Self-Organizing Neural Network for Pattern Recognition of Short Echo Time ^{1}H NMR Brain Spectra.

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Introduction

The aim of this study was to apply artificial neural network (ANN) analysis to discriminate between ^{1}H NMR brain spectra of inborn metabolic encephalopathies in children and normal volunteers.
The method used was a dimension reduction technique based on Kohonen ANN (Self-Organizing Map (SOM)) (1) which allows visualization of complex short echo time proton spectra into simple geometric relationship on a two dimensional display. The process is an unsupervised learning algorithm. It may be used to find clusters and the similarity between the input spectra.

Methods

Spectroscopy

Studies were performed using a 1.5 T MR Siemens SP63 system. Spectroscopy data were obtained using the stimulated echo acquisition mode (STEAM TE=20ms, TM=30ms, TR=1500ms, volume of interest = 8 ml) sequence in white matter. A spectrum was typically acquired in 256 scans. The study was conducted on 26 spectra (2) obtained from 10 children suffering from different lysosomal diseases (LD), 11 boys with X-linked adrenoleukodystrophy with various stages of disease from stage 0 to stage 3 ((X-ALD st0-st3) and 5 healthy children (control). The X-ALD st0 and 1 are children with no cerebral form of the disease and a child suffering from X-ALD st3 is a patient at the end stage of the disease.
The Hankel Lanczos Singular Value Decomposition HLSVD (3,4) method was applied to the time domain data to remove the dominating residual water resonance. After Fourier transform, phase and baseline correction of the spectra were done manually. To standardize the spectra, the intervals in the range of 0-4.5ppm was selected and normalized (each data point was divided by the sum of components in the selected region) with respect to N-acetyl-aspartate (NAA) signal at 2.0 ppm.

Artificial Neural Network

Analyses were carried out using the SOM Program Package (5) with MATLAB (6) which provides an objective way of conducting pattern recognition. The 271 data points in the region of 0 to 4.5 ppm of the 26 spectra were used in the input vector of SOM analyses. SOM consists of network neurons arranged on a hexagonal lattice grid (Figure 1). During the iterative process the algorithm performs an ordering of the neurons. Each neurons in the lattice stores a set of patterns which corresponds to a cluster center (Figure 2).

Results

The resulting patient map (Figure 1) shows that SOM is able to organize spectra in groups. Similar spectra are closer to each other in the grid than the more dissimilar ones. The position of each spectrum on the patient map correlates with the metabolic features characterizing the pathologies. The spectrum of a control child is presented in Figure 2, neuron (1,1). The LD spectra are grouped in the vicinity of high values of inositol and low values of NAA (Figure 2, neuron (1,5)). For X-ALD most patient spectra have an increase of lipids and a decrease in NAA (Figure 2, neuron(6,5)). Children at stages 0 and 1 of X-ALD are often found on the control neurons.

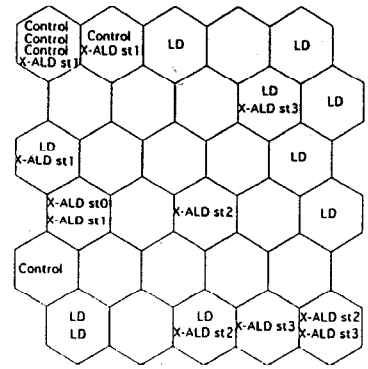

Figure 1: The resulting hexagonal grid patient map (6x5 neurons) obtained with SOM.

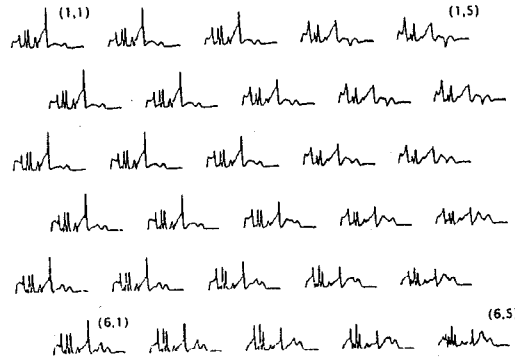

Figure 2: SOM of 26 ^{1}H NMR spectra. Each neuron in the hexagonal grid displays a different spectrum pattern.

Discussion

SOM has been applied to classify complex data spectra. The visual inspection of the SOM map shows the variations of the metabolic profiles in spectra. In some cases, the location of a patient in a specific neuron is unexpected (X-ALD st3, neuron (2,4)). Some overlap is noted between LD and ALD pathologies. Nethertheless, this approach constitutes an alternative way to analyze and compare quickly metabolic modifications in a small population of patients without having to process the signal areas of the metabolites in the spectrum.

Conclusion

We have demonstrated that using the pattern recognition capability of the SOM, we were able to classify into separate groups the LD and the X-ALD and the healthy children. These results show that SOM is a practical method for the automated interpretation of a limited number of spectra and could prove useful for rapid clinical classification.

References

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