Development of Computational Methods for B_1-Corrected Hyperpolarized ^{13}C MRI Human Studies

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Highlights:

Voxel-wise transmit B_1 field correction for hyperpolarized ^{13}C MRSI scans was developed and applied, yielding a more accurate quantification of pyruvate to lactate conversion rates (k_{PL}). The corrected k_{PL} estimations agree with simulations where over-flip leads to an underestimation of k_{PL}, whereas under-flip leads to overestimation.

Background and Motivation:

Hyperpolarized (HP) ^{13}C MR spectroscopic imaging (MRSI) enables quantitative monitoring of enzyme-catalyzed metabolism in human subjects. Using HP [1-^{13}C]pyruvate, the rate of conversion of pyruvate to lactate (k_{PL}) via lactate dehydrogenase (LDH) can be computed per voxel in patients with progressing liver metastases. However, ^{13}C surface transmit/receive (T/R) coils do not have a homogeneous B_1 excitation profile, resulting in a gradient of decreasing flip angles for voxels increasingly farther away from the coil. In calculating the k_{PL} for each voxel, the nominal flip angle can be corrected based off the coil's B_1 excitation profile. The goal of this project was to develop and test a novel computational framework to improve k_{PL} accuracy using B_1^+ correction in human studies.

Methods and Results:

Data from three patients are presented in **Table 1** with a representative case shown in **Figure 1**. The patients had liver metastases from varied cancer origins as listed in **Table 1**. For each scan, we acquired an axial T_1-weighted spoiled gradient-echo (LAVA) anatomical reference, as shown in **Figures 1(a)**, with the target lesion highlighted. In each scan, the ^{13}C T/R coil was placed on the patient's abdomen on the side closest to the target lesion to ensure coverage by the coil's T/R field. ^{13}C-pyruvate and ^{13}C-lactate signals were acquired with a 2D echoplanar spectroscopic imaging (EPSI) sequence over 1 minute with a temporal resolution of 3 seconds and a spatial resolution of 1.2 cm isotropic voxels.

In MATLAB, the spectral data were zero- and first- order phase corrected. Then, each metabolite was quantified as area under its spectral peak. An SNR filter with an empirically-determined threshold was applied to remove noise voxels. Similarly, voxels outside of the coil's sensitive region were excluded. The excitation profile of the ^{13}C T/R coil was previously measured from a phantom scan. In MATLAB, the previously measured excitation profile was aligned to the ^{13}C image based on fiducial locations (indicated with yellow dots) during the patient scan and shown in **Figures 1(b)**. The adjacent color bar indicates the scaling factor relative 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 to reflect the excitation profile. The k_{PL} maps were computed using an inputless two-site model [1]. The k_{PL} maps before and after the flip angle correction are shown in **Figures 1(c)** and **1(d)**, respectively. The k_{PL} values for selected voxels are also summarized in **Table 1** along with the percent difference.

Discussion:

The figure-8 coil provided adequate transmit power over the metastases despite B_1 inhomogeneity. In this study, over-flip led to an underestimation of k_{PL} (e.g. a -43.46% underestimation in Scan #2) whereas an under-flip led to overestimation (e.g. a +54.90% overestimation in Scan #2), which agree with simulations [1]. The B_1 correction methods developed in this study can improve quantitative accuracy of metabolism in human cancer. In future studies, we plan to utilize a fast B_1-mapping scheme for patient HP ^{13}C-pyruvate MRI [2].

References:

[1] Larson et al. NMR Biomed 2018.
[2] Tang et al. MRM 2019
[3] Ohliger et al. ISMRM 2016 Abstract.
4]. Sun et al. MRM 2018.

