# HYBRID PROTON/CARBON CONSTRAINED IMAGE RECONSTRUCTION FOR HYPERPOLARIZED METABOLIC IMAGING

Andreas Sigfridsson<sup>1</sup>, Kilian Weiss<sup>1</sup>, and Sebastian Kozerke<sup>1</sup>

<sup>1</sup>Institute for Biomedical Engineering, University and ETH Zurich, Zürich, Switzerland

### Introduction:

Spectroscopic magnetic resonance imaging of hyperpolarized compounds is a promising way of probing metabolic pathways in the in-vivo heart [1]. Despite many advances in fast spectroscopic imaging [2], spatial resolution remains limited by the constrained time-span of image acquisition and the rapid decay of the hyperpolarized signal. A particular challenge arises when using hyperpolarized pyruvate for cardiac metabolic imaging as the pyruvate signal in the blood pools may contaminate myocardium and hence can compromise kinetic modeling.

In the present work the method of spectral localization by imaging (SLIM) [3] is incorporated into image reconstruction to improve the spatial response of spectroscopic imaging of hyperpolarized substances. Using computer simulations and *in-vivo* data acquired in rat hearts upon injection of hyperpolarized  $[1-1^{13}C]$  pyruvate it is demonstrated that contamination from blood pool signals can be reduced by taking into account high-resolution proton images as a constraint in reconstruction.

## Methods:

<u>Theory</u>: The image is decomposed into separate compartments representing regions of the same signal origin (Fig. 1). The contributions to each point in the acquired k-space from each region is computed as

$$g_{ij} = \sum_{\text{compartment i}} e^{-ii}$$

for k-space position i and compartment j, and spatial position r. For each compartment j, only the spatial positions inside a compartment as defined based on the high resolution proton images are considered. Expressing the measurements in matrix form, P = GC, with P being the measured k-space data with elements  $p_i$  and C being the signal intensities in the compartments with elements  $c_j$ , the signal intensities can be recovered by solving this system of linear equations according to:

$$C = \left(G^{H}G\right)^{-1}G^{H}P$$



*Fig. 1.* Segmentation into three compartments.

Simulation: A segmentation of a rat heart (Fig. 1.) into myocardium, left and right ventricular blood pools was combined with the time curves obtained from a perfusion MRI measurement of a human heart to generate a synthetic data set. The segmentation was done on a 256x256 matrix covering a field of view of 60 mm, and the resulting data set consisted of 30 time points. From this data set, a *k*-space corresponding to a 30x60 matrix was extracted, and signal levels was computed both using the presented SLIM approach and by averaging within a region of interest (ROI).. The ROI-averaging approch consisted of Hamming-filtering and zero-filling the 30x60 *k*-space into a 256x256 matrix, followed by Fourier transform and averaging of the signal in the myocardial compartment. *In-vivo* measurements: The technique was evaluated on data acquired from a rat heart in a 9.4 T Bruker BioSpin 94/30 MRI system. The data consisted of a self-gated proton image of the same slice angulation and field of view as a dynamic carbon imaging sequence after injection of hyperpolarized  $[1-1^{13}C]$  pyruvate. The carbon imaging sequence included a spectral-spatial excitation pulse [2,4] that excited the slice with pyruvate, lactate and bicarbonate in an interleaved fashion with flip angles 10, 70 and 70 degrees, respectively. The time between each successive image was one second. The carbon imaging sequence used a matrix of 30x60, for a spatial resolution of 2x1 mm<sup>2</sup>.

#### **Results**:

The simulation time curves are shown in Fig. 2. The presented SLIM method yields accurate dynamic appearance (relative root-mean-square (rRMS) error 2%), whereas conventional ROI-averaging is clearly influenced by signal contamination from both the right and the left ventricle (rRMS error 23%). In the *in-vivo* experiment, the ROI-averaging technique produced higher values for the pyruvate compartment, compared to the SLIM technique (Fig. 3). This might be explained by contamination from the high pyruvate signal in the blood pool. The lactate and bicarbonate signal levels for both methods are comparable.

#### Discussion:

The data indicates that the SLIM approach may be less sensitive to the blood pool signal *in-vivo*. Issues related to inaccurate segmentation due to motion may be addressed by using a cardiac triggering during the carbon acquisition, and B1 field inhomogeneities may also be incorporated in the reconstruction step [5]. The SLIM technique holds potential in the setting of hyperpolarized metabolic imaging, where the spatial resolution is low and signal contamination compromises analysis of the metabolic processes. ROI-averaging (solid) vs SLIM (dashed)

#### References:

- 1. Golman et al., MRM 2008;59:1005–1013.
- 2. Cunningham, et al., JMR 2008; 193:139-146.
- 3. Hu et al., MRM 1988;8:314-322
- 4. Pauly et al., MRM 1993;29:376-782.
- 5. Löffler et al., JMR 1998;134:287–299.







Time [s] Fig. 3. In-vivo data. The ROI-averaging approach yields higher signal levels for the pyruvate, which could indicate contamination from the blood pool signal. The lactate and bicarbonate signal levels are comparable for both techniques.