Local-based Fuzzy Clustering for Segmentation of MR Brain Images

Jianzhong Wang, Lili Dou, Na Che, Di Liu, Baoxue Zhang and Jun Kong*

Abstract— **Accurate segmentation of magnetic resonance images (MRI) corrupted by intensity inhomogeneity is a challenging problem and has received an enormous amount of attention lately. On the basis of the local image model, we propose a different segmentation method for MR brain images without estimation and correction for intensity heterogeneity. Firstly, we obtain clustering context based on the distributing disciplinarian in anatomy that gray matter (GM) is always between white matter (WM) and cerebrospinal fluid (CSF) in brain, which ensure the three tissues exist together in each one. Then the size of the context is optimized by a minimum entropy criterion. Finally, FCM algorithm is independently performed in each context to calculate the degree of membership of a pixel to each tissue class. The proposed methodology has been evaluated for simulated images and shown the better results.**

I. INTRODUCTION

Magnetic resonance imaging (MRI) has many advantages over other diagnostic imaging modalities, such as high contrast between soft tissues, high spatial resolution and inherent 3D nature, thus has gained wide clinical applications [1]. A first step in medical image analysis is separation of the input image into meaningful regions, which could involve organ detection or tissue characterization. Currently, in many clinical studies segmentation is still mainly manual or strongly supervised by a human expert,which make the segmentation irreproducible and deteriorating the precision of the analysis of the segmentation. Hence, there is a real need for automated MRI segmentation tools. Unfortunately, there are mainly three considerable difficulties in segmenting MRI data: noise, partial volume effects (PVE) and intensity inhomogeneity. Intensity inhomogeneity, also referred to as bias field, appears as a continuous, slowly varying shadowing effect over the whole image, which causes intensities of the same anatomical structures be not constant. Although MRI images may appear visually uniform, such inhomogeneities can result in serious misclassifications when intensity-based segmentation techniques are used [2]. To eliminate or alleviate the adverse impact, two kinds of methods have been proposed for removing artifact signal inhomogeneities, namely, prospective and retrospective correction [3]. The prospective methods try to avoid this type of artifact in the acquisition process by using special hardware of specific sequences. Thus, it is unrealistic to compensate different scanned patients with a fixed estimated profile. The drawback restricts the validity of prospective correction methods.

Retrospective image processing methods have been more intensively developed, since they do not require special acquisition protocols and can be applied to removing both machine and patient-induced imhomogeneities. Various retrospectively approaches have been proposed to compensate the intensity inhomogeneities. Among them, surface fitting such as spline basis functions [4] and polynomials basis functions [5] via fitting a set of data points as closely as possible to the image brightness function. Correction is done by dividing computed surfaces voxel-by-voxel from the orginal image. However, the parameters of the basis functions or polynomials are estimated from manually or automatically selected reference points, which is either time consuming or unreliable. Homomorphic filters [6], assume that intensity inhomogeneity is a low-frequency signal that can be removed by a high pass filtering, while high-frequency details in MR images were also corrupted. The method based on Fuzzy C-means [9] minimizes the sum of class membership function and uses the first and second order regularization terms that ensure a smooth bias field. An extension of Fuzzy C-means based algorithm has been proposed in [10], where high robustness to salt and pepper noise and algorithm efficiency are the main benefits. Instead of working in the spatial domain, correction can be performed in wavelet domains [11] or Probability density functions domain. Such domains allow different uses of the assumptions made on intensity non-uniformity. Once data are corrected, they are transformed back to the spatial domain.

Multicontext fuzzy clustering (MCFC) is proposed in Literature [1]. Based on a novel image model which takes into account both artificial and inherent intensity inhomogeneities, multiple clustering contexts are generated for each pixel, and within a context, the C classes of tissues exist together and there are considerable pixels in each tissue class. Fuzzy clustering is independently performed in each context. The segmentation is no longer need the estimation and correction procedures for intensity inhomogeneities.

