Tissue Characterization by Fuzzy Clustering of Wavelet Denoised MRSI Data

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Contents

Introduction

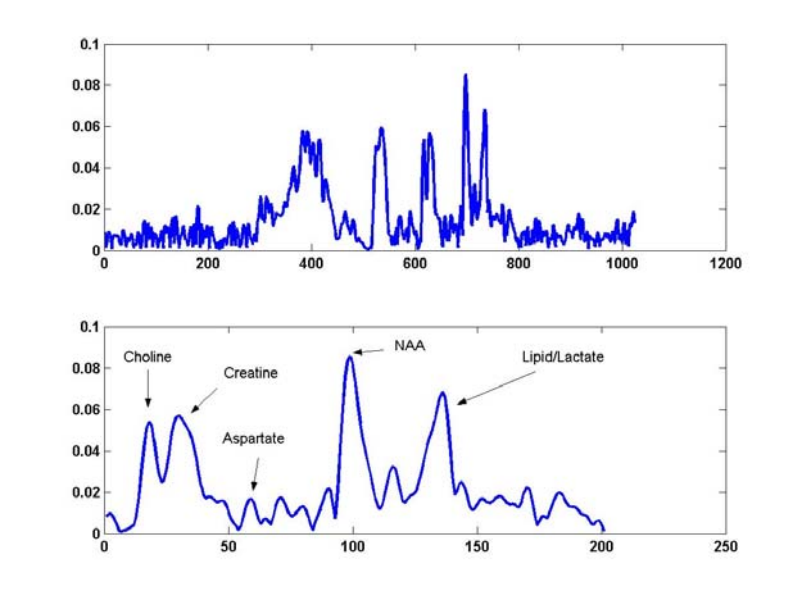
- Data acquisition in MRS
  - Use 3 gradients to localize a single voxel
  - Apply Fourier transform to FID signals to get spectra
- MRS Applications
  - ^{1}H : Tissue characterization
  - ^{31}P: Metabolism consideration, PH metry
  - ^{13}C, ^{19}F: Agent tracing,therapy evaluation

- ^{23}Na: Cellular environment consideration

- MRS Problems
  - Low SNR
  - Poor resolution
  - High sensitivity to magnetic field inhomogenities
  - Time consuming
  - Large amount of data

