Image segmentation by EM-based adaptive pulse coupled neural networks in brain magnetic resonance imaging

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A B S T R A C T

We propose an automatic hybrid image segmentation model that integrates the statistical expectation maximization (EM) model and the spatial pulse coupled neural network (PCNN) for brain magnetic resonance imaging (MRI) segmentation. In addition, an adaptive mechanism is developed to fine tune the PCNN parameters. The EM model serves two functions: evaluation of the PCNN image segmentation and adaptive adjustment of the PCNN parameters for optimal segmentation.

To evaluate the performance of the adaptive EM–PCNN, we use it to segment MR brain image into gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF). The performance of the adaptive EM–PCNN is compared with that of the non-adaptive EM–PCNN, EM, and Bias Corrected Fuzzy C-Means (BCFCM) algorithms. The result is four sets of boundaries for the GM and the brain parenchyma (GM + WM), the two regions of most interest in medical research and clinical applications. Each set of boundaries is compared with the golden standard to evaluate the segmentation performance. The adaptive EM–PCNN significantly outperforms the non-adaptive EM–PCNN, EM, and BCFCM algorithms in gray matter segmentation. In brain parenchyma segmentation, the adaptive EM–PCNN significantly outperforms the BCFCM only. However, the adaptive EM–PCNN is better than the non-adaptive EM–PCNN and EM on average. We conclude that of the three approaches, the adaptive EM–PCNN yields the best results for gray matter and brain parenchyma segmentation.

1. Introduction

Magnetic resonance imaging (MRI) provides high resolution images with differentiate tissues, based on the T1 local tissue parameters, T2 relaxation times and proton density. High quality MR images are not only indispensable to clinicians in diagnosis, treatment, and surgery planning, but also contain unique features that make them amenable to tissue segmentation and classification [1]. MRI is a non-invasive and powerful tool in the diagnosis of cerebral related disease, the monitoring of pathological changes and the establishment of preventive medical measures. Advances in modern brain MRI techniques enable the collection of large anatomical data sets in a short time. Brain tissue segmentation is an essential element of MRI analysis, and is important for data compression, quantitative analysis, registration, visualization and computer aided surgery [24]. Compared to acquisition, image processing and analysis are lengthy and labor-intensive. Although many segmentation techniques have been proposed for clinical applications, MRI approaches pose problems in the selection of the image features, the level of operator supervision, and the accuracy of tissue classification [6]. On the other hands, manual segmentation of brain tissues from series of 2D MR images is impractical in real applications. Thus, effective image segmentation algorithms are needed.

Image segmentation models can be grouped into three major types: statistical, structural, and hybrid [18]. In statistical models, the image is segmented based on the distribution of intensities within the intensity histogram. In structural models, the spatial relation between neighboring pixels is the basis for image segmentation. Hybrid models integrate two or more statistical and/ or structural classification models. A more detailed description of the three model types is given below.
1.1. Statistical models

Statistical models assume that each type of tissue is characterized by nearly uniform intensity. Therefore, the image intensity distribution is the basis for tissue classification. Statistical models can be further classified as non-parametric or parametric. In parametric statistical models, curve fitting algorithms are applied to fit the envelope of the histogram to a linear combination of various probability density functions. The estimated statistical parameters can then be applied for tissue segmentation [29]. Grabowski et al. (1999) proposed a mixture model for brain MRI tissue segmentation. First, a region-based model was employed to remove the skull. Then, Gaussian curve fitting was applied to the preprocessed histogram to segment the images into GM, WM and CSF [11]. Frisston et al. applied the expectation maximization (EM) algorithm to detect pixel intensity values using *a priori* knowledge of the histogram map characteristics of GM, WM, and CSF in normal subjects [10]. Lu et al. applied the EM algorithm to segment brain tissues in raw diffusion-weighted MR images [20]. In non-parametric statistical models, information on the probability distribution is not required for image segmentation. Hall et al. (1992) applied a non-parametric model Fuzzy C-Means (FCM) algorithm to three types of MR images (T1, T2, and Spin Density) for tissue classification [13]. One main drawback of the FCM algorithms was that the results were influenced by noises and artifacts. One major constraint to statistical models is that they only consider the intensity probability distribution. Since the spatial relationship between the pixels and their neighborhood is not included in the model, the global optimal solution is not guaranteed in cases involving spatial relationships.

