3-D Prospective Motion Correction for MR Spectroscopy

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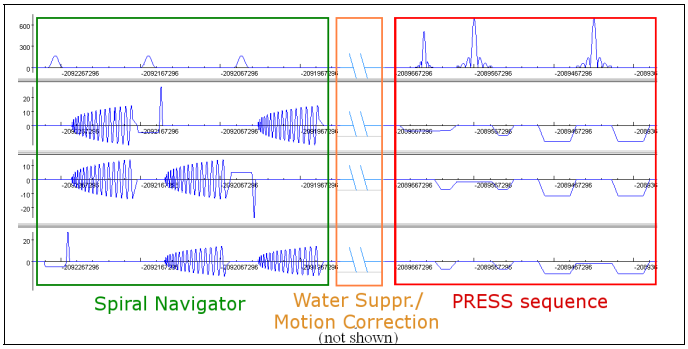
INTRODUCTION

Spectroscopy scans generally require averaging (over minutes) to obtain acceptable signal-to-noise ratio (SNR). Patient motion compromises the quality and reliability of the resulting spectra. Such concerns are particularly acute with subjects who have difficulty holding still, for instance young children or adults who are in pain or confused. Therefore, we implemented a single-voxel ^{1}H MR spectroscopy sequence with adaptive motion-correction based on the 3-dimensional prospective motion correction module for brain scans described in [1].

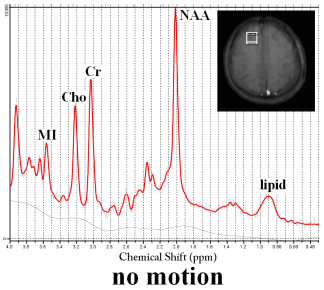
METHODS

We incorporated spiral navigators into a point-resolved spectroscopy (PRESS) [2] sequence (TE/TR=30/3000ms, BW=1.2kHz, 64 averages). Immediately prior to the water suppression module, three orthogonal, low-flip angle, low-resolution (32x32) spiral navigator scans are acquired. Navigator image reconstruction and motion estimation are performed during the water suppression module. The six rigid-body parameters (x, y and z translations and rotations) are estimated based on the navigator images using an extended Kalman filter [1, 3]. The effects of non-rigid motion are minimized by masking out areas, such as the neck and jaw, that can move non-rigidly with respect to the brain. For each TR period, the orientation and location of the MRS voxel are updated in order to maintain a constant voxel position relative to the (moving) brain. The pulse sequence is shown in the figure to the right. *In-vivo* studies were performed using three modes: (1) *baseline* without subject motion, (2) *non-navigated* scan with slow head rotation right to left (≈10°) and (3) *navigated* scan with approximately the same motion as in (2).

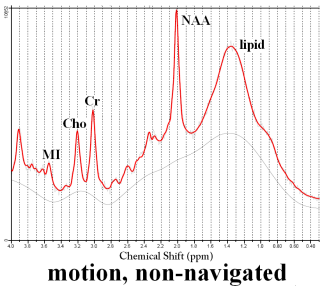


RESULTS

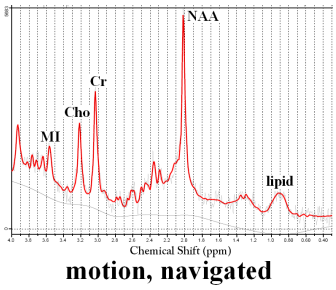
The figures below show right frontal white-matter spectra for the three cases: no motion (left), non-navigated with motion (center) and navigated with motion (right). The most notable difference between the two scans with motion is the large lipid peak in the non-navigated spectrum, caused by intersection of the (stationary) voxel with the skull / scalp for some of the larger rotations. The Table shows the percentage change of metabolite ratios relative to the no-motion case (baseline, or BL). The major metabolite ratios for the scan with motion compensation are within typical fitting errors (<8%, Cramer-Rao bounds), whereas non-navigated data show substantially larger differences (>10%). The total creatine line widths for the scan without motion and that with navigation are similar (0.032 and 0.038 ppm), whereas the line width is impaired when motion is present without navigation (0.048ppm).



no motion



motion, non-navigated



motion, navigated

	Non-navigated	Navigated
NAA/Cr (%BL)	13.5	-6.56
Cho/Cr (%BL)	-2.79	-3.98
MI/Cr (%BL)	-13.0	-7.65
Lipids/Cr (%BL)	+357	-49.8

DISCUSSION

The navigated spectrum is qualitatively and quantitatively very similar to the spectrum without motion, both in terms of metabolite ratios and line width. The absence of a large lipid peak in the navigated scan demonstrates that the voxel maintained its position relative to the (moving) brain, and therefore had no significant contributions from the skull. While the SNR was somewhat reduced in the navigated spectrum, the SNR can probably be recovered by correcting for phase errors due to residual motion within each voxel selection (PRESS) module. Conversely, the non-navigated spectrum is of poor quality and shows lipid contamination, a distorted baseline, and significant differences in metabolite values and poorer line width relative to the baseline scan. Consequently, the proposed MRS sequence with adaptive motion correction can improve spectral quality and reliability in the presence of subject motion.

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