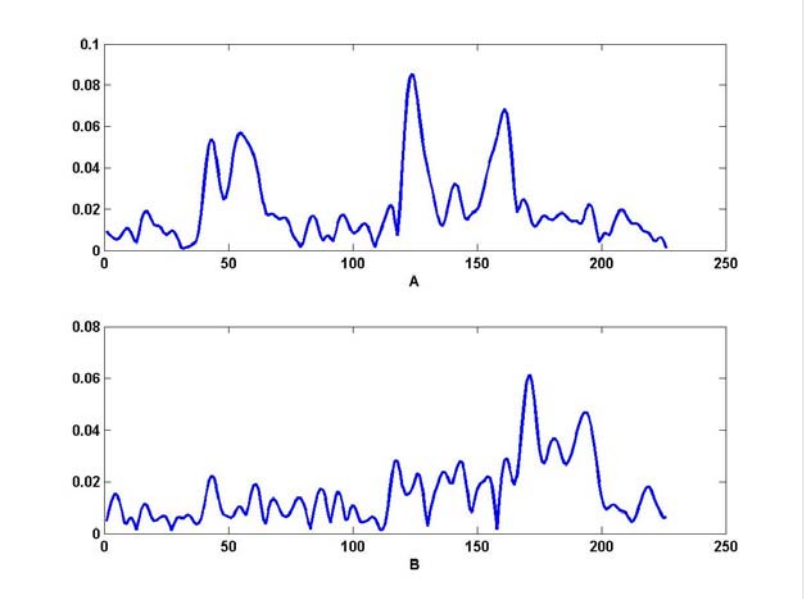
Tissue Characterization

- Our Goal
  - Detecting normal and abnormal tissues using their spectra

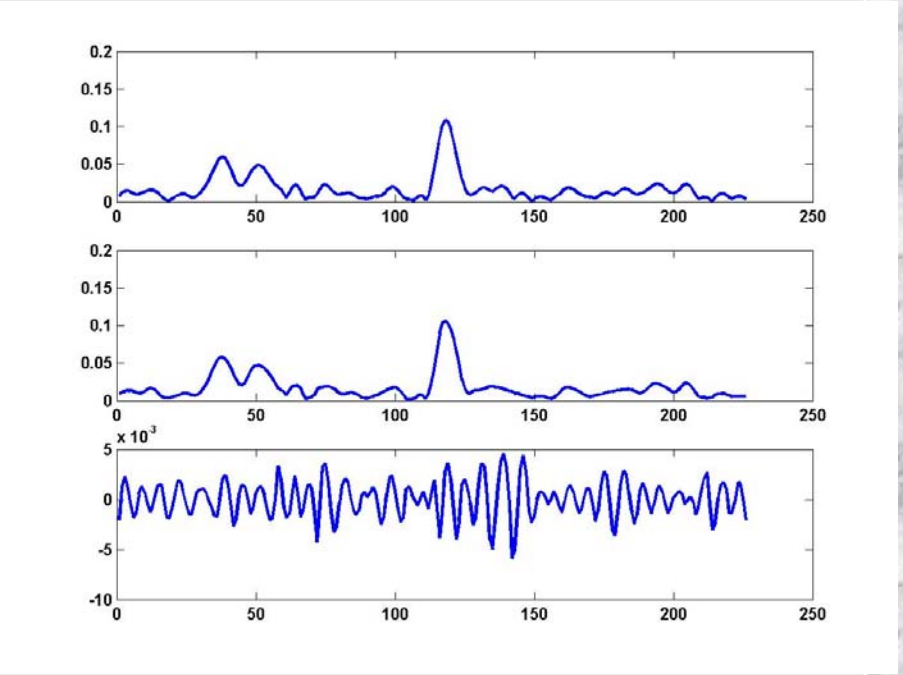


Methods

- Preprocessing
  - Classify spectra to brain and background regions
    - Background spectra have no fixed style
    - Correlation coefficient of background spectra is less than brain spectra

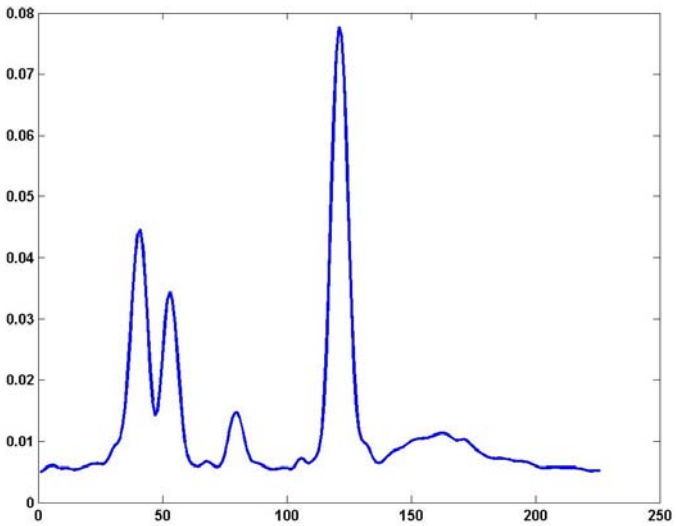


- Wavelet denoising
  - Find wavelet transform of the spectra
  - Compare details coefficients with a threshold
  - Remove details coefficients which are less than the threshold
  - Find inverse wavelet transform of the remaining coefficients



