Improving Fuzzy Algorithms For Automatic Magnetic Resonance Image Segmentation

E.A. Zanaty
College of Computer Science
Taif University, Saudi Arabia
zanaty22@yahoo.com

Sultan Aljahdali
College of Computer Science
Taif University, Saudi Arabia
aljahdali@tu.edu.sa

Narayan Debnath
Computer Science Department
Winona State University
ndebnath@winona.edu

Abstract: *In this paper, we present reliable algorithms for fuzzy K-means and C-means (FCM) that could improve MRI segmentation. Since the k-means or FCM method aims to minimize the sum of squared distances from all points to their cluster centers, this should result in compact clusters. Therefore the distance of the points from their cluster centre is used to determine whether the clusters are compact. For this purpose, we use the intra-cluster distance measure, which is simply the median distance between a point and its cluster centre. The intra-cluster is used to give us the ideal number of clusters automatically; i.e a centre of the first cluster is used to estimate the second cluster, while an intra-cluster of the second cluster is obtained. Similarly, the third cluster is estimated using the centre and intra cluster of the second cluster, so on, and only stop when the intra-cluster is smaller than a prescribed value.*

The suggested algorithms are evaluated and compared with established fuzzy K-means and C-means methods by applying them on simulated volumetric MRI and real MRI data to prove their efficiency. The application of these algorithms to a real MRI dataset cannot give us a quantitative measure about how much successful they are. As such, the segmentation results are judged visually by specialists.

Keywords: Medical imaging, Fuzzy clustering, Image segmentation.

1. Introduction

Magnetic resonance image segmentation has been proposed for a number of clinical investigations of varying complexity. Automatic segmentation of MR scans is very useful for research and clinical study of much neurological pathology. The accurate segmentation of MR images into different tissue classes, especially gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF), is important for the diagnosis and prognosis of certain illnesses. The automatic segmentation of brain MR images, however, remains a persistent problem. The major MR image segmentation problem with MR image is the corruption with inhomogeneity bias field. Several approaches have been proposed to address this limitation of intensity-based classification.

Clustering is one of the most popular classification methods and has found many applications in pattern classification and image segmentation [1-7]. Clustering algorithm attempts to classify a voxel to a tissue class by using the notion of similarity to the class. The fuzzy C-means clustering (FCM) algorithms have recently been applied to MRI segmentation [6-7]. Unlike the crisp K-means clustering algorithm [1-7], the FCM algorithm allows partial membership in different tissue class. Thus, FCM can be used to model the partial volume averaging artifact, where a pixel may contain multiple tissue classes [6]. A method of simultaneously estimating the intensity nonuniformity artifact and performing voxel classification based on fuzzy clustering has been reported in [7], where intermediate segmentation results are utilized for the the intensity nonuniformity estimation. The method uses a modified FCM cost functional to model the variation in intensity values and the computation of the bias field is formulated as a variational problem. However, in conventional FCM clustering algorithm, there is no consideration of spatial context between voxels since the clustering is done solely in the feature space.

K-means and C-means methods have several advantages such as: (1) it yields regions more homogeneous than those of other methods, (2) it reduces the spurious blobs, (3) it removes noisy spots, and (4) it is less sensitive to noise than other techniques. The final number of clusters is still always sensitive to one or two user-selected parameters that define the threshold criterion for merging. Though some compatibility or similarity measure is applied to choose the clusters to be merged, no validity measure is used to guarantee that the clustering result after a merge is better than the one before the merge. Partial results were stated in [8] to answer the questions: "Can the appropriate number of clusters be determined automatically? And if the answer is yes, how?" The number of clusters is determined by operating index procedures to whole data to determine the number of clusters before starting fuzzy methods. This will consume much time for finding the suitable number of cluster.

Therefore, two major problems are known with the K-means and FCM methods: (1) How to determine the number of clusters. (2) The computational cost is quit high for large data sets.

