

A Comparative Study of Segmentation Techniques used for MR Brain Images

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Abstract - In this paper we present a comparative study of MR brain image segmentation techniques. The aim of this study is to assess the robustness and accuracy of three most commonly used unsupervised segmentation methods k-means (KM), FCM and EM. KM is a well known hard segmentation method for quicker processing whereas FCM and EM are popularly used soft segmentation methods particularly for brain tissue models. Most of the neuroimage analyzing software employ one of these techniques as a preprocessing tool to enrich their subsequent processes. Based on the parameters similarity index and processing time, the performance of the methods on brain tissue segmentation are measured and compared. The similarity index calculation was done by using the 20 normal volumes and their gold standards available from IBSR. The rest of parameters are tested on the normal and abnormal brain volumes collected from scan centers and brain image pools. For normal and noiseless volumes all the three methods produced comparable results. FCM has an excellent performance over the anisotropic nature of volumes that are affected by partial volume effects (PVE) as well as diseased sets and EM was suitable for noisy sets, particularly volumes affected by intensity non-uniformity (INU) artifacts. KM, FCM and EM are rated in the given order in terms of processing time. This study is useful to choose a suitable method for computerizing brain diagnostic system.

Keywords: unsupervised classification, MR brain regions, K-Means, Fuzzy C Means, Expectation – Maximization.

1 Introduction

Segmentation plays an important role in biomedical image processing. It is often the starting point for other processes, including registration, shape analysis, visualization and quantitative analysis. In brain diagnostic system it is of increasing interest in the study of many brain disorders, pathologies detection, anatomy delineation, treatment planning and computer-aided neurosurgery. Three main regions of brain, white matter (WM), gray matter (GM) and cerebrospinal fluid (CSF) are the important subject of study in brain diagnostic system. Manual segmentation of these three brain tissue types by an expert is time consuming,

inconsistent and affected by operator bias as the volume of data involved in MRI studies is large. Hence automatic segmentation of brain regions will assist a physician to speed up in their diagnostic process.

Segmentation techniques are broadly classified into two types: supervised and unsupervised [1]. Supervised methods require the user interaction and thus known as semi-automatic. Unsupervised techniques are completely automatic and segment the regions in feature space with a high density. Unsupervised classification techniques like k-means (KM), fuzzy c-means (FCM) and Expectation-Maximization (EM) methods are well known automatic tools for brain diagnostic system. KM is a hard segmentation procedure that generates a sharp classification. It assigns each tissue either to a class or does not [2]. FCM utilizes the fuzzy theory in which a tissue can be classified into several classes at the same time but with different degree [3] [4]. It is considered to be the best method for the anisotropic nature of volumes that are affected by PVE where multiple tissues contribute to single voxel resulting in the blurring of tissue boundaries. EM algorithm is used to find the mixture of Gaussians that can model the data set, in which there is no prior knowledge about their density distributions on each MRI echo [5]. It is often used in estimation problems where some of the data are “missing” [6]. In this application, the missing data is knowledge of the tissue class.

Unsupervised methods employed for MR image segmentation often include original or a variant of these techniques to optimize the result that are reported in [7-15]. It is essential to know which method is to be adopted for the segmentation. There are very limited studies in the performance comparison of these methods. In this paper we present a comparative study of these unsupervised methods in terms of robustness, accuracy and complexity of segmentation output. In this work, the unsupervised classification methods were performed to classify the MR brain images into four main regions WM, GM, CSF and others. Others region includes the non-brain tissues like air, skull, scalp, fat, eyes, neck etc. Variety of brain images were taken to compare the performance of the methods. The visual inspection, similarity index and processing time are taken for the performance comparison. Initially they are tested on the original MRI volumes. Then the effects of these methods are checked on extracted brain portion. The brain is extracted

from the given original images using brain extraction algorithms (BEA). Finally the performances of the methods with the definite number of clusters are compared.