1.2. Structural models

In structural models, each tissue type is characterized by spatial clustering. The structural algorithms can be further classified as edge-based and region-based. In edge-based algorithms, the image is segmented by detection of the boundary between different tissue types. Edge-based algorithms are generally sensitive to the noise and artifacts [8,19]. Region-based algorithms compute the area of the tissues by choosing initial solution seeds and extending these areas until they are filled. Compared to edge-based algorithms, region-based algorithms are generally less sensitive to noise and artifacts. Fathi et al. (1999) added fuzzy logic the flood-fill algorithm for segmentation of brain MR images tissue into gray matter (GM), white matter (WM) and cerebrospinal fluid [9]. Niessen et al. (1998) combined an edge-based and a region-based structural method to classify brain MR image voxels as WM, GM, or CSF [23]. For image segmentation applications, algorithms that simulate biological mechanisms — such as pulse coupled neural networks (PCNN) — are drawn attention. The PCNN is inspired by the work of Eckhorn et al. [8]. It is an un-supervised neural network, which simulates the synchronous pulse bursts in cat’s visual cortex. PCNN’s are useful in image processing, especially image segmentation [22]. Applications include detection of the left ventricle boundary echocardiographic images, and tissue and organ segmentation of brain, abdomen, and lung magnetic resonance images [31]. Keller and McKinon used the PCNN to segment tissues and organs in brain and abdominal magnetic resonance images, respectively [17]. Murresan combined the PCNN with the Fourier transform in pattern recognition [22]. Moreno-Baron et al. integrated the PCNN with wavelets to quantify and analyze the sensor signals from an electronic tongue [21]. Li et al. applied the PCNN for a region-based image sensor fusion scheme [18]. Wang and Ma applied a multi-channel PCNN for multi-modality medical image fusion [34]. Ozen and Hassanien developed a PCNN-based segmentation algorithm to detect the boundaries of prostate tumors in transrectal ultrasound images [25]. Badr applied the PCNN to obtain signatures for brain lobe activity from single photon emission computerized tomography (SPECT) images as input for syntactic and semantic diagnosis [3]. The advantage of PCNNs is that the segmentation mechanism conforms to the clustering property of organs or tissues in medical imaging. The major drawback is the lack of a stopping mechanism, which leaves users to design ad-hoc stopping rules or arbitrarily assign the number of iterations [12,18].

1.3. Hybrid models

The idea of hybrid models is to integrate statistical and structural segmentation models for more robust results than what can be achieved with a single model. Tang et al. (2000) integrated the spectral analysis and intensity threshold technique for brain MR image segmentation [32]. Zhang et al. (2001) combined the Markov random field and the EM algorithm to segment the brain tissue into the WM and GM in brain MR images [36]. The main drawback of Markov random fields is that they are time-consuming [34]. Pluempitiwiryawej et al. developed a stochastic active contour scheme for cardiac MR image segmentation to solve problems with low contrast images of papillary muscles subject to turbulent blood flow by combining stochastic region-based and edge-based information [27]. To locate the modified Talairach cortical landmarks, Hu et al. proposed a model incorporating range-constrained thresholding and morphological operations to segment the planes containing the cortical landmarks [15]. Yan and Kassim applied an active contour algorithm for vessel segmentation in MR angiography images [25]. Ahmed et al. [2] proposed the Bias Corrected Fuzzy C-Means (BCFCM) algorithm to remove the effect of the noise and non-uniformities by integrating spatial neighborhood, with the histogram, and fuzzy logic techniques. Hou et al. [14] proposed a similar method, which employs the spatial neighborhood and in FCM approaches in the segmentation of brain MR images [14].

The BCFCM algorithm adds a spatial parameter to the objective function, which encourages the identical classification of adjacent pixels to reduce the interference caused by noise and non-

![Flow chart of the system.](image-url)
uniformities. Though BCFCM includes the spatial relationship, it does not consider distance between the pixel and its neighborhood. In PCNNs, the neighborhood interrelationship is assumed to follow a Gaussian distribution [35].