In this paper, a simple and effective segmentation method is presented to segment Resonance Brain Images Corrupted by Intensity Heterogeneity without estimation and correction for it. The rest of this paper is organized as follows. In Section 2, the local image model and conventional Fuzzy C-means algorithm are presented. Our proposed method is described in Section 3. Experimental and comparison results

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Jianzhong Wang and Baoxue Zhang are with the School of Mathematics and Statistics and Key Laboratory for Applied Statistics of MOE, Northeast Normal University, Changchun, China; (e-mail: wangjz019, bxzhang@nenu.edu.cn).

Lili Dou, Na Che,Di Liu and Jun Kong are with the Computer School and Key Laboratory for Applied Statistics of MOE, Northeast Normal University, Changchun, China; (e-mail: doull412, chen286,liud630, kongjun@nenu.edu.cn).

*Corresponding author. Tel.: +86 431 85696533; fax: +86 431 85696533

are presented in Section 4 and we conclude this paper in Section 5.

II. BACKGROUND

A. Local Image Model

A traditional approach to model intensity inhomogeneities in MRI images has been proposed in lectures[2] [6-7]. Bias field is commonly modeled as a continuous, slowly varying multiplicative over the image domain

$$y_i = \alpha_i x_i + n_i, x_i \in \{v_1, v_2, \ldots, v_c\} \tag{1}$$

where $y_i$and x_i are the observed and true intensity at the pixel i receptively; $n_i$is the measurement noise of independent white Gaussian distribution at pixel i; c is the desired number of tissue classes; $v_k$is true intensity for each tissue class k.

The modeling mentioned above can model the artificial intensity variations very well. But inherent intensity inhomogeneity is not considered in it. So in this paper we use the modal proposed by Chaozhe Z. Jiang et al [1], in which the intensity of inhomogeneities contains both artificial and inherent intensity inhomogeneities, as expressed

$$y_i = \alpha_i x_i + n_i, x_i \in \{v_1, v_2, \ldots, v_N\} \tag{2}$$

where y_i,x_i,n_i,and c are the same as mentioned above,N is the total number of pixels in the MR image. In this local model, artificial intensity inhomogeneity is modeled as bias field α_i. The true intensity v_i is used to model inherent intensity inhomogeneity, and it varies with the location i in the brain.

Clustering context is an important concept in the segmentation with intensity inhomogeneities. It is defined as a spatially connected subset of 2D MR images or 3D volume data. There are three assumptions for each context.

1. Bias field α_i, $1 \leq i \leq N$, is smooth and slowly varying.

From this assumption, the bias field α_i within a clustering context W can be approximately treated as a constant field: $\alpha_i \approx \alpha, \forall i \in W$.

2. Within a context, the c classes of tissues exist together and there are considerable pixels in each tissue class. Due to the complexity of brain tissue structure, which causes bends and twists of spatial distributions of tissues of WM, GM, and CSF, even a properly small size context can make this assumption solid. With this assumption, the cluster number, here it is equal to c, can be determined.

3. Within a context, all pixels of the same tissue have similar true intensities. According to the distributing disciplinarian in brain tissue: the pixels belonging to the same tissue are homogeneity, therefore they have similar intensities.

Because there are c classes of tissues in a clustering context W, the total number of true intensities in the context reduces to the fixed tissues number c: $x_i \in \{v_1, v_2, \ldots v_c\}, \forall i \in W$.

Therefore, (2) can be simplified in the local model:

$$y_i^j = x_i^j + n_i^j \tag{3}$$

where y_i^j is the observed intensity and x_i^j is the true intensity modulated by the bias field at pixel i in clustering context W_j; n_i^j is measurement noise at pixel i in W_j ; $v_k^j (k = 1, 2, \ldots c)$ is the approximate true intensity of the kth tissue in W_j ; α^j is a constant in context W_j; N_w is the total number of clustering contexts in volume data; and c is the desired number of tissues.

Based on this local model, the essential characteristics of the ideal image model, which was once corrupted by both artificial and inherent intensity inhomogeneites can be recovered. This facilitates any segmentation method.

