Neural Network Methods for Volumetric Magnetic Resonance Imaging of the Human Brain

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Abstract

Multimedia, including imaging and videoconferencing, is becoming the predominant mode of professional and technical communication. In the medical arena Multimedia Systems will have to deal with images of different types, including live videos of the participants in a video-conference, and still images or videos of radiological or MR (Magnetic Resonance) information. In the last thirty years there has been an explosion in our knowledge of the biochemical machinery of the nervous system. This knowledge has been primarily developed from invitro and invivo experiments in invertebrates and mammals. In the last few years with the advent of new imaging technologies such as Magnetic Resonance Imaging (MRI) and Positron Emission Tomography (PET) it has become possible to explore the integrated central nervous system (both biochemically and biophysically) in living humans. A major limitation in utilizing these techniques in an optimal fashion has been the lack of sophisticated image analysis systems which can extract the relevant information from the images in an automated or semiautomated manner. Brain MR images contain massive information requiring lengthy and complex interpretation (as in the identification of significant portions of the image), quantitative evaluation (as in the determination of the size of certain significant regions), and sophisticated interpretation (as in determining any image portions which indicate signs of lesions or of disease). In this paper we first survey the clinical and research needs for brain imaging. We discuss the state-of-the-art in relevant image analysis techniques. We then discuss our recent work on the use of novel artificial neural networks which have a recurrent structure to extract precise morphometric information from MRI scans of the human brain. Finally, experimental data using our novel approach is presented and suggestions are made for future research.

1 Introduction

Brain MRI scans contain massive information requiring lengthy and complex interpretation (as in the identification of significant portions of the image), quantitative evaluation (as in the determination of the size of certain significant regions), and sophisticated interpretation (as in determining any image portions which indicate signs of lesions or of disease). This complexity is compounded when it includes functional and biochemical assessment. A major limitation in utilizing Magnetic Resonance Imaging (MRI) and Positron Emission Tomography (PET) to explore the biochemical and biophysical functioning of the integrated central nervous system in living humans in an effective fashion has been the lack of sophisticated image analysis systems which can extract the relevant information from the images in an automated or semiautomated manner. Current state-of-the-art computerized tools and software lead to error rates exceeding 5-10% (MacFall 94) [30], which is too innacurate for the analysis of neuroanatomical and developmental changes of the human brain.

MRI brain morphometry is fundamental to large areas of medical research. In the work at Duke, we actively pursue research in MRI studies of neuroanatomical changes in basal ganglia and subcortical white matter, including the number, size, and severity of white matter disease (Figiel 91, McDonald 91, Krishnan 90) [11, 31, 24]. The purpose is to relate lesions with age. For instance in a set of 55 normal volunteers, we established that lesions occured with significant frequency above the age of 45 (Doraiswamy 94, Early 93) [7, 8]. We have conducted morphometric studies showing marked age dependent decline in caudate nuclei volume in subjects over 50 years of age (Krishnan 90, McDonald 91) [24, 31]. We have also compared cerebellar volumes in males and females, and shown that age dependency variation is statistically insignificant for cerebellar volume (Escalona 94) [9]. Other work conducted at Duke is related to MRI changes due to Alzheimer's disease (Early 93, McDonald 91) [8, 31], where long TR scans are analyzed for presence of signal hyperintensities in the basal ganglia and in deep white matter (McDonald 91).

This is just a sample of some ongoing work based on MRI brain morphometry. It uses advanced image segmentation software available from GE/CRD, Sun User's Group, and other organizations and research consortia. The imaging protocols we rely on are T1-weighted scans, T-2 weighted scans, Fast Spin echo and T1-weighted volume scans. Data is then analyzed using simple grid-square counting, and software tools such as *Voxtool* (which applies morphological processing techniques) and *MR Console* from GE. The techniques we use are also calibrated and tested using an anatomically realistic brain phantom.

While the grid-square counting method is highly accurate (with a calibrated error less than 1%), it is based on lengthy analysis by an expert and is totally impractical as the volume of available MRI scans becomes large, and when a statistically significant set of scans must be used to draw conclusions of scientific interest and clinical value. Other methods based on state-of-the-art tools and software lead to error rates (MacFall 94) [30] which are too high to accurately detect significant neurophysiological change in successive scans taken over time in a subject, or variations over a set of subjects in order to correlate observed properties or syndromes. Additionally, research in functional MRI is now being developed at Duke both in the Medical Center's Departments of Psychiatry and Radiology, and in the Department of Psychology. We are interacting with these groups to bring the power of new image processing methodology to bear on the problems they are addressing. Thus it is now essential to research new methods for MRI morphometry which will combine high accuracy and fast processing, compatible with the high volume of data which is now available.

Recurrent neural networks which we discuss in this paper have very strong potential as effective and efficient tools for brain MRI segmentation, since they can combine methods akin to those of morphometric techniques as practiced by experts, together with high volume parallel computation. In the next section we review MRI segmentation methods. In Section 3 we discuss the basic mathematical tool that will be used in this work: the Random Neural Network model and its adaptation to the MRI brain morphometry problem using a recurrent geometric network. Section 4 discusses the classification method which we propose and some experimental results. Conclusions and additional reserch directions are discussed in Section 5.

