# An Automated Algorithm for Combining Multivoxel MRS Data Acquired with Multicoils

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## Introduction

Although widely available, multicoils are not widely used in multivoxel MRS studies. This is in large part due to the lack of an automated algorithm that combines the data acquired by the individual coils as is available in MRI. The combination of multivoxel MRS data acquired with multicoils should yields improvement in SNR, which is spatially dependent and theoretically can range from one to the square root of the number of coils. In order to achieve this improvement, it is required to phase-correct, and combine the multivoxel data sets correctly<sup>1</sup>. Manual combination of multivoxel MRS data can be prohibitively time consuming. Therefore, a key element in the adoption of this method would be the availability of an automated algorithm which combines the individual data acquired by each separate coil into a combined weighted dataset. We have developed a fully automated algorithm which utilizes the frequency-domain fitting method of LCModel<sup>2</sup> to analyze the individual datasets and to determine the weighting factors for each individual spectrum. Herein we demonstrate the results of applying this algorithm to data acquired from a phantom containing metabolites and *in vivo* data acquired from the brain of normal volunteers.

### **Materials and Methods**

The studies were performed using a 3T scanner (Signa LX, General Electric, Waukesha, WI) equipped with a body coil (length 53 cm, diameter 55 cm) for RF transmission and a custom designed head phased array coil containing four coils for receiving. Spectra were recorded with PRESS sequence, TR/TE of 2000/35 ms,  $16\times16$  array, FOV of 24 cm, slice thickness of 1 cm, and 512 time points. The scanning time was 8:40 minutes. LCModel fitting was applied on the multivoxel data from each receiver. Then, all of the information required for the combination was extracted from the LCModel output files. The phase corrections factors were read and used to phase each of the individual spectra, and the metabolite areas were used to determine the weighting factor for each spectrum. The weighted complex spectrum for each voxel,  $S_{wi}$ , was constructed from the four component spectra  $S_i$  and the area of a particular metabolite,  $W_i$ , found by LCModel, chosen separately for each voxel. The algorithm searches for the peak that was found to be present in a majority of the spectra (from each coil) at each spatial location. In cases where more than one met this criterion, the algorithm chose the peak that had the best fit as judged by the SD of the area of the fit by LCModel. The SNR of the weighted dataset was compared with that of each of the individual sets and an interleaved dataset, in which for each spatial location the best spectrum out of the individual spectra was chosen.

### **Results and Discussion**

The method presented here is completely automated, and no user interaction is required once the algorithm is initiated. The total process of analyzing and combining the four  $16 \times 16 \times 512$  individual datasets and of analyzing the resulted complex combined dataset by LCModel took ~100 min (using a SPARC 10 workstation). The combination of MRS data acquired from a phantom and the brains of normal volunteers yielded improved SNR in all voxels. In both cases, the average improvement in SNR compared to that in the interleaved set was 1.4. In the spherically symmetric phantom, the theoretical SNR improvement of two-fold was achieved in three central voxels where the sensitivities of the coils were almost similar. As predicted, the average improvement of SNR in the central voxels of the weighted set over the interleaved set (SNR<sub>weighted</sub>/SNR<sub>individual</sub>=1.74±0.02, n=9 voxels) was significantly higher (p<0.005) than that of the peripheral voxels (SNR<sub>weighted</sub>/SNR<sub>individual</sub>=1.34±0.09, n=24 voxels). In the brain, spectra obtained from the ventricles of the brain show no metabolites while those of the brain show clearly the presence of NAA, Cr and Cho at 2.0, 3.0 and 3.2 ppm, respectively. The NAA areas in the weighted CSI set, calculated by LCModel, were higher than that in each of the CSI data recorded by the individual coils and the interleaved set (Figure 1). Moreover, the distribution of NAA was more homogeneous and therefore less dependent on the reception profile in the weighted set than in the individual sets.

#### Conclusions

Multi-coils have gained wide use in conventional MR imaging due to the accessibility of an automated combination algorithm which preserves the SNR of the individual coils and provides increased spatial coverage over individual coils. We believe that the approach described here offers similar advantages in the analysis of multivoxel MRS data acquired with phased array coils.



 References:
 1) Wald LL, et al. Magn. Reson. Med 1995; 34: 440.

 2) Provencher SW, Magn. Reson. Med 1993; 30: 672.

**Figure 1.** NAA area maps calculated from (A) the dataset acquired by the dominant coil (B) the weighted data set (B). (C) The improvement in SNR of the weighted dataset over the interleaved dataset, in which for each spatial location the best spectrum out of the individual spectra was chosen.