Development of Computational Methods for B1-Corrected Hyperpolarized C-13 MRI Human Studies

Philip Lee[1,2], Hsin-Yu Chen[2], Jeremy W Gordon[2], Peder EZ Larson[1,2], Mark Van Criekinge[2], Michael Ohliger[2], Duan Xu[1,2], John Kurhanewicz[1,2], Robert A Bok[2], Pamela Munster[3], Daniel B Vigneron[1,2]

[1]UCB/UCSF Bioengineering Graduate Group, San Francisco, CA; [2]UCSF Departments of Radiology & Biomedical Imaging and Medicine, San Francisco, CA; [3]UCSF Department of Medicine, San Francisco, CA

Background and Motivation:

Hyperpolarized (HP) ^{13}C MR spectroscopy (MRS) allows for quantitative monitoring of metabolites in tissues. Using HP ^{13}C-pyruvate, the rate of conversion between pyruvate and lactate (k_{PL}) can be computed per voxel in patients with progressing liver metastases. However, ^{13}C transmit/receive (T/R) coils do not have a homogeneous B1 excitation profile, resulting in a gradient of decreasing flip angles for voxels increasingly farther away from the coil. In computing the k_{PL} for each voxel, the nominal flip angle needs to be corrected based off the coil's B1 excitation profile. The goal of this project was to develop and test a novel computational framework to correct HP k_{PL} images for B1 variations in human studies.

Methods and Results:

A 56-year-old male patient with pancreatic neuroendocrine tumor liver metastases was imaged on August 28, 2018 with HP ^{13}C-pyruvate. An axial T1-weighted LAVA image with the target lesion highlighted is shown in **Figure 1(a)**. The ^{13}C T/R coil was placed on the patient's right side, closest to the lesion. ^{13}C-pyruvate and ^{13}C-lactate signals were acquired with an echoplanar spectroscopic imaging sequence over 1 minute with a temporal resolution of 3 seconds and a spatial resolution of 1.2 cm voxels. In MATLAB, each metabolite peak was integrated over time. An SNR filter with an empirical threshold of 1.2×10^{11} AU was applied to remove noise voxels. Similarly, voxels outside of the coil's sensitive region were removed.

The excitation profile of the ^{13}C T/R coil was previously acquired with a phantom. In MATLAB, using coil fiducial markers, the excitation profile was rotated to its orientation during the patient scan and shown in **Figure 1(b)**. The adjacent color bar indicates the scaling factor applied to the nominal flip angle for each voxel. The nominal flip angles for pyruvate and lactate of 10° and 20°, respectively, were scaled for individual voxels based off the excitation profile. With the corrected flip angles and the SNR-filtered ^{13}C-pyruvate and ^{13}C-lactate signals, a k_{PL} image was computed using an inputless two-site model [Larson et al. NMR Biomed 2018], both with and without the corrected flip angles, shown in **Figure 1(c)** and **(d)**, respectively. **Figure 2** displays the percent changes after applying the flip-correction. Voxels with >150% change are binned together.

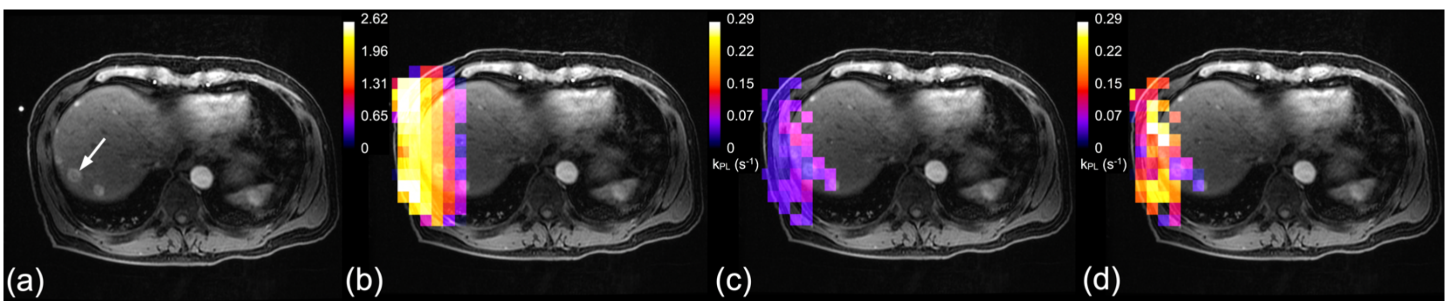

Figure 1. (a) An axial T1-weighted LAVA image with the target cancer lesion highlighted. ***(b)*** The excitation profile of the ^{13}C T/R coil. ***(c)*** k_{PL} values without the flip-correction. ***(d)*** k_{PL} values with the flip-correction.

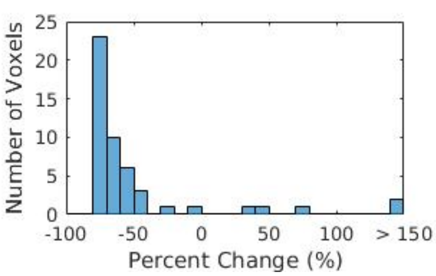

Figure 2. A histogram of the percent changes after applying the flip-correction.

Discussion:

In this study, most tissue voxels in close proximity to the coil received a higher flip angle than intended. The findings agree with simulations [Figure 4, Larson et al. NMR Biomed 2018] where over-flip leads to an underestimation of k_{PL}, whereas under-flip leads to overestimation. The B1 correction methods developed in this study can improve quantification of metabolism in human cancer.

References:

[1] Larson et al. NMR Biomed 2018. [2] Ohliger et al. ISMRM 2016 Abstract.