2 Magnetic Resonance Image Segmentation Methods

Normal brain MRI segmentation includes separation of brain parenchyma and cerebrospinal fluid, while abnormal brain MRI segmentation involves separation of tumor. Any computerized segmentation method has to have the following two factors: (1) the characteristics of different ROI (regions of interest) that the segmentation is based on; (2) the mathematical and computational approach the method takes. Multispectral MR images are often used for better segmentation [36].

The following feature characteristics of brain tissues in MRI have been used for segmentation: image pixel intensity [37], edge and contour [29, 23], anatomical brain structure [27], and texture contents [10, 34]. A number of computational approaches have been adopted for extraction of these features, including:

- Unsupervised segmentation such as k-means clustering [5], fuzzy c-means clustering [21], unsupervised Hopfield neural networks [1].
- Supervised segmentation, including model-based and rule-based segmentation [27], statistical image analysis [28], supervised neural networks using cascade correlation [21], and the random neural network [10].

The most simple and widely used method for MRI segmentation is based on intensity thresholding, contouring or edge detection, combined with some enhancement techniques. These usually do not fully take advantage of MR image properties and of knowledge about the brain. Dawant et al. [6] use least square fitting to correct intensity variations before neural network classifiers are used to separate white and gray matter. The intensity corrections make gray and white matter further apart in the multi-spectral phase space, so that the neural network classifier can better separate them. However, the result depends on user selected sample points and it is vulnerable to errors in those samples. Kennedy et al. [23] compute intensity differentials and contours for evaluation of normal and pathologic brain anatomy. Dynamic contours or "snakes" are also used for brain MRI segmentation [29]. Supervised segmentation methods including k-nearest neighbors clustering proposed by Clarke et al. [5] give better rusults. Hall et al. [21] compared several neural network and fuzzy clustering methods in terms of segmentation performance, learning method (supervised vs. nonsupervised), computational complexity and importance in diagnostic process. Their results suggest that fuzzy c-means and feedforward cascade correlation generally performs better than other algorithms, though the neural network algorithms covered by their investigation are limited. Z. Liang et al. [28] develop a statistical method that characterizes tissue regions with a Markov random field. First the class parameters are estimated using maximum likelihood fitting with expectation-maximization (EM) algorithm, then the segmentation is performed using the maximum *a priori* probability (MAP) algorithm. C. Li et al. [27] use a knowledge-based approach for tissue labeling and tumor identification. They define specific models and design very detailed processes for separation of skull, white and gray matter, mainly based on shape and connectivity. The complicated model definition and need of *a priori* knowledge are the limitations of this method. Amartur et al. [1] propose to use Hopfield neural networks for nonsupervised segmentation of MRI, where the segmentation is formulated as the minimization of an energy function. However this approach is not robust and is subject to local minima, and it does not take into account any structural.

There are limitations to many of these segmentation methods. The model-based and rule-based methods usually require a large set of heuristic rules. Model-based methods may put restrictions on MR images they classify, e.g. connectivity of tissues [29]. Statistical classification usually requires *a priori* assumptions on the distribution, and complicated estimation of parameters. Robustness is also a weak point for almost all the segmentation methods.

3 Recurrent pulsed random networks

The research we conduct uses a recurrent neural network model: this is due to the need for explicitly representing detailed granular interdependencies, as well as topographical properties and symmetries in MRIs. These cross dependencies relate properties of local neighbourhoods, or of separate regions, in a complex manner which requires network feedback. Our neural network model (Gelenbe 89, 90, 93) [12, 13, 16] captures the essence of this behavior in a recurrent network of n neurons.

In this model [12] positive and negative signals circulate between neurons. Positive signals represent excitation, while negative signals represent inhibition. A negative signal reduces by 1 the potential of the neuron to which it arrives (i.e. it "cancels" an existing signal) or has no effect on the signal potential if it is already zero, while an arriving positive or signal adds 1 to the neuron potential. The potential at a neuron is constituted only by positive signals which have accumulated, and which have not been cancelled by negative signals. Each neuron accumulates signals as they arrive, and can fire if its total signal count or potential at a given instant of time exceeds a threshold. Then the neuron fires at random intervals with an exponential distribution of constant rate. These signals go out to other neurons, or back to itself, or to the outside of the network. The model also allows for depletion of potential over time when the neuron does not receive further signals.

In this model, signals can either arrive to a neuron from the outside of the network (exogenous signals) or from other neurons. Each time a neuron fires, a signal leaves it, depleting the total potential of the neuron. A signal which leaves neuron i heads for neuron j with rate $w^+(i,j)$ as a positive signal, or as a negative signal with rate $w^-(i,j)$, or it departs from the network. A neuron is capable of firing and emitting signals if its potential is strictly positive. External stimuli are represented by exogenous positive signals which arrive to the $i-th$ neuron in a Poisson process of rate $\Lambda(i)$, and negative signals which arrive to the $i-th$ neuron according to a Poisson process of rate $\lambda(i)$. The diring rate $r(i)$ of a neuron is the sum of all of its outgoing signal emission rates. This model has very useful features:

- it represents more closely the manner in which signals are transmitted in a biophysical neural network where they travel as voltage spikes rather than as fixed signal levels,
- it is computationally efficient due to the product form solution,
- it has a computationally fast learning algorithm (Gelenbe 93),
- it is easy to simulate, since each neuron can be simply represented by a counter,
- it represents neuron potential and therefore the level of excitation as an integer, rather as a binary variable, which leads to more detailed information on system state.

