IMPROVED HYBRID SEGMENTATION OF BRAIN MRI TISSUE AND TUMOR USING STATISTICAL FEATURES

S. Allin Christe¹, K. Malathy² and A. Kandaswamy³

^{1,2}Department of Electronics and Communication Engineering, PSG College of Technology, Coimbatore, India

E-mail: allin_christy@yahoo.co.in¹, er.malathy@gmail.com²

³Department of Bio-Medical Engineering, PSG College of Technology, Coimbatore, India

E-mail: hod@bme.psgtech.ac.in³

Abstract

Medical image segmentation is the most essential and crucial process in order to facilitate the characterization and visualization of the structure of interest in medical images. Relevant application in neuroradiology is the segmentation of MRI data sets of the human brain into the structure classes gray matter, white matter and cerebrospinal fluid (CSF) and tumor. In this paper, brain image segmentation algorithms such as Fuzzy C means (FCM) segmentation and Kohonen means(K means) segmentation were implemented. In addition to this, new hybrid segmentation technique, namely, Fuzzy Kohonen means of image segmentation based on statistical feature clustering is proposed and implemented along with standard pixel value clustering method. The clustered segmented tissue images are compared with the Ground truth and its performance metric is also found. It is found that the feature based hybrid segmentation gives improved performance metric and improved classification accuracy rather than pixel based segmentation.

Keywords:

K-Means, Fuzzy C-Means, Fuzzy Kohonen Means Clustering, Distance of Clustering, Von Dongen Index

1. INTRODUCTION

Image segmentation which is a method of subdividing an image into its constituent parts. It is challenging part to play in many medical imaging application. It still remains and probably will remain for long the key problem of image analysis. It plays a major role in many medical imaging applications like automating or facilitating the delineation of anatomical structures and other regions of interest. It plays a vital role in numerous biomedical-imaging applications such as the quantification of tissue volumes, diagnosis and computer integrated surgery[1][2]. Many approaches have been proposed for the segmentation of brain tissues (MR Image textures)[3] and tumors, for instance, classical, statistical, structural, fuzzy, and neural networks based techniques[4].A number of segmentation methods have been used in MRI during past decades, with limited success[5]. In medical image segmentation clustering is the most popular method which partitions a data set into a group of similar characteristics in which FCM clustering is found most suitable for MRI segmentation[6]. But an MRI image which is widely corrupted by noise, RF inhomogeneity and partial volume effects it cant be clearly represented by a membership function especially in the transitional regions. The FCM algorithm uses a knowledge-based classification and tissue labeling approach to initially segment MR brain images and added an expert system to locate tissue presence by matching it with a prior model [7] and it was shown to be superior on normal brain but worse on abnormal brains with edema, tumors etc. and also found that FCM is over sensitive to noise. K-means

clustering is also competitive learning clustering algorithm used in fMRI[8]. However, the transitional regions between tissues in MRI images are not clearly defined and the noise in the image will leads to further degradation with segmentation. In order to overcome the disadvantages fuzzy methods are integrated with Kohonen's competitive algorithm, and a new hybrid method using conventional pixel and proposed statistical feature based segmentation are done and shown that feature based segmentation provides improved results.

The rest of this paper is organized as follows. Section 2 briefly introduces the concepts involved in clustering algorithm like K-Means, FCM and hybrid segmentation algorithm (FKM). The proposed methods are discussed in section 3. Performance Metrics is discussed in section 4. In section 5 we present experimental results. Finally we summarize and conclude in section 6.

2. CLUSTERING APPROACHES

The clustering segmentation algorithms used here are K means, FCM and hybrid FKM. A point belonging to only one cluster is K means. A point belonging to more than one cluster is Fuzzy c means but overlapping may occur in FCM. This problem is overcome by fuzzy kohonen means algorithm i.e. a point belonging to more than one cluster with certain probability.

2.1 K-MEANS

The <u>K-means algorithm</u> assigns each point to the cluster whose center (also called centroid) is nearest. The center is the average of all the points in the cluster i.e., its coordinates are the arithmetic mean for each dimension separately over all the points in the cluster. The algorithm steps are:

- 1. Choose the number of clusters, k and determine the cluster centers.
- 2. Assign each point to the nearest cluster center based on minimum distance as in Eq.1.

