EXTRACTION OF MAGNETIC RESONANCE SPECTROSCOPIC IMAGING CHARACTERISTICS USING WAVLET TRANSFORM

Z.Torbatian[1], H. Soltanian-Zadeh[2]
[1]Control and Intelligent Processing Center of Excellence, Electrical and Computer Engineering Department, University of Tehran, Tehran 14395-515,Iran
[2]Image Analysis Laboratory, Radiology Department, Henry Ford Health System, Detroit, MI 48202, USA
e-mail: z.torbatian@ece.ut.ac.ir, hszadeh@ut.ac.ir

Abstract-**Magnetic Resonance Spectroscopic Imaging (MRSI) provides useful information about chemical properties of the tissue. In this paper, a new method was developed based on dyadic Wavelet transform to extract metabolite information of MRSI spectra like N-acetyl aspartate (NAA), Choline (Cho) and Creatine (Cr). After differentiation of brain signals from background, the Wavelet coefficients were processed in order to detect peaks. It was tested and evaluated on simulated data and real data of 10 patients. The accuracy of proposed method was 86% and 72% for simulated data and real data respectively.**

Keywords **- Magnetic Resonance Imaging (MRSI), metabolite, Wavelet Transform (WT), Spline Wavelet**

I. INTRODUCTION

Magnetic Resonance Spectroscopic Imaging (MRSI) is a non-invasive technique that may offer promising results in diagnosis characteristics of tumors [1]-[10]. MRSI measures biochemical metabolites like N-acetyl aspartate (NAA), Choline (Cho), Creatine (Cr), and Lipid-Lactate (Lip-Lac) of the tissue. The peak area like Cho, Lip_Lac and area ratios like Cho/Cr, Cho/NAA are proposed to be effective in diagnosis the grade and type of tumors [1]-[4] and differentiation of radiation necrosis from recurrence tumors [5]-[6]. Cho, taking part in membrane construction, is increased in tumors because of cell proliferation [1]. NAA, involved in neuron and axons, decreases in tumors because of neuron defects [1]. Cr, contained in energy production, is expected to increase in tumors because of energy exhaustion while weakly supported by data [1].

Based on metabolite benefits in diagnosis of brain abnormalities, the metabolite peak characteristics should be extracted at first. The low SNR MRSI spectra are sensitive to inhomogenities of magnetic filed, so extensive processing is needed for feature extraction [11]. Noise reduction, baseline correction and differentiation of brain signals from background can be mentioned as the preprocessing steps [11]. The metabolite characteristics like peak values, peak area and bandwidth can be extracted from modified signal.

Wavelet transform (WT) has been widely used in analyzing biomedical signals like MRSI [8], [11] and Electrocardiogram (ECG) [12]-[13]. Wavelet analysis outperforms conventional methods in metabolite determination [11] and R peak detection [12]. WT decomposes signals into different resolutions (scales) based on Wavelet basis. Using Wavelet coefficients at different scales with various noise and artifact effects provides better analysis results [13]. In [11], after some preprocessing steps, the wavelet coefficients of modified signal are compared with a threshold in order to extract metabolite peaks. Defining an appropriate threshold would be challenging and may be sensitive to baseline drift. To detect R peak in ECG signal, a multi-scale procedure is done on wavelet coefficients that makes the process to be less sensitive to baseline drift and noise effect [12]-[13].

The aim of this work is to extract MRSI metabolites like NAA, Cho and Cr using a dyadic Wavelet transform. After differentiation of brain signals from background based on signal energy, the signal is processed directly to extract metabolites without any other pre processing. Simulated data are developed to evaluate proposed method efficiency. The results calculated for real data of 10 patients (provided at Henry Ford Health (HFH) System, Detroit, MI) are compared with those derived from Eigentool software developed at HFH [14] to complete evaluation.