This paper addresses these problems for dealing with the shortcomings of existing fuzzy methods. We present alternative K-means and FCM algorithms that could improve MRI segmentation. The algorithms

incorporate spatial information into the membership function and the validity procedure for clustering. We use the intra-cluster distance measure, which is simply the median distance between a point and its cluster centre. The number of the cluster increases automatically according the value of intra-cluster. For example when a cluster is obtained, it uses this cluster to evaluate intra-cluster of the next cluster as input to the FCM or K-means and so on. It stops only when the intra-cluster is smaller than a prescribe value. The most important aspect of the proposed algorithms is actually to work automatically. Alterative is to improve automatic image segmentation. The performance of the proposed method is illustrated using simulated volumetric MRI and real MRI. Due to the reference of real MRI dataset being unknown to measure how much our algorithms are successful, specialists opinion is considered.

The rest of this paper is organized as follows: Section 2 describes the MRI segmentation problem. The proposed K-means clustring algorithm and fuzzy c-means are presented in sections 3, 4 respectively. Experimental comparisons are given in Section 5. Finally, Section 6 gives our conclusions.

2. The MRI Segmentation Problem

The basic idea of image segmentation can be described as follows. Given a set of data $X=\{x_1,x_2,…,x_N\}$ and a uniformity predicate P, we wish to obtain a partition of the data into disjoint nonempty groups $\{v_1,v_2,…,v_k\}$ subject to the following conditions:

(1) $\bigcup_{i=1}^{k} v_i = X$

(2) $v_i \bigcap v_j = \phi, \quad i{\neq}j$

(3) $P(vi)=TRUE, \quad i=1,2,…,k$

(4) $P(vi \bigcup vj) = FALSE, \quad i{\neq}j$

The first condition ensures that every data value must be assigned to a group, while the second condition ensures that a data value can be assigned to only one group. The third and fourth conditions imply that every data value in one group must satisfy the uniformity predicate while data values from two different groups must fail the uniformity criterion.

To obtain a 3D MR image, the positional information about the tissues must be recorded. This involves isolating the source of each component of the MR signal to a particular voxel using the technique of spatial encoding. In MR imaging, spatial encoding is achieved by performing slice selection in one direction (e.g. the z-axis), frequency encoding in another direction (e.g. the x-axis), and phase encoding in the third direction (e.g. the y-axis). In slice selection, a narrow bandwidth is applied in the presence of a z-axis linear gradient field. Since the resonance frequency of a proton is proportional to the applied magnetic field,

the presence of a gradient field means that only a narrow slice in the body will have a resonant frequency within the bandwidth of the resonant frequency [9-10]. MR image segmentation involves the seperation of image pixels into regions comprising different tissue type. All MR images are affected by random noise. The noise comes from the stray current in the detector coil due to the fluctuating magnetic fields arising from random ionic currents in the body or the thermal fluctuations in the detector coil itself. More discussion can be seen [11]. When the level of noise is significant in an MR image, tissues that are similar in contrast could not be delineated effectively, which causes error in tissue segmentation. More sophisticated techniques would be needed to reconstruct the image from incomplete information [12-14]. A 3D image can be obtained from many consecutive 2D slices.

3. The Proposed K-means Clustering Algorithm

K-means clustering is one of the simplest unsupervised classification algorithms [1-3]. The procedure follows a simple way to classify the dataset through a certain number of clusters. The algorithm partitions a set of N vector $X=\{x_j, j=1,…,N\}$ into C classes v_i, $i=1, …, C$, and finds a cluster centre for each class c_i denotes the centroid of cluster v_i such that an objective function of dissimilarity, for example a distance measure, is minimized. The objective function that should be minimized, when the Euclidean distance is selected as a dissimilarity measure, can be described as:

$$P = \sum_{i=1}^{C} \left(\sum_{k, x_k \in v_i} \left\| x_k - c_i \right\|^2 \right), \qquad (1)$$

where $\sum_{k, x_k} \left\| x_k - c_i \right\|^2$ is the objective function within group i, and $\left\| x_k - c_i \right\|$ is a chosen distance measure between a data point xk and the cluster centre c_i.

The partitioned groups are typically defined by a $(C \times N)$ binary membership matrix $U=(u_{ij})$, where the element uij is 1 if the j-th data point xj belongs to group i, and 0 otherwise. That means:

$$u_{ij} = \begin{cases} 1 & if \left\| x_j - c_i \right\|^2 \leq \left\| x_j - c_k \right\|^2 \\ 0 & otherwise \end{cases}, \text{ for each } k \neq i \qquad (2)$$

$$c_i = \frac{\sum_{x_j \in c_i}^{N} x_j}{R_i}, \qquad (3)$$

where Ri is number of data point in class v_i.

