Fast Analysis Of 1H Magnetic Resonance Spectroscopic Imaging Data: An Artificial Neural Network Based Approach.

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INTRODUCTION: Accurate quantification of the MRSI-observed regional distribution of metabolites involves relatively long processing times. This is particularly true in dealing with large amount of data that is typically involved in multi-center clinical studies. To significantly shorten the processing time, we have implemented an Artificial Neural Network (ANN) based approach to quantify phase corrected (as opposed to magnitude) spectra. This method was tested on simulated and normal human brain data. The metabolite area ratios for normal subject data were compared with line fitting (LF) method and published values.

METHODS: Data acquisition: Two-dimensional MRSI was acquired on a 3 T Philips Intera scanner using the PRESS localization and 24x24 phase encoding steps. The sequence parameters were TR = 1500ms and TE = 39ms, spectral width = 2000 Hz, number of points = 1024, and slab thickness = 12 mm. Unsuppressed water spectra with identical sequence parameters except for 12x12 phase encoding steps were acquired for automatic phase correction and inter-voxel spectral alignment.

Preprocessing: Spectral preprocessing and phase correction were performed as suggested in [1 & 2]. The spectra were corrected for B0 inhomogeneity using water reference deconvolution [3]. A Wiener filter approach was developed and implemented to make the deconvolution procedure more effective in the presence of varying amount of noise in the spectrum. Particularly at low TE, the baseline removal is a crucial step for accurate quantification, due to the presence of broad macromolecular resonances. Baseline correction was implemented as a preprocessing step, using Wavelet shrinkage [4].

Quantitation: Radial basis function neural networks (RBFNN) were used for the spectral quantitation. RBFNN (Fig. 1) were preferred over the Multilayer Perceptron (MLP) due to their faster training speeds. The normalized peak of interest, which is automatically identified from the input spectrum based on *apriori* information about position and local gradient information, is given as input to the network. The network outputs are the amplitude, linewidth and proportion of Lorentzian in the peak. These parameters are used in computing the area under the peak. The networks were trained with simulated data sets using the Voigt lineshape (linear combination of Lorentzian and Gaussian). Following parameter variations were used in training: i) Full width at half maximum (FWHM): 1.9531– 13.6719 Hz; ii) proportion of Lorentzian: 0-1; iii) Amplitude: 0 -1.5. Gaussian noise equivalent to 3% of the maximum signal amplitude was added to the input peaks, to make the networks more robust. The basis functions were selected by training a Gaussian mixture model for the input data set with the Expectation Maximization algorithm [5]. The optimal number of basis functions was set using an early stoppage criterion. Since the peaks are identified locally in each spectrum, there is no *apriori* information about the length of input vector to the RBFNN. To take care of this problem, multiple RBFNN's with wide range of input vector lengths were trained. The RBFNN with input vector length closest to identified peak is automatically chosen for quantification. Separate RBFNN's were trained to account for the overlapping peaks, as shown in Fig 2. This step significantly improved the accuracy of estimation of the peak parameters for Cr and Cho.

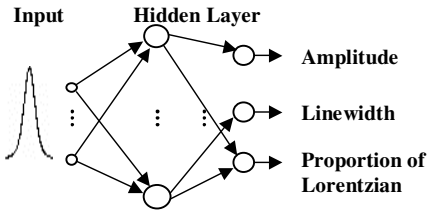

Fig1: RBFNN for quantification of peaks

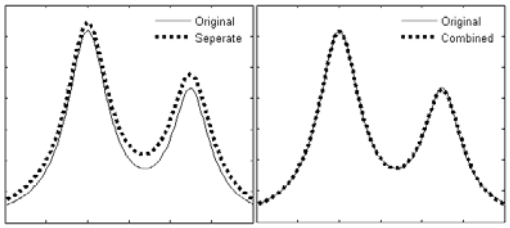

Fig 2: Estimation without (left) and with (right) overlap

Area Ratios	NAA/Cr	Cho/Cr
RBFNN	1.58 (0.13)*	0.90 (0.08)*
LF [2]	1.60 (0.11)*	0.95 (0.08)*
Published [6]	1.59	0.96

Table 1: *Area Ratios for NC (N = 7). Values reported as mean (std). * implies values statistically insignificant.*

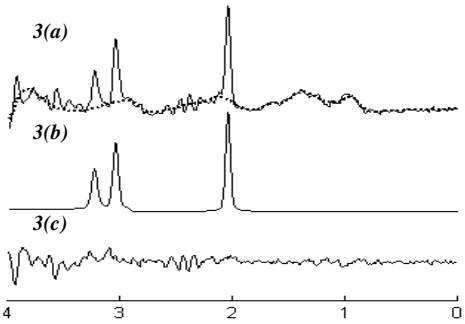

Fig 3(a): *processed input spectrum (solid), estimated baseline (dash),* ***3(b):*** *estimated spectrum,* ***3(c):*** *error in estimation.*

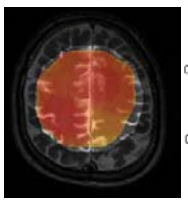

Fig 4: NAA metabolite map.

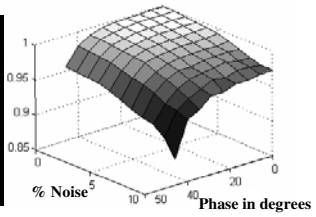

Fig 5: Correlation coefficient. for area.

CONCLUSION: An accurate, robust, automatic and fast method for quantification of MRSI data based on RBFNN is presented. This is the first study to use ANN for quantitation of phased spectra as opposed to magnitude spectra. Results show that this method is comparable to the LF method. The computational time on a typical PC was around 15-20 seconds compared to 30-40 minutes for line fitting methods. This method is amenable to implementation in parallel computing environment, reducing the time even further and making real time analysis practical.

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