Accurate construction of brain tissues depends on accurate segmentation of the original MR images. Because of the large volume of images, it is impractical to conduct the segmentation manually. Therefore, an effective segmentation algorithm is highly needed. In this paper, we propose a hybrid automatic segmentation algorithm that integrates the statistical expectation maximization (EM) model and the structural PCNN model. The EM algorithm determines the required number of iterations for each type of tissue. Meanwhile, the EM output is used to adaptively adjust the PCNN model parameter. The proposed EM-based adaptive PCNN (adaptive EM–PCNN) automatically segments brain MR images into WM, GM and CSF. In experiments, the performance of the EM–PCNN is compared with that of the non-adaptive EM–PCNN, the EM and another hybrid model (the BCFCM). Both algorithms share the same structure, except that the non-adaptive EM–PCNN does not have a parameter adjustment mechanism.

2. System architecture

Fig. 1 gives a flow chart for the system architecture. The system works in two stages. In the first stage, the original input image is first enhanced using a non-isotropic spreading filter [30]. The non-isotropic spreading filter increases the signal-to-noise ratio by reducing the noise while simultaneously preserving the edges [26]. Then, Region-of-Interest (ROI), the intracranial tissues, is extracted from the original MR images. In the second stage, the ROI is segmented into WM, GM and CSF. Since the WM and parenchyma (GM + WM) are the areas of the greatest interest in clinical applications, those tissues are used for segmentation measurements. Then, the Jaccard similarities of each segmented area and the golden standard are derived as measures of the segmentation performance. As further performance verification, the adaptive EM–PCNN segmentation performance is compared with the performance of the non-adaptive EM–PCNN, the EM and another hybrid model (the BCFCM). Fig. 2 shows an example of image enhancement by the non-isotropic spreading filter. Fig. 2a and b shows the original MR image and the processed image. A close-up view shown in Fig. 2c and c illustrates the effect of enhancement.

2.1. Stage 1: image pre-processing

The purpose of the first stage is to enhance and extract the intracranial tissues within the MR image. The output image is further segmented into WM, GM and CSF. In this paper, the non-isotropic spreading filter and the revised Watershed algorithm are applied to enhance the MR images and remove the non-intracranial tissues [6,30]. Fig. 2 shows an example of image enhancement by the non-isotropic spreading filter. Fig. 2a and b shows the original MR image and the processed image. A close-up view shown in Fig. 2c and c illustrates the effect of enhancement.

For intracranial tissue extraction, experimental results showed that the revised Watershed can completely separate the skull from the intracranial tissues. No further algorithms such as morphological processing are required for this task. A detailed explanation of the intracranial tissue extraction is given below.

Step 1: Fig. 3a shows the MR image input. First, the gradient of the input image is calculated. Then, the gradient image is subjected to the complementary operation. Fig. 3b shows the output of the complementary operation, with the corre...
Step 2: The step 1 output undergoes the watershed algorithm to segment the image into basins. Fig. 3d shows the watershed algorithm output. Fig. 3e shows a close view of a section of Fig. 3d. The white dotted lines are the borders of the basins. Since the output images are over-segmented, merging will be required during post-processing.

Step 3: If all of the intensity level in two adjacent basins fall within the assigned pre-flooding height, these two basins are merged. Fig. 3f shows the binary output of the basin-merging process.

Step 4: Only the object with the biggest area in Fig. 3f is reserved. The reserved area is mapped back to the original MR image. The mapped image (Fig. 3g) shows the intracranial tissues.

2.2. Stage 2: image segmentation

The adaptive EM–PCNN, a hybrid automatic image segmentation algorithm combining the EM algorithm and PCNN, is used to segment the intracranial tissues into WM, GM and CSF. In clinical applications, WM and parenchyma (GM + WM) are the two targets of greatest interest and the CSF is generally not at interest. Therefore, the WM and parenchyma (GM + WM) segmentations are used to measure the performance. A brief description of the EM–PCNN algorithm is given below.

Step 1. The intracranial image intensity histogram is calculated. The EM is applied to the histogram to estimate the distribution parameters for WM, GM and CSF portions of the image. From these, thresholds for classification of the WM, GM and CSF can be derived.

Step 2. The PCNN is applied to segment the brain MR image. When the histogram of the PCNN segmentation exceeds a threshold, the segmented area in that iteration includes two types of tissues. In this case, the PCNN back up a previous iteration.

Step 3. A feedback mechanism is used to adjust the PCNN parameter to reduce the expansion of the segmented area in the next iteration. After the next iteration, the PCNN parameter is reset to its original value.