2 Methods

2.1 KM algorithm

KM is one of the simplest unsupervised algorithms to classify a given data set through a certain number of clusters (assume k clusters) fixed a prior.

This algorithm is composed of the following steps with a data set $x_i, i=1,2,...,n$.

- Step 1: Initialize the centroids $c_j, j=1,2,...,k$
- Step 2: Assign each data point to the group that has the closest centroid
- Step 3: When all points have been assigned, calculate the positions of the k centroids
- Step 4: Repeat Steps 2 and 3 until the centroids no longer move. This produces a separation of the data points into groups from which the metric to be minimized can be calculated.

This algorithm aims at minimizing an objective function, in this case a squared error function.

The objective function is given by

$$J = \sum_{j=1}^k \sum_{i=1}^n \|x_i^{(j)} - c_j\|^2 \quad (1)$$

where $\|x_i^{(j)} - c_j\|^2$ is a measure of intensity distance between a data point x_i and the cluster center c_j . For simplicity, the Euclidean distance is used as the dissimilarity measure.

2.2 FCM algorithm

This algorithm employs fuzzy portioning such that a data point can belong to all groups with different membership grades between 0 and 1. This method is frequently used in pattern recognition. The aim is to find cluster centers that minimize a dissimilarity (objective) function. The objective function is given by:

$$J_m = \sum_{i=1}^n \sum_{j=1}^c u_{ij}^m d_{ij} \quad (2)$$

where $m \in [1, \infty]$ is a weighting exponent, $u_{ij} \in [1, 0]$ is the degree of membership x_i in the cluster j , x_i is the i^{th} of d -dimensional measure data, c_j is the d -dimensional center of the cluster and d_{ij} is the Euclidean distance between i^{th} data point (x_i) and j^{th} centroid (c_j).

The fuzzy portioning is carried out through an iterative optimization of the objective function given in equation (2), with the update of membership u_{ij} and the cluster centers c_j by:

$$u_{ij} = \frac{1}{\sum_{k=1}^c \left[\frac{d_{ij}}{d_{ik}} \right]^{\frac{2}{m-1}}} \quad (3)$$

$$c_j = \frac{\sum_{i=1}^n u_{ij}^m x_i}{\sum_{i=1}^n u_{ij}^m} \quad (4)$$

This procedure will stop if the improvement of objective function over previous iteration is below a threshold value, $\mathcal{E} \in [1, 0]$. By iteratively updating the cluster centers and the membership grades for each data point, FCM iteratively moves the cluster centers to the “right” location within a data set.

The detailed algorithm of FCM as proposed by Bezdek [4] is:

- Step 1: Randomly initialize the membership matrix $U = [u_{ij}]$, $U^{(0)}$ that has a constraint equation given by

$$\sum_{i=1}^c u_{ij} = 1, \forall j = 1, \dots, n \quad (5)$$

- Step 2: At k -step, calculate the centroids and objective function by using the equations (4) and (2) respectively.
- Step 3: Update $U^{(k)}$, $U^{(k+1)}$ by using the equation (3).
- Step 4: If stopping criteria exist then stop; otherwise return to Step 2.

2.3 EM algorithm

The EM algorithm for image segmentation is based on modeling the image as a Gaussian mixture model (GMM), where, the parameters of the model are not known a prior (missing data), and it utilize the estimation theory (incomplete data) to estimate the missing data [5] [16].

The data model is then represented by [17]:

$$f(x_i / \phi) = \sum_{k=1}^K p_k G(x_i / \theta_k) \quad (6)$$

where K is the number of classes that need to be extracted from the image, $\theta_k \forall k = 1, 2, \dots, K$ is a parameter vector and its of the form $[\mu_k, \sigma_k]$ such that μ_k, σ_k are the mean and standard deviation of the distribution of k , respectively, p_k is

the mixing proportion of class k ($0 < p_k < 1, \forall k = 1, \dots, K$ and $\sum_k p_k = 1$), x_i is the intensity of pixel i , and $\phi = \{p_1, \dots, p_k, \mu_1, \dots, \mu_k, \sigma_1, \dots, \sigma_k\}$ is called the parameter vectors of mixture that is the missing data. The EM algorithm utilizes the maximum log-likelihood estimator (ϕ_{ML}) to estimate the value of ϕ .

