

Motion Artifact Removal in J-Difference Editing -- Is Phase Correction of Individual Acquisitions Enough?

P. Bhattacharyya¹, M. Brown², M. Lowe¹, and M. Phillips¹

¹Cleveland Clinic, Cleveland, OH, United States, ²Siemens Medical Solutions

Introduction

Previously, we have shown that it is important to monitor and account for the effects of motion in J-difference edited MRS¹. A common method for accounting for the loss of signal amplitude due to phase incoherence caused by motion is to apply a phase correction to individual acquisitions prior to signal averaging². Because subject motion causes a phase shift between subsequent acquisitions, phase correction of individual acquisitions increases the signal-to-noise ratio in the final spectra. When performing similar phase correction prior to signal averaging in J-difference GABA editing, we show that while the metabolite signal fluctuation is reduced, the final edited spectra still suffer from motion artifact. We propose to retrospectively discard motion-corrupted portion of the data and use the scan prior to the onset of motion in order to possibly retrieve edited spectrum of good quality. We have adopted a water signal based interleaved navigator approach to track motion.

Methods

MR scans were performed using a 3 Tesla Siemens whole body Trio scanner (Erlangen, Germany). A single subject was scanned several times with a MEGA-PRESS sequence³ having water signal based interleaved navigator. The scan parameters for the 30×30×30 mm³ single voxel spectroscopy at occipital cortex were: TR = 3000 ms, TE = 68 ms, water suppression bandwidth = 35 Hz, editing pulse frequency = 1.90 ppm, editing frequency-selective pulse bandwidth = 41 Hz, NEX = 72, total acquisition time = 7 min 12 sec. The subject was instructed to move head during specific periods of the scan. Data were acquired in a shot by shot basis, and the first eight measurements were ignored in order to ensure steady state magnetization. The interleaved navigator was set up as in Thiel et al⁴, in which the same sequence is repeated within one repetition time but without any water suppression. Data analysis was done using jMRUI software package⁵. Phase correction of the subspectra prior to averaging was performed in two different ways: (i) using the residual water phase information, and (ii) using the NAA from the scans that had no effect on the NAA peak. The data were summed into 8 bins of 8 acquisitions each in order to get a reasonable statistics of NAA and Cr signal amplitudes.

Results and Discussion

The time course of signal amplitudes of both NAA and Cr are plotted in Fig. 1 for (a) without any phase correction, (b) using residual water for phase correction, and (c) using NAA for phase correction. The fluctuation in NAA signal amplitude (Fig. 1(i)) is reduced from 24.10 ± 0.13% in (a) to 12.20 ± 0.32% in (b) and 7.30 ± 0.24% in (c). The Cr signal amplitude fluctuation (Fig. 1(ii)) reduced from 28.80 ± 1.06% in (a) to 12.90 ± 0.46% in (b) and 9.20 ± 0.34% in (c). Reduction in signal fluctuation indicates that the signal drop due to motion is largely compensated for by phase correction prior to averaging of signals.

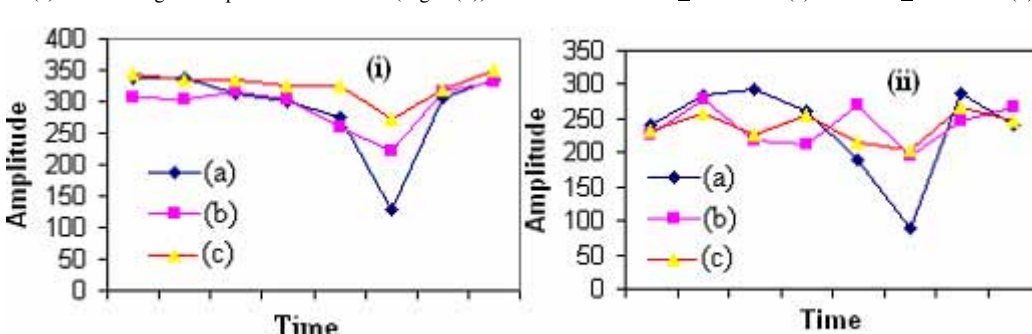


Fig. 1. Temporal fluctuation of (i) NAA and (ii) Cr signals with and without phase correction prior to signal averaging.

peaks in Fig. 2(b) indicates extremely poor editing during motion. As shown earlier¹, only the portion of the data prior to motion has good editing and should be used. Hence only the spectrum shown in Fig. 2(c) is a reliable GABA edited spectrum with efficient editing.