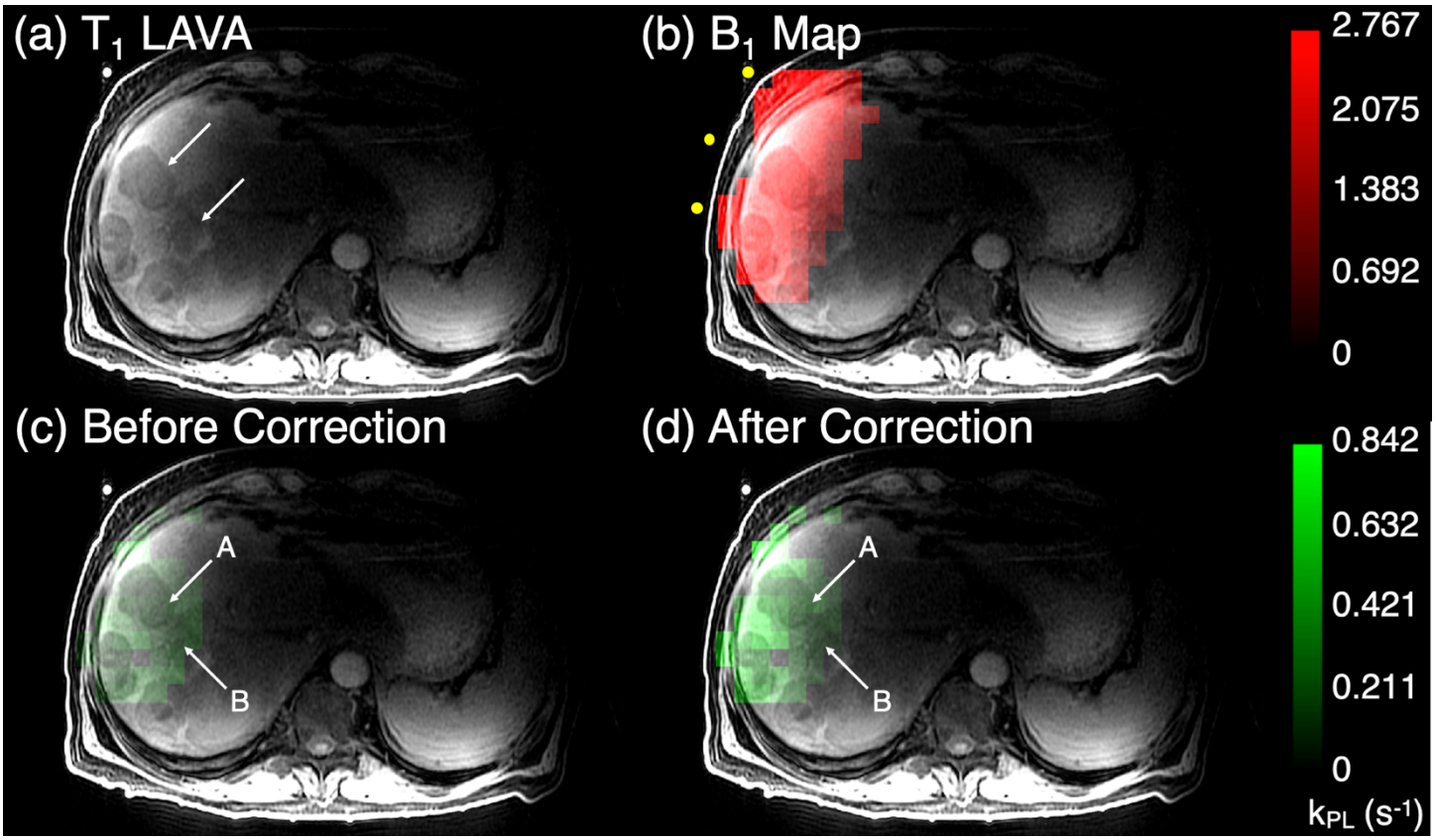

Figure 1. Scan #2 is shown in this figure. ***(a)*** An axial T1-weighted LAVA image with the target cancer lesions highlighted. ***(b)*** The excitation profile of the ^{13}C T/R coil. ***(c)*** k_{PL} values before the flip angle correction. ***(d)*** k_{PL} values after the flip angle correction. Over-flipped tumor voxel A had an initial k_{PL} estimation of 0.055 s^{-1} but was corrected to 0.097 s^{-1}. Under-flipped tumor voxel B had an initial k_{PL} estimation of 0.099 s^{-1} but was corrected to 0.064 s^{-1}.

Scan #	Cancer Origin	Flip Correction Scaling	k_{PL} Before Correction (s^{-1})	k_{PL} After Correction (s^{-1})	% Difference
1	Neuroendocrine	1.00	0.054	0.054	0.00
		1.47	0.043	0.081	-46.10
		1.90	0.032	0.090	-65.06
2	Cholangiocarcinoma	*1.47*	*0.055*	*0.097*	*-43.46*
		0.70	*0.099*	*0.064*	*+54.90*
		1.57	0.063	0.126	-50.25
3	Cholangiocarcinoma	1.70	0.026	0.059	-56.94
		1.07	0.027	0.029	-8.50
		1.10	0.030	0.034	-12.82

Table 1. Selected voxels with their specific flip correction scaling factors and their estimated k_{PL} values before and after the correction. A voxel with a scaling factor above 1.00 was over-flipped, that is, it experienced a flip greater than the nominal flip angle. Hence, its flip angle needed to be scaled higher. Voxels that are highlighted in the above figure are italicized.