 $d_j = \|x_i - w_{ij}\|^2 i = 1, 2, \dots, N, j = 1, 2, \dots, K$ (1) where d_j is the distance between input and weight vector, N is the number of input elements, K is the number of clusters, x_i is the input vectors, w_{ij} is the weight from input node i to output node j.

- 3. Re-compute the new cluster centers.
- 4. Repeat the two steps no 2 and 3 until some convergence criterion is met (usually that the assignment hasn't changed).

The main advantages of this algorithm are its simplicity and speed which allows it to run on large datasets. Beacuse of the crisp classification it does not ensure that the result has a global minimum of variance [9] but it maximizes inter-cluster (or minimizes intra-cluster) variance, since of its hard cluster it is not suitable for MRI because it is intrinsically blurry but fuzzy clustering is most suited for some segmentation because it retains the more information of the original image.

2.2 FUZZY C-MEANS CLUSTERING

In fuzzy clustering is a method where large data is grouped into clusters in which each point has a degree of belonging to clusters, as per it membership rather than belonging completely to just one cluster. The data points that are nearer to the centre have high degree of membership than the points on the edge of a cluster have a lesser degree [6]. The fuzzy c-means algorithm steps are:

- 1. Random initialization of inputs to the clusters C.
- 2. Calculate centroid V_i for each cluster, using Eq. 4.
- 3. Using objective function in Eq. 2 find the coefficients of the cluster for each point
- 4. Repeat steps 2 and 3 until the algorithm has converged (that is, the coefficients change between two iterations is no more than ε , the given threshold).

The objective function is minimized when pixels close to centroids are assigned high membership values and low membership values assigned to pixel far from centroid.

The standard FCM objective function is given in Eq.2 $J_m(U,V) = \sum_{j=1}^{N} \sum_{i=1}^{C} u_{ij}^m d^2(X_j, V_i)$ (2)
where, $\mathbf{X} = \{\mathbf{X}_1, \mathbf{X}_2, \dots, \mathbf{X}_N\}$ is a p × N input data matrix,

where, $\mathbf{X} = \{\mathbf{X}_1, \mathbf{X}_2, \dots, \mathbf{X}_j, \dots, \mathbf{X}_N\}$ is a p × N input data matrix, where p represents the dimension of each feature vector, and N represents the number of feature vectors. C is the number of clusters. U_{ij} is the membership function of the jth data in ith cluster C_i and d is the distance between input and centroid. The membership function is expressed in Eq. 2

The membership function is expressed in Eq.3

$$U_{ij} = \frac{1}{\sum_{k=1}^{c} \left(d(x_j, v_{ij}) \middle| d(x_j, v_k) \right)^{2/(m-1)}}$$
(3)
$$V_i = \frac{\sum_{j=1}^{N} (u_{ij})^m x_j}{\sum_{j=1}^{N} (u_{ij})^m} \ i = 1, 2, \dots, C$$
(4)

where m is a weighting exponent on each fuzzy membership, which controls the degree of fuzziness. A measurement of similarity between X_i and V_i is given in Eq. 5.

$$d^{2}(X_{j}, V_{i}) = ||X_{j} - V_{i}||^{2}$$
(5)

The results of this algorithm depends upon the initial choice of weights but it minimizes intra-cluster variance. Similar to K means it also has a local minimum. It needs a large data set and requires a large CPU time for its processing.