II. METHODOLOGY

A. Quadratic Spline Wavelet

Quadratic Spline Wavelet is an appropriate tool in detecting peaks like R, P and T peaks in ECG signal [12]-[13], therefore it may be beneficial in detecting metabolite peaks in MRSI signals. The Fourier Transform of proposed spline wavelet is as follows:

$$\hat{\Psi}(\omega) = i\omega\left(\frac{\sin\frac{\omega}{4}}{\frac{\omega}{4}}\right)^4 \qquad (1)$$

which results the following low pass ($H(\omega)$) and high pass ($G(\omega)$) filters:

$$H(e^{i\omega}) = e^{i\omega/2}(\cos\omega/2)^3 \qquad (2)$$
$$G(e^{i\omega}) = 4ie^{i\omega/2}(\sin\omega/2)$$

The equivalent frequency response of filter ($Q_j(e^{i\omega})$) bank at scale j is (3)

$$Q_j(e^{i\omega}) = \begin{cases} G(e^{i\omega}) \\ G(e^{i2^{lk-1}\omega}).\prod_{l=0}^{j-2} H(e^{i2^l\omega}) \end{cases}$$

It offers generalized linear phase filters at different scales with central point delay equal to $2^{j-1}-1$ [13]. The frequency responses of equivalent filters at different scales are shown in Fig. 1. As shown, the spline filters cover different frequency ranges at different scales. The spline wavelet produces a positive maximum-negative minimum pair called modulo maxima in the presence of uniphase wave at different scales. The zero crossing point of modulo maxima refers to the peak location with some delays. This delay increases at higher scales. The wavelet coefficients of a simulated signal at scale 1 to 4 are shown in Fig. 2.

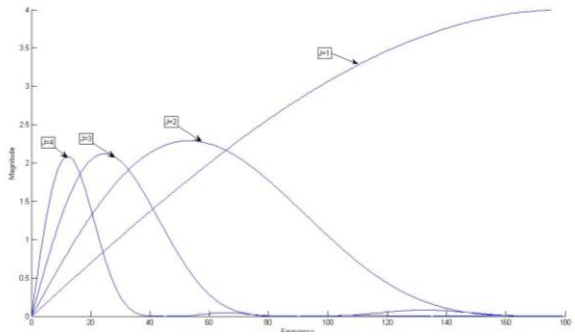

Fig. 1. Frequency response of equivalent filters at different scales (*j*).

B. Proposed method

The metabolite peaks are usually appeared on specific locations in the MRSI signal. Therefore, a region of interest (ROI) is defined for the signal to be processed. To differentiate brain signals from background, the ROI energy of each signal is computed and compared with a threshold. A signal with normal metabolites called reference signal is selected among brain signals. Considering frequency responses of equivalent filters at scale 1 to 4, we worked on wavelet coefficients of scale 2 because it covers a moderate range of frequency. The equivalent filter is a band pass filter which suppresses noise and removes baseline effect in processing. Therefore, the wavelet coefficients of ROI at scale 2 are computed. Then positive maximum-negative minimum coefficients are detected by thresholding and are paired based on their distances producing modulo maxima. The zero crossing points of modulo maxima with a delay refer to the locations of peaks in the ROI. The metabolite peaks are usually the dominant peak in their neighbors. After detecting peaks in ROI and considering reference signal, a specific range is defined to detect NAA as the dominant peak in that area. The detected NAA peak of each signal is transferred to the location of reference signal NAA in order to align signals automatically. Then narrower ranges are considered for Cho and Cr peaks based on reference signal in order to detect two other metabolites.

III. RESULTS

The proposed method is tested and evaluated using real data and simulated data. MRSI spectra of 10 patients were processed to produce metabolite maps.

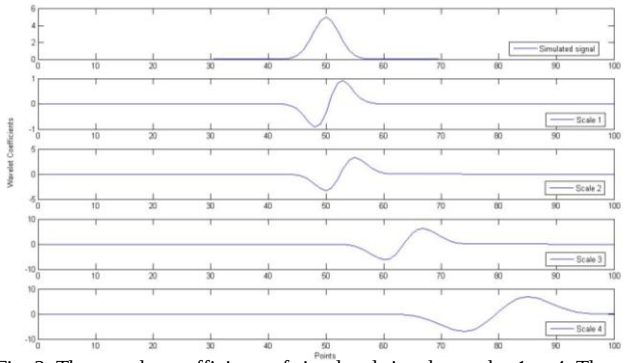

Fig. 2. The wavelet coefficients of simulated signal at scales 1 to 4. There are delayed modulo maxima at different scales representing peak location.

For MRSI simulation, NAA, Cho and Cr peaks were simulated using Gaussian functions with random widths, amplitudes, and locations in order to create main signal [11]. The background signal created using a number of Gaussian functions with appropriate width, location and amplitude was added to the main signal [11]. The final simulated signal was produced by adding white Gaussian noise to the signal [11].The metabolite detection for a real data is shown in Fig. 3. For simulated data, the areas of detected metabolites (NAA, Cho, and Cr) were compared with their actual values. To evaluate method performance on real data, the results were compared with the metabolites derived from Eigentool Software [14]. The accuracy of detection for real and simulated data are reported in Table I. The calculated metabolite maps for one patient are shown in Fig. 4.