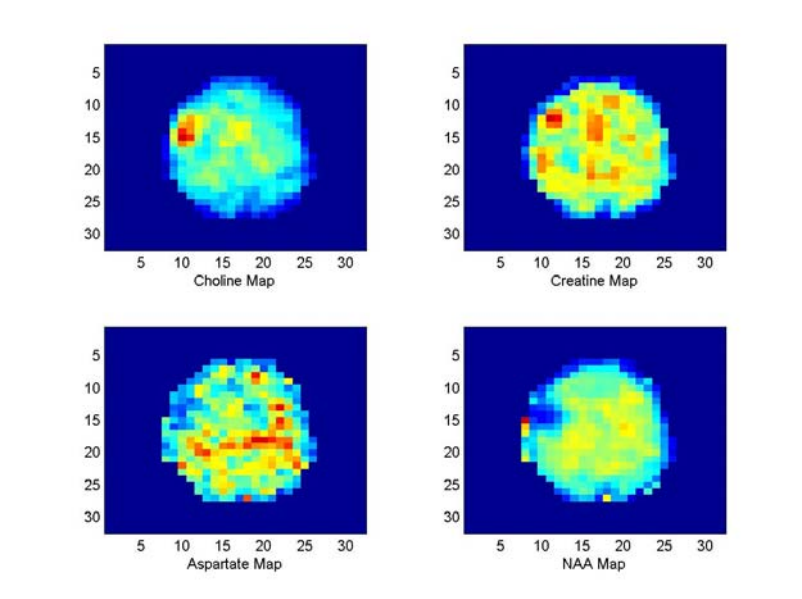
- Peak Detection
  - We specify the limits of each metabolite using the reference spectrum

  (the reference spectrum is the mean of spectra in a slice)
  - The metabolites' limits can be specified by finding local minima and maxima of the reference spectrum



Feature Extraction

- The whole spectrum
- The areas under peaks of Choline, Creatine, Aspartate and NAA
- The areas under peaks of Choline, Creatine and Aspartate normalized to the area under peak of NAA



- Clustering
  - Applying Fuzzy c-Means

Number of clusters = 4

$$u_{ik} \in [0,1], \quad 1 \le i \le c, 1 \le k \le n$$

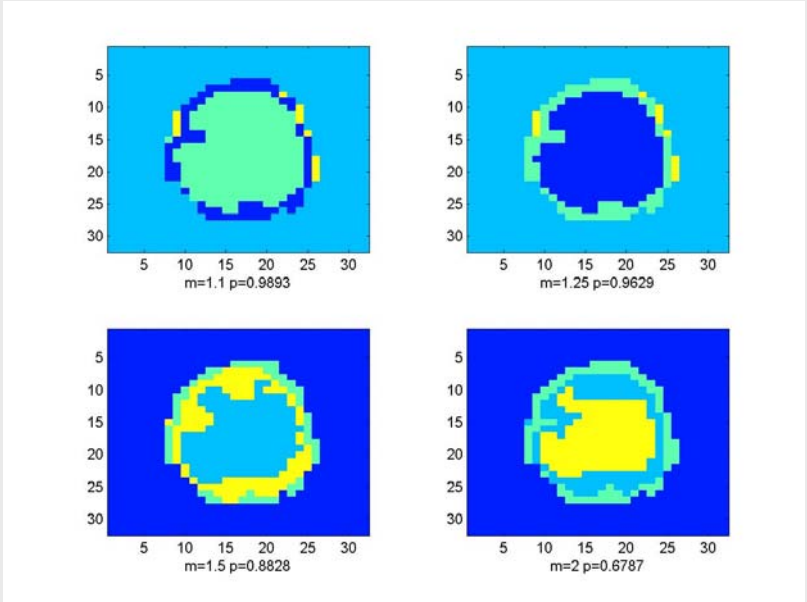
$$\sum_{i=1}^{c} u_{ik} = 1, \quad 1 \le k \le n$$

$$\sum_{k=1}^{n} u_{ik} > 1, \quad 1 \le i \le c$$

$$J_m(U,v) = \sum_{k=1}^{n} \sum_{i=1}^{c} (u_{ik})^m \left| x_k - v_i \right|^2$$