2.3 FUZZY K MEAN SEGMENTATION

In order to overcome the difficulties in K-means and FCM algorithm we combine the K-means with fuzzy clustering. The fuzzy k-means algorithm minimizes the within-class sum square errors [16][17] under the following conditions:

$$\sum_{k=1}^{C} m_{ik} = 1 \quad i = 1, 2, \dots n$$

$$\sum_{i=1}^{n} m_{ik} > 0 \quad k = 1, 2, \dots c$$
(6)

$$m_{ik} \in \{0,1\}, i = 1,2,...,n; k = 1,...,c$$
 (7)

It is defined by the following objective function:

$$J = \sum_{i=1}^{n} \sum_{k=1}^{c} m_{ik}^{\varphi} d^{2}(X_{i}, C_{k})$$
(8)

Where m_{ik} is the membership function, n is the number of data, c is the number of classes, c_k is the vector representing the centroid of class k given in Eq.10, x_i is the vector representing individual data i and $d^2(x_i, c_k)$ is the squared distance between x_i and c_k distance, which for simplicity further denoted by d^2_{ik} . φ is the fuzzy exponent which ranges from $(1,\infty)$. It determines the degree of fuzziness of the final solution i.e., the degree of overlap between groups. With $\varphi = 1$, the solution is a hard partition. As φ approaches infinity the solution approaches its highest degree of fuzziness. The minimization of the objective function J provides the solution for the membership function given in Eq. 9

$$m_{ik} = \frac{d_{ik}^{2(\emptyset-1)}}{\sum_{j=1}^{c} d_{ij}^{2(\emptyset-1)}} = 1, 2, \dots, n; k = 1, \dots, c$$
(9)
$$c_k = \frac{\sum_{j=1}^{n} m_{ik}^{\varphi} X_i}{\sum_{i=1}^{n} m_{ik}^{\varphi}} k = 1, 2, \dots, c$$
(10)

The fuzzy k-means algorithm steps are:

- 1. Choose the number of classes k, with $1 \le k \le n$ and fuzziness exponent φ , with $\varphi > 1$.
- 2. Choose the distance in the variable-space with d_{ik}^2 .
- 3. Choose a value for the stopping criterion ε (ε = 0.001 gives reasonable convergence)
- 4. Initialize $m_{ik} = m_{ik}^{(0)}$, e.g. with random memberships or with memberships from hard k-means partition.
- 5. At iteration it =1,2,3 (re) calculate $C_k=C_k^{(it)}$ using Eq.10 and $m_{ik}^{(it-1)}$ using Eq.9.
- 6. Re-calculate $m_{ik}=m_{ik}^{(it)}$ and $C_k^{(it)}$. If numerical overflow would occur with d_{ik} close or equal to 0, m_{ik} is set to 1.
- 7. Compare $m_{ik}^{(it)}$ to $m_{ik}^{(it-1)}$. If $||m_{ik}^{(it)} m_{ik}^{(it-1)}|| < \varepsilon$, then stop if objective function reached; otherwise return to step 5.

By integrating the FCM cluster with Kohonen means clustering algorithm FKM can deal with overlapping gray scale intensities and not clearly defined borders between tissues successfully.

FCM algorithm is also sensitive to noise and outliers, but FKM segmentation improves segmentation, though it performance degrades when applied to noise corrupted images but which could be improved on pre-processed data.

3. PROPOSED METHOD

The proposed method consists of four stages as shown in Fig.1. Initially corrupted MRI image are pre-processed. After performing pre-processing, the statistical features are extracted and clustering done. The clustered segmented images are compared with the Ground truth images of the MR brain tissues. MR Images which are normally corrupted by disturbances like Gaussian and RF in-homogeneity are to be pre-processed. The pre-processing operation consists of three stages like denoising, registration, RF inhomogeneity correction. Denoising using adaptive window method is used to remove the Gaussian noise present in the gray scale images and color images. Registration is warping subject's brain images to a standard space, by

matching grey matter in these images, to a grey matter reference. This approach reduces the confounding effects of non-brain (e.g. scalp) structural variability on the registration. MR images which are usually corrupted by a smooth, spatially varying artifact that modulates the intensity of the image (bias). These artifacts, although not usually a problem for visual inspection, can impede automated processing of the images. Thus a bias corrected version gives more uniform intensities within the different types of tissues.

The above pre-processing stages of registration, bias correction are performed using Statistical Parametric Mapping (SPM5)[10]. The pre-processed image is skull removed using a Brain Extraction Tool (BET) and only the internal tissue are made ready for further segmentation process. The internal tissues are clustered using pixel based method and statistical feature based method. To overcome the difficulty of the segmentation of images involving complex random tissue patterns, we propose a statistical feature based Fuzzy K means clustering algorithm.

