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Segmentation of central nervous system tumor images with neural networks*

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Abstract

Tumor image segmentation represents a crucial step not only in the diagnosis of the disease but also in its evaluation and monitoring of treatment. In the present work, neural networks are used to recognize the presence of tumoral tissue in central nervous system on magnetic resonance images generated by *in vivo* spectroscopy and relaxometry. Relaxation data was validated and categorized by means of spectroscopic data, used as a sort of virtual biopsy. Neural networks were trained with the relaxation data in a supervised mode, assuming three categories for the tissue: tumoral, normal or unaffected and liquid or necrosis. Segmentation performed in this way correlates closely to other methodologies previously developed, shortening drastically the processing time what makes it very useful in its clinical application.

Key words: Image segmentation; *in vivo* spectroscopy; neural networks; relaxometry; tumor.

Segmentación de imágenes de tumores de sistema nervioso central mediante técnicas de redes neuronales

Resumen

La segmentación de imágenes de tumores representa un paso crucial no solamente en el diagnóstico de la enfermedad en su evaluación y monitoreo durante el tratamiento. En el presente trabajo, las redes neuronales son utilizadas para reconocer la presencia de tejido tumoral sobre imágenes de resonancia magnética generadas por espectroscopia *in vivo* y relaxometría. Los datos de relajación fueron validados y categorizados mediante el uso de la información espectroscópica. Las redes neuronales fueron entrenadas con los datos de relajación en modo supervisado, suponiendo tres categorías para el tejido: tumoral, normal o no afectado y líquido o necrosis. La segmentación realizada en esta forma correlaciona muy bien con la obtenida por otras metodologías desarrolladas previamente, disminuyendo dramáticamente el tiempo de procesamiento, lo que la hace una técnica muy útil para su aplicación clínica.

Palabras clave: Espectroscopia *in vivo*; redes neuronales; relaxometría; segmentación de imágenes; tumor.

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Introduction

Magnetic Resonance Spectroscopy (MRS) is a non-invasive tool that allows distinguishing brain malignant tumors from non-anaplastic tumors (1). Metabolic maps can be obtained by the Chemical Shift Imaging (CSI) technique but they lack the spatial resolution necessary for therapy considerations (2, 3). Relaxation studies have been used long ago for the assessment of tumors, being the T_2-map of a tissue often used as a basis for interpreting clinical images (4). The combination of both techniques allows for the determination of nosologic maps with appropriate spatial resolution to establish, through segmentation, an accurate determination of Gross Target Volume or GTV commonly used in radiotherapy treatment planning. Neural networks have been extensively used for pattern recognition and classification. In the present work, it is proposed the use neural networks to obtain nosologic maps using information coming from MRS and Relaxometry.

Materials and Methods

CSI was performed axially to obtain spatial distributions of metabolite concentration across the lesion, TE= 30 ms and VOI of 96 cm^3 (80 x 80 x 15 mm). Relaxometry studies were performed using the standard multiecho sequence (CPMG) with 16 echoes, with a base echo time TE = 22 ms and 8 axial slices 5 mm thick centered at the tumor. The relaxation image parameters were set according to CSI voxel matrix; two slices were included within the CSI matrix. The spectroscopy data analysis was performed based on relative values. The critical Cho/NAA ratio value for which a tissue was considered malignant was 1.3 or over. The spectra were considered atypical if the Cho/NAA ratio had a value between 0.9 and 1.29 and normal or unaffected below 0.9. Necrosis was established when all the metabolites intensities were low. For the analysis of relaxation data, a special image processing algorithm was developed to extract the magnetization decays for different regions of interest or ROI´s coming from within a CSI voxel. All the decay patterns coming from a particular CSI voxel were classified according to the state of the tissue (normal, pathologic, necrotic or edema) determined by the CSI spectrum as explained before. In this way CSI information was used as a sort of virtual biopsy for each voxel as shown in Figure 1. The structure of the neural network used in this work was of the perceptron type (5). It included two hidden layers consisting of three neu-