This algorithm is given in the following two steps:

1. The Expectation (E) step
Compute the expected value of Z_{ik} by using the current estimate of the parameter vector ϕ .

$$Z_{ik}^{(t)} = \frac{p_k^{(t)} G(x_i / \theta_k^{(t)})}{f(x_i / \phi^{(t)})} \quad (7)$$

where Z_{ik} is the posterior probability that given x_i , x_i comes from class k . The posteriori probability satisfies the constraints, $(0 \leq Z_{ik} \leq 1, \sum_k Z_{ik} = 1, \sum_i Z_{ik} > 0, 1 \leq i \leq N, 1 \leq k \leq K)$. x_i is the value of the pixel i . $G(x_i / \theta_k)$ is the probability of pixel i and is a member of class k .

2. The Maximization (M) step
Use the data from the expectation step as if it were actually measured data.

$$\mu_k^{(t+1)} = \frac{\sum_{i=1}^N Z_{ik}^{(t)} x_i}{\sum_{i=1}^N Z_{ik}^{(t)}} \quad , \quad (8)$$

$$\sigma_k^{2(t+1)} = \frac{\sum_{i=1}^N Z_{ik}^{(t)} (x_i - \mu_k^{(t+1)})^2}{\sum_{i=1}^N Z_{ik}^{(t)}} \quad , \quad (9)$$

$$p_k^{(t+1)} = \frac{\sum_{i=1}^N Z_{ik}^{(t)}}{N} \quad . \quad (10)$$

The following steps summarize the EM algorithm for image segmentation.

- Step 1: The number of classes K and the image I are provided to the system
- Step 2: The initial estimation of parameter $\phi^{(0)}$ is estimated based on the histogram of the image and the number of classes.
- Step 3: Perform the E-step and M-step iteratively until convergence is reached. At each iteration the E-step computes the class

probability of each pixel based on the current estimation of $\phi^{(t)}$. M-step computes the new expectation of $\phi^{(t+1)}$ based on values computed in the previous E-step. After convergence the maximum estimator of ϕ is produced.

Step 4: Use ϕ_{ML} as a classifier to generate the classification matrix C .

Step 5: Assign label to each class based on the classification matrix C and generate the segmented image.

2.4 Evaluation parameters

Both qualitative and quantitative validations are considered for the performance evaluation. The qualitative evaluation is simply the visual inspection of the result done by the four experts of the field. For this qualitative study, the four regions of interest background, CSF, GM and WM are displayed in black, dark gray, light gray and white color respectively.

Next the level of agreement index and processing time are considered for quantitative evaluation. Jaccard coefficient is chosen as the level of agreement measure. The Jaccard coefficient (J) [18] is given by:

$$J(A, B) = \frac{A \cap B}{A \cup B} \quad (11)$$

where A and B are two data sets. The value J varies from 0 for complete disagreement to 1 for complete agreement, between A and B .

2.5 Preprocessing

The brain extraction is a necessary step before segmentation. Indeed pixels lying outside the brain contour and which are not of interest (skin, fat, bone and air) share intensity with the region of interest. This leads to a mystifying conclusion of segmentation result. Numerous brain extraction algorithms are available. We used our brain extraction algorithms (BEA) [19] [20] to extract the brain from T1-w and T2-w MR scans respectively.

3 Materials

We have used 46 datasets obtained from the following sources for our experiments.