Since the K-means method aims to minimize the sum of squared distances from all points to their cluster centers, this should result in compact clusters. We use the intra-cluster distance measure, which is simply the median distance between a point and its cluster centre. The equation is given as:

$$\text{intra} = midean(\sum_{i=1}^{C} \sum_{x \in c_i} \|x - v_i\|^2) \qquad (4)$$

Therefore, the clustering that gives a minimum value for the validity measure will tell us what the ideal value of k is in the K-means. Then the number of cluster is known before estimating the membership matrix.

The proposed K-means clustering algorithm consists of the following steps:

Step1: Select a subset from the dataset and initialize the cluster centers c_i, $i =1,…,C$.

Step 2: C=2 the initial number of cluster, C_{max}=the maximum number of cluster.

Step 3: Determine the membership matrix U according to Eq.(2) using C= C_{max} it is seleced arbitrary.

Step 4: Compute the objective function according to Eq.(1). Goto step 8, if either it is below a certain tolerance value or its improvement over previous iteration is below a certain threshold.

Step 5: Update the cluster centers c_i, $i=1,…, C$ using Eq.(3).

Step 6: Obtain center v_1.

Step 7: Goto step3 and use v_1 centers as input c number of cluster to obtain center v_2.

Step 8: Use v_2 to calculate the intra distance according to the above equation (4), stop if intra is smaller than a prescribe value.

Step 9: C= C+1, return to step 3, until C =Cmax

Step 10 : Stop.

4. The Propsed Fuzzy C-Means Algorithm

Fuzzy C-means clustering (FCM), also known as fuzzy ISODATA, is a data clustering algorithm in which each data point belongs to a cluster to determine a degree specified by its membership grade. Bezdek [1] has proposed this algorithm as an alternative to earlier K-means clustering. FCM partitions a collection of N vector x_i, $i=1,…,N$ into C fuzzy groups, and finds a cluster centre in each group such that an objective function of a dissimilarity measure is minimized. The major difference between FCM and K-means is that FCM employs fuzzy partitioning such that a given data point can belong to several groups with the degree of belongingness specified by membership grades between 0 and 1. In FCM, the membership matrix U is allowed to have not only 0 and 1 but also the elements

with any values between 0 and 1. This matrix satisfies the constraints:

$$\sum_{i=1}^{C} u_{ij} = 1, \forall j = 1,..., N \qquad (5)$$

The objective function of FCM can be formulated as follows:

$$P(u, v_1, ..., v_C) = \sum_{i=1}^{C} \sum_{j=1}^{N} u_{ij}^{m} \|x_j - c_i\|^2, \qquad (6)$$

where u_{ij} is between 0 and 1; c_i is the cluster centre of fuzzy group i, and the parameter m is a weighting exponent on each fuzzy membership (in our implementation, we set it to 2). Fuzzy partitioning is carried out through an iterative optimization of the objective function shown above, updating of membership uij and the cluster centres c_j by:

$$c_i = \frac{\sum_{j=1}^{N} u_{ij}^{m} x_j}{\sum_{j=1}^{N} u_{ij}^{m}} . \qquad (7)$$

$$u_{ij} = \frac{1}{\sum_{k=1}^{C} \left(\frac{\|x_j - c_i\|}{\|x_j - c_k\|} \right)^{2/(m-1)}} . \qquad (8)$$

Simlar to K-means method, we use the intra-cluster distance measure, which is simply the median distance between a point and its cluster centre as shown in Eq. (4)

The proposed FCM clustering algorithm is composed of the following steps:

Step1: Select a subset from the dataset and initialize the cluster centers c_i, $i =1,…,C$.

Step 2: C=2 the initial number of cluster, C_{max}=the maximum number of cluster, it is seleced arbitrary.

Step 3: Initialize the membership matrix U with random values between 0 and 1 such that the constraints in Eq.(5) are satisfied.

Step 4: Calculate fuzzy cluster centers c_i, i=1,…, C using Eq.(7).