Step 4. The probability distributions parameters EM generated are used as a fitness function to evaluate the number of iterations for each type of tissue.

Since the proposed algorithm contains an adaptive mechanism, it is named adaptive EM–PCNN. A more detailed description of the adaptive EM–PCNN in brain MR image segmentation is given below.

Fig. 4a and b shows the example of an intracranial MR image and its histogram, respectively. Three peaks in the histogram show
the mode of three types of tissues. Most published literatures in the fields of medical image processing used Gaussian distribution to model the tissues (organs) since Gaussian distribution naturally fits the behavior of tissues (organs) in the acquired images. The EM algorithm has a closed-form M-step for the mixture distributions with Gaussian components fitted by maximum likelihood estimation (MLE) [4]. Therefore, EM algorithm with the basis of Gaussian distribution is employed. Since there are three types of tissues in the MR images, three is set as the number of Gaussian distribution in EM algorithm. Fig. 4c shows the results of curve fitting to the distributions. The black dashed line represents the combination of the estimated starts from small areas with high intensity and gradually expand is commonly modeled by a Gaussian equation. The segmentation of the matrix

where $\hat{\theta}(t)$ is the decay weight (or time constant); $\theta(t)$ is the threshold value in the last iteration; $V_0$ is the normalized constant; $Y(t-1)$ is the output image in the last iteration.

Then, each neuron in the dynamic threshold is compared with its corresponding internal energy $U(t)$. If $U(t) > \theta(t)$, then the corresponding output neuron is equal to 1. Otherwise, it is equal to 0. Each iteration updates the internal activation of the neuron ($U(t)$) and the output for every neuron in the network ($Y(t)$), based on the stimulus signal from the image ($S$) and the previous state of the network ($Y(t)$). The dynamic threshold ensures that activated PCNN output expands smoothly in spatial domain.

Conventional PCNNs cannot expand the segmented area adaptively [25]. This causes the algorithm to overshoot when the segmented area reaches the borders of a different type of tissue, leading to segmentation of two types of tissue in a single iteration. Under such case, the histogram of the segmented area covers the threshold of two types of tissues. Fig. 6 shows one typical example of the overshoot effect, which leads to the poor classification performance. The misclassification occurs when the iteration is crossing the threshold of WM and GM and the threshold of the GM and CSF, which is shown as the point $a$ and the point $b$ in Fig. 6, respectively.

In a PCNN, the value of the decay weight $\alpha_B$ is inverse proportion to the expansion rate of the segmented area. To solve the problem of the misclassification caused by the overshoot, we adjust adaptively the expansion rate of the PCNN by varying value of $\alpha_B$. While the segmented area crossing the border of different tissues, the value of the $\alpha_B$ is reduced to slow down the expansion rate of the segmented area. After then, the value of the $\alpha_B$ returns to the preset rate. The steps of the algorithm are described as follows.

1. From the EM output, we can calculate the intersection of the distributions of two types of tissues as the threshold of WM and GM and the threshold of the GM and CSF. Those two thresholds in histogram are statistically optimal solution to separate tissues. Fig. 7 shows the optimal threshold based on the EM.
2. For each iteration, the segmented area dilates along the profile of the previous iteration. Then, the corresponding histogram intensity slides down from the previous iteration. If the range of the histogram intensity covers the threshold, it means the segmented area over expands in that iteration. Fig. 8 shows one example of the overshoot in one iteration. The $\alpha_B$ is then reduced with proportion to the percentage of the number of overshoot pixels. Since the $0 < A/B < 1$, $\alpha_B$ must be greater than 0 and less than $\alpha_0$. Its value is given by

where $\alpha_B$ is the adjusted decay weight; $A$ is the number of pixels with intensity at or exceeding the threshold; $B$ is the number of
pixels segmented during the current iteration; $\alpha_0$ is the preset decay weight.

3. Return the segmented area back to the previous iteration and rerun the PCNN with the adjusted decay weight $\alpha_B$.

4. After this iteration, reset the decay weight back to the original value $\alpha/DC^2$, then go to Step 2.

Fig. 9 shows a flow chart for the adaptive algorithm. Since the segmentation measurements do not include the CSF, iteration can stop when the intensity of the segmented area exceeds the CSF/GM threshold (line b in Fig. 6).

The neural network parameters are interactively selected and verified. Table 1 lists the set of parameters applied in this paper.

