

# Reproducibility Evaluation of Spatially Resolved Liver $^{31}\text{P}$ Metabolism Using a Dual Tuned 8-channel $^{31}\text{P}/^1\text{H}$ Coil

A. Panda<sup>1,2</sup>, S. R. Jones<sup>1,2</sup>, and U. Dydak<sup>1,2</sup>

<sup>1</sup>School of Health Sciences, Purdue University, West Lafayette, Indiana, United States, <sup>2</sup>Department of Radiology and Imaging Sciences, Indiana University School of Medicine, Indianapolis, Indiana, United States

**Introduction:** A multi-channel phased-array  $^{31}\text{P}$  coil can be used to acquire regional changes in the  $^{31}\text{P}$  metabolite concentration of the whole liver [1]. This information can then be used for diagnosis and follow-up of various liver diseases [2]. However, changes in the placement of the coil position, separation between the anterior and posterior coils, and spectroscopic grid placement during the scan can significantly affect the acquired data [3]. In this abstract we present a preliminary investigation on quality and coverage of a dual-tuned 8-channel phased-array  $^{31}\text{P}/^1\text{H}$  coil presented in [1]. The aim of this work was to examine the methods (acquisition and processing) to minimize data variability from coil placement and spectroscopic imaging setup, correct for coil sensitivities, and evaluate variability in the data from one scan to another for whole liver  $^{31}\text{P}$  2D MRSI.

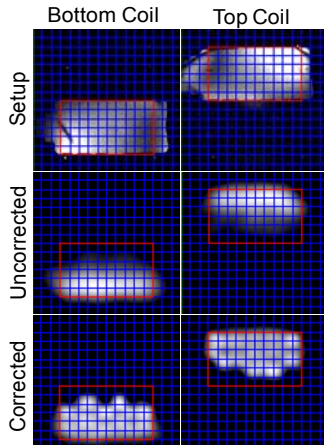


Figure 1: Uncorrected and corrected sensitivity maps for the top and bottom coil.

sequence: TE 2.3ms, TR 1s, FOV 400x400x30 mm<sup>3</sup>, nominal voxel size 25x25x30 mm<sup>3</sup>. Each FID was acquired with 2048 points and a bandwidth of 5000 Hz. The acquisition took about 24 min for 30 weighted averages. The first point of each FID was used to determine the relative phases of each coil and to phase adjust the data before combining the signal. An exponential filter of 25 Hz line-broadening and first order phase correction was applied to the combined signal.

Coil sensitivity correction maps for both the anterior and posterior coil plates (each containing four  $^{31}\text{P}$  channels) were computed individually by calculating the area under the peak from the  $^{31}\text{P}$  spectrum of a homogenous 10 liter 25 mM potassium phosphate monobasic phantom.

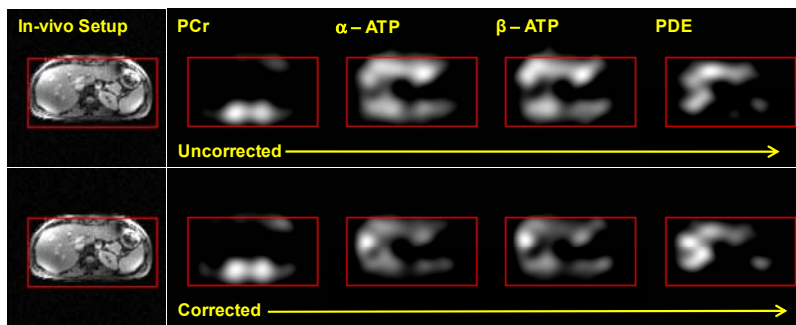


Figure 3: Uncorrected and Corrected MRSI in-vivo data.

and corrected sensitivity maps obtained for the anterior and posterior plates of the coil. Figure 2 shows the results of this sensitivity correction on the full phantom data. The sensitivity map analysis shows that usable data can be obtained for a maximum depth of 18 cm. Figure 3 shows the results of coil sensitivity correction on *in vivo* data. We see a moderate increase in the signal at the middle and decrease in the noise at the edges after the correction. From data variability analysis it was concluded that within 5 cm of either of the coils the relative concentrations are within 20% of each other. However, farther away the variability increases to about 40% between two scans. Correction of coil sensitivities seems to have little to no effect on correcting for the variability.

**Conclusion:** Various techniques that have worked successfully in minimizing the data variability from coil placement and spectroscopic planning are presented. Effects of coil sensitivity and a possible algorithm to correct for it are discussed. Correction of sensitivity had a moderate improvement on signal for *in vivo* data, but did not change the variability between two scans. The metabolite concentration data from voxels closer to the coil showed less variability than voxels farther away in longitudinal scans, due to the higher SNR of spectra closer to the coil. Improving the SNR with 3D CSI might give a better reproducibility between scans.

**References:** [1] A. Panda et al., Proc. ISMRM 2009, 17:475; [2] S. Solja et. al. Liver International, Vol. 25, 2005; [3] J. James et al., Proc. ISMRM 2009, 17:615.

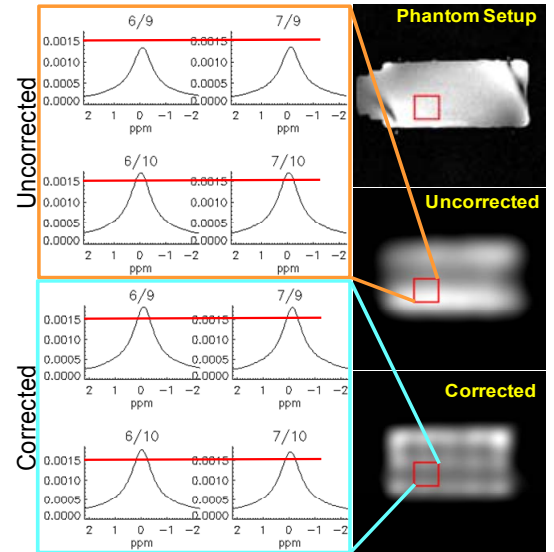


Figure 2: Uncorrected and corrected MRSI for a Phantom.

**Results/Discussions:** Figure 1 shows the original uncorrected