Step 5: Compute the cost function (objective function) according to Eq.(6). Goto step 9, if either it is below a certain tolerance value or its improvement over previous iteration is below a certain threshold.

Step 6: Compute a new membership matrix U using Eq.(8).

Step 7: Obtain center v_1.

Step 8: Goto step3 on the subset with c number of cluster to obtain center v_2.

Step 9: Use v_2 to calculate the intra distance according to the above equation (4), stop if intra is smaller than a prescribe value.

Step 10 : *C= C+1*, return to step 3, until *C =Cmax*

Step 11: Stop.

5. Experimental and Comparative Results

The experiments were performed with several data sets on a PC with a P4 2.4GHZ CPU, 256 MB of RAM and performed in MATLAB. Our expremint includes one on simulated MR and another on real MR brain data consisting of several classes. The advantages of using digital phantoms rather than real image data for validating segmentation methods include prior knowledge of the true tissue types and control over image parameters such as modality, slice thickness, noise and intensity inhomogeneities. We used a high-resolution T1-weighted MR phantom with slice thickness of 1mm, 3% noise and no intensity inhomogeneities, obtained from the classical simulated brain database of McGill University [15]. Two transverse slices drawn from the simulated MR data are shown in Fig(1a), (1b), and (1c). MRI has several advantages over other imaging techniques enabling it to provide 3-dimensional data with high contrast between soft tissues (see Fig.(1a)). However, the amount of data is far too much for manual analysis/interpretation and this has been one of the biggest obstacles in the effective use of MRI. Segmentation of MR images into different tissue classes, especially gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF), is an important task. Brain MR images have a number of features, especially the following: Firstly, they are statistically simple: MR Images are theoretically piecewise constant with a small number of classes. Secondly, they can have relatively high contrast between different tissues. Unlike many other medical imaging modalities, the contrast in an MR image depends strongly upon the way the image is acquired.

(a)   (b)
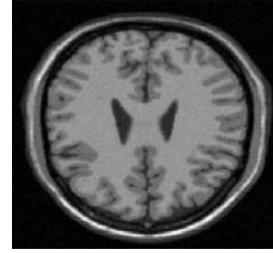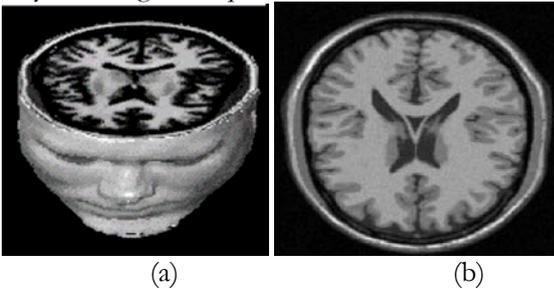
(c)

Fig.(1): Test images: a) 3D simulated data, b) and c) two original slices from the 3D simulated data (slice91, and slice100).

The quality of the segmentation algorithm is of vital importance to the segmentation process. The comparison score S for each algorithm is proposed in [16], which defined as:

$$S = \left| \frac{A \cap A_{ref}}{A \cup A_{ref}} \right|$$

(13)

where A represents the set of pixels belonging to a class as found by a particular method and Aref represents the set of pixels belonging to the very same class in the reference segmented image (ground truth).

5.1 MRI segmentation results

Here we compare the evaluation of our proposed methods to the standard fuzzy K-means and c-means (FCM) methods when they are applied to simulated MR and real MR data.

Experiment on the simulated MR data

Table (1) shows the corresponding average percentage of accuracy scores of the individual segmentation methods, after applying them to the simulated MR data (two slices of the segmented 3D MR volume).

The volume was reduced in size to 181 ×108 × 90 to reduce the high computational cost. A qualitative representation of the segmentation results is shown in Figs. (2), and (3). The figures show two slices of the segmented 3D MR volume.

Experiment on the real MR data

Table (2) shows the corresponding accuracy scores of the four methods for the nine classes of real images (real brain image with nine classes, for example see class0 in Fig. (1a)). Obviously, the proposed K-means and FCM methods are more stable and achieve much better performance than the standard K-means and FCM for most classes. Our methods work automatically while in case of the standard K-means and FCM, the number of cluster is manually determined.

