

MRSI BRAIN TUMOR CHARACTERIZATION USING WAVELET AND WAVELET PACKETS FEATURE SPACES AND ARTIFICIAL NEURAL NETWORKS

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ABSTRACT

Magnetic Resonance Spectroscopic Imaging (MRSI) is a non-invasive technique for assessing biochemical fingerprint of tissue composition. The need to differentiate between normal and abnormal tissues and determine type of abnormality before biopsy or surgery motivated development and application of MRSI. There are several technical reasons that make the brain easier than other organs to be examined with MRSI. This paper presents our proposed methods and results for the analysis of the brain spectra of patients with three tumor types (Malignant Glioma, Astrocytoma, and Oligodendroglioma). After extracting features from MRSI data using wavelet and wavelet packets, we use artificial neural networks to determine the abnormal spectra and the type of abnormality. We evaluated the proposed methods using clinical and simulated MRSI data and biopsy results. The MRSI analysis results were correct 97% of the time when classifying the spectra of the clinical MRSI data into normal tissue, tumor, and radiation necrosis. They were correct 72% and 83% of the time when determining tumor types using the clinical and simulated MRSI data, respectively.

1. INTRODUCTION

One of the recent and important applications of nuclear magnetic resonance technology is Magnetic Resonance Spectroscopic Imaging (MRSI). This technique is used for noninvasive determination of biochemical properties of tissue useful for diagnosis and treatment evaluations [1]. To this end, certain parameters are extracted from the voxel spectra by applying complicated analysis on them [2]. In recent years, a variety of investigations and research have been reported on the diagnostic applications of these signals. In particular, proton MR spectroscopy has been used to detect and characterize abnormal tissue. As in imaging, there are technical reasons that make the brain imaging easier than other organs: motion artifacts are

minor, shimming is relatively easy to perform, and there is no detectible lipid in normal brain tissue [2]. In addition, due to non-invasive property of this method, it could be a good candidate for brain diagnostics. In brain MRSI data, detecting and extracting the peaks related to certain metabolites such as creatine (Cr), choline (Cho), and N-Acetyl Asparatine (NAA) are of significant importance [1]. Cr is involved in energy production in cell mitochondria. Cho takes part in membrane and neurotransmitter synthesis. NAA is contained only in neurons. Different kinds of brain lesions have certain effects on these metabolites [2]. Our goal in this research was to detect and segment tissue abnormalities by extracting the biochemical features related to these peaks in the MRSI data of brains with tumors. As discussed above, each of these metabolites has a specific role in the brain tissue and based on available clinical data, each brain lesion will have different effects on these metabolites. Therefore, applying appropriate processing methods to the MRSI data can be useful in differentiating between normal tissues and tumors and between different tumor types. Our final goal is to develop novel processing methods to determine the type of abnormality automatically.

2. METHODS

2.1. Preprocessing

2.1.1. Noise Reduction Using Wavelets

For many signals, the low-frequency content is the most important part. It is what gives the signal its identity. The high-frequency content, on the other hand, imparts flavor or nuance. In wavelet analysis, we often speak of approximations and details. The approximations are the high-scale, low frequency components of the signal. The details are the low-scale, high frequency components [3]. The noise components of a noisy MRSI signal have most of their significant coefficients in detail parts of the wavelet transform domain. We apply wavelet transform,

vanish the noise coefficients by thresholding the detail components and take the inverse transform of the remaining coefficients to get denoised data. The thresholding method compares details coefficients with a threshold estimated using Donoho's proposition:

$$T_i = C\sigma_i \quad (1)$$

where T_i is the threshold for the i -th level of denoising and σ_i is the median of absolute value of details in the i -th level, divided by 0.6754 [3]. We gave C a value of 3 and applied thresholding for 3 levels using `coiflet3` wavelet.

