

Tissue Characterization by Fuzzy Clustering of Wavelet Denoised MRSI Data

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Abstract

A relatively new method of MR techniques, known as MRS, is an efficient approach to specify chemo-physical structures of living organs, invasively. Proton Magnetic resonance spectroscopy is used to detect abnormal tissues widely. In this paper we propose wavelet based denoising method and apply fuzzy clustering to the extracted features of spectra to detect background, normal, semi-cancered and cancered tissues. The results show that the ratios of the area under peaks of choline, creatine and Aspartate to the NAA for the cancered tissues are greater than healthy tissues.

Key words – MRS, Wavelet Transform, Denoising, Feature Extraction, Clustering, Fuzzy.

1. Introduction

Magnetic Resonance Spectroscopy (MRS) is a relatively new, efficient and non-invasive method to detect chemo-physical structures of living organs [1]. It has some clinical applications such as investigation of cancered tissue, active regions in the brain, propagation of drug or temperature in the body and PH metry. However, MRS is time consuming and needs complex and heavy cost processing because of high sensitivity to magnetic field

inhomogenities, low SNR and large amount of data.

In this paper we propose a method to reduce MRS data noise using wavelet transform. Then we consider the area under some important metabolites' (Choline, Craetine, Aspartate, NAA) peaks as features that can be extracted from MRS data (Fig.1). We detect 4 clusters for brain voxels applying fuzzy c-Means clustering to the ratio of the area under the peak of Choline, Creatine and Aspartate to the area under the peak of NAA

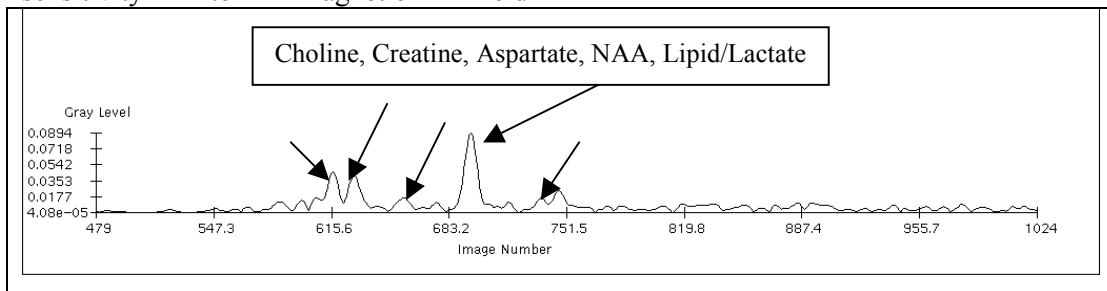


Fig 1. A sample spectrum and the positions of some metabolites in the brain.

2. Methods

2-1. Denoising

Noise reduction using wavelet transform [2,3] is based on this fact that each part (signal and noise) of a noisy signal has its own coefficients in the wavelet transform of noisy signal. Thus if we can vanish the coefficients belonging to the noise and take inverse transform of the remained coefficients, we have denoised data.

We use a thresholding method to specify noise coefficients, i.e., comparing details

coefficients with a threshold which can be estimated using Donoho's proposition [4].

$$T_j = C\sigma_j \quad (1)$$

where T_j is the threshold for the j th level of denoising and σ_j is the median of absolute value of details in the j th level, divided by 0.6754.

We gave C a value of 3 and applied thresholding for 2 levels and used 'Reverse Biorthogonal 1.3' as the mother wavelet.