Table (1): Segmentation accuracy of individual methods on MRI volume dataset.

Methods	accuracy
	MRI volume
K-means	0.55394
The proposed k-means	0.58341
FCM	0.52531
The proposed FCM	0.604318
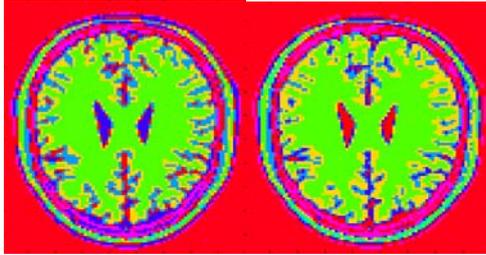
(a)　　　　　　(b)
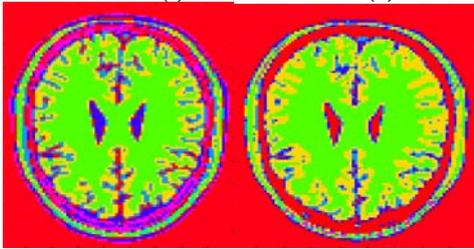
(c)　　　　　　(d)

Fig(2): Segmentation results for the slice (z=100) on a simulated data using methods: (a) K-means, (b) FCM, (c) the proposed K-means, (d) the proposed FCM

(a)　　　　　　(b)

(c)　　　　　　(d)

Fig(3): Segmentation results for the slice (z=91) on a simulated data using methods: (a) K-means, (b) FCM, (c) the proposed K-means, (d) the proposed FCM.

5.2 Specialists Judgment

In this section, two real T2-weigthed MRI images (data1 and data2) are obtained as test sets from the x-ray Department (Faculty of Medicine), as shown in Figs (5a-5c). The anatomical model used to generate real brain MRI data consist of tissue volumes, one for each tissue class (white mater (WM) within the brain parenchyma, gray matter (GM) within the brain parenchyma, cerebro spinal fluid (CSF) surrounding the brain and within the ventricles, fatty tissue (FAT), Skull bone (does not include sinuses), SKN (mostly skin)).

The voxel values in these volumes reflects the proportion of tissue presented in the voxel, in the range [0,255] as shown in Fig.(4). We take the opinion of five medical doctors with PhD degrees. They have some knowledge about the number of clusters in the images. Which each slice with six classes consists of 384×512 pixels. Qualitative representation of the segmentation results for two real MRI image are shown in Figs. (6) and (7) using the segmentation methods. The application of these algorithms to a real MRI dataset cannot give us a quantitative measure about how they are successful. As such, qualitative assessment of the segmentation results is judged visually.

We present qualitative comparison results of the segmented image methods, where the opinion of doctors from x-ray department has been considered. In the case of data2, all of them show that the proposed methods give better results, as shown in Table (3), which a value/reference of the proposed FCM is the best and the established K-means is the worst method.

Table(2): Segmentation accuracy (%) of four methods on brain classes.

	Class1	Class2	Class3	Class4	Class5	Class6	Class7	Class8	Class9	Over all
K-means	62.96	57.53	77.84	91.61	66.47	77.18	85.96	43.60	99.15	77.36
FCM	53.52	64.38	75.19	89.30	62.76	29.09	83.09	6.76	98.95	73.73
The proposed k-means	67.55	61.14	78.83	100.0	67.96	61.87	89.21	51.27	97.26	66.55

After that, the standard FCM, and K-means methods respectively misclassified some parts of gray matter into white matter. In contrast, the proposed methods can yield satisfactory result, which is more compatible with human visual perception.