The state of the network is represented by the state q_i of each neuron which is a probability, i.e. a real number between 0 and 1.

Theorem 1 *(Gelenbe 89, 90) For the recurrent random neural network, the probability that neuron i is excited (or firing) is given by:*

$$q_i \equiv \lambda^+(i)/[r(i) + \lambda^-(i)], \tag{1}$$

where the $\lambda^+(i), \lambda^-(i)$ for $i = 1, \ldots$, n satisfy the system of non-linear simultaneous equations:

$$\lambda^+(i) = \sum_j q_j r(j) p^+(j,i) + \Lambda(i), \qquad \lambda^-(i) = \sum_j q_j r(j) p^-(j,i) + \lambda(i) \tag{2}$$

Equation (1) can be interpreted as a sigmoid function which transforms the rates $\lambda^+(i), \lambda^-(i)$ at which excitation and inhibition pulses arrive to the neuron, into the probability q_i that the neuron is excited. (1) and (2) constitute the basic non-linear calculus used to apply this model to various tasks. In (Gelenbe 93, 94) it is shown that (1) and (2) always have an unique solution.

3.1 Geometric recurrent neural networks for MRI brain morphometry

In this section we describe a neural network structure which relates closely to the MRI which we must process and whose contents need to be identified. For this reason, and because of the close link between the internal functions of the network and its geometric organization, we will all it a "Geometric recurrent neural network". This network is composed of several layers. The layer structure does not imply a feed forward structure. Indeed, in general our network layers have internal inter-neural interaction. Thus recurrence will be intrinsic to each individual layer. The mathematical model used for this integrated multilayer and recurrent neural network will be the pulsed random neural network we have describe above so that we can take advantage of its convenient mathematical properties leading to efficient network analysis and network learning.

The neurons in each layer L_i relate directly to pixel positions (x, y) on the brain MRI scan. We denote by $N_i(x, y)$ the neuron in position (x, y) of layer L_i, while $q_i(x, y)\varepsilon[0, 1]$ represents its state. Each $N_i(x, y)$ interacts with other neurons in the same layer via weights representing excitation, denoted by $w_i^+(x, y, d, D)$, or inhybition denoted by $w_i^-(x, y, d, D)$. Here d refers to a particular direction from (x, y), while D refers to a Euclidean distance. For instance, d can encode the 8 main directions (N, NE, E, SE, S, SW, W, NW) wit the integers 1, ..., 8. Thus (x, y, d, D) will designate a specific neuron position. For instance $(x, y, 1, 1)$ designates the neuron position $(x, y + 1)$, while $(x, y, 3, 2)$ designates the neuron position $(x + 2, y)$. A useful subclass of networks will only use local interconnects. The simplest case is when $D \leq \sqrt{2}$ so that we are dealing with strictly local connections from a neuron to its immediate neighbours in all eight principal directions.

For inter-layer connections, neuron $N_i(x, y)$ in the $i-th$ layer will interact with $j-th$ layer neurons by excitatyion or inhibition weights denoted by

$$w_{ij}^+(x, y, d_{ij}, D_{ij}), w_{ij}^-(x, y, d_{ij}, D_{ij}), \tag{3}$$

respectively. Notice that the distances and directions for neuron interconnects between layers will depend in general on the layers (i, j), hence the parameters d_{ij} and D_{ij}. The network weights will be chosen as a result of a learning algorithm which uses the image I, and hints provided by the expert user. Thse hints may be progressively stored in various network layers. Some of the weights can be fixed a priori, as for instance around the edges of the image, or for parts of the image which have a well known structure.

Each layer L_i of neurons interacts with the expert user (or with several expert users). Each layer is a rectangular grid which maps exactly into the set of pixels in the brain image. Specifically, layer L_i is specialized in the $i - th$ specific tissue type which we denote by $T(i)$. The expert clamps neuron $N_i(x, y)$ to value $q_i(x, y) = 1$ (for instance by using the mouse, or an electronic pencil coloring an area) if pixel (x, y) is clearly identified by the expert user as belonging to an area where the tissue is of type $T(i)$. If the tissue at (x, y) is clearly identified as not being of type-i, then $N_i(x, y)$ is set to value $q_i(x, y) = 0$. If the tissue at position (x, y) is not identified clearly as being $T(i)$ or not, then the value of neuron $N_i(x, y)$ can be set to a value 0.5 to indicate uncertainty, or to some other value to indicate the related likelihood. For an n-neuron recurrent random network, we have shown that the learning algorithm (Gelenbe 93) [16] is of computational complexity at most $O(n^3)$. We expect have designed learning algorithms of complexity no more than $O(D^2n)$ for single layer networks, and of complexity $O(D^2nL)$ where L is the number of layers and D is the distance in local connectivity. This is done by exploiting the locality of the interconnection of the network. Further performance improvements will be sought by efficient use of parallel processing.

