

## Enhanced unsupervised segmentation of multispectral Magnetic Resonance images

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**Abstract.** Image segmentation is an established necessity for an improved analysis of Magnetic Resonance images. Neural network-based clustering has been shown in literature to yield good results, yet the possibility of transforming the input feature space in order to enhance the clustering process has gone largely unexplored. In this paper we focus on brain imaging and present a new algorithm for unsupervised segmentation of multi-spectral images, based on the research, through neuro-fuzzy techniques, of an optimized space in which to perform clustering. Tests performed on both real and simulated MR images show promising results, encouraging the application to different medical targets and further investigation.

### 1. Introduction

The introduction of advanced medical imaging techniques has dramatically improved the quality of brain pathology diagnosis and treatment. In particular, Magnetic Resonance imaging (MRI) allows the acquisition of three-dimensional, high resolution and highly detailed images of brain anatomy, with unparalleled soft tissue contrast with respect to other medical imaging modalities.

To fully exploit the potentialities of these medical imaging techniques, the development of image processing tools such as segmentation, which allows the identification and quantitative evaluation of brain structures and lesions in a non-invasive manner, is fundamental.

Many approaches to MRI segmentation, both supervised and unsupervised, have been proposed in literature [1]. Among the unsupervised segmentation techniques, both the K-means algorithm and its fuzzy equivalent, C-means, have been employed, as well as unsupervised learning neural networks. In particular, neural network-based clustering has yielded good results [2][3], yet the possibility of transforming the input space in order to facilitate segmentation has been largely unexplored.

In this paper we propose a new, unsupervised algorithm for multi-spectral MR image segmentation. In our method, classical Kohonen map-based clustering is enhanced through the search of an optimized space in which to operate the clustering.

The paper is organized as follows: in Section 2, system architecture is described; while results are reported in Section 3. Conclusions and possible further developments are illustrated in Section 4.

## 2. Methodology

In the proposed technique, each input is a slice of the image dataset, which undergoes a number of sequential processing steps: preprocessing, clustering, error backpropagation, and classification. Magnetic resonance imaging is a tomography technique, i.e. each image comprises a number of slices, each corresponding to a given slice of tissue; following the pulse repetition period (TR) and parameters related to the applied radio-frequency magnetic field, it is possible to obtain images with different contrast, each reflecting a different parameter regulating the relaxation of the excited tissues. In this paper, we consider multispectral datasets comprising three images (also referred to as channels) weighted by spin-lattice time constant T1, spin-spin time constant T2 and proton density (PD). After the clustering process, each cluster is manually interpreted and assigned to a proper tissue class.

### 2.1 Preprocessing

Preprocessing aims at improving the quality of each input image and reducing the computational burden for subsequent analysis steps. Specifically, since skull and other extracranial tissues are usually of scarce clinical interest in most MRI studies, they were discarded, along with the background, as described by the preprocessing technique proposed in [4].

Subsequently, each voxel in the input image is assigned a six-dimensional feature vector, which comprises the gray level intensities of the corresponding pixel in the three channels, as well as the mean intensities calculated in a 3x3 neighborhood of the pixel in each channel. This aims at compensating the effects of random noise, while minimizing the loss of resolution. All feature vectors are normalized prior to segmentation by subtracting the mean and dividing by the standard deviation, where the mean and standard deviation are estimated independently for each slice.

### 2.2 Clustering

The proposed network architecture consists of two fully interconnected layers; the first layer, composed of computing elements (neurons) of order zero (perceptron) with linear activation function, is followed by a second layer of computing elements of order two (radial basis), with gaussian activation function.

Let  $\mathbf{X}$  be the input pattern,  $\mathbf{H}$  the output of the hidden layer and  $\mathbf{Y}$  the output of the network. Moreover, let  $\mathbf{W}$  and  $\mathbf{C}$  be the weight vectors of the first and second layer, respectively. In order to jointly optimize both layers, training is carried out in two steps [5]. In the first step, the second layer is trained using the standard Kohonen rule for unsupervised learning (while the first layer is not trained): at each iteration, the winning neuron's centers are adjusted according to

$$\Delta c_{ji} = \eta_c \cdot (h_i - c_{ji}) \quad (1)$$

whereas the weights of the neighboring neurons are updated according to

$$\Delta c_{ji} = \eta_c \cdot f_{neigh} \cdot (h_i - c_{ji}) \quad (2)$$

In fact, though the idea of preserving input space topology in network output space topology has limited sense in a 2x2 network, we have found that this update does enhance the system's performance.