Twenty coronal T1-w datasets of normal subjects were obtained from the Internet Brain Segmentation Repository (IBSR) developed by Centre for Morphometric Analysis (CMA) at Massachusetts General Hospital. Some of these datasets were affected by INU artifacts. Twelve datasets of both T1-w and T2-w MRI Head Scans were collected from KGS Advanced MR and CT Scans, Madurai, Tamilnadu, India. The MRI Datasets were acquired on a Siemens 1.5T

scanner between April 2007 and September 2007. Fourteen abnormal datasets are available at ‘The Whole Brain Atlas’ (WBA) website maintained by the Department of Radiology and Neurology at Brigham and Women’s Hospital, Harvard Medical School, the Library of Medicine, and the American Academy of Neurology. These datasets had anisotropic nature of voxels with stack of slices of size 256 256. These were used to test our methods on datasets with abnormalities.

4 Results and Discussions

The three methods are implemented in Matlab 6.5 and tested on the images chosen from the material pool. The experiments were performed in a 1.73 GHz Intel Pentium dual-core processor, Windows XP with 1GB RAM.

Initially the qualitative performance of methods on original MR scan is done. For the original image given in row 1 of Fig.1, some of the surrounding fatty regions are classified as WM by all the methods. The other regions like GM and CSF are misclassified by the KM and EM methods whereas the FCM classified them correctly. While applying the methods on extracted brain portion of the original image, they all gave the acceptable results as given in row 2 of Fig.1. This type of testing was made with several scans and found that the segmentation on extracted brain produced accurate results. Hence for the further validation, the methods were applied on the brain portion extracted from the MR scans.

Then an abnormal T2-w image was tested and the results are shown in Fig.2. This T2-w image has more blurred region boundaries and a sample is pointed by the rectangle. KM method over segments the WM region by treating some of CSF and GM pixels enclosed within the rectangle as WM pixels as shown in Fig.2c and vice versa by EM method

because it under segments the WM region as shown in Fig.2e. FCM segments WM accurately.

One more attribute of FCM is that it tends to cluster data into equal sized clusters and never left any region as blank. The results for FCM shown in Fig.3 proved this. The segmentation result of KM (Fig.3c) and EM (Fig.3e) methods have no region for WM but FCM (Fig.3d) segmented all the regions correctly and are comparable with the manual segmentation (Fig.3b).

Then the methods were tested on 20 normal datasets collected from IBSR. Manual segmentation of four regions is available for these datasets and was used as “gold standard” for our comparison. The Jaccard coefficient, J value computed between each method and gold standard of 20 datasets is given in Table 1, region wise. Performance of EM was best for GM and CSF and low for WM segmentation due to under segmentation capability for WM region. It missed most of the WM regions near the end of the brain.

Next we estimated time of processing for each method. The processing time for KM is approximately 0.75 s/slice, FCM $\approx$ 2.5 s/slice and EM $\approx$ 7.5 s/slice. The increasing value of execution time is due to the computational complexity of the methods.

The performance of these methods depends on the initial positions of the centroids. For the KM method, they are placed as much as possible far away from each other. FCM using the U, randomly initialized matrix to compute initial centers. Instead of this random selection, the initial cluster centers could be decided as the mean of the image density partition (depending upon the number of clusters). This will yield better results and quicken the process. But EM method fails to utilize the strong spatial correlation between neighboring pixels due to the GMM which assumes that all the pixels distributions are identical and independent.