The purpose of feature extraction[11] is to reduce the original data set by measuring certain properties, or features, that distinguish one input pattern from another. Instead of using the gray level value of a given pixel, a feature vector is extracted from the original image and a partition of the feature vectors into different regions is performed. This is done by grouping data points in the feature space with the same similarity into clusters based K-means, FCM and FKM segmentation methods.

In this paper, a novel method of the statistical features like histogram based features and Gradient-based parameter features which can define the property of the image are extracted from the input image. Histogram is computed from the intensity of the pixel without considering any spatial relations. Some of the histogram features considered here are mean brightness, variance, skewness and kurtosis are found using the Eqns. (11) to (14).

$$\mu = \sum_{i=1}^{Ng} i. p(i)$$
(11)
2. Variance:

$$\sigma^{2} = \sum_{i=1}^{N_{g}} (i - \mu)^{2} p(i)$$
3. Skewness: (12)

 $\mu_3 = \sigma^{-3} \sum_{i=1}^{N_g} (i - \mu)^3 p(i)$ (13)

4. Kurtosis

 $\mu_4 = \sigma^{-4} \sum_{i=1}^{N_g} (1-\mu)^4 p(i) - 3$ (14)

Where p(i) is a normalized histogram vector, $i = 1, 2, N_g$ and N_g denotes the number of intensity levels. The histogram based features are extracted from the processed image. Extracted features are shown in Fig.2.

The Gradient-based parameter features derived from the gradient magnitude map of the image are Mean absolute gradient, Variance absolute gradient, Variance absolute gradient, Skewness of absolute gradient and Kurtosis of absolute gradient which are calculated for a neighborhood of 3x3.







Fig. 2 Histogram based features: (a) mean, (b) variance, (c) skewness, (d) Kurtosis

They are calculated by using the Eqns. (15) to (18): 1. Mean absolute Gradient: $GrMean = \frac{1}{M} \sum_{i,j \in ROI} ABSV(i,j)$ 2. Variance: (15) $GrVariance = \frac{1}{M} \sum_{i,j \in ROI} (ABSV(i,j) - GrMean)^2$ (16) 3. Skewness $GrSkewness = \frac{1}{\left(\sqrt{GrVariance}\right)^2} \frac{1}{M} \sum_{i \in POI} (ABSV(i, j) - GrMean)^3$ (17)4. Kurtosis $GrKurtosis = \frac{1}{(\sqrt{GrVariance})^4} \frac{1}{M} \sum_{ij \in ROI} (ABSV(i,j) - Grmaen)^4 - 3$ (18)

(18)

where ABSV is a absolute gradient value, ROI is a region of interest. The gradient based features are extracted from the processed image. Extracted features are shown in Fig.3.



Fig.3. Absolute gradient based features: (a) Gr.mean, (b) Gr.variance, (c) Gr.skewness, (d) Gr.Kurtosis

From the six extracted features, the features with more energy values selected for clustering and fed as data input for further clustering. The clustering based segmentation algorithms like K means, FCM and FKM is performed using pixel-based and statistical feature based method, and segmented into white matter, Gray matter and CSF and tumor. The results of segmented tissue output are also validated by a performance metrics for the above mentioned algorithms based on distance based clustering with the available ground truth and only a qualitative assessment done for tumor results as no ground truth available for it.

4. DATA ACQUISITION

The algorithms are implemented in MATLAB v 7.1 and evaluated on both simulated T1w MRI scans of a MNI digital brain phantom and real datas. The simulated MRI data was generated with noise levels of 0%, 1%, 3%, 5%, 7%, 9%, and with RF intensity inhomogeneity (INU) of 0%, 20% and 40%. Entire data set downloaded but for processing only five images was considered for each combination of noise and intensity nonuniformity for a total of ninety random images obtained from Brainweb. Brainweb is maintained by the Brain Imaging Center at the Montreal Neurological Institute[12]. Each generated image simulated are T1 weighted single channel MRI scan using the SFLASH (Spoiled FLASH) pulse sequence collected in the transaxial direction. The parameters for each generated image were as follows: TR, 18 ms; TE, 10 ms; flip angle, 30°; FOV, 256 mm x 256 mm; number of slices (contiguous), 256; slice thickness, 1 mm; in-slice resolution 1 mm x 1 mm and also real MR Image data from Internet Brain Segmentation Repository (ISBR) database[13].A performance analysis of the segmented data was also done with its available ground truth.