Fig. 10 illustrates how the adaptive PCNN handles overshooting. The pixels in the right hand side of the threshold in Fig. 8 remain, which is shown as Fig. 10a. The overshoot area is segmented in the next iteration, which is shown as Fig. 10b.

Fig. 11 shows how the segmented area and its corresponding histogram progress in a typical series of iterations. The histograms show that the intensity of the segmented area decreases from the previous iteration. The binary diagrams show the segmented area in each iteration.

Fig. 12 shows how the segmented area accumulates in a typical series of iterations. The progress of the segmented area, which dilates along the profile from the previous iteration, displays the PCNN's property of the structural models.

For each iteration, we applied conditional probability in the histogram to classify the segmented area by type. In histogram-based classification, we classify the segmentation output as CSF, GM, or WM using the MLE conditional probabilities of the three tissue types given a specific iteration. The conditional probabilities can be derived from the EM output and the upper and lower histogram bounds for each segmentation iteration. A more detailed description of the MLE approach can be found in [28,30]. In Table 2, $P(A)$ denotes the MLE conditional probability of tissue type $A$ given a specific iteration, where $A$ can be CSF, GM or WM. The formula for $P(A)$ is

$$P(A) = \text{Weight}(A) \times \text{Cdf}(A)$$

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\alpha_L$</td>
<td>2.01</td>
</tr>
<tr>
<td>$V_L$</td>
<td>2.01</td>
</tr>
<tr>
<td>$\alpha_F$</td>
<td>3.01</td>
</tr>
<tr>
<td>$V_F$</td>
<td>1.0</td>
</tr>
<tr>
<td>$\alpha_0$</td>
<td>0.08</td>
</tr>
<tr>
<td>$V_0$</td>
<td>10</td>
</tr>
<tr>
<td>$\beta$</td>
<td></td>
</tr>
</tbody>
</table>

Fig. 9. Flow chart of adaptive PCNN algorithm.

Fig. 10. An example of overshoot.
where \( A \) is CSF, GM or WM; Weight (\( A \)) is the ratio of the number of type \( A \) pixels to the sum of pixels of all tissue types, which can be derived from the EM output; \( Cdf(A) \) is the cumulative density function of tissue \( A \) on the range extending from the lower bound to the upper bound. 

The results in Table 2 show that the first 4 iterations are classified as WM. From the 5th to the 13th iterations, the segmented area is classified as GM. After the 13th iteration, the segmented area is classified as CSF.

Fig. 13 shows an example of the input image and the golden standard for locating WM, GM, and CSF. The EM–PCNN has the properties of both the statistical and structural models. Fig. 13b shows an example of the classification output of the adaptive EM–PCNN.

In this paper, the performance evaluation of the adaptive EM–PCNN is compared with that of the non-adaptive EM–PCNN, expectation maximization (EM), and hybrid BCFCM models. As a statistical model in its own right, EM can be applied independently of the PCNN for automatic image segmentation [7]. In the EM implementation in this paper, the pixels in the MR images are classified solely based on the thresholds \( a \) and \( b \), as shown in Fig. 6. A pixel is classified as GM if its intensity is at least \( b \) but lower than \( a \), and as WM if its intensity is equal to or higher than \( a \).

The BCFCM is based on the Fuzzy C-Means (FCM) algorithm, which has been applied with some success in MR soft tissue segmentation and partial volume estimation [16]. The FCM strategy is to minimize the following objective function \( J \) with respect to the membership function \( u \) and the centroids \( v_i \):

\[
J = \sum_{i=1}^{c} \sum_{k=1}^{N} w_{ik} |x_k - v_i|^2
\]

where \( N \) is the set of histogram pixel intensities; \( p \) is a weighting exponent on each fuzzy membership; \( w_{ik} \) and \( x_k \) are the membership value and the image intensity at location \( k \); \( v_i \) is the centroid of class \( i \).

FCM assumes that the images are spatially invariant. In Bias Corrected Fuzzy C-Means (BCFCM), the so-called “neighborhood effect” [2] acts as a regularizer and biases the solution toward piecewise-homogeneous labeling. The BCFCM employs a term which makes the label of a pixel dependent on the labels of other pixels in its neighborhood. The modified objective function is given by

\[
J = \sum_{i=1}^{c} \sum_{k=1}^{N} w_{ik} |x_k - v_i|^2 + \frac{\alpha}{N_k} \sum_{i=1}^{c} \sum_{k=1}^{N} w_{ik} \left( \sum_{x_r \in N_k} |x_r - v_i|^2 \right)
\]

where \( N_k \) is the set of neighboring pixels in window \( x_k \); \( N_k \) is the number of the elements in \( N_k \). \( \alpha \) is weight of the neighbors term.

