Water sidebands removal in spectral fitting

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Target Audience: MR spectroscopists with interests in GABA, glutamate, glutamine, and spectroscopic quantification.

Introduction: GABA editing sequences need many averages to attain a usable snr for the GABA signal. These averages should be added coherently to avoid loss of snr and to avoid line shape distortions. The residual water signal is a reliable reference to correct for phase and frequency shifts but a balance must be struck between a strong reference and possible contamination of the spectrum by residual water sidebands and background signals. Since eddy current correction, coherent addition and residual water removal are closely connected, an undesirable line shape of the residual water will impair removal of water sidebands and can further cause baseline distortions. We implemented a concerted eddy current correction and water removal scheme to optimally correct the spectral data and remove the residual water. This method has been tested using GABA editing experiments performed on 141 normal volunteers.

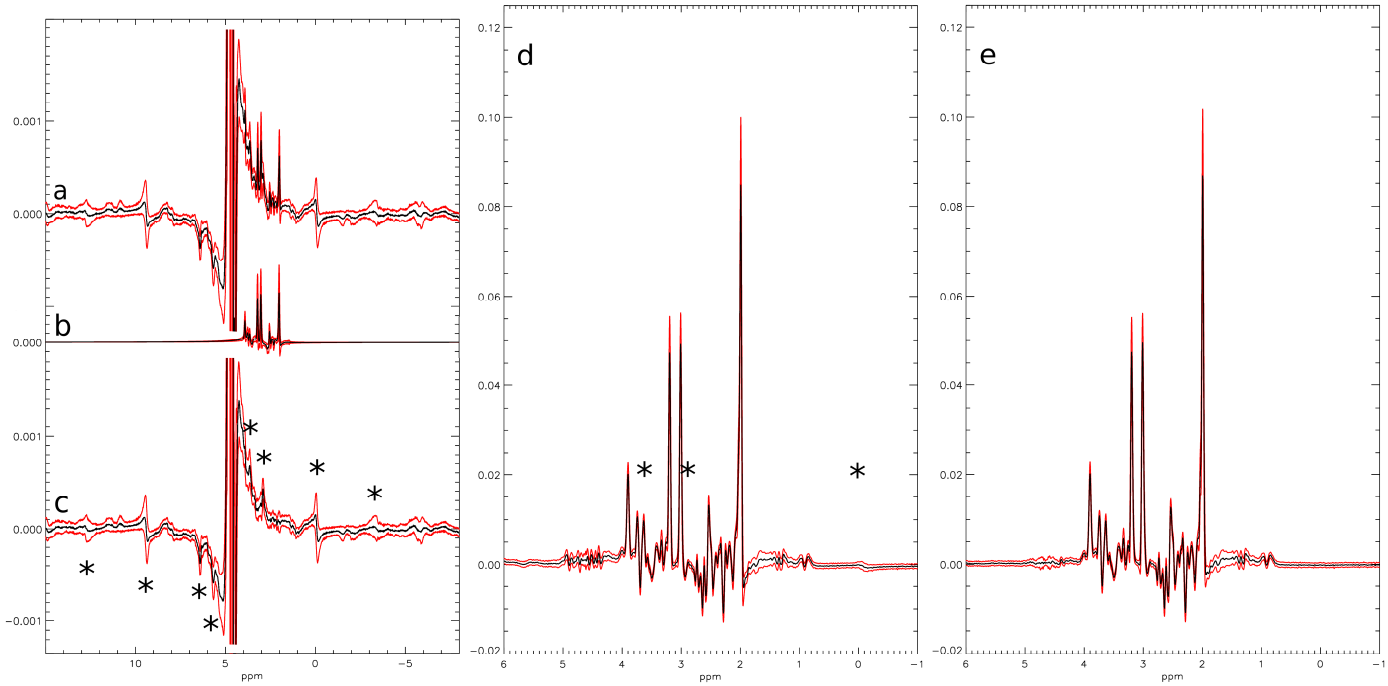

Figure 1. a) Unsuppressed water reference. **b)** HSVD fit to water suppressed last 8 acquisitions. **c)** Unsuppressed water reference minus metabolite spectrum revealing the water sidebands (* in figure). **d)** Uncorrected spectrum after HSVD water removal. The water sideband locations are marked by '*'. **e)** Corrected spectrum after HSVD removal. In a, b, and c, the amplitudes have been normalized by the average unsuppressed water amplitude. In d, and e, the amplitudes have been normalized by the average suppressed water amplitude. Black lines are the average, red lines the standard deviation from 141 subjects.

Methods: 141 volunteers were scanned on a 3 Tesla whole body scanner (GE, Milwaukee, WI, 14M4 platform). The spectroscopy voxel was placed immediately superior to the ventricles, NS = 768, TR/TE = 1500/68 ms, NEX = 2. The GABA editing pulse (1) covers both GABA β-H2 and the M4 macromolecules. It was switched on and off during even- and odd-numbered scans. A total of 768 water-suppressed (ws) edited and un-edited FID pairs were acquired for a total of 20 minutes. At the end of the sequence 16 acquisitions are taken without water-suppression (nws), averaged-in-scanner by nex=2 and saved as 8 separate acquisitions.

The data was processed as follows: The 8 nws reference scans were fitted with a single lorentz-gauss line shape and phase- and frequency- corrected before adding them together. At the end of the ws acquisitions, closest to the nws acquisitions, 8 scans were phase- and frequency- corrected in the same manner and added together to create a spectrum with the same metabolite amplitude as in the nws signal but with much weaker water artifacts. With an HSVD (2) (nroots=64) algorithm this signal was fitted and peaks in the metabolite range of 1.5 to 4.2 ppm were selected (see Fig. 1b). This fitted signal was then subtracted from the nws reference signal to reveal all sidebands (Fig 1c). The fit (HSVD nroots=64) to this signal is used to correct the phase and frequency of all the data by multiplying with a complex exponential: exp(-i*phase(fit)). To add all the acquisitions the corrected data are fitted to the residual water with a single lorentz-gauss line to correct phase and frequency. The HSVD algorithm is then used again to remove the residual water from the summed data (nroots=32, only components +/- 0.3 ppm from water frequency and greater than 1/500 of the maximum signal strength.). The effectiveness of the method was tested by comparing the averaged spectra of the corrected and the uncorrected data from 141 subjects as shown in figure 1 d and e.

Results and Discussion: Removal of the metabolite signals from the reference scan revealed two sidebands covered by the stronger metabolite signals. Correcting the data for the sidebands removes them from the water suppressed data as can been seen from the isolated sideband in Fig 1d and 1e at 0 ppm. The eddy current correction also improved the residual water removal by the HSVD (Fig 1d and e in the range 4.2 – 5 ppm) and improved the baseline visibly at and lower than 4ppm. Precise quantification becomes increasingly important when the number of subjects is large so as to increase statistical power for genetic correlation studies. Even small artifacts can introduce statistical bias that skews genetic correlations. Finally, the correction introduced here also improves the line shape of the metabolites which leads to further quantification improvements.

References: 1. Sailasuta P. et al, Proc ISMRM 9:1011 (2001). 2. de Beer R, van Ormondt D.. NMR Basic Princ Prog 1992:26:201–248