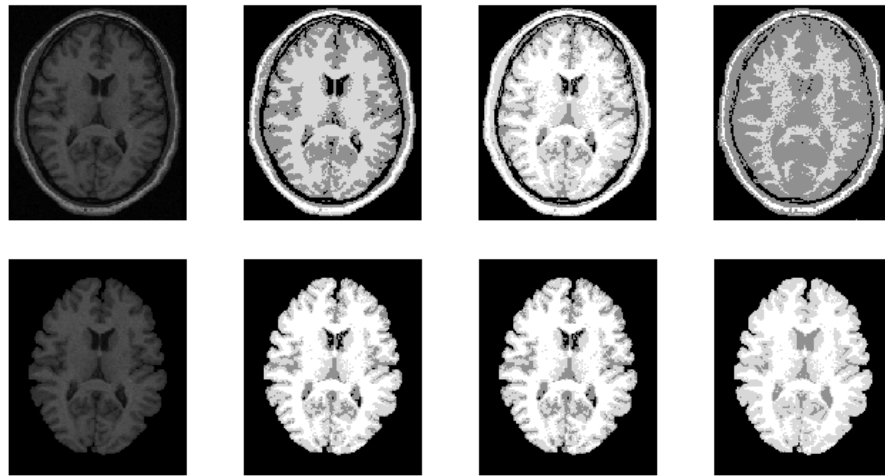


Figure 1. Segmentation result of KM, FCM and EM on original head scan (Row 1) and on the brain extracted from the original using our BEA (Row 2). The original head scan is in column 1 of row 1 and the extracted brain is in column 1 of row 2. The four regions WM (white in color), GM (light gray), CSF (dark gray) and others (black in color) of head and brain obtained by KM are in column 2, FCM are in column 3 and EM are in column 4 respectively.

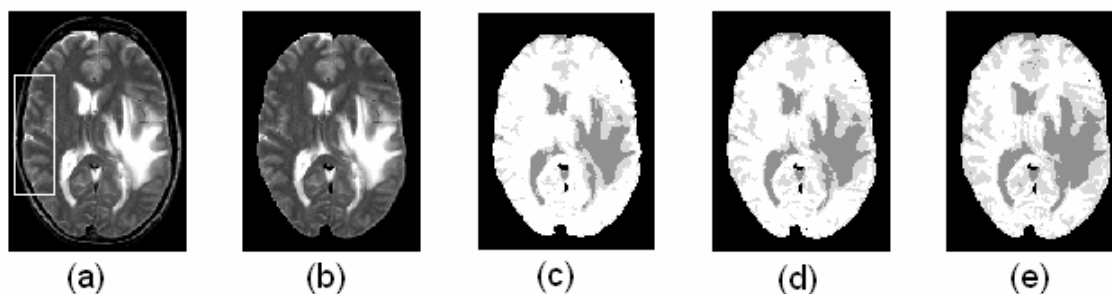


Figure 2. Segmentation results of abnormal T2-w scan (WM in white, GM in light gray, CSF in dark gray and others in black) (a) Original scan with a rectangle to compare the results (b) Extracted brain portion done by our BEA (c) KM segmentation (d) FCM Segmentation (e) EM Segmentation

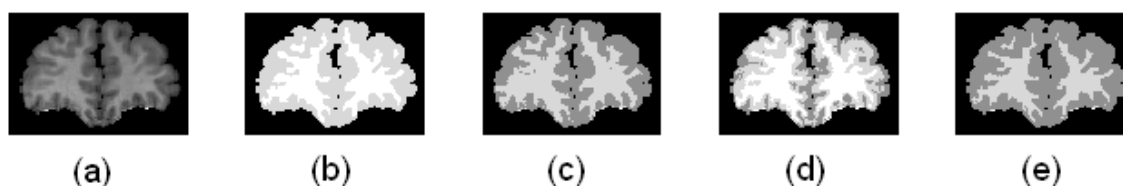


Figure 3. Segmentation results of posterior end of head (WM in white, GM in light gray, CSF in dark gray and others in black) (a) Original brain (b) Manual segmentation (c) KM segmentation (d) FCM Segmentation (e) EM Segmentation

5 Conclusions

In this work we have made a comparative study of the performance of three segmentation methods KM, FCM and EM. Experiments were carried on the original MRI head scans and skull stripped brain. The classification results were found to be better in skull stripped brain. Performance of these methods on 20 volumes in classifying WM, GM, CSF and others showed region specific results. EM performed better in classifying CSF and GM and others while KM did well for WM. Therefore the overall performance of EM is better and comparable with manual extraction of gold standard. In some cases segmentation is just a tool that leads the subsequent process and is not depending on the accuracy of the result. The fastest KM method is suitable for that type of segmentation. For the anisotropic volumes with blurred region boundaries, the methods KM and EM have a chance to miss or misclassify one or more regions. But FCM never misses a region. So FCM is more appropriate for these types of volumes and even for abnormal sets. FCM outperforms other methods in terms of robustness across the variety of scans and number of regions. Based on accuracy and

processing time, FCM can yield better result than the other two.