IV. DISCUSSION

In this work, a novel method based on WT was introduced for MRSI processing. It does not need any preprocessing that may change or lose some of data information and aligns spectra automatically respect to reference signal. It is expected to be faster than previous method [11] because no modified signal is required to be produced. It performed well on simulated data, whereas the proposed method results for real data were not as accurate as [11]. Multi scale processing [12] can be suggested as an alterative to improve performance. In this way, the detection is started from scale 4 (containing the least noise effect) and ends at scale 1 (having the least delay respect with peak location). It may be also helpful to smooth spectra after peak detection to calculate more accurate peak area. Utilizing match wavelet basis instead of spline basis may improve the performance. Match wavelet basis are designed based on spectra characteristics and may remove the delay between zero crossing point of modulo maxima and the peak.

V. CONCLUSION

MRSI metabolites have shown high potential in diagnosis brain abnormalities. Extracting accurate metabolite characteristics would be important in MRSI processing.

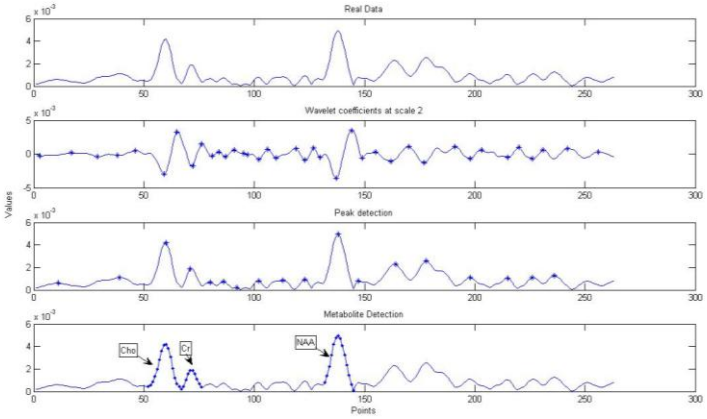

Fig. 3. Metabolite detecting procedure for a real data. The first one is the ROI related to a real data. Modulo maxima detection is shown in the second subplot. The third subplot shows the detected peaks. The NAA, Cho and Cr ranges are shown in the last subplot.

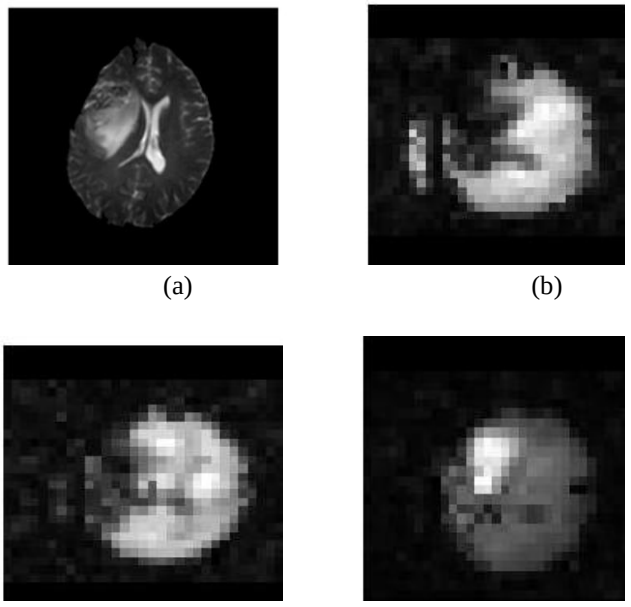

Fig. 4. A 30-year –old man with right frontal brain tumor. a) T2-weighted image. b) NAA metabolite map, c) Cr metablbolite map, d) Cho metabolite map. The decrease of NAA, Cr and increase of Cho represents abnormal region.

TABLE I
Accuracy of metabolite detection for real and simulated data

	Real MRSI data			Simulated MRSI data		
Metabolite	NAA	Cho	Cr	NAA	Cho	Cr
Detection Accuracy	70%	72%	76%	92%	70%	97%

In this paper, a Wavelet based method was proposed to detect main metabolite peaks in MRSI signal without any preprocessing. It is not sensitive to baseline drift and can be developed to produce more accurate results using appropriate Wavelet basis. The extracted features can be used to differentiate brain abnormalities and manage treatment.

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