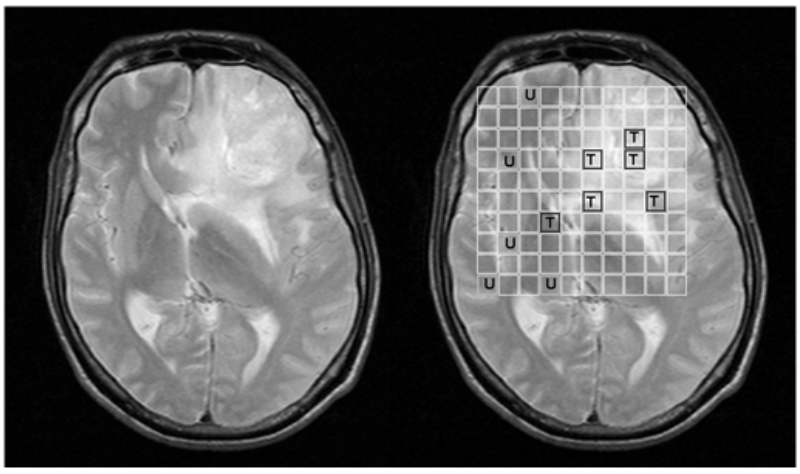

Figure 1. Left, T_2-weighted multiecho image. Right, CSI grid used indicating voxels that correspond to pathologic tissue (T) and normal or unaffected tissue (U).

rons sisting of three neurons each one and an output layer consisting of two neurons, as shown in Figure 2. To provide an input with enough time resolution to separate the different decay patterns, at least twenty bits were used. All exponential decay patterns were normalized to intensity one for the first echo time and in order to convert them to a binary number, i.e., for the neural network input, a threshold value previously determined was used in the following way: any time the decay pattern was above the threshold value a logic one was assumed, otherwise a logic zero. Since the relaxation decay data were only sampled for eight echo times, interpolation was needed. The threshold value was chosen to discriminate between different decay patterns, i.e., the value that imposes the highest differences in the number of significant bits among the decay patterns for the total number of input bits selected. Training was performed using the back-propagation algorithm in supervised mode only (6). To obtain the nosologic map resulting from the neural network classification the following gray palette was used: gray to indicate tumor tissue, white to indicate normal or unaffected tissue and black to indicate edema or necrotic tissue.

Results and Discussion

Analysis of the normalized decay patterns suggested a threshold value of 0.3 to obtain the binary input of the neural network. Since the CSI voxel size included as much as 500 relaxometry voxels, the number of patterns that can be used to train the neural network was about 3000, using only those CSI voxels with a well defined diagnosis, i.e., Cho/NAA ratio above 1.3 to indicate for tumoral tissue, less than 0.9 for normal or unaffected tissue and low metabolite concentrations for necrotic tissue. Some considerations have to be done in the number of iterations for the back propagation used to train the neural network in supervised mode. In Figure 3, the error as a function of the number of iterations during the training of the neural network is represented. This learning plot indicates that there is a global error rise for a certain number of iterations, about 2000, and after that point further training does not improve any better the accuracy of the prognostic, i.e., the global error remains around 50%, the neural network have equal chances to classify correctly. By contrast, for a single pattern, the neural network can reduce the error as low as possible with a number of it-

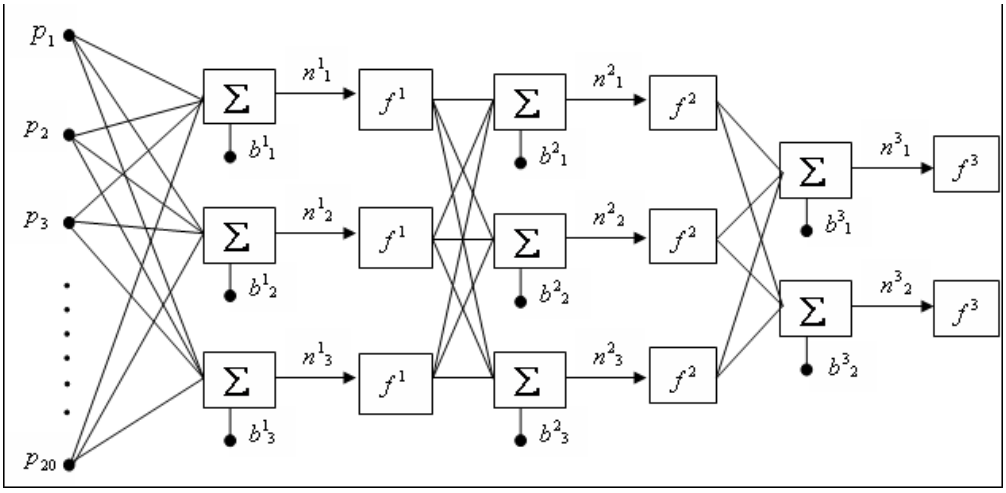

Figure 2. Neural network structure used in this work. Two hidden layers with three neurons each and an output layer with two neurons.