4 The classification method

The method we use for classifying the contents of an image assumes that the image contains a finite set of M regions $R_1, \ldots, R_M$ which we wish to identify. Even though in many cases the sum of all regions will cover the whole image, this is not assumed in our approach, so that an image may contain areas outside of the regions of interest which we will not wish, or be able to.

Each region in an image will be composed of possibly non-contiguous areas. Furthermore, we postulate that a region is characterized by its detailed granular properties, including grey levels, but especially by local dependencies between neighboring pixels. Our proposed method for classifying the contents of and image is outlined below:

- We set up M recurrent neural networks $L_1, \ldots, L_M$, each of which is specialized in capturing the properties of one of the regions.
- Each network L_i is trained with a learning algorithm, using a set of input samples which are known to belong to the region R_i
- Then when the whole contents of that particular or similar image need to be classified, each of the M networks is applied to the image as follows.
- The image is decomposed into blocks of small size (i.e. of size much smaller than the image itself). Each small block of pixels in the image is classified as belonging to some region R_i, if the neural network which provides the best match for that region (in a sense which will be made precise in the sequel) is network L_i.
- If none of the M networks provides a sufficiently good match for block of pixels, then that block is set aside as not being classified into any of the M regions being considered.

This approach will classify a finite number of regions, and it assumes that a sufficient number of "certified" samples of these regions must already be available. There are numerous application areas where one knows in advance what one is seeking in an image and the issue is then to identify these regions in an accurate and highly automated manner. This approach will be effective for the accurate classification of anatomically significant regions within brain MRI scans. For each network L_i, the weights have to be learned from a certified sample of pixels which belong to region R_i. This will be carried out with the RNN's learning algorithm. For an n-neuron random network we have shown (Gelenbe 93 [16]) that the fully connected RNN learning algorithm is of computational complexity $O(n^3)$. Due to the local connections involved in the networks we use in this work, the actual complexity of learning for the networks which we use is linear in the size of the network.

The network structure described above and which we use in this work is illustrated in Figure 1. As indicated previously, connections between neurons are limited to the eight nearest neighbors, Rather than constructing a network covering the whole image, we have found it to be both much more efficient and sufficiently accurate to implement each L_i as a small 5×5 neuron network. Each of these networks is trained as follows.

We take a small number of 5×5 sample blocks of pixels which are representative of region R_i as the training set for L_i. The input to neuron $N_i(x,y)$ is the corresponding observed pixel gray level $I(x,y)$ from the sample block, and the target value to be attained by the neuron state $q_i(x,y)$ as a result of the learning algorithm is also the encoded version of corresponding pixel value $I(x,y)$ in the sample block. The sum of squared differences between the states of L_i's neurons when they are fed the block B's pixel values, and the pixel values themselves are used as the error function E_i for the training algorithm:

$$E_i = \frac{1}{2} \sum_{(x,y)\,\in\,B} [I(x,y) - q_i(x,y)]^2 \tag{4}$$

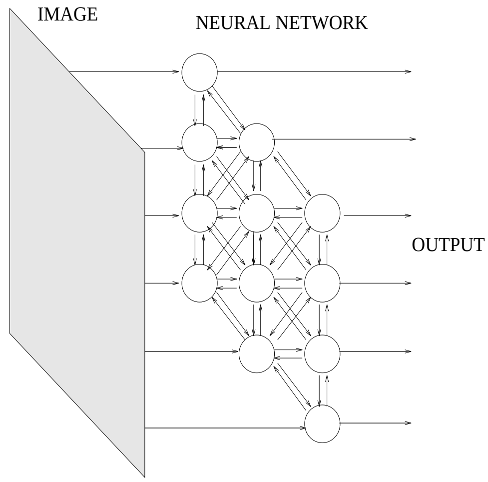

Figure 1: Illustration of the RNN structure we use for region classification. In practice we use 5×5 neural grids and image blocks for the RNN classifier.

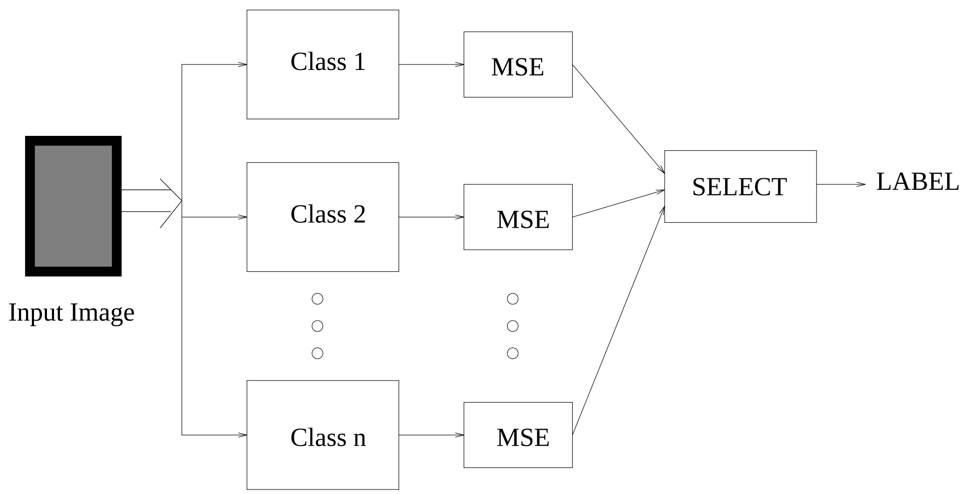

Figure 2: Block diagram of RNN processor.