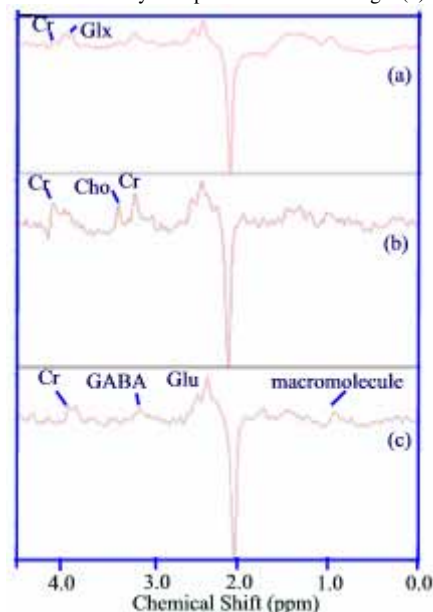


Fig. 2. Edited spectrum for (a) all acquisitions, (b) acquisitions during motion, and (c) acquisitions prior to motion

The final edited spectrum obtained by phase correction prior to signal averaging still suffers from poor spectral editing due to motion. Using the amplitude of the unsuppressed navigator water signal as indicator of motion¹ (which matches with the controlled motion pattern in the study), the dataset was divided into (a) total scan duration, (b) during motion, and (c) prior to motion. The edited spectra from the three datasets are shown in Fig. 2. The presence of strong Cr and Cho

Even though phase correction prior to averaging significantly reduced the fluctuation of metabolite signal amplitude by reducing the signal drop due to motion, the final edited spectrum showed almost no improvement. By using data from several scans we estimate a 3% drop in unsuppressed navigator water signal amplitude as the cutoff beyond which the data should be discarded. This cut-off is expected to vary from system to system and should be estimated for the specific system. We also compared unsuppressed navigator water, residual water, NAA and Cr signal amplitudes as ways of tracking subject motion. Unsuppressed water is much more efficient in tracking motion because of its much higher signal amplitude. Retaining more residual water to follow its signal amplitude evolution may cause unwanted baseline distortion.

Conclusions

While phase correction of individual measurements acquired in a shot by shot basis significantly reduces the signal fluctuation caused by motion in the sub-spectra, it does not remove motion artifact from the final edited spectrum. Thus phase correction of individual acquisitions is not sufficient to remove motion artifacts in J-difference editing. An independent approach must be adopted to track and further analyze motion corrupted data. Interleaved navigator approach is an effective way of tracking motion and discarding motion corrupted data. The magnitude of signal drop beyond which the data should be discarded needs to be estimated.

References

1. P. Bhattacharyya, M. Lowe, M. Phillips, and M. Brown, Proc. Intl. Soc. Mag. Reson. Med. **14** (2006).
2. G. Zhu, D. Gheorghiu, and P.S. Allen, *NMR Biomed.* **5**, 209-211 (1992).
3. M. Mescher., H. Merkle, J. Kirsch, M. Garwood., and R. Gruetter, *NMR Biomed.* **11**, 266-272 (1998).
4. T. Thiel, M. Czisch, G.K. Elbel, and J. Hennig, *Magn Reson Med.* **47**, 1077-1082 (2002).
5. A. Naressi, C. Couturier, J.M. Devos, M. Janssen, C. Mangeat, R. de Beer, and D. Graveron-Demilly, *Magma*, **12**: 141-152 (2001).