

# Magnetic Resonance Spectroscopy using Multiple Receive Coils

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## Introduction

Many clinicians routinely use multiple receive coils for *magnetic resonance imaging* (MRI) studies of the human brain. In conjunction with these exams, it is often desired to perform proton *magnetic resonance spectroscopy* (MRS) experiments to quantify metabolites from a region of interest. An MRS absorption spectrum can be generated for each coil element, however interpreting the results from each channel is a tedious process. Combining MRS absorption spectra obtained from an experiment in which multiple receive coils are used simplifies clinical diagnosis. Techniques for combining MRS absorption spectra from multiple receive coils have been proposed(1),(2), and a new technique similar to these approaches will be introduced.

## Methods

Data was collected using a 1.5 T General Electric (GE) Signa MR scanner equipped with a high bandwidth (1MHz) data acquisition subsystem and a TwinSpeed gradient coil capable of 40 mT/cm at a maximum slew rate of 150T/m/s. Conventional *point resolved spectroscopy* (PRESS) and *stimulated echo mode* (STEAM) pulse sequences were used with an 8-channel domed head coil (MRI Devices) to acquire the data. Data was collected from the GE MRS phantom, which contains a solution of known concentrations of metabolites commonly found in the human brain, and a number of human subjects under approved institutional review board agreements. Raw data from each experiment was saved and processed off-line using MATLAB.

## Results

For each single-voxel MRS scan, a set of non-water-suppressed reference data was collected along with a corresponding set of water-suppressed data for which water was suppressed using a *chemical shift selective* (CHESS) technique(3). Each data set was phase corrected using a phase-correction vector created from the reference data. Residual water was removed from the phase-corrected water-suppressed data by subtracting an appropriately scaled and phase-corrected reference data set.

A Fourier transform of the windowed, phase-corrected water-suppressed data set with residual water removed was used to generate the MRS absorption spectra from each receive coil. The absorption spectra for each receive coil were then combined using a weighted averaging process, where the weights for each spectra were determined from the peak magnitude value of the reference data received at each receive coil. In this manner, stronger signals which yield spectra with higher signal-to-noise ratios are weighted more than weaker signals.

## Discussion and Conclusion

Experiments using both PRESS and STEAM conducted on the GE MRS phantom for an 8 cm<sup>3</sup> voxel located at the center of the phantom with a conventional single-channel quadrature head coil vs. the 8-channel head coil showed that the signal-to-noise ratios of creatine peaks from MRS absorption spectra were comparable and differed by less than 5%.

A representative MRS scan of a human subject as shown in Fig. 1 yields the multiple absorption spectra shown in Fig. 2. Parameters for this scan were: TE: 144 msec., TR: 1500 msec., 8 cm<sup>3</sup> voxel, 16 reference frames, 128 water-suppressed frames, with a scan time of 3 minutes and 48 seconds. Applying the reference weighted spectrum averaging technique for combining MRS absorption spectra from multiple receive coils provides the spectrum shown in Fig. 3. This result is similar to that obtained from a single-channel quadrature head coil and is clinically acceptable.

## References

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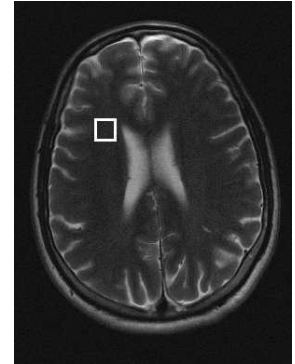


Fig. 1. 8-channel MR image of human brain.

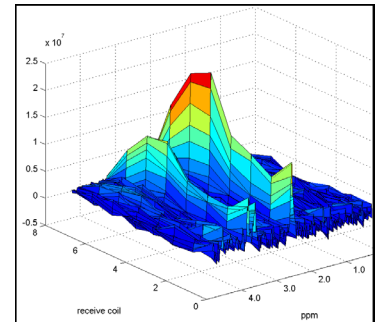


Fig. 2. "Stacked" MRS absorption spectra of individual coil elements for region indicated in Fig. 1.

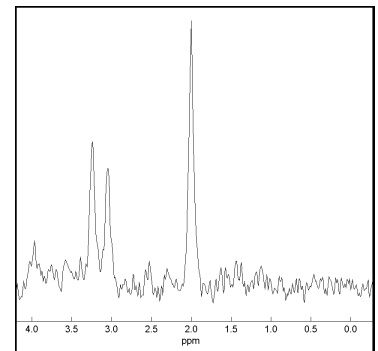


Fig. 3. MRS absorption spectrum generated by combining multiple spectra shown in Fig. 2.