Baseline Correction in MR Proton Spectroscopy Using Bi-exponential Separation

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Synopsis

An accurate quantification of MR spectroscopy has been compromised by a non-zero baseline. We experienced the same issue in our single voxel proton MR spectroscopy of a brain. We noticed that there was a fast-relaxing signal in the temporal signal which could contribute to the baseline. The fast-relaxing component was easily removed by bi-exponential fitting due to a large difference in the relaxation rate between the fast and slow-relaxing components. The effectiveness of this method for the baseline correction was confirmed through brain MR spectroscopy at the motor cortex using both the spin echo and stimulated echo sequences.

Introduction

An accurate quantification of MR spectroscopy has been compromised by a non-zero baseline. We experienced the same issue in our single voxel proton MR spectroscopy of a brain. The MR spectroscopy analysis program in the MRI console required a manual selection of spectral ranges for the baseline. However, it was difficult to find out the spectral regions that were confidently at the baseline. Our application is to compare the spectral quantity on the brain's motor cortex before and after a physical exercise and therefore the spectral baseline has to be corrected accurately. We developed a fully automated method of correcting the spectral baseline as a preprocessing step.

Methods

Our approach is based on an observation that the time domain signal decayed very fast in the first few samples followed by a slower relaxing signal. The fast-relaxing signal will be broad in the frequency domain spectrum and will serve as a background baseline. Therefore, we modeled the signal S(t) as a bi-exponential relaxation with a fast and slow relaxation rates, R_{fast} and R_{slow}: $S(t)=S_{fast}(t)+S_{slow}(t)$, where $S_{fast}(t)=S_{0fast}\exp(-R_{fast}t)$, and $S_{slow}(t)=S_{0slow}\exp(-R_{slow}t)$. S_{0fast} and S_{0slow} are the signal amplitude at t=0 of each component. The fast-relaxing component contributed to the baseline and hence it was subtracted from the acquired signal S(t), resulting in a baseline-corrected signal $S_{cor}(t)$, i.e., $S_{cor}(t)=S(t)-S_{fast}(t)$. The overall processing steps are summarized in a diagram shown in Fig. 1. A Matlab program was programed using the 'fit' function with the 'exp2' model for the bi-exponential curve fitting. Proton MR spectroscopy data were collected from the brain of healthy participants using single voxel-selective spectroscopy sequences at 3T with a 20-ch head&neck RF coil. An automated shimming was used for more reliable reproducibility. The voxel was selected at the motor cortex that was localized using a foot-stimulating task fMRI. We tested different selection of the motor cortex that was centered at the bilateral and the right lateral location. The spin echo (PRESS) [1] and stimulated echo (STEAM) [2,3] sequences were tested with an echo time of 30 ms and 20 ms, respectively. Using the selected sequence and the voxel location, the MR scan was repeated twice with one day interval in each subject. After the first day's scan, the subject was asked to exercise for about an hour on a treadmill. Quantification of spectral peaks were obtained after the baseline correction using the AMARES method with the default database for starting values and prior knowledge of the proton brain spectra in jMRUI 6.0 beta. [4]

Results

The voxel location for the bilateral and the right motor cortex is shown in Fig. 2. The signal and spectra from these voxels of a representative participant are shown in Figures 3 and 4 for the spin echo and stimulated echo sequences, respectively. As expected, the spin echo signal was greater than the stimulated echo. However, the temporal signal relaxed with a strange pattern in the bilateral location of the voxel as marked in Fig. 3 and this pattern was observed in most of the participants with variable degree from the bilateral voxel with the spin echo sequence. In contrast, the stimulated echo signal relaxed bi-exponentially independent of the voxel location. The average R_{fast} and R_{slow} in Fig. 3 were 992 s^{-1} and 20.8 s^{-1} for the spin echo and those in Fig. 4 were 1105 s^{-1} and 30.0 s^{-1} for the stimulate echo. The average composition of the fast component was 0.58 and 0.69, for the spin echo and stimulated echo, respectively. R_{fast} was greater in the stimulated echo than the spin echo, which might be attributed partially to the shorter echo time of the stimulated echo. The big difference in the relaxation rates and a balanced composition made the bi-exponential fitting very reliable. The spectral peak amplitudes were reduced after the baseline correction as shown in Fig. 5.

Discussion

The fast-relaxing component was not observed in proton and phosphorous spectroscopy of leg muscles in our other experiments. The fast-relaxing component observed in the brain will need more investigation for its source and meaning. There was a report to attribute the baseline to large molecules in the brain tissue. [5]

Conclusion

The proton MR signal from a brain had two relaxation components and they were easily separated using a bi-exponential curve fitting due to a large difference in the relaxation rates and a balanced composition of the fast-relaxing component. It was confirmed that the fast-relaxing component contributed to the baseline and the signal subtracted with the fast-relaxing component was successfully removed from the baseline. Once the initial fitting parameters were set, the baseline correction was fully automated without a further manual adjustment.