Training is carried out using the RNN learning algorithm [16] for each sample block B selected for region R_i. Thus network L_i "learns" the characteristics of R_i by storing them in its weights.

If we have M regions to be classified in the image, for each region R_i we train a net L_i so that it stores interconnection weights which will allow it to mimic region i. Once the training process is complete, the M networks are used as follows:

- We scan all the blocks of the image to be processed and feed every block of the image into every one of the networks $L_1, \ \ldots, n$.
- A block in the image is classified as belonging to region j if L_j gives the smallest mean squared error between the block and the output of each of the networks (Figure 2) – as long as this error remains below an acceptable threshold. Otherwise the algorithm will not classify that particular block.

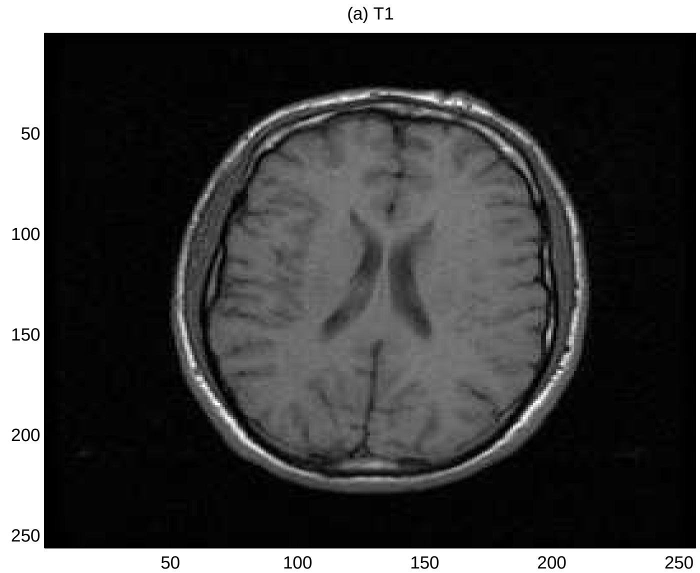

Figure 3: A T_1 MR image before being processed by our method

4.1 Experimental results

We have applied this method to the classification of grey matter from MR images of the human brain as shown on Figures 3, 5, and 7. The results we obtain correspond to a classification of the grey matter regions of the brain, or equivalently to the segmentation of the MRI into grey matter (R_1) and white matter (R_2) regions.

Current MRI technology obtains multispectral characteristics of the image: T1, T2 (relaxation time) and PD (photon density) images. Information extracted from these multispectral images can then be used for 3D reconstruction and visualization of the brain for medical purposes. For instance, quantified tissue volumes are frequently used for clinical studies in neuroradiology leading to information about neuropathology or in neuropsychiatry. Measurement of tissue volumes is used specifically for diagnosing disorders. A specific example is provided on Figures 3, 5 and 7 for T_1, T_2 and PD images.

In order to apply the classification method we propose, we first carry out a simple grey level histogram analysis so as to reduce the depth of the image, and filter out irrelevent surrounding area. Then we pick up training sets for different the different regions which we want to classify. These training sets composed of 5×5 pixel blocks are used to train the different geometric recurrent networks. In practice, our results have been obtained by training the network assigned to a specific region with 12 training blocks taken from the grey matter and white matter regions.

Our experimental results confirm that when the geometric RNN is trained for a certain region, it then consistently gives an output which is very close to the input block, as long as the input block is taken from the region for which it has been trained. Otherwise the network's output exhibits a very significant difference with the input block as shown on Figures 9 and 10. We have used this fact to classify the regions of the brain from the MRI scans, by feeding each block in the image into each of the two trained RNN classifiers as described previously. The class that gives the smallest mean squared error between the pixel values of the block being tested and the RNN output is selected to determine the regions to which each block belongs. Figures 4, 6, 8 show the results of our classifier for grey matter on the T_1, T_2 and PD images. Excluding the regions' borders, the empirically observed percentages of correct classification (the probability that the MSE from the orrect classifier is larger than that from the wrong classifier) are $P_1 = 98.41\%$, for the region of Class 1, and $P_2 = 98.64\%$ for the region of Class 2. These percentages are very similar to those that are known to be obtained by a human expert

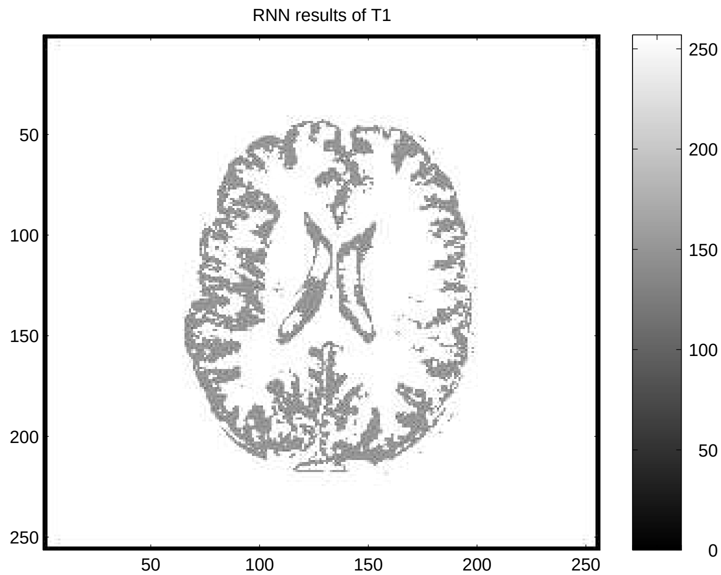

Figure 4: Result of RNN processing for the T-1 MRI image.

