Navigators Improve Accuracy of Quantitative Sodium MR Imaging Compromised by Head Motion During with Long Acquisition Times

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Purpose: Quantitative sodium (^{23}Na) MR imaging [1] provides valuable measurements of early local changes of cell density in applications such as monitoring the response of brain tumors to fractionated radiation treatment [2]. A 10-min acquisition is required to achieve a biologically relevant spatial resolution at a signal-to-noise ratio sufficient for quantification [3]. Patient motion is likely to occur within such long scan times. Stimulations show that even small intra-acquisition motion compromises quantification, although the decrease in image quality is not visually apparent. Exploiting the relatively long repetition time (TR) required for quantitative sodium imaging, we present a method to collect navigators embedded within the flexible twisted projection imaging (flexTPI) sequence as a means of detecting and correcting intra-acquisition motion with no time penalty.

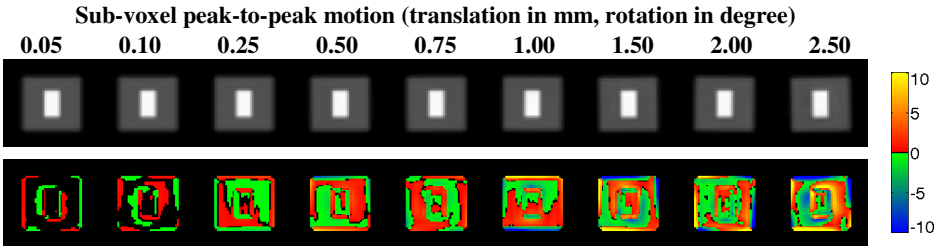

Figure 1 Selected cross-section of simulated data with intra-acquisition movement (top), and percent difference relative to motion free data (bottom).

Methods: A numerical phantom comprised of a central region of cerebrospinal fluid (CSF; 2.6 x 4.9 x 2.6 cm^3, 145 mM, T_2 = 55 ms) surrounded by tissue (10 x 10 x 10 cm^3, 36 mM, biexponential T_2 of 60% 2.5 ms and 40% 14 ms) was used to investigate the effect intra-acquisition movement. The k-space data corresponding to a 10-min flexTPI acquisition[3] were simulated with random, smoothly varying 3D translations (peak-to-peak 0.05-2.5mm) and 3D rotations (peak-to-peak 0.05°-2.5°) during the acquisition. Images reconstructed from the data were then converted to TSC bioscales, and the percent signal difference from the motion-free acquisition was computed.

The flexTPI sequence was modified to acquire a series of low-resolution navigator images along with the conventional projection imaging data. Navigator data were collected following each conventional flexTPI readout in each TR with a different set of flexTPI trajectories to image the same field of view (FOV) repeatedly but at a lower resolution. This navigated flexTPI sequence was used to acquire two quantitative ^{23}Na imaging datasets (**A** and **B**) at 9.4 Tesla on an healthy volunteer, with each dataset containing three separate acquisitions, one each for quantification, B0 correction and B1 correction, respectively. Scan time for each acquisition was 9 minutes 45 seconds with T_R = 160 ms, where 3657 projections were collected for flexTPI imaging with radial fraction = 0.32, gradient strength = 0.49 mT/m, nominal resolution = 3.3 mm, TE = 0.26 ms (TE = 1.26 for B0 acquisition). Meanwhile, navigator data were collected at a temporal resolution of 70s (438 projections, radial fraction = 0.22, gradient strength = 0.49 mT/m, 8 mm resolution). Dataset **A** was collected with the experienced subject who remained as still as possible, while dataset **B** was collected with the subject deliberately coughing at 2, 4, 6, and 8 minutes during each acquisition.

Motion parameters were derived from the navigator data using the AIR image registration package [4]. For motion correction, all flexTPI imaging data were aligned in k-space with respect to the first navigator data where the subject remained stationary. Images reconstructed with ($\mathbf{B_{nav}}$) and without ($\mathbf{B_{unc}}$) motion correction were then converted into TSC maps. Difference maps ($\mathbf{B_{unc}} - \mathbf{A}$ and $\mathbf{B_{nav}} - \mathbf{A}$) were computed to evaluate the performance of motion correction on quantification of tissue sodium concentration (TSC) in the human brain.

Results and Conclusion: Figure 1 shows grayscale and % error cross-sections through the phantom for different simulated motions. Although the grayscale images are visually identical, significant quantification errors are clearly appreciated in the difference images. The errors are most pronounced near high-contrast borders, but also extend into homogenous regions. Acceptable errors of less than 5% of the TSC bioscale could only be obtained for the smallest movements (<0.25 mm/deg maximum translation/ rotation).

Figure 2 shows the quantification results for human imaging. While the three TSC maps (**A**, $\mathbf{B_{unc}}$, $\mathbf{B_{nav}}$, unit: mmol/L tissue) are visually indistinguishable, $\mathbf{B_{unc}} - \mathbf{A}$ reveal significant quantification error due to motion, especially along contrast borders. Error were greatly reduced after correcting for intra-acquisition motion ($\mathbf{B_{nav}} - \mathbf{A}$).

The addition of navigators to the flexTPI sequence enabled intra-acquisition motion detection and correction for improved accuracy of quantitative sodium imaging without any increase in scan time. This strategy may allow longer acquisitions to obtain higher spatial resolution.

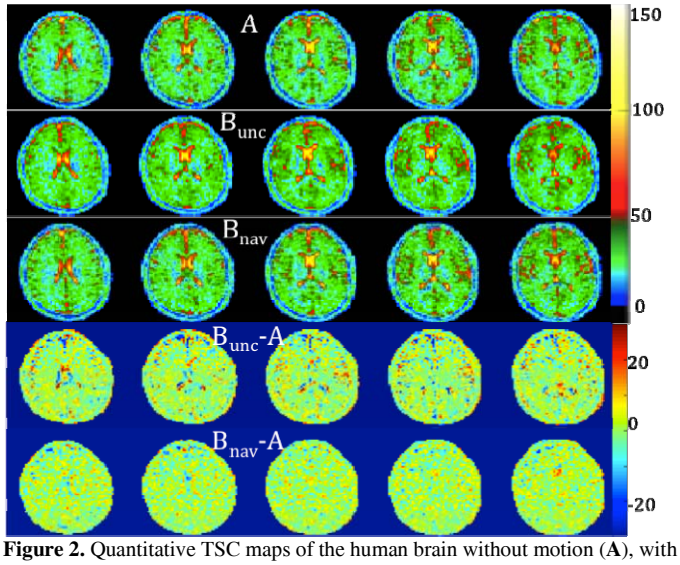

Figure 2. Quantitative TSC maps of the human brain without motion (**A**), with discrete coughing and no motion correction ($\mathbf{B_{unc}}$), with discrete coughing and motion correction ($\mathbf{B_{unc}}$), and their difference maps show significantly reduced quantification errors due to motion after correction.

References: [1] Lu et al., Magn Reson Med 2010; 63:1583–1593. [2] Thulborn et al., Neuroimag Clin N Am 2009; 19: 615-624. [3] Atkinson et al.,Magn Reson Med 2011; 66:1089-1099. [4] Woods et al., J. Comput Assist Tomography 1998; 22:139-152.

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