Automatic Detection of Lipid Peaks in MR Spectroscopic Image Data using Artificial Neural Networks

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Introduction: Presence of lipids in brain parenchyma may indicate the active de- or re-myelination in multiple sclerosis (MS). Magnetic resonance spectroscopic imaging (MRSI) can provide tissue biochemical information *in vivo*. Manual examination of each voxel for the presence of lipid peak in MRSI data is tedious due to the number of voxels. This problem becomes more acute in multicenter clinical trials where large data need to be analyzed. To alleviate this problem, we have developed an automatic and rapid procedure that based on artificial neural networks (ANN) for identification of lipid peaks in MRSI data.

Methods: Data Acquisition: Proton MRSI data was acquired on 1.5 T scanner with a spin echo sequence with variable TR (maximum of 1000 ms) and TE equals to 30 ms. Acquisition was localized to centrum semiovale region in brain with approximately 100 mm (A/P) x 100 mm (R/L) x 15 mm (S/I) volume. Three chemical shift selective (CHESS) pulses for water suppression and eight outer volume suppression pulses for minimizing extramenengeal tissue contamination were incorporated into the sequence. Other acquisition parameters were: spectral bandwidth=1000 Hz, number of complex points=256, FOV=240x240 mm^2, and number of phase-encoding steps=32x32. In addition, water unsuppressed MRSI data were also acquired with identical parameters as the metabolite data, except for 16x16 phase-encoding steps, for automatic spectral processing [1]. Localizer image was acquired to generate a mask of the spectroscopic volume-of-interest (VOI). Spectral preprocessing and phase correction were performed as suggested in ref [1]. RBFNN: The radial basis function neural network (RBFNN) can be represented by the parametric model [2]: $y_k = \sum_{c=1}^{m} w_{ck}\phi_c\left(\|\mathbf{x}-\boldsymbol{\mu}_c\|\right)$ where $\mathbf{x}$ is an input MR spectrum, w_c's are the network weights and m is the number of basis functions; ϕ_c is the basis function of the network and in case of the Gaussian function it is defined as [3] $\phi_c(\mathbf{x}) = \exp(-\|\mathbf{x}-\boldsymbol{\mu}_c\|^2 / 2\sigma_c^2)$ where $\boldsymbol{\mu}_c$: vector determining the center and σ_c: width of the basis function ϕ_c. The characteristic set $\{\boldsymbol{\mu},\sigma\}$ of the Gaussian basis functions are determined from a set of input training vectors. The network weights in the output layer are computed using *input-output* paired training data sets. Network Training: RBFNN is trained with randomly selected spectra with and without presence of lipids peaks. Spectral length ranged from 0.8 to 1.8 ppm is given as input to the network for training. The error function minimized during the training is $E(w) = \frac{1}{2}\sum_{n=1}^{N}\left[\sum_{i=1}^{m} w_i\varphi_i(\mathbf{x}^n) - t^n\right]^2$ where t^n is the targeted output for input vector $\mathbf{x}^n$, m (=10) is the number of basis functions and N (=150) is the number of spectra used for training. Voxels with bad spectral quality are automatically identified and discarded for analysis as described in ref. [4].

Fig. 1: Schematic representation of RBFNN processing for lipid peak identification in the spectrum

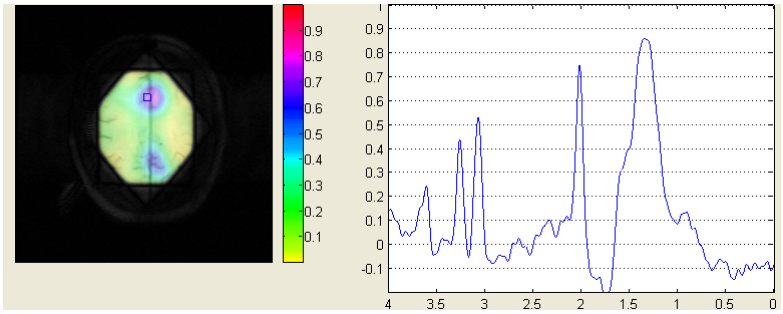

Fig. 2: Left: Overlay of the map of RBFNN output values for all voxels on localizer VOI. Right: Spectrum from the voxel (shown as blue color box on the map) with network output value 0.75 has shown the presence of lipid

Results & Discussion: Figure 1 shows the schematic representation of lipid peak identification using the RBFNN. From the input spectrum, RBFNN analyzes the spectral region between 0.8-1.8 ppm to determine the presence of lipid peak. The output is a normalized value between 0 and 1. Output value close to zero indicates no lipid peak and close to one represents the presence of very strong lipid peak in the spectrum. For all the data, spectrum with output value above 0.7 showed presence of lipid peaks. This threshold value is determined based on the observation made from large number of voxels. Overlay of the smoothed output values for all voxels on localizer image is shown in fig. 2. Spectrum showed in fig. 2 is from the voxel with RBFNN output value 0.75. Presence of strong lipid peak can be observed. This method was applied in the analysis of MRSI data of primary progressive multiple sclerosis (PPMS) patients as part of multicenter clinical trial [4].

In conclusion, RBFNN can be an accurate, robust and automatic tool for rapid detection of lipid peaks in MRSI data.

References: [1] Doyel et al, J Magn Reson, 1995. [2] Bhat et al. JMR, 2006. [3] Bishop CM, Oxford Press, 1995. [4] Sajja et al, Mult Scler, 2008.