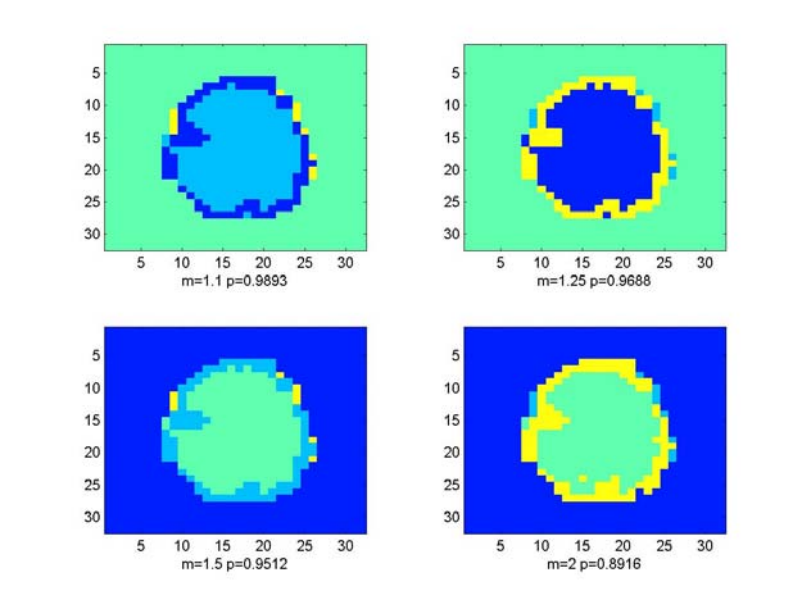
- The whole spectrum results

m = 1.1, 1.25, 1.5, 2



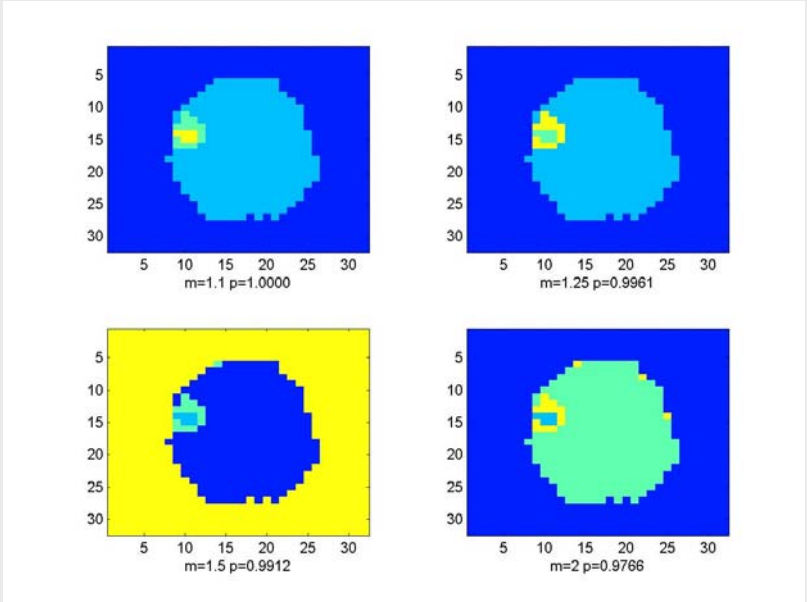
- The areas under each metabolite results

m = 1.1, 1.25, 1.5, 2



- The normalized areas results

m = 1.1, 1.25, 1.5, 2



Conclusion

- Wavelet transform can be used to reduce the noise of MRS Data.
- The areas under peaks of Choline, Creatine, Aspartate and NAA can be used to detect abnormal tissues.
- The areas under peaks of Choline, Creatine, Aspartate normalized by NAA are suitable features to detect abnormal tissues.

Discussion

- The imaginary parts of spectra may be useful to classify the spectra.
- Wavelet transforms can be used to improve the peak detection routine.
- A priori knowledge (medical) may be used to determine the optimal number of features.
- A priori knowledge (medical) may be used to improve interpretation of the results.

Thank You