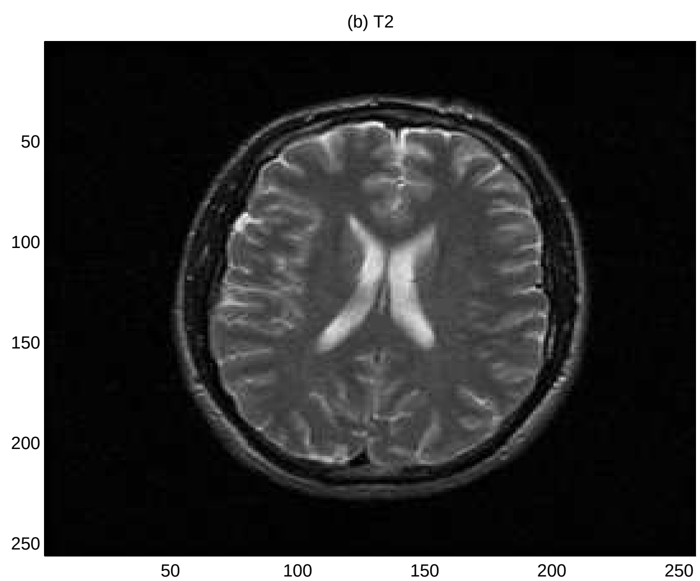

Figure 5: A T2 MR image before being processed by our method

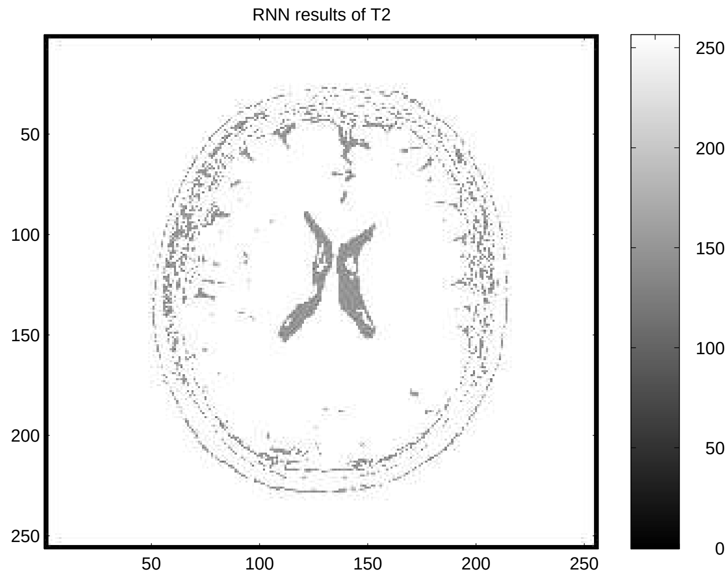

Figure 6: Result of RNN processing for the T2 MRI image.

