Wavelet-Based Methods for Analysis of Magnetic Resonance Spectroscopic Imaging (MRSI) Data

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Abstract
MRSI is an efficient approach to specify chemo-physical structures of living organs non-invasively. In this paper, we propose and evaluate wavelet-based signal processing methods to extract features of these signals for diagnostic purposes. After preprocessing using wavelet, i.e., denoising, baseline correction to the signal, and separating background signals from the biological ones, we use wavelet transform coefficients for detecting peaks. The results in clinical and simulated data show superiority of the proposed methods compared to the previous methods. The new methods generate results that are more accurate than those of the previous ones about 10% on average.

Introduction
One of the recent and important applications of nuclear magnetic resonance technology is Magnetic Resonance Spectroscopic Imaging (MRSI). This technique is used for non-invasive determination of biochemical properties of the tissues that are useful for diagnosis and treatment evaluation [1]. To this end, certain parameters are extracted from the voxels spectra by applying complicated analysis on them. For example, peaks related to different metabolites are distinguished and their characteristics such as peak areas and area ratios are estimated. Analysis of MRSI requires complex and extensive processing because of its high sensitivity to magnetic field inhomogenities and low SNR [2, 3].

The MRSI data used in this study are from the brain tissues of 7 patients. In the brain MRSI data, separating and extracting the peaks related to certain metabolites such as creatine (Cr), choline (Cho), and N-Acetyl Asparatine (NAA) are of significant importance. NAA is the dominant peak in normal adult brain spectra. It is accepted as a neural and axonal marker whose physiological role is currently unknown. Reduced NAA has been observed with many neurological diseases that cause neuronal and axonal degeneration. Cr has been considered to be stable enough to be used as an internal reference in reporting relative concentrations of other brain metabolites, but recent findings suggest that this assumption should be used with care. Cho takes part in membrane and neurotransmitter synthesis. In adult brain, an increase in the Cho peak area is associated with Alzheimer's disease, chronic hypoxia, post liver transplant and epilepsy, while a decrease is seen in hepatic encephalopathy [2].

The aim of this study is to use MRSI for more informed diagnosis, where they are ambiguous from the diagnostic images and/or the available clinical information. This paper presents four

new methods based on wavelet transform for automatic and non-invasive determination of the tissue biochemistry from MRSI.

Proposed Methods

Preprocessing: **a) Noise Reduction:** The signal and noise components of a noisy MRSI signal have most of their significant coefficients in separate parts of the wavelet transform domain. We apply wavelet transform, vanish the noise coefficients, and take the inverse transform of the remaining coefficients to get denoised data. To be efficient, we apply the denoising algorithm to a region of interest in the MRSI data. **b) Baseline Correction:** There are several that may introduce distortions to the baseline. For example, a delay between RF excitation and the beginning of the collection period produces a rolling baseline, even after appropriate phase correction for the delay [4]. For reliable evaluation of peak areas, all distortions must be as flat or as well defined as possible. Care must be taken with baseline correction due to the possible distortion of the signal intensities. As discussed the factors with most effect on this distortion are related to hardware and will appear in low frequencies of signal [3]. Therefore we have developed a method for correcting baseline by thresholding the low frequency wavelet coefficients. **c) Background Removal:** The MRSI data in the background has low amplitude wavelet coefficients [5]. We discriminate the tissue spectra from the background spectra by comparing the reconstructed signals after thresholding their wavelet coefficients.

Processing: Due to the low SNR (Signal to Noise Ratio) of the MRSI data, automatic determination of the peaks locations is not simple [3]. We threshold the wavelet coefficients and reconstruct a signal from the remaining coefficients. This signal contains the peaks without minor details that prevent automatic estimation of the peaks locations. We estimate the peaks locations from this signal. Then, we calculate the peaks features using the original signal that contains all the information. The features extracted for each peak are: peak area, maximum value, bandwidth, and mean value of the wavelet coefficients in the peak region. The threshold value depends on MR scanner and patient conditions. Our approach calculates it automatically using the mean value of wavelet coefficients for each patient.

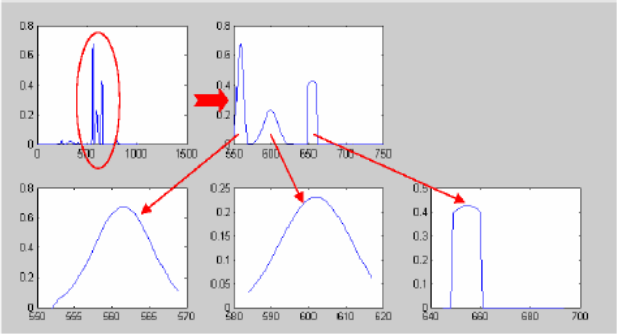

Figure 1: Results of separating peaks of a simulated MRSI signal by the proposed method.