The neighborhood effect acts as a regularizer and biases the solution toward piecewise-homogeneous labels. This feature is particularly useful for segmenting scans corrupted by salt and pepper noise [2]. Fig. 14a–c illustrate the segmentation output by non-adaptive EM–PCNN, EM and BCFCM, respectively.

The segmentation output of the EM–PCNN is visibly closer to the golden standard than that of the BCFCM. However, visual inspection alone does not show that the adaptive EM–PCNN outperforms the EM and non-adaptive EM–PCNN. Statistical analysis is required for performance verification. The following section describes the statistical analysis in detail.

2.3. Performance evaluation

In this paper, Jaccard similarity is employed as the index for performance evaluation. The formula of Jaccard similarity is given:

\[
J(S_1, S_2) = \frac{|S_1 \cap S_2|}{|S_1 \cup S_2|}
\]

where \( S_1 \) is the golden standard; \( S_2 \) is the segmented area; \( \cap \) is intersection operator; \( \cup \) is union operator.

The golden standard \( S_1 \) is the binary tissue images defined by the BrainWeb. \( S_2 \) is segmentation output either from adaptive EM–PCNN, non-adaptive EM–PCNN, EM or BCFCM. The range of the Jaccard similarity falls from 0 and 1. The higher of the Jaccard similarity means the segmented area matches more with the golden standard. Single-tailed paired-samples t-tests are conducted to verify whether the proposed adaptive EM–PCNN outperforms significantly other three methods.

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**Table 2**

<table>
<thead>
<tr>
<th>Iteration</th>
<th>( P(CSF) )</th>
<th>( P(GM) )</th>
<th>( P(WM) )</th>
<th>Result</th>
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</thead>
<tbody>
<tr>
<td>1</td>
<td>0.00000</td>
<td>0.00000</td>
<td>0.00043</td>
<td>WM</td>
</tr>
<tr>
<td>2</td>
<td>0.00000</td>
<td>0.00118</td>
<td>0.17389</td>
<td>WM</td>
</tr>
<tr>
<td>3</td>
<td>0.00000</td>
<td>0.00852</td>
<td>0.08720</td>
<td>WM</td>
</tr>
<tr>
<td>4</td>
<td>0.00000</td>
<td>0.01150</td>
<td>0.01757</td>
<td>WM</td>
</tr>
<tr>
<td>5</td>
<td>0.00000</td>
<td>0.03084</td>
<td>0.00929</td>
<td>GM</td>
</tr>
<tr>
<td>6</td>
<td>0.00004</td>
<td>0.06971</td>
<td>0.00255</td>
<td>GM</td>
</tr>
<tr>
<td>7</td>
<td>0.00011</td>
<td>0.07650</td>
<td>0.00026</td>
<td>GM</td>
</tr>
<tr>
<td>8</td>
<td>0.00030</td>
<td>0.08605</td>
<td>0.00003</td>
<td>GM</td>
</tr>
<tr>
<td>9</td>
<td>0.00050</td>
<td>0.05147</td>
<td>0.00000</td>
<td>GM</td>
</tr>
<tr>
<td>10</td>
<td>0.00135</td>
<td>0.04867</td>
<td>0.00000</td>
<td>GM</td>
</tr>
<tr>
<td>11</td>
<td>0.00188</td>
<td>0.02147</td>
<td>0.00000</td>
<td>GM</td>
</tr>
<tr>
<td>12</td>
<td>0.00302</td>
<td>0.01145</td>
<td>0.00000</td>
<td>GM</td>
</tr>
<tr>
<td>13</td>
<td>0.00137</td>
<td>0.00214</td>
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<tr>
<td>14</td>
<td>0.00541</td>
<td>0.00338</td>
<td>0.00000</td>
<td>CSF</td>
</tr>
<tr>
<td>15</td>
<td>0.00470</td>
<td>0.00094</td>
<td>0.00000</td>
<td>CSF</td>
</tr>
</tbody>
</table>
Fig. 11. Progression of the segmented area and corresponding histogram. (a) First iteration, (b) second iteration, (c) third iteration, (d) fourth iteration, (e) fifth iteration, (f) sixth iteration, (g) seventh iteration, (h) eighth iteration, (i) ninth iteration, (j) tenth iteration, (k) eleventh iteration, (l) twelfth iteration, (m) thirteenth iteration, (n) fourteenth iteration, (o) fifteenth iteration.
Fig. 12. Accumulation of the segmented area. (a) First iteration, (b) second iteration, (c) third iteration, (d) fourth iteration, (e) fifth iteration, (f) sixth iteration, (g) seventh iteration, (h) eighth iteration, (i) ninth iteration, (j) tenth iteration, (k) eleventh iteration, (l) twelfth iteration, (m) thirteenth iteration, (n) fourteenth iteration, (o) fifteenth iteration.