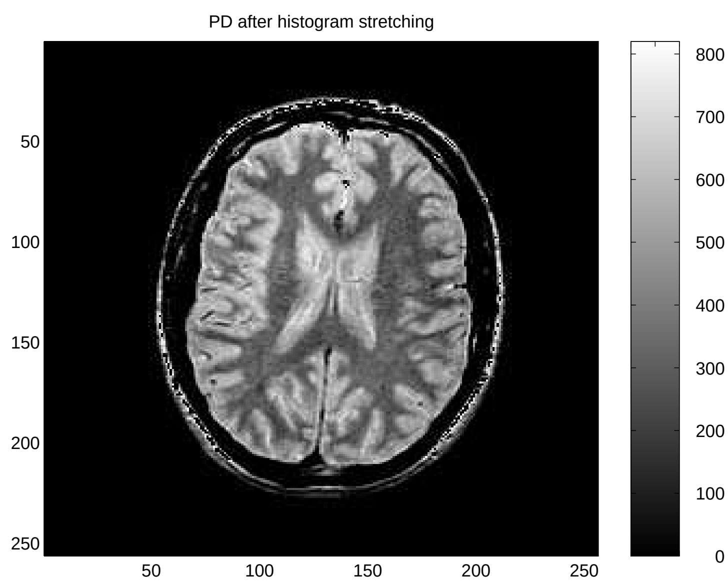

Figure 7: A PD weighted MR image before being processed by our method

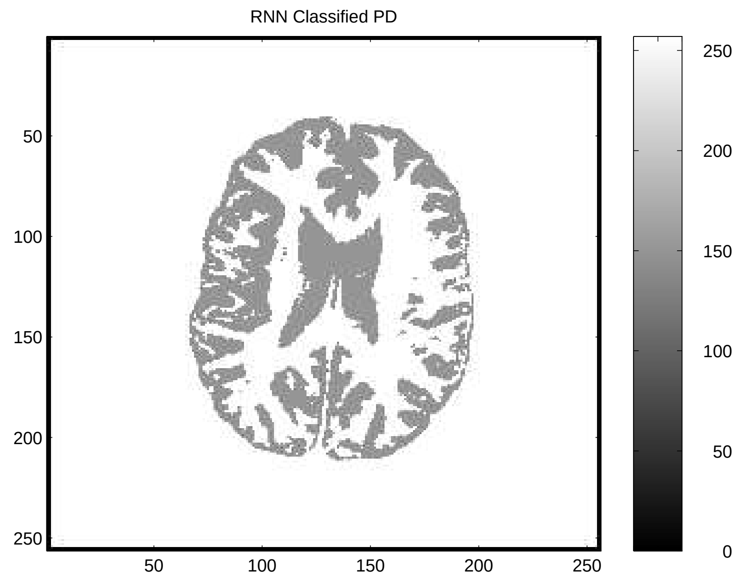

Figure 8: Result of RNN processing for the PD MRI image.

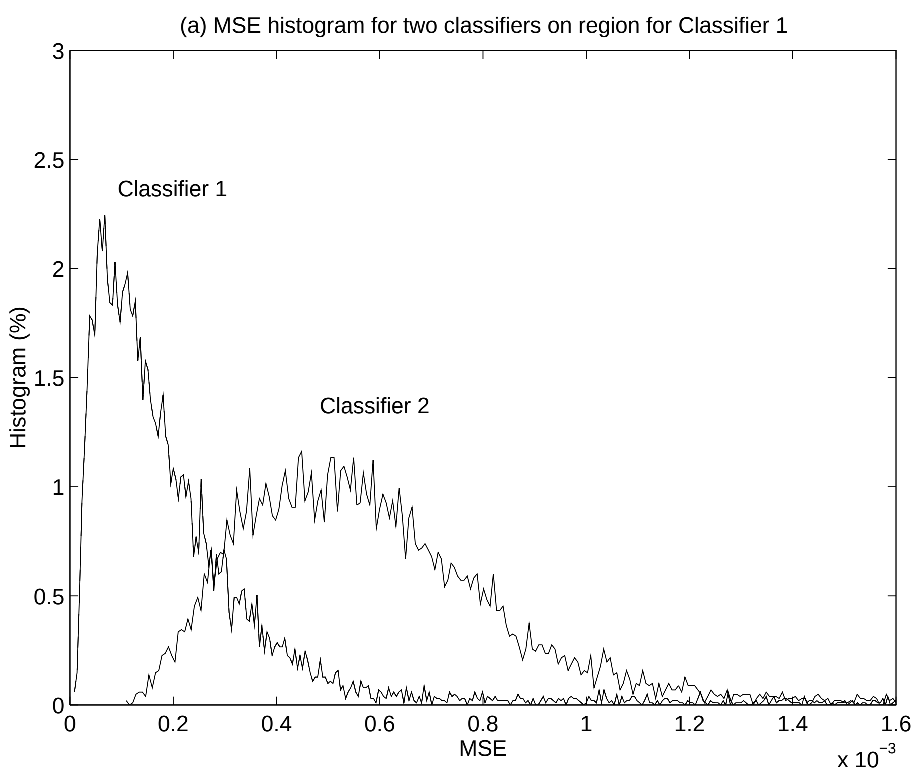

Figure 9: Histogram of the Mean Squared Error (MSE) for the two trained RNN classifiers (Class-1 and Class-2) on the region of Class 1.

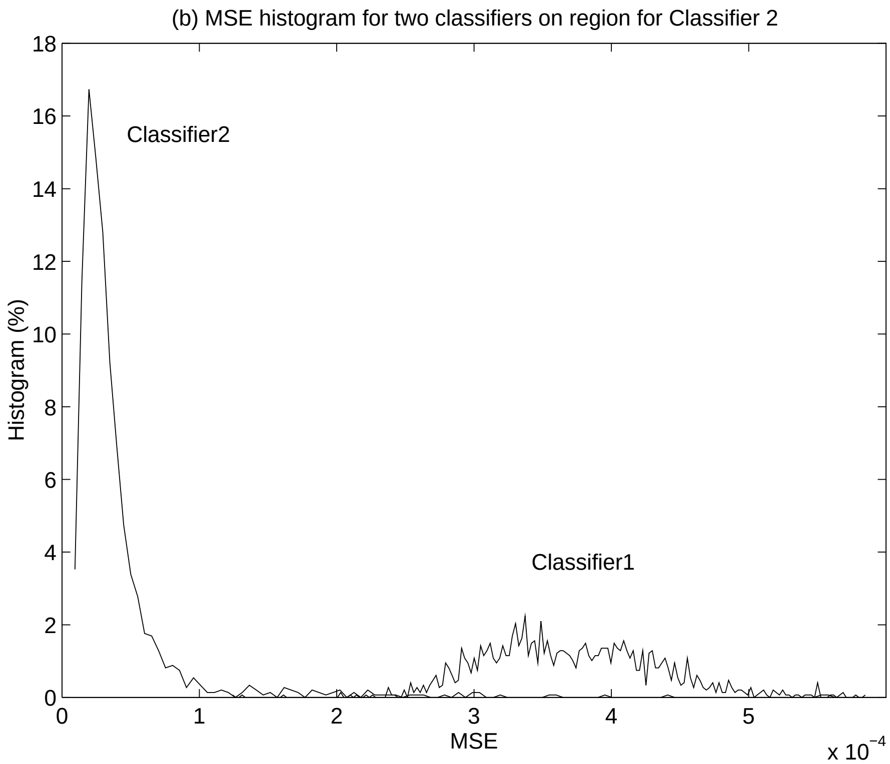

Figure 10: Histogram of the Mean Squared Error (MSE) for the two trained RNN classifiers (Class-1 and Class-2) on the region of Class 2.