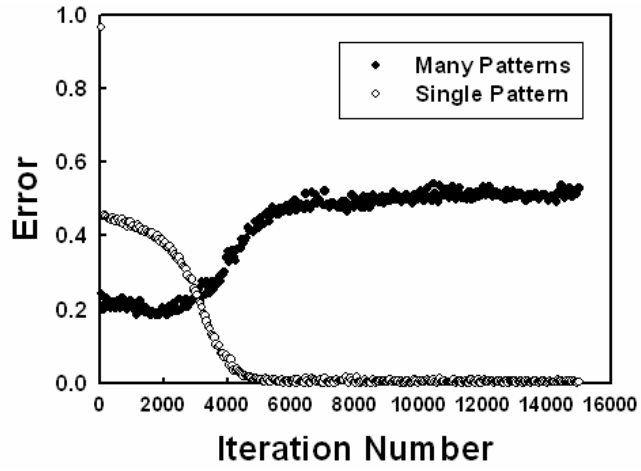

Figure 3. Learning plot for the neural network. Black circles correspond to the global error obtained for a training with many patters and white circles represent the error for a training made with a single pattern.

erations sufficiently high. For all the cases analyzed in this work 2000 iterations were used, which guaranteed that the global error remained around 20%, with an average processing time of approximately 5 minutes. To validate the neural network classification, nosologic maps so obtained were compared with maps using the same type of information, i.e. relaxation data, obtained with a methodology previously derived (7) that uses an Inverse Laplace Transform algorithm (ILT) to determine the transversal relaxation rate spectra for each CSI voxel and correlates it with the spectroscopic information coming from that CSI voxel. An example of the comparison is shown in Figure 4. An analysis of the figure reveals a great level of correspondence between both maps, although the map obtained with neural network exhibits less detail and is limited to only three gray levels. In all the cases analyzed in this work by both methods the correspondence was always above 80 %. There is an intrinsic problem in both methods that comes from the partial volume problem (8, 9), i.e., the CSI voxel is too big that it always contains more than a tissue type, and both methods handle this problem in a different way. The neural network method estimates a sort of "decay time" to convert the decay pattern to a binary number. It is easy to see that different combinations of exponential functions could give almost the same binary number mixing tissue information. This suggests introducing different ways to codify the decay pattern. Another difference exist in the processing time, the neural network method takes about 5 minutes for the training while the ILT method takes about the same time for a single relaxation rate spectrum to be obtained and many relaxation rate spectra are needed to establish the correlation of relaxation rates with spectroscopic data. This result points in favor of using the neural network method to obtain nosologic maps in a reasonable time, particularly when a high number of images have to be analyzed as happens in 3D treatment planning for radiotherapy or radiosurgery.

Conclusions

The methodology presented in this work clearly yields nosologic maps that allow for the segmentation of brain tumor images with appropriate spatial resolution for therapeutical needs. Its use can be extended to combine images obtained from other modalities, such as diffusion weighted images.

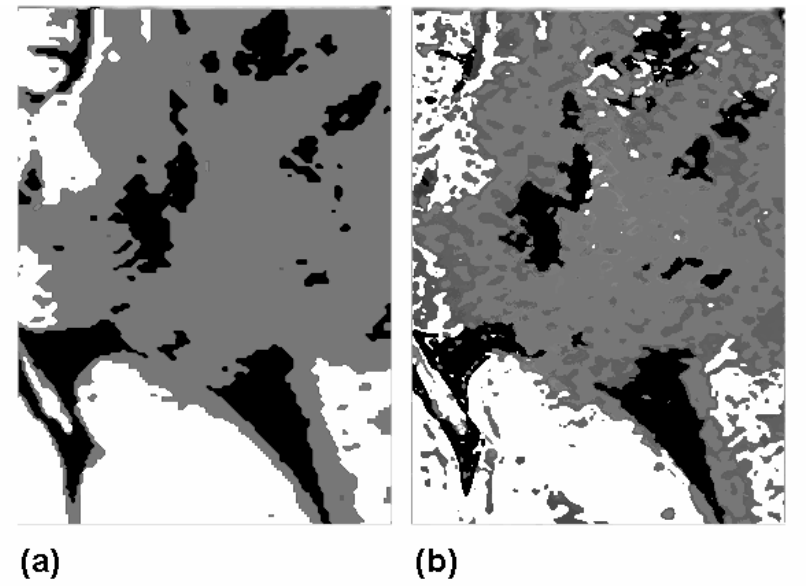

Figure 4. Comparison of (a) nosologic map obtained with neural network trained in supervised mode and (b) nosologic map obtained by inverse Laplace transform method [7]. Correspondence is of 86.1 % for this example.

Finally, fusion of spectroscopic information with images coming from other MR modalities such as relaxometry or diffusometry seems to be the best way to assess a confident segmentation of the tumor image.

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