SVD 8-Channel Coil Combine for 2D Chemical Shift Imaging (CSI) MRI

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Introduction

Magnetic Resonance Spectroscopy (MRS) can be used to study Traumatic Brain Injury (TBI), a condition that results in serious neurological and neuropsychological dysfunction, often without obvious signs of external injury or findings on conventional MRI and CT imaging. MRS, and in particular Chemical Shift Imaging (CSI), is able to detect relative abundances of key metabolites such as phosphocreatine (PCr), N-acetylaspartate (NAA), lactate (Lac), and choline (Ch) in small volumetric regions of the brain. It is has been shown that damaged neuronal tissue has a decreased ratio of NAA to PCr, with the ratio being predictive of outcome in TBI (Yeo, 2006).

CSI has many limitations. The 3D voxel size for each spectrum is low resolution (1.5 cm x 1.5 cm x 1.5 cm) due to both scanning time and signal strength limitations. Also, spectra collected by CSI must be processed extensively to remove baseline signals (mostly H_2O) and correct for phase. Currently, CSI data for the brain is being collected by 8 head channel coils in order to improve resolution and signal strength. The typical method of combining raw data from multiple coils is by the sum-of-squares method (Wright, 1997). However, this method has limitations. Extra processing steps for determining coil sensitivity and for zero-order phasing are required during the coil combine process. Furthermore, sum-of-squares methods cause loss of phase information prior to analysis and quantification of metabolites.

Singular Value Decomposition (SVD), a signal processing technique that provides the dominant mode signal, can used to combine time decay signals from multiple channel coils by obtaining the optimal coil combination weights objectively (Sandgren, 2005). The advantages of SVD over the sum-of-squares method include preservation of phase-information, automatic zero-order phasing, no need of *a priori* information about coil sensitivity, and separation of signal from noise in low signal-to-noise situations. We have recently implemented an 8-channel coil combine SVD technique on a 2D phantom dataset with results presented.

Methods

Analysis of multiple channel CSI data via SVD is a multi-step process. First, data are collected with a multiple channel coil using a phase-encoded 2D CSI acquisition sequence. Next, the phase-encoded FIDs are Fourier transformed in both spatial dimensions and shifted to the proper orientation. For each voxel, FIDs from each coil are imported into an $m \times n$ matrix, **A** (m = # of coils, n = # of time samples). The matrix is predominately rank one and can be decomposed via SVD where the first right singular vector of **A** (i.e. dominant mode in time) is set as the FID for the voxel of interest whereas the first left singular vector provides the optimal weight of coils. Singular values are inspected to verify the strength of the dominant mode and ensure the rank of matrix **A** is one. The combined time-domain data is then sent to LCModel for analysis and quantization (Provencher, 1993). Estimated ratios NAA, Ch, and Lac with PCr are reported for each voxel along with estimated standard deviations expressed in percent of the estimated concentrations.

Results

Sample data were collected with a 2D CSI sequence of a cylindrical phantom on a 1.5T GE HDx EXCITE clinical scanner with an 8 channel head coil provided by GE. Axial data were acquired with the following parameters: 12×12 acquisition matrix, voxel size = 3.375 cm^3, TE = 144 ms, TR = 1 sec, and NEX = 2. Raw data were then transferred to a remote workstation where the phase-encoded FIDs were Fourier transformed in both spatial dimensions and shifted to the proper orientation. All data were then analyzed via the SVD method and SAGE (GE MRS processing suite), which combines data from multiple coils by the sum-of-squares method. Singular values were examined, verifying strength of the dominant mode and the rank of the matrix. Both sets of processed data were then sent to LCModel for analysis. Voxels contained within the phantom (i.e. no partial volume effects) were selected for statistical analysis of signal-to-noise ratio (SNR), metabolite concentration ratio, and standard deviation of metabolite ratios. Results are reported in **Table 1**.

The ratios of metabolites to PCr were expected to be near equivalent for both SVD and sum-of-squares since the data was acquired from the same phantom. However, SNR was expected to differ based on method of analysis. A one-tailed T-test of the means showed analysis by SVD had a statistically significant higher SNR than analysis by the sum-of-squares method ($p < 0.05$). Furthermore, inspection of standard deviations for average metabolite ratios across the phantom suggests that analysis by SVD provides more consistent spectra for analysis (lower variance).

	SVD		SAGE (sum-of-squares)	
	Mean	**St. dev**	**Mean**	**St. dev**
SNR*	13.03	4.93	10.75	3.96
NAA/PCr	1.385	0.020	1.410	0.022
Ch/PCr	0.355	0.005	0.355	0.006
Lac/PCr	0.357	0.023	0.390	0.026

Table 1. * *indicates p-value < 0.05*

Conclusions

Preliminary analysis of SVD coil combine versus sum-of-squares coil combine shows advantages for the SVD-based technique. SVD provides a statistically significantly higher SNR than conventional methods of analysis. Furthermore, analysis of metabolites shows that the SVD method provides consistent evaluation over the region contained within the phantom. These analyses also show that, without any *a priori* knowledge, SVD successfully deals with the problems of determining coil sensitivity and of correcting for zero-order phase.

In the future, SVD analysis will be extended to 3D CSI data sets in both phantom and human subjects. SVD analysis could provide a very useful tool for the analysis of MRS data collected on TBI patients, where motion artifact, low SNR, and coil sensitivity are serious issues affecting the quality of spectra.

References

Provencher SW. "Estimation of metabolite concentrations from localized *in vivo* proton NMR spectra." *Magn Reson Med.* **30**: 672 (1993).

Sandgren N, Stoica P, Frigo FJ, Selen Y. "Spectral analysis of multichannel MRS data." *J. Magnetic Resonance*. **175**: 79-91 (2005).

Wright SM, Wald LL. "Theory and Application of array coils in MR spectroscopy." *NMR Biomed.* **10(8)**: 394-410 (1997).

Yeo RA, Phillips JP, Jung RE, Brown AJ, Campbell RC, Brooks WM. "Magnetic Resonance Spectroscopy Detects Brain Injury and Predicts Cognitive Functioning in Children with Brain Injuries." *J. Neurotrauma*. **23**: 1427-1435 (2006).