carrying out manual volumetric analysis of brain MR images.

5 Conclusions and further research

Brain cortical region is integral in all aspects of motor, sensory and cognitive function, and is divided into functional and structural regions which are delineated by folds on the outer surface (the sula) and by the limiting planes. These regions are important in a variety of neurological and psychiatric disorders such as schizofrenia, learning disability, attention deficit disorder, depression, aphasias, etc. The novel imaging methods we investigate can lead to automated techniques to identify and quantify cortical regions of the brain. Our neural network based research will lead to software tools which are usable by the radiologist, the clinician and the medical researcher. This is very likely to help advance our understanding of the neuroanatomical substrate of important disorders, as well as of normal brain development. Furthermore our research can result in novel methods for processing and interpreting Functional MRI. The work presented in this paper constitutes progress in these directions, however there are many further directions which need to be investigated. Some of them are outlined below.

In many important areas of image processing – as with MRI or computed tomography – it is of particular interest to deal with three dimensional images (in addition to two dimensional ones). In this case, we propose to investigate the use of a three-dimensional "grid" of neurons $N(x, y, z)$. All of the preceding discussion carries over to this case, and each "layer" can be used to describe cross sections of the image, or be upgraded to three dimensions. When weights, as well as the state of each neuron, become important output information of the networks, it may become important to revisit the primitives which are allowed in the network. The conventional network primitives – namely excitation and inhibition between neurons – do not allow some neuron k to interact directly with some the synaptic weights which link some other neuron i to a third neuron j. The effect of pre-synaptic potential is well known in biological neurons, but hardly developed in artificial neural networks. We will investigate its use for image processing in this research.

In the work described in this paper, we have made use of a simple quadratic error function to learn the weights. In fact, in many cases it may be necessary to include in the error function terms which relate to the expert advice, as well as *a priori* information about the weights. For instance, our previous work on image textures (Atalay 1991, 1992, 1992b) shows that a texture with a granular and isotropic (insensitive to the direction) structure will necessarily result in weights which are independent of direction, but which include both an excitatory and inhibitory component. Thus we need to consider learning algorithms which are based on error functions which include information concerning the weights, as well as derivative information in the images (contours) while conventional learning functions are based on error functions containing only image and neuron state information. Similarly we would include the expert's advice, as initially entered into some layers i, by specifying values $V_i(x, y)$ for the neuron states in certain areas A_{ik} of network layer i. This leads to new error functions and new learning algorithms.

Another important issue concerns image compression. Brain MR images typically range in volume from a quarter to one million pixels of 12 or 16 bits. The massive data involved with several sections, multiple sections over time, or functional MR imaging of several sections of the human brain, becomes a serious impediment to efficient data storage, transmission and processing. Thus it is essential to find ways to meaningfully compress this information. Archival versions of images will need to be stored uncompressed for medical and legal purposes, on very large volume and relatively slow access devices. However, meaningfully compressed images should then be stored for fast transmission and access.

The segmentation techniques we investigate, themselves lead to a compressed version of the MR image, where each pixel is now replaced by a label which describes the region it belongs to. This can easily lead to a 4–to–1 compression, or more, in "depth" or number of bits per pixel. However we could also investigate "spatial" techniques based on neural networks, similar to the methods we have recently investigated for video-compression (Gelenbe 1994, 1996) [18, 20]. These methods can contribute anywhere from 16–to–1 to 4–to–1 compression very efficiently and in a computationally fast manner. Our research will examine the resulting "image quality" and whether it can then result in accurate volumetric analysis. These approaches will also be compared with commercial standards for compression and their resulting image quality.

In the future, much research in MRI will concern functional studies of the brain. Functional MRI requires the analysis of changes within a brain image over a period of time described as a series of MRI's taken over several crossections during an experiment. In such images, motion is a major issue for several reasons. The subject being scanned cannot remain perfectly still during the experiments being conducted. As a result image processing must detect and compensate for this motion. The scans are being taken in order to detect significant changes in the images in relation to the functional experiment which is being conducted. Thus change or motion detection is at the center of MR image interpretation in Functional MRI. Certain changes (such as observed blood pulsing in relation to heart beat) are not necessarily significant in such images. Thus such changes need to be detected and factored out of the image interpretation. Thus future research will also have to investigate motion detection and motion compensation in the context of Functional MRI in order to detect and interpret the functionally significant changes in successive images. This work will call upon the methodology and advanced neural techniques which we have already developed for "intelligent" videoconferencing [18, 20].

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