2.1.2. Noise Reduction Using Wavelet Packets

De-noising is one of the interesting applications of wavelet packet analysis. The wavelet packet de-noising procedure involves four steps: 1) computing the wavelet packet decomposition of signal x at level N . 2) For a given entropy, computing the optimal wavelet packet tree. 3) Thresholding of wavelet packet coefficients. This threshold is a reasonable first approximation for most cases. However, it should be refined by trial and error so as to optimize the results to fit particular analysis and design criteria. We used SURE (Stein's Unbiased Risk Estimate) method in which the threshold equals [3]:

$$T = \sqrt{2 \log_e(n \log_2(n))} \quad (2)$$

where n is the number of samples in the signal. This method works well if the signal is normalized in such a way that the data fit the model $x(t) = f(t) + e(t)$, where $e(t)$ is a Gaussian white noise with zero mean and unit variance. Due to the nature of our signals they could be modeled in this way, therefore we used this thresholding method for 3 levels using `Daubechie10` wavelet. 4) Computing wavelet packet reconstruction based on the original approximation coefficients at level N and the modified coefficients.

2.1.2. Baseline Correction

There are several factors 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 [5]. Therefore, we have developed a method for correcting baseline by thresholding the low frequency wavelet coefficients.

2.2. Feature Extraction

2.2.1. Wavelet Transform

Due to the low SNR (Signal to Noise Ratio) of the MRSI data, automatic determination of the peaks locations is not simple [2]. One major advantage afforded by wavelets is the ability to perform local analysis – that is, to analyze a localized area of a larger signal [3]. We use wavelet transform (`Daubechie10`) for analyzing the local areas related to each peak and segregate metabolite peaks by thresholding the wavelet coefficients and finally 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 the wavelet coefficients.

2.2.2. Wavelet Packets

The wavelet packet method is a generalization of wavelet decomposition that offers a richer range of possibilities for signal analysis [3]. In wavelet analysis, a signal is split into an approximation and a detail. The approximation is then split into a second-level approximation and detail, and the process is repeated. In wavelet packet analysis, the details as well as the approximations can be split [3]. This offers the richest analysis: we applied wavelet packets algorithm to our signal for 3 levels (`Daubechie10`) and extracted the statistical parameters such as mean, maximum, and variance values of the coefficients of each sub-band. We used these statistical parameters as other features extracted from the signal. In this way, we had features expressing the whole signal characteristics despite the above method, in which we only used the features related to specific regions of the signal (metabolite peaks).

2.3. Classification

Artificial Neural Networks (ANN's) are one of the most common classifiers used in MRSI processing [6]. We used multilayer perceptron neural networks to classify the features extracted from the spectra. As mentioned before, we applied two processing methods to extract features from the signals. The first method using wavelet transform extracted the features related to metabolite peaks and the second one extracted several features expressing the whole signal characteristics. We used these two classes of

features in various sets to find the best features describing each lesion.

In order to train the network and verify its ability to distinguish between different tumor spectral features we divided the available data into 2 sets. The first set was used for training and the remaining set was used for testing.

2.4. MRSI Data

To test and evaluate the proposed methods, we used clinical and simulated MRSI data. The clinical data were the MRSI and biopsy results from the brains of seven patients (mean age = 43, range = 38-50, two female, five male) affected by three types of tumors (Malignant Glioma, Astrocytoma, Oligodendroglioma) and focal necrosis. The MRSI data were acquired using a 1.5 T MRI System (GE Signa).

To generate the simulated MRSI data, we constructed three main peaks for the brain metabolites 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. We also used the available clinical data and the effect of each brain lesion on the spectra to simulate the spectra related to each lesion.

3. EXPERIMENTAL RESULTS

Denosing results show about 5dB and 7dB SNR improvement using wavelets and wavelet packets, respectively. Therefore using wavelet packets could remove the available noise in MRSI signals better than wavelets.

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. Alternatively, a high-pass filter was applied to the signal whose results were 24% less effective than our proposed method.

