direct IDEAL after simulations with 50 noise realizations. While both reconstruction methods yield comparable SNRs, the metabolite ratios from k-space IDEAL deviate significantly from the truth.



**Figure 3.** Comparison of a fully sampled Direct IDEAL dataset individually reconstructed for each species with a 4X accelerated dataset reconstructed with CS Direct IDEAL (top) and their respective line profiles (bottom). At this acceleration factor, high SNR, low NRMSE, and off-resonance suppression are still retained.