3. Experimental setup and performance evaluation

Images for performance analysis were acquired from BrainWeb's public domain simulated image database with T1 modality and slice thickness 1 mm. Gray level variations arising from noise and inhomogeneities were added to the gold-standard phantom images [5]. The selected images suffered from six levels (0%, 1%, 3%, 5%, 7%, 9%) of noise and 2 levels (0%, 20%) of background inhomogeneity, making for a total of 12 levels of image quality. The noise distribution followed a Gaussian probability density function with

Fig. 13. Segmentation output as determined by golden standard and by adaptive EM–PCNN. (a) Input image and golden standard and (b) segmentation output by adaptive EM–PCNN.
Fig. 14. Segmentation output by non-adaptive EM–PCNN, EM and BCFCM. (a) Segmentation output by non-adaptive EM–PCNN, (b) segmentation output by expectation maximization and (c) segmentation output by BCFCM.

Fig. 15. Images simulated at various noise levels (0%, 5% and 9%).
**Table 3**

Results of Jaccard similarity comparison.

<table>
<thead>
<tr>
<th>Algorithm</th>
<th>Mean</th>
<th>Standard deviation</th>
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<tbody>
<tr>
<td></td>
<td>Gray matter</td>
<td>Brain parenchyma</td>
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<tr>
<td>Adaptive EM–PCNN</td>
<td>0.80239</td>
<td>0.97062</td>
</tr>
<tr>
<td>Non-adaptive EM–PCNN</td>
<td>0.78356</td>
<td>0.97058</td>
</tr>
<tr>
<td>EM</td>
<td>0.78784</td>
<td>0.97009</td>
</tr>
<tr>
<td>BCFCM</td>
<td>0.77547</td>
<td>0.96287</td>
</tr>
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</table>

**Table 4**

Paired \(t\)-test of Jaccard similarity (\(\alpha = 0.05\)).

<table>
<thead>
<tr>
<th></th>
<th>Mean</th>
<th>Standard deviation</th>
<th>95% Confidence interval</th>
<th>Significant Level</th>
<th>Results</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Lower</td>
<td>Upper</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gray matter</td>
<td></td>
<td></td>
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<tr>
<td>Adaptive EM–PCNN vs. Non-adaptive EM–PCNN</td>
<td>0.01883</td>
<td>0.06693</td>
<td>0.01527</td>
<td>0.000</td>
<td>Accept (H_1): (\mu_1 &gt; \mu_2)</td>
</tr>
<tr>
<td>Adaptive EM–PCNN vs. EM</td>
<td>0.01455</td>
<td>0.11384</td>
<td>0.00850</td>
<td>0.000</td>
<td>Accept (H_1): (\mu_1 &gt; \mu_2)</td>
</tr>
<tr>
<td>Adaptive EM–PCNN vs. BCFCM</td>
<td>0.02692</td>
<td>0.10888</td>
<td>0.02113</td>
<td>0.000</td>
<td>Accept (H_1): (\mu_1 &gt; \mu_4)</td>
</tr>
<tr>
<td>Brain parenchyma</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adaptive EM–PCNN vs. Non-adaptive EM–PCNN</td>
<td>0.00004</td>
<td>0.00125</td>
<td>-0.00002</td>
<td>0.00011</td>
<td>Accept (H_1): (\mu_1 &gt; \mu_2)</td>
</tr>
<tr>
<td>Adaptive EM–PCNN vs. EM</td>
<td>0.00053</td>
<td>0.01518</td>
<td>-0.00028</td>
<td>0.00013</td>
<td>Accept (H_1): (\mu_1 &gt; \mu_2)</td>
</tr>
<tr>
<td>Adaptive EM–PCNN vs. BCFCM</td>
<td>0.00775</td>
<td>0.01518</td>
<td>0.00695</td>
<td>0.00086</td>
<td>Accept (H_1): (\mu_1 &gt; \mu_4)</td>
</tr>
</tbody>
</table>

**Table 5**

Computational time (unit: seconds).