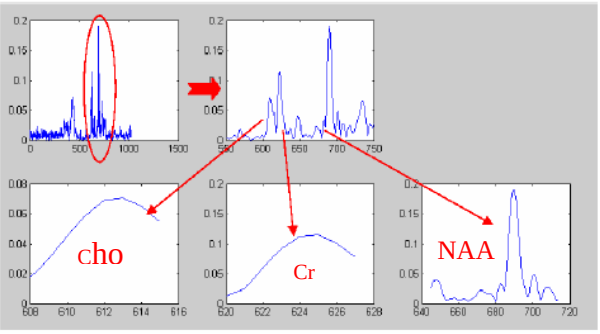

Figure 2: Results of separating metabolite peaks of a real MRSI signal by the proposed Method.

Experimental Results

To test and evaluate the proposed methods, we used real MRSI data and also simulated the MRSI data as follows. First, the three main peaks for the brain metabolites are constructed using

Gaussian functions. We compiled these peaks with random width, amplitude, and location, and with a background signal. To create the background signal, we used appropriate number of Gaussian functions with appropriate width, location, and amplitude. Finally, we added white Gaussian noise to the inverse Fourier transform of the spectra and reconstructed the results into the simulations.

Peak identification results obtained from the simulated and real data are shown in Figs. 1-2, respectively. Note that the proposed method has segregated the peaks correctly. This method detects 77%-96% of the peak areas (see Table1) and compared to other methods is about 6-10% more accurate.

Table 1: Accuracy percentage of peak detection for real and simulated MRSI data, applying our proposed method.

data	real MRSI data			simulated MRSI data		
peaks	Cho	Cre	NAA	Cho	Cre	NAA
Accuracy percentage of peak detection	88	90	96	77	80	86

Denoizing results are given in Table 2. Note that focusing the noise reduction process to specific region of the spectra has improved the SNR up to about 40dB.

Table 2: Comparison of the SNRs of the original and denoised spectra. (First method: applying the denoising algorithm to the whole signal. Second method: applying the denoising algorithm to the region of interest).

SNR Values / Methods	SNR for Entire Original Signal (dB)	SNR for Region of Interest of Original Signal (dB)	SNR for Entire Original Signal after Denoising (dB)	SNR for Region of Interest of Original Signal after Denoising (dB)
First Method	10.2	16.14	14.54	14.45
Second Method	10.2	16.14	11.63	53.6

To evaluate the baseline correction, we calculated the correlation between the baselines removed in neighboring signals after applying the proposed wavelet-based method. The result was more than 83% on average for about 1000 signals. In another approach, a reference signal, acquired before the main measurement, was compared with the signal to correct the distortion related to baseline [4]. This method was more accurate than our proposed method but our method did not need the reference signal. Alternatively, a high-pass filter was applied to the signal whose results were 24% less effective than our proposed method (see Table 3).

Table 3: Correlation percentage between the baseline removed in neighboring signals after applying our method compared to a conventional method (The conventional method applies a high pass filter to the signal). Both methods were applied to all of the 7 patients (140 signals of each patient).

Cases / Methods	Correlation percentage for Patient1	Correlation percentage for Patient2	Correlation percentage for Patient3	Correlation percentage for Patient4	Correlation percentage for Patient5	Correlation percentage for Patient6	Correlation percentage for Patient7
Our method	72.7	89	92.3	74.6	85.7	81	88.2
Conventional method	50.6	65.2	69.9	52.6	57.8	53.3	64.7

To evaluate the background removal algorithm, we applied the proposed method to 3000 signals (1000 background signals and 2000 head signals). The results were 92.0% correct. We also applied the method to the simulated signals (100 background and 200 brain signals). The results

were 97.3% correct (see Table 4). Compared to the previous methods, the proposed method showed 8.3% improvement [6].

Table 4: Results of our algorithm for distinguishing the background signal from head signals as applied to real and simulated MRSI data. For real and simulated data, the accuracy is about 92% and 97%, respectively.

Data / Signals	Real MRSI data			Simulated MRSI data		
	Number of signals	Number of correctly distinguished signals	Number of incorrectly distinguished signals	Number of signals	Number of correctly distinguished signals	Number of incorrectly distinguished signals
Head signals	2000	1821	179	200	194	6
Background signal	1000	939	61	100	98	2

Discussion

We introduced novel methods for preprocessing and processing of the brain MRSI data. Our attempt in the preprocessing step was to reduce the signal distortions and prepare it for the main process. In the processing step, we could segregate the peaks correctly and therefore extracting their specifications such as peak area, max value, and bandwidth. Our experimental results were about 10 percent more accurate than those of the previous techniques. In this work, we separated the peaks and extracted their features. Other methods may be developed to encompass the whole signal and extract some other features from it.

Conclusion

MRSI utilizes conventional imaging hardware to measure a wide spectrum of metabolites, providing useful additional information about the tissue biochemistry. In this paper, we developed and evaluated four preprocessing and processing methods for these signals, which were more accurate compared to the previous methods. For the future work, we will employ these methods and the corresponding extracted features to classify different brain abnormalities. In addition, we are planning to extend our approach to process MRSI signals from other organs and use it as an automatic and non-invasive diagnostic method for different diseases.

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