5. PERFORMANCE ANALYSIS

In order to evaluate the accuracy of tissue segmentation some of the segmentation performance parameters based on ground truth based evaluation[14] are used here. The idea of this is to measure the difference between the machine segmentation and the ground truth (ideal result). They are defined as

1) Under segmentation which represents the percentage of negative false segmentation given by (UnS): N_{fp} / N_n .

2) Over segmentation which represents the percentage of positive false segmentation given by (OvS): N_{fn} / N_p.

3) Incorrect segmentation representing the total percentage of false segmentation given by (InC): $(N_{fp} + N_{fn}) / N$.

where N_{fn} is the number of pixels that do not belong to a cluster and are segmented into the cluster. N_{fp} is the number of pixels that belong to a cluster and are not segmented into the cluster. N_p is the number of all pixels that belong to a cluster, N_n is the total number of pixels that do not belong to a cluster and N is the total number of pixels. From these segmentation parameters a relative error is calculated using the Eq.(19)

$$Relative \ error = \frac{(measured \ value) - (ground \ truth \ value)}{(ground \ truth \ value)}$$
(19)

Since the algorithms are clustering based algorithm a parameter based on distance clustering is also used for validation which is based on matching the clusters of the two clustering. Considering two different segmentations C_1 and C_2 of the same image, we associate each region $C_i \cap Cj$ as maximum only if $C_1=C_2$. The distance of clustering is calculated by using the Eqns (20), (21).

$$a(c_1, c_2) = \sum_{c_j \in c_i} \max \left| c_j \cap c_i \right|$$
(20)

$$a(c_2, c_1) = \sum_{c_i \in c_2} \max \left| c_j \cap c_i \right| \tag{21}$$

where, C_i belongs to set C_1 and C_j belongs to set C_2 . From this distance of clustering, an Von Dongen index[15] is found using the Eq. (22)

$$D(c_1, c_2) = 2n - a(c_1, c_2) - a(c_2, c_1)$$
(22)

where n is the size of cluster.From which the overall cluster performance based on similarity measure is found using Eq.(23)

$$P = 1 - \frac{[a(c_1/c_2) + a(c_2/c_1)]}{2n}$$
(23)

whose range should be between 0 and 1. A value of 1 implies a perfect matching., i.e., two identical clusters.

The overall classification accuracy of segmentation of the entire data set A is also found using Eq. (24)

$$CA(A_i) = \frac{t}{r} \cdot 100 \tag{24}$$

where t is the number of sample cases correctly classified, and n is the total number of sample cases. As feature based segmentation provides improved results for the brain tissues it is also applied on pathological images. The tumor segmented results are shown in Fig.7, Fig.8 in which K means, FCM output shows some extra tissue matters present which is removed in FKM.

6. RESULTS AND DISCUSSION

The effectiveness of the proposed approach is experimentally determined using the datasets and ground truth images for the MR Image Textures (brain tissues) such as White Matter, Gray Matter and Cerebral Spinal Fluid downloaded from Brain Web MR Simulators and also from Internet Brain Segmentation Repository (ISBR) database. The proposed algorithm is implemented and applied using MATLAB on a P-IV machine. Fig.4 shows a sample of brain MR image sand their ground truth images are shown in Fig.5. The pre-processed image is shown in Fig.6.