B. Fuzzy C-means Algorithm

Fuzzy C-means (FCM) originally introduced by Bezdec (1981) as an improvement of the hard k-means algorithm, which is one of the most widely used fuzzy clustering techniques [12],The idea of the FCM is to partition n data points into c clusters by minimizing the following objective function:

$$J(\mu, \nu) = \sum_{k=1}^{c} \sum_{i=1}^{n} \mu_{ik}^m d^2(x_i, \nu_k) \tag{4}$$

subject to: $\sum_{k=1}^{c} \mu_{ik} = 1$,where μ_{ik} indicates the membership degree to which data point x_i belongs to kth cluster, m is the weighting exponent (in our study, $m = 2$), and ν_k is the fuzzy cluster center for cluster. μ is the $c \times n$ fuzzy c-partition matrix, and ν is the matrix of prototypes of the clusters. Using the Euclidean norm, the distance metric d measures the vector distance of a feature vector from a cluster center in the feature space, i.e.:

$$d^2(x_i, \nu_k) = \|x_i - \nu_k\|^2 \tag{5}$$

The objective function is minimized when data points close to the center of their clusters are assigned high membership values, and low membership values are assigned to data points far from the center. The membership functions and cluster centers are updated by the following expressions:

$$\mu_{ik} = \sum_{j=1}^{c} \left(\frac{d(x_i, \nu_k)}{d(x_i, \nu_j)}\right)^{-\frac{2}{m-1}} \tag{6}$$

and

$$\nu_k = \frac{\sum_{i=1}^{n} \mu_{ik}^m x_i}{\sum_{i=1}^{n} \mu_{ik}^m} \tag{7}$$

In implementation, matrix ν is randomly initialized, μ and ν then and are updated through an iterative process using (6) and (7), respectively.

III. METHODOLOGY

In order to keep the competence of the whole algorithm for overcoming the impact of the intensity inhomogeneity, the crucial point is that the contexts generating for all pixels should satisfy the three assumptions. For the first assumption, we can consider the bias field in one context is uniform if the context size is as small as possible. Because the pixels belong to the same tissue are homogeneity, so they are extremely similar, which make assumption 3 satisfy. From the second assumption, it is used to generate the contexts based on the tissue distributing disciplinarian in anatomy that GM is always distributing between WM and CSF . We can ensure

that the third tissue must exist in the context if the WM and CSF are confirmed existing together in a context and there are considerable pixels.

As we discussed above, To satisfy the above assumptions, the context size should be properly decided. On the principle that all the three tissues exist together in the context we use shannon entropy as a homogeneity measurement to optimize the size of the clustering context. Our method relies on the assumptionsentropy value grows with increasing of the intensity of bias field [13]. On this assumption, entropy is a good measure of the field smoothness which can be minimized for each context in order to overcome the bias problem. All the contexts can be generated adaptively in this method and the membership degree calculated by FCM in each context will be more reliable.

We can conclude our method as follows:

1. A global threshold segmentation algorithm is used to obtain the WM image and CSF image of the processing MRI.

2. Based on the distributing disciplinarian in anatomy that GM is always between WM and CSF in brain, the two images obtained from the first step can be regarded as the reference to judge whether the two matters exist together in a clustering context, and to confirm that all the three tissues exist together.

3. The Shannon entropy is used as a homogeneity measurement to optimize the size of the clustering context.

4. According to the suitable of FCM algorithm for the uncertainty and fuzziness of gray-scale image, FCM algorithm is independently performed in each context to calculate the degree of membership of a pixel to each tissue class.

A. Context generation method

To make sure each context contains three tissues, we need to obtain white matter image (I_{wm}) and cerebrospinal fluid image (I_{csf}) of the processing MRI by an initial segmentation algorithm. For not requiring high accuracy of the segmentation result, the global threshold method is selected as our initial segmentation.