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Table 1: The Jaccard coefficient (similarity measure) obtained for the segmentation techniques KM, FCM and EM for the brain regions CSF, GM, WM and others on the 20 Normal data sets from the IBSR.

S.No	Volume	CSF			GM			WM			Others		
		KM	FCM	EM	KM	FCM	EM	KM	FCM	EM	KM	FCM	EM
1	1_24	0.0426	0.0394	0.0764	0.4913	0.475	0.541	0.7113	0.7069	0.6977	0.999	0.9989	1
2	2_4	0.0268	0.0274	0.0302	0.4221	0.4195	0.432	0.5825	0.5874	0.5303	0.9992	0.9992	1
3	4_8	0.0535	0.0518	0.1086	0.4568	0.4589	0.4811	0.6199	0.6352	0.5937	0.999	0.999	1
4	5_8	0.042	0.0397	0.1373	0.4804	0.4739	0.5719	0.6581	0.6557	0.6217	0.999	0.999	1
5	6_10	0.0636	0.061	0.1789	0.4877	0.4721	0.5767	0.6955	0.696	0.6796	0.9989	0.9989	1
6	7_8	0.0456	0.0423	0.0754	0.5445	0.5335	0.5579	0.7506	0.7524	0.7258	0.9989	0.9988	1
7	8_4	0.0552	0.0481	0.1017	0.5138	0.4963	0.5505	0.7001	0.6987	0.6917	0.9985	0.9984	1
8	11_3	0.078	0.0702	0.1729	0.5556	0.5338	0.6355	0.7596	0.7592	0.7165	0.9986	0.9985	1
9	12_3	0.052	0.045	0.2257	0.539	0.5168	0.6328	0.7827	0.7721	0.7277	0.9983	0.9982	1
10	13_3	0.0258	0.0234	0.0857	0.52	0.4876	0.689	0.7553	0.7446	0.7354	0.9993	0.9992	1
11	15_3	0.0524	0.0553	0.1206	0.3919	0.4018	0.4499	0.5077	0.5206	0.4887	0.9986	0.9987	1
12	16_3	0.0485	0.0439	0.1092	0.4594	0.4513	0.548	0.5954	0.5977	0.5696	0.9992	0.9992	1
13	17_3	0.0587	0.054	0.1108	0.4872	0.4772	0.5285	0.7202	0.7202	0.6865	0.9994	0.9994	1
14	100_23	0.0291	0.026	0.0745	0.5216	0.4879	0.6382	0.7401	0.7348	0.7029	0.9985	0.9984	1
15	110_3	0.0651	0.0554	0.1536	0.5565	0.5249	0.6209	0.71	0.7076	0.665	0.9992	0.9991	1
16	111_2	0.0388	0.0352	0.0801	0.4994	0.4788	0.5715	0.7187	0.709	0.7004	0.999	0.9989	1
17	112_2	0.0522	0.0457	0.1135	0.5482	0.5228	0.6162	0.7161	0.7159	0.6739	0.9991	0.9991	1
18	191_3	0.0421	0.0371	0.0653	0.5488	0.5248	0.5633	0.7493	0.7485	0.6919	0.999	0.9988	1
19	202_3	0.0311	0.0283	0.1549	0.5392	0.5184	0.6062	0.761	0.7538	0.7336	0.9975	0.9975	1
20	205_3	0.0445	0.0394	0.1561	0.5458	0.5234	0.5956	0.762	0.7577	0.7178	0.9978	0.9977	1
Average:		0.0474	0.0434	0.1166	0.5055	0.4889	0.5703	0.6998	0.6987	0.6675	0.9988	0.9987	1.0000

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