On the other hand, data1 is more complicated than data2, so the judgment on this data becomes more difficult. In this case, all doctors show that the proposed FCM segmentation method gives better results. Although, the proposed K-means, standard FCM, and K-means methods, respectively misclassified some parts of gray matter into white matter, the proposed method still obtained better results than standard FCM and K-means methods. We rearrange the reference according to majority of doctors after seeing the different results as shown in table (3). The rank total is computed through computing the average percentage between the two data when using one method. The percentage is assumed, where reference 1,2,...,6 take percentage 60,50,...,10 respectively.
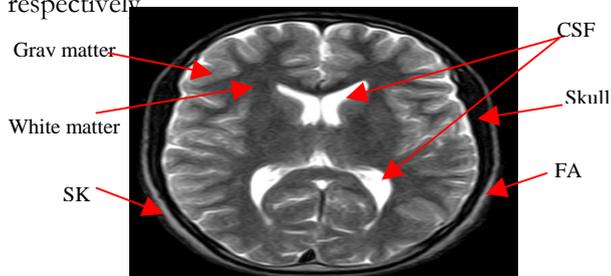
Fig. (4): The anatomical model for real MRI image.
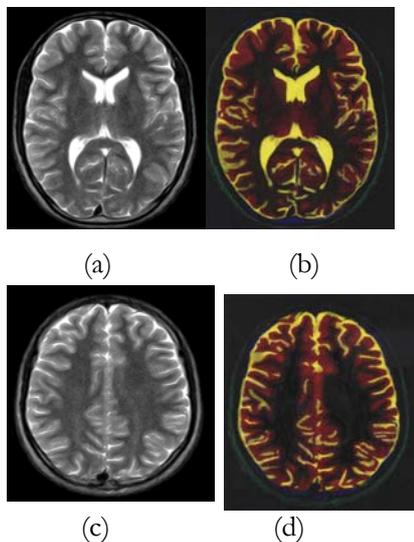
Fig. (5): MRI image. a) Original image of data1 image, b) manual segmentation of the image shown in (5a), c) Original image of data2 image and d) manual segmentation of the image shown in (5c).
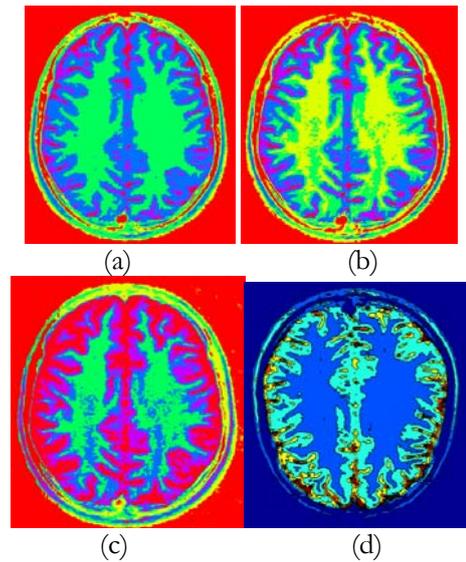
Fig. (6): Segmentation of real MRI image (data2): a) K-means, b) FCM, c) The proposed K- means, d) The proposed FCM.
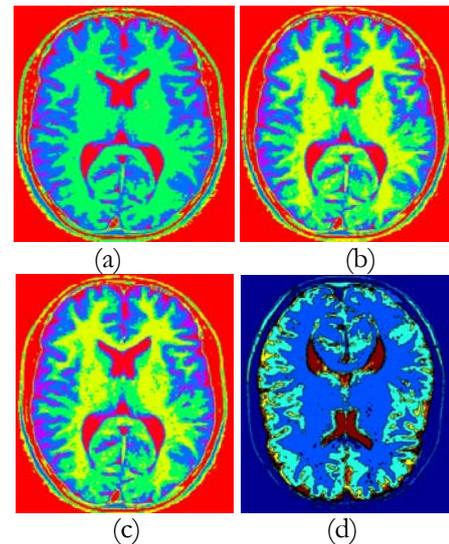
Fig. (7): Segmentation of real MRI image (data1): a)K-means, b) FCM, c) The proposed K-means, d) The proposed FCM.

Table (3): The rank of data1 and data2.

	Methods	Rank data 1	Rank data 2	Rank total
Individual methods	K-means	1	2	2
	FCM	2	3	3
	The proposed K-means	2	1	1
	The proposed FCM	1	1	1

6.Conclusion

A method for improving image segmentation has been presented. Rather than tuning a method for the best possible performance, it works automatically and can indeed improve the segmentation accuracy over the existing methods. The algorithms incorporate spatial information into the membership function and the validity procedure for clustering. They have estimated accurate clusters automatically even without prior knowledge of the true tissue types and the number of cluster of given images.