We need calculate the minimal circumscribed rectangle of the brain in the image and select this part as the processing image at first, which make each context contain tissue pixels as many as possible and ensure the accurate segmentation result of each context. And then the image is divided into eight average contexts that four rows and two columns. Because the image is approximate symmetry in the vertical orientation and the sizes of different images (except background) are diverse, so two columns and four rows are more reasonable and widely applicable. Finally the global threshold segmentation algorithm is used in each context respectively to obtain the final three tissue images.

The results of initial segmentation are shown in Fig.1 (a) shows a simulated MR image that corrupted with 40% intensity inhomogeneities. (b) is the result of initial segmentation. A-D are Four contexts under consideration located on different areas and the magnified drawing of regions A-D are shown in Fig.2 Form region A and C we can see if the context contain two tissues WM and CSF, it must also contain GM. Otherwise, as region B and D, GM and WM or GM and CSF exist together, we can not confirm the third tissue must exist.

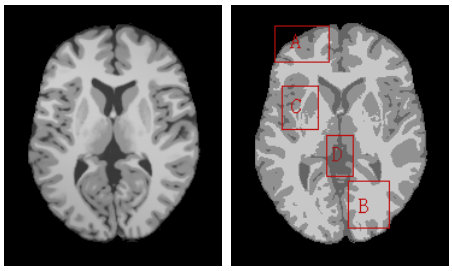
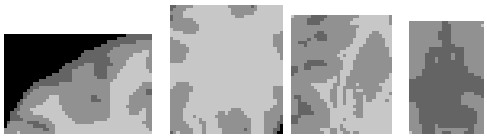


Fig. 1. (a)simulated MR image (b)initial segmentation.



(a) (b) (c) (d)

Fig. 2. (a-d)are the magnified drawing of regions A-D in Fig.1(b)

TABLE I
SIMILARITY INDEX FROM INITIAL SEGMENTATION

	ρ_{csf}	ρ_{wm}	ρ_{gm}
0%	0.9110	0.9605	0.9395
20%	0.9120	0.9594	0.9385
40%	0.9117	0.9547	0.9347

By comparing with the "ground truth", the similarity indices of the initial segmentation for image with 0%, 20%, and 40% intensity inhomogeneities are listed in Table I. The similarity index value of each tissue is greater than 90%.Therefore, we can judge whether the WM and CSF exist together in a context by image I_{wm} and I_{csf}, and to confirm that whether all the three tissues exist together.

Using the information from I_{wm} and I_{csf}, the ratio of the CSF and WM in the whole image can be calculated as:

$$r_{csf} = \frac{N_{csf}}{M \times N} \tag{8}$$

$$r_{wm} = \frac{N_{wm}}{M \times N} \tag{9}$$

where N_{csf} and N_{wm} are the numbers of CSF and WM respectively. M and N are the width and height of the image.

The steps of the contexts generating can be described as follows:

Step 1: Generation of the first context.

Firstly, define a rectangular window with an initial size of $m \times n$, the point $I_{csf}(1,1)$ is the upper left corner of the rectangular. cr_{csf} is the ratio of CSF in the rectangular, which is defined as equation (10). In order to guarantee the quantity of CSF in the context, the values of m and n are increased until $cr_{csf} \geq r_{csf}$.

Secondly, in the image I_{wm}, using the updated values of m and n as the size of the rectangular, the point $I_{wm}(1,1)$

is the upper left corner of the rectangular.cr_{wm} is the ratio of WM in the rectangular, which is defined as equation (11). So increasing the values of m and n until $cr_{wm} \geq r_{wm}$ to ensure WM exists in this context and there are considerable pixels.

$$cr_{csf} = \frac{CN_{csf}}{m \times n} \tag{10}$$

$$cr_{wm} = \frac{CN_{wm}}{m \times n} \tag{11}$$

where CN_{csf} and CN_{wm} are the pixel number of CSF and WM in the context.

Thirdly, the entropy of this rectangular is calculated. Then the size of this rectangular is enlarged with increasing the value of m and n constantly and calculates the entropy of each one, from these contexts we choice the one has the minimum entropy value as the first context, its size is the updated values of m and n.