Acknowledgements

Data collection at HMRC has been supported by a PGP grant of IALS at UMASS Amherst.

References

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Figures

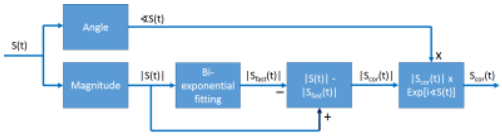

Fig. 1. A diagram of the baseline correction processing. The acquired time signal S(t) and the corrected signal $S_{cor}(t)$ are in a complex format. The bi-exponential fitting is applied to the amplitude of the complex signal, i.e., |S(t)|. The amplitude of the fast-relaxing signal is subtracted from the amplitude of the input signal. The corrected signal in the complex format is constructed from the baseline-corrected amplitude and the phase of the input signal, i.e., <S(t).

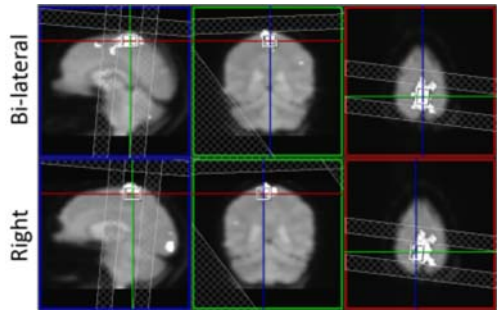

Fig. 2. The spectroscopy voxel is marked on the orthogonal slices of echo planar images overlaid with fMRI activation for the bilateral motor cortex of feet. The crossed stripes represent the presaturation bands that were applied only to the spin echo sequence because it was not available for the stimulated echo sequence. The volume of the selected voxel was 20(AP)x16x16 mm^3.

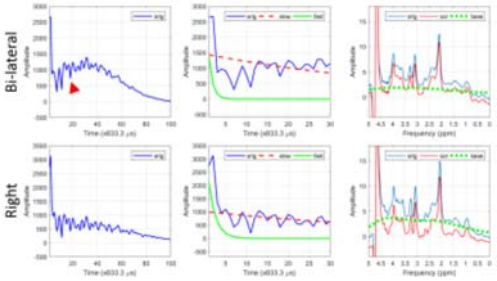

Fig. 3. Spectroscopy signals and spectra obtained at 2 different locations of motor cortex using the spin echo sequence. The left two columns are the temporal signal shown only for the leading samples. The right most column is the real component of the spectrum. R_{fast} was 1272 s^{-1} and 711 s^{-1} at the bilateral and right motor cortex, respectively. The composition of the fast component, $S_{0fast}/|S(0)|$ was 0.49 and 0.70, at the bilateral and right motor cortex, respectively. The temporal signal from the bilateral location dipped after the fast–relaxing signal as marked by a red arrow head.

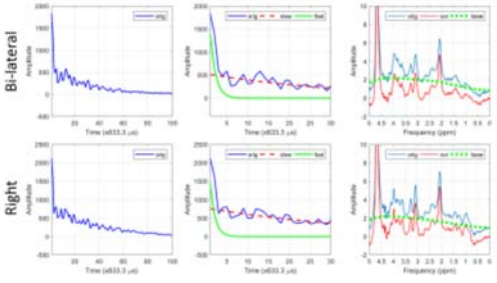

Fig. 4. Spectroscopy signals and spectra obtained at 2 different locations of the motor cortex using the stimulated echo sequence. The left two columns are the temporal signal shown only for the leading samples. The right most column is the real component of the spectrum. R_{fast} was 945 s^{-1} and 1064 s^{-1} at the bilateral and right motor cortex, respectively. The composition of the fast component, i.e., $S_{0fast}/|S(0)|$ was 0.73 and 0.65, at the bilateral and right motor cortex, respectively.

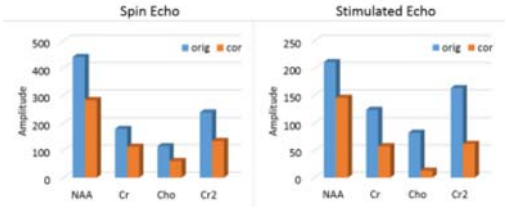

Fig. 5. Quantification of major spectral peaks shown in Figs. 3 and 4 in which the NAA (N-acetyl aspartate), Cr (Creatine), Co (Cholin), and Cr2 peaks are located at 2.07, 3.07, 3.26, and 3.94 ppm, respectively. All the spectral peaks were reduced in its amplitude after the baseline correction. The reduction of the spectral amplitude was not uniform over the spectral peaks. The reduction was progressively increased as the peaks approached the water peak at 4.7 ppm as expected from the baseline curve shown in Fig. 4.