<table>
<thead>
<tr>
<th>Algorithm</th>
<th>Mean</th>
<th>Standard deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adaptive EM–PCNN</td>
<td>1.69838</td>
<td>0.29321</td>
</tr>
<tr>
<td>Non-adaptive EM–PCNN</td>
<td>1.63638</td>
<td>0.24904</td>
</tr>
<tr>
<td>EM</td>
<td>1.45354</td>
<td>0.24313</td>
</tr>
<tr>
<td>BCFCM</td>
<td>2.41587</td>
<td>0.31245</td>
</tr>
</tbody>
</table>

The results show that the adaptive EM–PCNN outperforms the non-adaptive EM–PCNN, the EM and the BCFCM on average. Single-tailed paired \(t\)-tests were conducted to determine whether the adaptive EM–PCNN outperformed the non-adaptive EM–PCNN, EM and BCFCM. Therefore, we tested the hypothesis:

\[ H_0 : \mu_1 = \mu_2 \]
\[ H_1 : \mu_1 > \mu_2 \]

where \(\mu_1\) is the Jaccard similarity between the adaptive EM–PCNN and the golden standard; \(\mu_2\) is the Jaccard similarity between the non-adaptive EM–PCNN (EM or BCFCM) and the golden standard.

Table 4 shows the output of the paired \(t\)-test at a significance of \(\alpha = 5\%\). A confidence interval with a lower limit greater than 0 implies that the null hypotheses \(H_0\) should be rejected. Acceptance of the alternative hypotheses \(H_1\) implies that the adaptive EM–PCNN performs significantly better in segmentation than the chosen benchmark (the non-adaptive EM–PCNN, EM or BCFCM). In gray matter segmentation, results show that adaptive EM–PCNN significantly outperforms the non-adaptive EM–PCNN, the EM and the BCFCM. For brain parenchyma segmentation, the adaptive EM–PCNN is significantly better than only the BCFCM.Though the adaptive EM–PCNN is better than the non-adaptive EM–PCNN and the EM on average, the difference does not reach significance.

Fig. 16 shows an example of 3D reconstruction of images segmented by the adaptive EM–PCNN with 1° noise and 20° background non-uniformity. Since the brain parenchyma is a 3D solid...
GM mode. Fig. 15b provides the same visualization effect as the brain parenchyma.

4. Conclusions

This paper presents an automatic hybrid image segmentation model that integrates the EM and the PCNN for automatic segmentation of brain MR images. In addition, an adaptive EM-based PCNN algorithm is proposed to fine tune the PCNN parameter choice. The EM is first applied to brain MR image histograms to estimate the distribution parameters for the WM, GM and CSF regions. The estimated parameters serve as a fitness function for tissue classification. In addition, the thresholds derived from the EM output are used to adaptively adjust the rate of expansion of the segmented area, thus enhancing the classification quality.

The performance of the adaptive EM–PCNN is compared with that of the non-adaptive EM–PCNN, EM and BCFCM. Results show that the adaptive EM–PCNN significantly outperforms the other three algorithms in gray matter segmentation. In brain parenchyma segmentation, the adaptive EM–PCNN significantly outperforms the BCFCM. Though the adaptive EM–PCNN is also better on average than the non-adaptive EM–PCNN and EM, the differences do not reach significance. Overall, the adaptive EM–PCNN outperforms the other three algorithms in GM/brain parenchyma segmentation.

In this paper, the integration of the EM and PCNN demonstrates how fully automatic image segmentation can be achieved with the adaptive functionality. Since the PCNN algorithm is iterative, the results raise the possibility that in the future, similar automated, adaptive segmentation approaches can be implemented with other iterative segmentation techniques. The operation and performance achieved with various choices of segmentation algorithm and adaptive design is a direction for future research.

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References

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