2-2. Feature Extraction

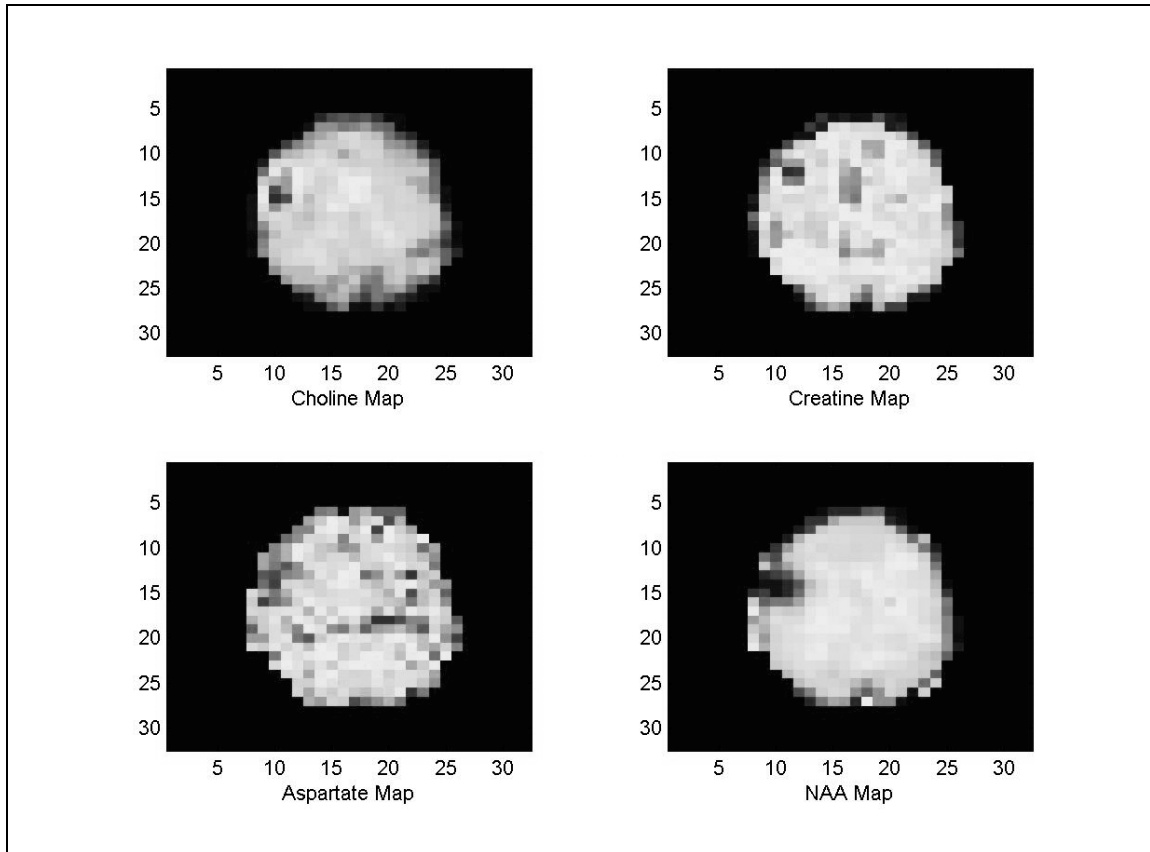


Fig 2. The map of 4 metabolites concentrations in the brain.

Each spectrum indicates some metabolites peaks of its source (related voxel), as seen in Fig 1.

We developed an automated algorithm to detect peaks of metabolites and use their areas as a feature of the related spectrum. A map of each metabolite's concentration is shown in Fig 2. It seems the position of tumor is placed in the upper-left region of the image.

We use the ratio of the sum of area under the peaks of Choline, Creatine and Aspartate to the area under the peak of NAA as the feature of each spectrum to be used by fuzzy clustering.

2-3. Clustering

We use the fuzzy c-Means clustering [5] to classify image voxels into normal, semi-cancered, cancered and background.

3. Results

A noisy spectrum and its denoised version are shown in Fig 3. It should be noted that

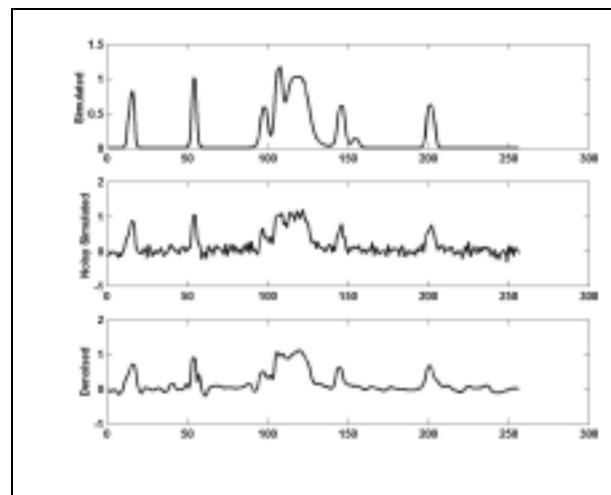


Fig 3. A simulated spectrum, noisy simulated spectrum and denoised simulated noisy data.

our proposed method, broads the flat parts of noisy data and keeps the edges.

The result of fuzzy c-Means clustering shows the location of normal, semi-cancered, cancered and background voxels (see Fig 4). The membership values for 94% of the brain voxels to their clusters are greater than 0.75, which implies the high degree of confidence for the extracted features and clustering result.

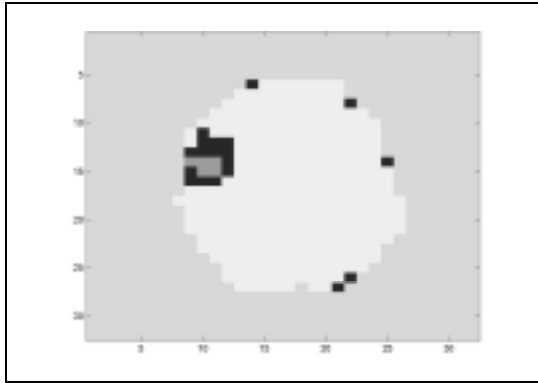


Fig 4. The result of clustering, showing normal, semi-cancered, cancered and background.

4. Discussion and Conclusion

We employ the wavelet transform to reduce MRS data noise successfully and consider the ratio of the sum of area under the peaks of Choline, Creatine and Aspartate to the area under the peak of NAA as features for each spectrum. Applying fuzzy c-Means to this feature vectors yields classification of brain tissues as normal, semi-cancered, cancered and background with the high membership values for the voxels.

As we explained in the beginning of this paper, MRS has a high sensitivity to the magnetic field inhomogenities. It should be noted that a priori knowledge about the brain physiology an function will improve efficiency of feature extraction and interpretation the clustering result and their applications for medical decision-making and therapy.

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