Contrarily to the second layer, the first layer is trained using error back-propagation. In supervised learning schemes, the error is given by

$$E = \sum_p \alpha_p \left\| \mathbf{Y}^p - \mathbf{T}^p \right\|^2 \quad (3)$$

where  $\mathbf{T}^p$  is the user-supplied target associated to the  $p^{\text{th}}$  training pattern and  $\alpha_p$  represents the relative importance of each training pattern (here assumed equal to 1 for every pattern). In this case, the target is determined by associating each input pattern with the winning neuron; so that, supposing  $j$  the index of the winning neuron,  $\mathbf{t}_k^p$  is equal to 1 for  $k=j$  and 0 otherwise. Intuitively, this corresponds to searching a linear transformation of the feature space, requiring that input patterns be as close as possible to the associated centroids. The hidden layer is then trained using the classical delta rule for training. In particular, it can be derived from equation (3) that

$$\frac{\partial E}{\partial w_{ji}} = \sum_p \alpha_p \sum_j (\delta_j^{1p} \cdot x_i^p) \quad (4)$$

where  $p$  denotes the  $p^{\text{th}}$  input pattern and

$$\begin{aligned} \delta_j^{1p} &= \delta_j^{2p} \cdot \frac{G'(z_j^p)}{z_j^p} \cdot (h_i - c_{ji}) \\ \delta_j^{2p} &= y_j^p - t_j^p \end{aligned} \quad (5)$$

where  $\mathbf{z}_j^p = \left\| \mathbf{H}^p - \mathbf{C}_j^p \right\|$ . The weights of the first layer are then updated according to

$$\Delta w_{ij} = -\eta_w \cdot \frac{\partial E}{\partial w_{ij}} \quad (6)$$

In the present study, the first layer consists of 4 computing elements with linear activation function. Thus, not only the hidden layer performs a linear transformation of the input space, but it also reduces the dimensionality of the feature space. This allows obtaining, in average, better experimental results than when all features are retained in the clustering step. The second layer has 4 computing elements, arranged in a 2 by 2 topology. Four clusters are sufficient to discriminate between the three

tissue classes (white matter, gray matter and cerebrospinal fluid) that can be found in normal brain parenchyma (i.e. after the removal of extrameningeal tissues).

The network is separately trained for each slice to account for intensity inhomogeneities across different slices by randomly selecting 2000 pixels per slice as training set. A Gaussian neighborhood function  $f_{neigh}$  equal either to  $0.01 \cdot e$  (lateral and underlying neighbors) or  $0.01 \cdot e^{-2}$  (diagonal neighbor) is used for unsupervised training. An adaptive learning coefficient, initially set to 0.0001 for the first layer ( $\eta_w$ ) and 0.001 for the second one ( $\eta_c$ ), is used: if the error increases,  $\eta$  is decreased and weight values are set to those of the previous iteration, whereas if the error decreases below a predefined threshold,  $\eta$  is increased. Finally, training is stopped when a predetermined number of iterations, equal to 500 in this study, is reached.

### 3 Results

In this section, the results obtained using both simulated MR images and normal volunteers' scans are illustrated.

#### 3.1 Simulated MR images

The use of simulated images eases the task of validating a segmentation method as a reproducible and known ground truth is available. Moreover, it allows to separately test the proposed segmentation method stability against intensity inhomogeneities and random noise [6]. The simulated datasets were made available by the Brainweb institution<sup>1</sup> [7]. All multichannel datasets comprise 181x217, 12 bit gray level T1-weighted, T2-weighted and PD-weighted images with 1.0 mm slice thickness.

For the purpose of this study, three reference slices were selected. Since in this case the ground truth is known a priori, each cluster is associated with the most probable tissue class using maximum likelihood estimation; in this way, an upper bound to the performance of the proposed clustering technique is determined. A representative slice is shown in Figure 1. To evaluate the results, 20 trainings for each reference slice were performed with different random initial conditions for the centers of the neurons in the second layer (a diagonal matrix was used to initialize first layer weights).

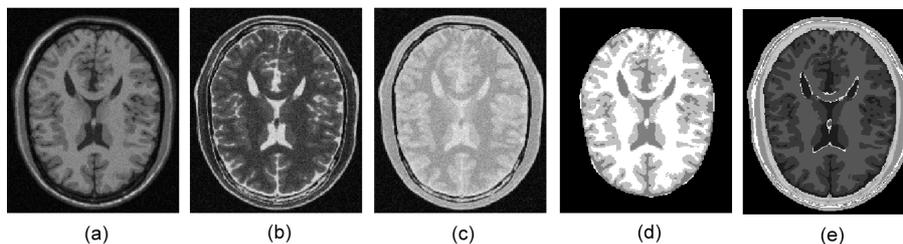


Figure 1. A representative slice from the simulated datasets (noise 5%, intensity inhomogeneity 0%) and the corresponding segmentation. (a) T1-weighted image, (b) T2-weighted image, (c) PD-weighted image, (d) result of the clustering procedure, (e) ground truth.