Step 2: Context optimization based on entropy-minimization algorithm

Firstly, with the value of m fixedness, initialize the value of n. The point $I_{csf(1,n+1)}$ and $I_{wm(1,n+1)}$ are regarded as the upper left corner of the rectangular, respectively. Do the same as mentioned in step 1 to calculate the size and the position of the next context.

Secondly, keeping the value of m stable, the size of rectangular is enlarged constantly with increasing the value of n , and several rectangles can be obtained by this way. From these rectangles we select the one with the minimum entropy value as a context. Repeating this operation until all the columns in the m rows are contained in the context. The last context in the m rows should be incorporated with the above context if it contains few numbers of WM and CSF, which is necessary to guarantee the quantity of WM and CSF in each context.

The above two steps were repeated until the contexts required for all pixels are generated.

B. Local Segmentation

After we get all contexts according to the method mentioned above, FCM algorithm perform the classification independently in each context to calculate the degree of membership of a pixel to each tissue class.

FCM algorithm can be summarized as follows: Initialize class centroid values,$\{v_k\}_{k=1}^{c}$. And beginning from the second context, use the clustering results of $\{v_k\}_{k=1}^{c}$ from the previously generated context as the initial cluster centroids.

Update the membership matrix with (6).

Update the cluster centroids with (7).

As we know, initialization is very important for meaningful clustering results and reduction of computation time. The centroids in two neighboring contexts are approximately equivalent Because of the two neighboring contexts are quite similar, so we using the clustering results from the previous context as the initial values in current context, which can reduce the computational time and improve the accuracy. After FCM is performed in all the contexts, maximum membership principle is used to obtain the final segmentation result.

IV. EXPERIMENTS

The proposed algorithm was implemented in Matlab on a PC with Intel Pentium 4 2.66GHz processor and 512M RAM. It was tested on simulated MRI images obtained from the Brain Web Simulated Brain Database at the McConnell Brain Imaging Center of the Montreal Neurological Institute (MNI), McConnell University.

Four different indices (false positive ratio r_{fp}, false negative ratio r_{fn} ,similarity index ρ [14] and misclassification error MCR) are exploited for each of three brain tissues as quantitative measures to validate the accuracy and reliability of our method.

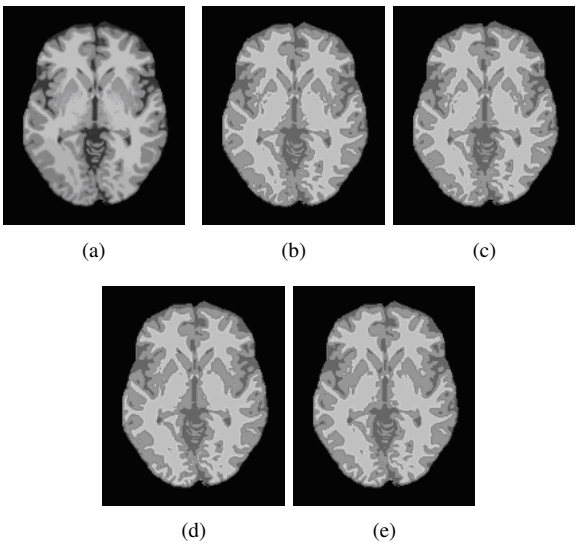


Fig. 3. (a) simulated MRI. (b)FCM segmentation. (c)MCFC segmentation.(d)our segmentation (e)The ground truth.

TABLE II

THREE INDICES FROM SIMULATED DATA.

method	indices	CSF	GM	WM
FCM	r_{fp}	16.68	9.14	11.52
	r_{fn}	12.56	13.17	7.39
	ρ	85.68	88.62	90.73
MCFC	r_{fp}	4.97	3.81	10.67
	r_{fn}	2.89	9.62	3.25
	ρ	96.11	93.08	93.29
our method	r_{fp}	5.31	1.50	5.53
	r_{fn}	2.14	5.59	1.67
	ρ	96.33	96.38	96.97

The brain image in Fig.3 (a) is a slice of the simulated 3-D volume with 40 %intensity inhomogeneity. The segmentation results of the standard FCM, MCFC are shown in (b) and (c) respectively. Using our proposed algorithm, the segmentation result is shown in Fig.3 (d). The "ground truth" of Fig.3 (a) is shown in (e). From the segmentation results in Fig.3, we can visually see that our method is more accurate especially in the transition area between WM and GM or GM and CSF. Table II shows the quantitative experimental results.