Extensive experiments using MR images generated by the BrainWeb simulator [15] and real MR data have been used to evaluate the proposed methods. Due to the use of soft segmentation, the proposed FCM algorithm is able to give a good estimation of tissue volume in the presence of inaccurate tissues.

Although the proposed K-means method misclassified some parts of gray matter into white matter, it still achieves better results than the standard K-means and C-means in the case of real MR images. By comparing the proposed methods with established one, it is clear that our algorithms can estimate the correct tissues much more accurately than the established algorithms. Furthermore, the proposed methods to clustering turn out to be particularly interesting because, due to partial volume effects during acquisition, pixel values at the borders between volumes of interest correspond to mixtures of different anatomical tissues.

Future research in MRI segmentation should strive toward improving the accuracy, precision, and computation speed of the segmentation algorithms, while reducing the amount of manual interactions needed. This is particularly important as MR imaging is becoming a routine diagnostic procedure in clinical practice. It is also important that any practical segmentation algorithm should deal with 3D volume segmentation instead of 2D slice by slice segmentation, since MRI data is 3D in nature.

References

[1] JC. Bezdek , "Pattern recognition with fuzzy objective function algorithms", Plenum Press, New York, 1981.

[2] AWC. Liew, SH. Leung, WH. Lau, "Segmentation of color lip images by spatial fuzzy clustering", IEEE Trans. Fuzzy System, Vol. 11, pp. 542-549, 2003.

[3] AWC. Liew, Leung SH, Lau WH., "Fuzzy image clustering incorporating spatial continuity", IEE Proceedings-Vision, Image and Signal Processing, Vol. 147, pp.185-192, 2000.

[4] LK. Szeto, AWC. Liew, H. Yan, SS.Tang, "Gene expression data clustering and visualization based on a binary hierarchical clustering framework", Special issue on "Biomedical Visualization for Bioinformatics", Journal of Visual Languages and Computing, Vol. 14, pp.341-362, 2003.

[5] S .Wu, AWC. Liew, H.Yan, "Cluster analysis of Gene expression data based on self-splitting and merging competitive learning", IEEE Trans. on Information Technology in Biomedicine, Vol. 8, pp. 5-15, 2004.

[6] DL. Pham, JL.Prince, "Adaptive fuzzy segmentation of magnetic resonance images", IEEE Trans. Med. Imag., Vol.18, pp.737-751, 1999.

[7] AWC. Liew, H.Yan, "An adaptive spatial fuzzy clustering algorithm for MR image segmentation", IEEE Trans. Med. Imag., Vol. 22, pp.1063-1075, 2003.

[8] M.T.El-Melegy, E.A.Zanaty, M.R.Girgis and Walaa M.Abd-Elhafiez," On cluster validity indexes in fuzzy and hard clustering algorithms for image segmentation" IEEE international conference on computer vision, Vol. 6, VI 5-8, 2007.

[9] DW. Chakeres, P.Schmalbrock, "Fundamentals of magnetic resonance imaging", Williams & Wilkins, Baltimore, 1992.

[10] RB. Buxton, "Introduction to functional magnetic resonance imaging-principles and techniques", Cambridge University Press, 2002.

[11] A.W.C. Liew and H. Yan, "Current Methods in the Automatic Tissue Segmentation of 3D Magnetic Resonance Brain Images", Medical Imaging Reviews, Vol. 2, pp. 91-103, 2006.

[12] H. Yan, JC. Gore, "An efficient algorithm for MR image reconstruction without low spatial frequencies", IEEE Trans. Med. Imag., TMI-9, pp. 184-179, 1990.

[13] H. Yan, M. Braun, "Image reconstruction from Fourier domain data sampled along a zig-zag trajectory", Magnetic Resonance in Medicine, Vol.18, pp. 405-410, 1991.

[14] H. Yan, "Signal processing in magnetic resonance imaging and spectroscopy", Marcel Dekker Inc., 2002.

[15] BrainWeb: "Simulated Brain Database", McConnell Brain Imaging Centre, Montreal Neurological Institute, McGill.

[16] D.Q. Zhang, and S.C. Chen, "A novel kernelized fuzzy c-means algorithm with application in medical image segmentation," Artif. Intell. Med, Vol.32, pp.37–50, 2004.