<sup>1</sup> available online at <http://www.bic.mni.mcgill.ca/brainweb/>

It is worth noting that, with very low levels of noise, better results can be obtained excluding mean intensities from the input features. In Figure 2 the percentage of correctly classified pixels with and without a post-processing filter (consisting simply in the re-classification of isolated pixels) are shown; though numerical results increase only modestly with the post-processing filter, the visual quality of segmentation is enhanced (figures omitted for brevity). Typical standard deviation values (for trials with equal noise and intensity inhomogeneity) were around 0.5 %, and in any case never above 1.5%.

### 3.2 Real MR images

The proposed technique was also validated on MR images of normal volunteers. A representative dataset, shown in Figure 3, was provided by the Center for Morphometric Analysis at Massachusetts General Hospital<sup>2</sup>.

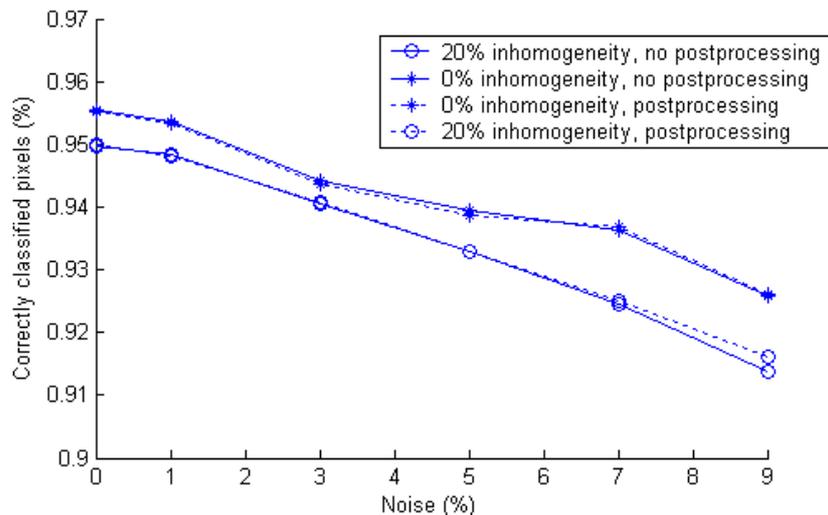


Figure 2. Clustering results with varying levels of noise and intensity inhomogeneities.

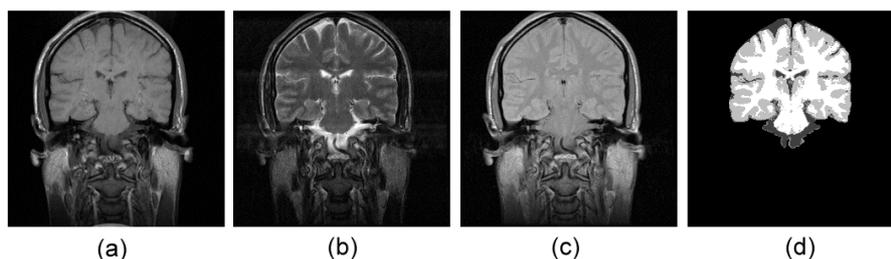


Figure 3. Results of the clustering procedure on a slice from the normal volunteer's scan. (a) T1-weighted image, (b) T2-weighted image, (c) PD-weighted image, (d) clustering.

<sup>2</sup> available online at <http://neuro-www.mgh.harvard.edu/cma/ibsr>

All scans were acquired at the NMR Center of the Massachusetts General Hospital with a 1.5 Tesla General Electric Signa MR system. Three spin echo sequences were considered in this study: a T2-weighted (TR 4200/TE 104.32/flip angle  $90^\circ$ ), a T1-weighted (TR 700/TE 20/ flip angle  $90^\circ$ ) and a PD-weighted (TR 2500/TE 13.04/flip angle  $90^\circ$ ) sequence. All slices are 256x256, 8 bit gray level images with 0.859375 mm inplane resolution, 6.0 mm thickness and 1.0 mm interslice gap.

#### **4 Conclusion and future works**

In this paper, a novel approach to the segmentation of multispectral cerebral MR images is proposed, which enhances the unsupervised clustering capabilities of a Kohonen self-organizing map with a linear transformation of the input space. The proposed technique was evaluated on both simulated and real MR images, showing promising performances both from a qualitative and quantitative point of view. Furthermore, being the proposed technique fully unsupervised, and the results substantially independent of the initial network conditions, it constitutes an effective remedy to the issue of intra- and inter-observer variability, which is a major drawback of supervised or manual segmentation techniques.

Future efforts will be devoted to the further testing of the proposed technique, both from a qualitative and quantitative point of view, and to its application to the study of brain pathologies, in particular to brain tumor diagnosis and follow-up.

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