Fig 5: GT of WM, GM and CSF of Sample Image



Fig.6. Pre-processed image for 0% , 5% noise with 0% RF INU



Fig 7: Pixel based segmented outputs: WM, GM and CSF respectively, row 1:K means, row 2: FCM, row 3 : FKM





Fig 8: Feature based segmented outputs: WM, GM and CSF respectively, row 1:K means, row 2: FCM, row 3 : FKM



Fig 9: Feature based segmented outputs of a tumor, column 2:K means, column 3: FCM , column 4 : FKM



Fig 10: Feature based segmented outputs of another tumor, column 2:K means, column 3: FCM , column 4 : FKM

A sample T1w input image of noise level 0% and 5% with 0% INU are shown in Fig.4. The above algorithms are tested for all noise level with 0% and 20% INU for a slice thickness of 1mm and 3mm. Pixel based segmented results for K-Means, FCM and FKM are shown in Fig.7. The feature based segmented results for K- Means, FCM and FKM are shown in Fig.8 which shows an improved result compared to pixel based segmentation.

The cluster performance measure p is calculated by comparing the segmented results with the ground truth images. A sample of the metrics for slice 1 mm is tabulated in Table 1 and Table 2.

Table.1. Pixel based segmentation Performance measurefor0% RF INU and various noise levels

Images	Performance measure p	K means	FCM	FKM
T1_1mm_ pn0_rf0	White	0.6895	0.7034	0.7668
	Gray	0.5912	0.6792	0.7548
	CSF	0.5852	0.6925	0.7433
T1_1mm_ pn3_rf0	White	0.5973	0.6876	0.7523
	Gray	0.5762	0.6523	0.7412
	CSF	0.5518	0.6634	0.7278
T1_1mm_ pn5_rf0	White	0.5423	0.6534	0.7318
	Gray	0.5678	0.6231	0.7243
	CSF	0.5323	0.6254	0.6996

Images	Performance measure p	K means	FCM	FKM
T1_1mm_ pn0_rf0	White	0.7045	0.7356	0.8090
	Gray	0.6573	0.7003	0.7848
	CSF	0.6369	0.7245	0.7978
T1_1mm_ pn3_rf0	White	0.6656	0.6934	0.7867
	Gray	0.6052	0.6745	0.7746
	CSF	0.5978	0.6856	0.7580
T1_1mm_ pn5_rf0	White	0.6245	0.6756	0.7712
	Gray	0.5924	0.6610	0.7500
	CSF	0.5750	0.6534	0.7314

 Table.2. Feature based segmentation Performance measure for

 0% RF INU and various noise levels

From Table1 and Table 2 and also from the Fig. 7 and Fig. 8 it is clear that FKM gives better segmentation results rather than K-means and FCM for both pixel based and feature based segmentation. Our proposed statistical feature based FKM gives improved segmentation results rather than pixel based segmentation.



Fig.10 Under Segmentation

Fig.10 is an error plot of under segmentation for all algorithms. It is observed that FKM gives less under segmentation when compared to K means and FCM.



Fig.11 Over Segmentation



Fig.12 Incorrect Segmentation

From the Fig 11 and 12 which are error plots of over segmentation and incorrect segmentation for all algorithms it is clear that FKM gives minimum error for over and under segmentation respectively when compared to K means and FCM.







Fig. 14 Feature based classification accuracy

Fig.13 and Fig.14, is a plot of classification accuracy for pixel based and feature based for all noise level and for all the tissues. It shows that FKM gives better classification accuracy value compared to K-means and FCM.

6. CONCLUSION

In this work we have implemented an improved segmentation for the given MRI brain image datasets into its important tissues like gray matter, white matter, cerebrospinal fluid and tumor. According to the experimental results the proposed statistical feature hybrid FKM clustering gives better segmentation results rather than pixel based segmentation. It is also shown both pixel and feature based method hybrid FKM gives better segmentation results rather than K means and FCM. The proposed feature based method gives improved overall classification accuracy of 84.12% for all noise levels compared to 82.5% of pixel based method. Our method is implemented and tested for T1w images only, but the same could be extended for T2w and PD images. This work gives an improved tissue accuracy which would be added feature in estimation of volume changes in the tissues which leads to pathological problems. The extension of this work would be to improve segmentation with new improved features.

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