The results of classifying the extracted features into three classes (tumor, necrosis, and normal) for both of the methods are shown in Tables 1-2. As can be seen, we used different sets of the features for training and testing the networks to find the best features. In the case of wavelet features (which are peak features) we obtained the best accuracy when we used peak area ratios, which was 90% for the test data (see Table 1). We also used different sets

of wavelet packets features separately to find the best features in this domain. The results of classifying these features show about 7% improvement compared to the previous features. This shows that these features can describe the spectra and the effects of lesions on them better than the previous ones. The best features in this group, as seen in Table 2, were the maximum and mean values of the coefficients of each sub-band of wavelet packets in level 3. The accuracies of the networks trained with these features were 95.6% and 95% for the maximum and mean, respectively. When we used both of these features for training the network, we obtained a higher accuracy at 97.3%.

In the next step, we used artificial neural networks to classify the tumor spectra into 3 types (Glioma, Oligodendroglioma, and Astrocytoma). Due to the sample size limitation, we used a leave one out method for training and testing of the network. We used the best features obtained in the previous methods (maximum and mean values of the coefficients of each sub-band of wavelet packets domain in level 3). The classification accuracy results were: 71% for Glioma, 75% for Oligodendroglioma and 69% for Astrocytoma. We also used the simulated spectra for each brain tumor type for training and testing of the network. The classification accuracy results were: 82% for Glioma, 85% for Oligodendro-glioma, and 83% for Astrocytoma.

4. SUMMARY

We have developed and applied novel processing methods to extract useful features from the MRSI signals and classify the spectra of the brain tumors. We considered two denoising methods using wavelets and wavelet packets to suppress the noise. The results of using wavelet packets were about 2 dB superior to those of the wavelets. We also removed the baseline distortions from the signals. Then, we applied the two preprocessing methods to prepare the signals for feature extraction. In the feature extraction step, we applied wavelets and wavelet packets as two separate methods. After applying the extracted features from each method to ANN, we obtained superior results using wavelet packets features extracted from the entire signal than the wavelet features extracted from the peaks. This suggests that brain lesions affect the entire signal in addition to the metabolite peaks. The best features were the maximum and mean values of the coefficients of each sub-band of wavelet packets in level 3. We also classified the tumor spectra into three types using the best features obtained. The classification results showed 72% accuracy for the clinical data and 83% accuracy for the simulated data.

5. CONCLUSION

MRSI signals can improve diagnosis of brain lesions based on their information about tissues biochemical construction. We developed and applied new algorithms for these signals. We were able to extract useful information for detecting and characterizing different brain lesions. The results indicate that the proposed methods extract from the MRSI data the effects of each brain lesion on the metabolites. Therefore, the proposed methods have the potential to non-invasively determine the type of the brain tumor. Future work needs to include more patients and other brain lesions. Feature extraction method needs to be optimized to improve the overall accuracy of the proposed approach. Because this approach is the only non-invasive method for biochemical identification, it has a great potential for brain diagnosis and may replace the conventional invasive methods such as biopsy [6].

6. REFERENCES

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Table 1. ANN classification accuracy using the features extracted by the wavelets. Networks were trained and tested for different sets of features. The features were peak areas, peak area ratios, maximum values of the peaks, and peak widths.

Features	No. of Features	Network Structure	Overall (%)	Tumors (%)	Radiation Necrosis (%)	Normal Tissue (%)
All	15	15-20-3	88	94	86	85
Peak areas	3	3-5-3	89	92	86	88
Area Ratios	6	6-5-3	90	96	85	91
Max values	3	3-7-3	82	87	88	72
Peak widths	3	3-7-3	76	65	73	91
Peak areas + Area Ratios	9	9-12-3	87	96	85	82
Max values + Area Ratios	9	9-12-3	82	80	91	75
Peak widths + Area Ratios	9	9-12-3	81	75	78	92

Table 2. ANN classification accuracy using the features extracted by the wavelet packets. Networks were trained and tested for different sets of features. The features were maximum, variance, and mean values of the coefficients of each sub-band in level 3.

Features	No. of Features	Network Structure	Overall (%)	Tumors (%)	Radiation Necrosis (%)	Normal Tissue (%)
All	24	24-12-3	96.6	98	96	96
Max	8	8-10-3	95.6	96	95	96
Variance	8	8-10-3	85	82	90	84
Mean	8	8-10-3	95	95	98	93
Max + Mean	16	16-10-3	97.3	98	97	97