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An efficient neural network based method for medical image segmentation

Nima Torbati, Ahmad Ayatollahi*, Ali Kermani

Department of Electrical Engineering, Iran University of Science and Technology, Tehran, Iran

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ABSTRACT

The aim of this research is to propose a new neural network based method for medical image segmentation. Firstly, a modified self-organizing map (SOM) network, named moving average SOM (MA-SOM), is utilized to segment medical images. After the initial segmentation stage, a merging process is designed to connect the objects of a joint cluster together. A two-dimensional (2D) discrete wavelet transform (DWT) is used to build the input feature space of the network. The experimental results show that MA-SOM is robust to noise and it determines the input image pattern properly. The segmentation results of breast ultrasound images (BUS) demonstrate that there is a significant correlation between the tumor region selected by a physician and the tumor region segmented by our proposed method. In addition, the proposed method segments X-ray computerized tomography (CT) and magnetic resonance (MR) head images much better than the incremental supervised neural network (ISNN) and SOM-based methods.

1. Introduction

Medical image analysis plays a key role in computer aided diagnosis (CAD) systems. It involves fundamental steps like enhancement, segmentation, registration and visualization, among which segmentation which divides an image into its constructed regions is the first step in many medical image analyses [1]. Medical images are often corrupted by noise due to several reasons. The first one is that different imaging modalities use different acquisition techniques; secondly, during the acquisition the image is formed under the influence of different physical phenomena and finally, specific technical limitations that accompanies each imaging modality. Several methods such as edge detection, thresholding, region growing, clustering and artificial neural networks (ANN) have been proposed for segmenting medical images. Edge detectors, like canny [2], are not suitable for segmenting medical images. One reason is that medical images are usually corrupted by noise. However, edge detectors determine edges with the local information in the neighborhood of a pixel. Therefore, real edges are never formed in medical images [3]. So, pre-processing steps are needed to reduce the noise effect.

Intensity distribution in medical images is so complex that makes it difficult to determine the threshold value. Thus thresholding methods on their own are not suitable, and they have to be combined with other methods [4].

By using predetermined similarity criteria, region growing methods gather pixels or sub-regions from larger regions. Successful methods such as those proposed in [5,6] suffer from sensitivity to the selection of initial seed points.

Clustering is a popular method for medical image segmentation. Among clustering techniques, the fuzzy *c*-mean (FCM) [8] has received much attention since it preserves more information from the original image compared to other segmentation methods [7,9,10].

Artificial neural network (ANN) has been widely used in medical image analysis fields such as segmentation, data compression, image enhancement and noise suppression [11,12]. Multilayer perceptron (MLP), self-organizing maps (SOM), Hopfield and pulse coupled neural networks have been also utilized for medical image segmentation [13–18,29,30]. SOM network is one of the most suitable networks used for segmentation. This is an unsupervised network based on the competitive learning and discovering topological structure hidden in the input data for visual display in one or two dimensional spaces [19]. Two great advantages of the SOM based segmentation methods are unsupervised training and fast learning. There are some disadvantages to segmentation methods which use this network. The first drawback is that increasing the number of neurons in this network does not usually result in a better segmentation performance. The second disadvantage is that they need high dimensional input space with empirical features for an optimal performance [20]. And finally that they cannot segment images with heavy noise successfully.

* Corresponding author. Tel.: +98 912 137 4823.
E-mail address: ayatollahi@iust.ac.ir (A. Ayatollahi).

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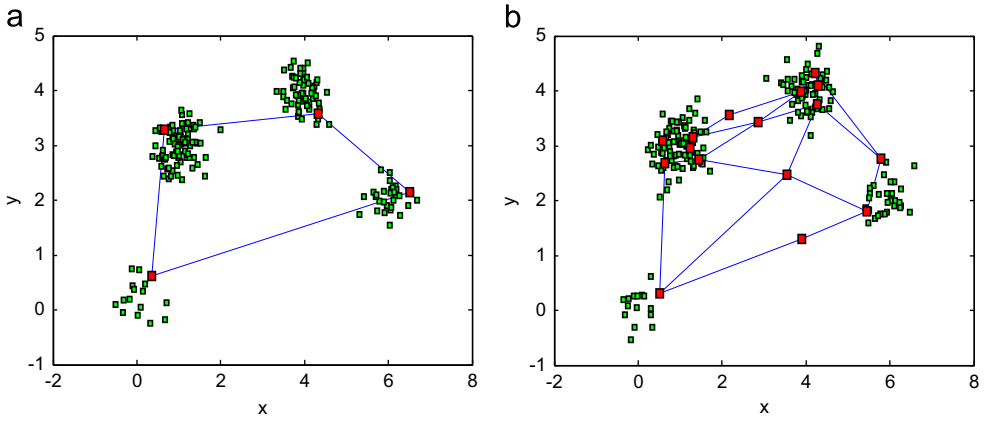

Fig. 1. (a) Classification result of the 2×2 SOM network. (b) Classification result of the 4×4 SOM network. (For interpretation of the references to color in this figure, the reader is referred to the web version of this article.)

