

Contamination reduction in the reconstruction of SLIM (CORRECT-SLIM) and its application to quantitative cardiac ^{31}P -CSI

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Purpose:

Usually spectra encoded by chemical shift imaging (CSI) are reconstructed using a Fourier transform to a regular grid of pixels or voxels. In contrast to that Spectral Localization by IMaging (SLIM) [1] takes the shape of different compartments (organs) into account as a prior knowledge and determines the spectra for these irregularly shaped compartments. Spectral Localization with Optimal Pointspread function (SLOOP) [2] clarified the spatial origin of the reconstructed SLIM signals by adding the concept of spatial response functions and proposed criteria to optimize the acquisition. The purpose of this work was to propose a method that takes advantage of the knowledge of the spatial response function to reduce contamination in the reconstruction of SLIM. Furthermore the method was applied to quantitative cardiac ^{31}P spectroscopy where signal contaminations from the chest wall pose a severe problem.

Methods:

CORRECT SLIM uses the knowledge of the spatial response function of a SLIM/SLOOP reconstruction to reduce the possible contamination from an adjacent compartment. Figure 1 illustrates the basic idea of CORRECT SLIM for the example of human myocardial spectroscopy. Figure 1a shows an image of a short axis slice through the left ventricle of a healthy volunteer. In figure 1b, the segmentation of this slice into compartments like left ventricular (lv) myocardium, lv blood, right ventricular (rv) blood etc. is demonstrated. The spatial response function of the SLIM/SLOOP reconstruction for lv myocardium is illustrated in figure 1c. Extended regions of the chest wall contribute to the myocardial signal (1d). The aim of a myocardial signal without contamination from the chest wall could be reached if a solution corresponding to the SRF of 1d could be subtracted from the SLIM solution. Because of the limited resolution of the CSI experiment and the orthogonality of the difference to the SLIM/SLOOP solutions, the solution corresponding to the SRF of 1d has to be approximated by another one shown in 1e. By subtracting the result corresponding to 1e from the SLIM/SLOOP solution (1c) a CORRECTED SLIM solution (1f) is created. Iteratively the contamination of CORRECT SLIM solution can be further reduced by subtracting the approximated myocardial SRF in the compartment of the chest wall from the previous CORRECT SLIM step.

CORRECT SLIM was implemented using IDL and tested on 15 ^{31}P 3D CSI data sets of healthy volunteers (age 52 ± 11.2 years, min 31, max 67 years) using 3 iterations. Using an external standard as a reference the metabolite concentrations of PCr and gATP have been quantified absolutely.

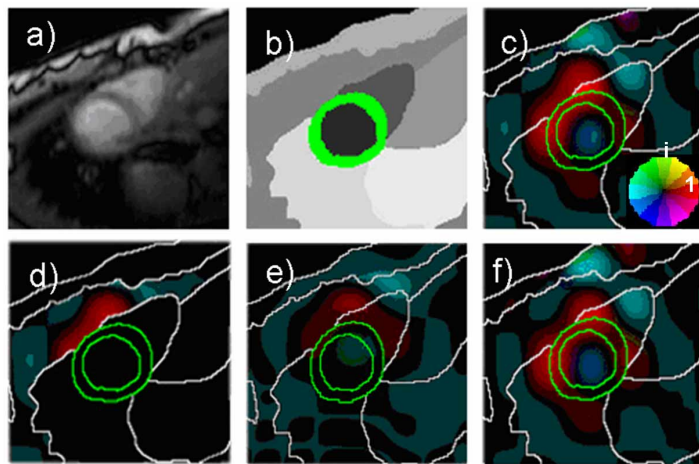


Fig 1: a) short axis view of the heart, b) segmentation into compartments, c) SRF of the SLIM/SLOOP reconstruction, d) spatial origin of chest wall contamination to the myocardial SLIM/SLOOP spectrum, e) low resolution approximation of the contamination shown in 1d, f) SRF of the CORRECT SLIM reconstruction

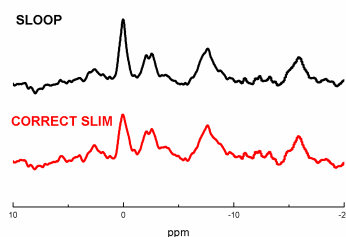


Fig 2: Myocardial ^{31}P spectra reconstructed by SLIM/SLOOP or CORRECT SLIM, respectively.

Results:

For human myocardial ^{31}P spectroscopy CORRECT SLIM could decrease the maximum contamination (normalized integral of the SRF) from the chest wall by $56.2\% \pm 7.6\%$ compared to the SLIM/SLOOP reconstruction. An example of resulting myocardial spectra is shown in figure 2. In all spectra the measured PCr concentration is $11.3\% \pm 38.1\%$ smaller for CORRECT SLIM compared to SLIM/SLOOP while for gATP a decrease of $9.3\% \pm 28.5\%$ could be observed. The absolute values changed for PCr from (values in mmol/kg wet weight) 8.7 ± 2.5 to 7.2 ± 2.6 and for ATP from 4.6 ± 0.9 to 4.2 ± 1.4 .

Conclusion:

CORRECT SLIM allows to decrease the contamination from neighbouring compartments in CSI spectra. In the example of myocardial ^{31}P spectroscopy the signal contamination from the chest wall was significantly reduced. The standard deviation for the absolute PCr and ATP values could not be reduced.

References:

- [1] Hu XP, Levin DN, Lauterbur PC, Spraggins T. Magnetic Resonance in Medicine 8: 314-322 (1988)
- [2] von Kienlin M, Mejia R. Journal of Magnetic Resonance 94: 268-287 (1991)