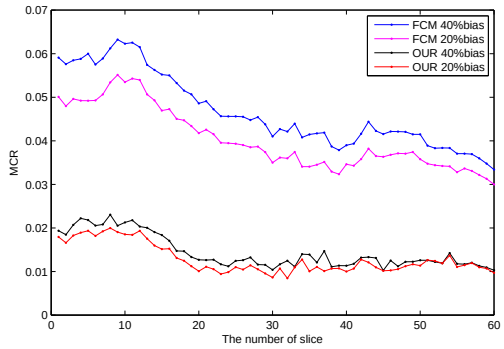


Fig. 4. MCR from slices 71 to 130 in the simulated brain image sequence.

TABLE III

THREE INDICES FROM SIMULATED DATA.

bias value	indices	CSF	GM	WM
20%bias	r_{fp}	0.0402	0.0095	0.0485
	r_{fn}	0.0201	0.0573	0.0024
	ρ	0.9702	0.9657	0.9752
40%bias	r_{fp}	0.0431	0.0144	0.0508
	r_{fn}	0.0214	0.0603	0.0066
	ρ	0.9681	0.9617	0.9720

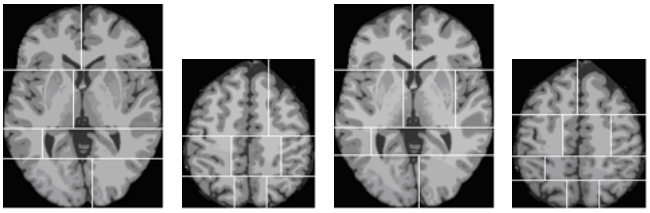
To illustrate precise and veracity of our method,we do experiment on sixty images from slice 71 to 130 in the simulated brain image sequence that corrupted by 20% and 40% intensity inhomogeneities respectively. We also apply standard FCM and our proposed method to the sixty images for comparison. The MCR are shown in Fig.4. It clearly demonstrates that our method has a better performance than FCM at the different bias field level.The average validation result:false positive ratio r_{fp}, false negative ratio r_{fn}, and similarity index ρ of the sixty images are shown in Table III.From Table III, we can find that Though the image are corrupted by 40% intensity inhomogeneities, the similarity indices of all the tissues are still larger than 96%,which indicates an excellent agreement between our segmentation results and the "ground truth".

TABLE IV

SIMILARITY INDEX FROM INITIAL SEGMENTATION

	20%bias	Entropy20%bias	40%bias	Entropy20%bias
CSF	97.04	97.47	97.06	97.14
GM	95.53	95.78	95.69	95.77
WM	96.23	96.61	96.01	96.10

From Table IV we can see the effect of entropy optimization to segmentation. The similarity index obtained by entropy optimization is higher than validation result without optimization. Fig.5 shows the result of context generation is usually different for the same MRI slice corrupted with different level bias field. We could see the proposed algorithm will get more contexts for the image with greater migration. However on the premise of ensuring assumption 1 and 2 satisfaction, our method make the number of contexts be minimum as much as possible which improve the ability of overcoming intensity inhomogeneities as well as the operation speed.



(a) (b) (c) (d)

Fig. 5. (a,b) the context generation on the simulate brain slices with 20% bias field. (c,d) the corresponding results with 40% bias field.

V. CONCLUSIONS

In this paper, we proposed a theoretically simple and practically effective approach to automatic tissue classification This algorithm can satisfy the assumptions well, so reliability of clustering results in the context can be guaranteed. The algorithm has been applied to the segmentation of MR brain structures with intensity heterogeneities. And the computational time of our proposed method is much smaller than other algorithms.

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