To overcome the first problem of SOM networks, an incremental method has been proposed in [15]. But, in fact, increasing the number of neurons in the first layer of a SOM network does not decrease the segmentation accuracy. This comes from the concept of SOM network as shown in Fig. 1. This figure shows a two-dimensional (2D) feature space with four classes. The red quadrangles denote neurons and the blue lines show the interconnections between the neurons. The feature space is classified by 2×2 and 4×4 SOM networks in Fig. 1(a) and (b), respectively. Both networks have classified the space properly, however neurons in Fig. 1(b) display the topological structure of the input better than the neurons in Fig. 1(a). As can be observed, the dense classes have more neurons. Therefore, increasing the number of neurons in a SOM network results in an enhanced classification. But considering Fig. 1(b), if the neuron lying in a specific cluster does not join other neurons in that cluster, the samples near that neuron are incorrectly classified as extra clusters. As a result, the problem of the SOM is not the initial selection of the number of neurons but merging these neurons properly. In other words, after the segmentation is done, a post-processing step is required to unite the neurons belonging to a specific cluster.

Tucci et al. proposed a new structure for SOM networks based on a new neuron model [21]. In this network called FIR-SOM, each neuron acts as a finite impulse response (FIR) system. In a trained FIR-SOM network with constant filter coefficients, neurons of the first layer present a moving average (MA) filter regardless of the underlying input distribution. This property makes the network more robust against noise and sparse samples in the input space.

In order to rectify the drawbacks of segmentation methods based on the SOM network, we propose a merging MA-SOM (MMA-SOM) method for segmenting two dimensional medical images. The proposed method utilizes MA-SOM network to segment medical images. After that, a merging process is initiated to connect the objects of a joint cluster together. Then a two dimensional (2D) discrete wavelet transform (DWT) is used to build the input feature space of the network. The experimental results show that MA-SOM discovers the pattern of the input image properly, and is robust against noise. The segmentation results of breast ultrasound images (BUS) demonstrate that there is a significant correlation between the tumor region selected by a physician and the tumor region segmented by our proposed method. In addition, the proposed method segments X-ray computerized tomography (CT) and magnetic resonance (MR) head images much better than the incremental supervised neural network (ISNN) [20] and SOM network based methods.

The rest of the paper is organized as follows: Section 2 describes FIR-SOM networks and introduces the proposed method; Section 3 presents the experimental results, and the two last sections discuss the concluding remarks of the paper.

2. The proposed MMA-SOM segmentation algorithm

Each neuron in a FIR-SOM network is defined as a FIR system of order M. The weight vector $\omega(t)$ is shown by the linear combination of the last M values of input $x(t)$ as

$$\omega(t) = \sum_{k=1}^{M} a_k(t)x(t-k), \tag{1}$$

where $[a_1(t), a_2(t), \ldots, a_M(t)]$ are the samples of the impulse response of the system and $t = 1, 2, \ldots$ represents the time steps.

In SOM networks, all neurons receive the same input sample $x(t)$ at any training step. However, in FIR-SOM networks, each neuron receives a personalized input sequence that is influenced by its neighbors' cooperation. Therefore, in order to obtain the trace of the last M values of the input $x(t)$ to the neuron i, each neuron is associated with a set of M trace vectors $[x_i(t-1), x_i(t-2), \ldots, x_i(t-M)]$. These vectors build the following trace matrix:

$$X_i(t) = [x_i^1(t), x_i^2(t), \ldots, x_i^M(t)]. \tag{2}$$

In this FIR system, the trace and weight vectors represent the input and output, respectively. Thus, if the columns of the trace matrix $X_i(t)$ represent the sequence of the last M inputs to neuron i, the weight vector ω_i of the neuron can be shown as

$$\omega_i(t) = \sum_{k=1}^{M} a_i^k(t)x_i^k(t) = X_i(t)a_i(t), \tag{3}$$

where each neuron i has its own set of FIR coefficients $[a_i^1(t), a_i^2(t), \ldots, a_i^M(t)]$. At each training step, it is necessary to perform a single step time shift of the trace vectors. This is obtained by a shift of the trace matrix $X_i(t)$ as follows:

$$\hat{X}_i^{t+1} = [x(t), x_i^1(t), \ldots, x_i^{M-1}(t)], \tag{4}$$

where $\hat{X}_i^{t+1}$ represents the trace matrix after a single step time shift of the trace vectors. At each training step, the trace matrix is updated by the following equation:

$$X_i(t+1) = X_i(t) + \eta_{ci}(t)(\hat{X}_i^{t+1} - X_i(t)), \tag{5}$$

where c is the wining neuron; and $\eta_{ci}(t)$ is a neighborhood function:

$$\eta_{ci}(t) = \exp\left(\frac{-d^2(c,i)}{2\sigma^2(t)}\right) \tag{6}$$