ISSN: 2277-3754
International Journal of Engineering and Innovative Technology (IJEIT)
Volume 1, Issue 2, February 2012

Brain Tumor Segmentation of Contras Material Applied MRI Using Enhanced Fuzzy C-Means Clustering

Hari Prasath S.P, G.Kharmega Sundararaj, A.Jayachandran
spharipprasath@gmail.com, megaminindia@gmail.com, jaya1jaya1@gmail.com

Abstract*— This paper focuses on the image segmentation, which is one of the key problems in medical image processing. A new medical image segmentation method is proposed based on Enhanced fuzzy c- means (EFCM) algorithm and YCbCr color model. Firstly, we convert the contrast applied MRI into YCbCr color model then classify the image into the region of interest and background using EFCMs algorithm. The method is capable of solving unable exactly contoured lesion objects problem in MRI image by adding the color-based segmentation operation. The key idea of color-converted segmentation algorithm with EFCMs is to solve the given MRI image by converting the input gray-level image into a color space image and operating the image labeled by cluster index. Over all, the proposed technique produce more accurate results compare with other techniques.

Index Terms— **MRI, brain tumor, FCM, gradient, Color-converted segmentation algorithm, K-means clustering technique, Lesion, Tumor.**

I. INTRODUCTION

Imaging is a basic aspect of medical sciences for visualization of anatomical structures and functional or metabolic information of the human body [1]. Structural and functional imaging of human body is important for under-standing the human body anatomy, physiological processes, function of organs, and behavior of whole or a part of organ under the influence of abnormal physiological conditions or a disease [2,3]. For the last two decades, radiological sciences have witnessed a revolutionary progress in medical imaging and computerized medical image processing, some important radiological tools in diagnosis and treatment evaluation and intervention of critical diseases have much significant improvement for health care. So, medical imaging in diagnostic radiology is evolving as a result of the significant contributions of a number of different disciplines from basic sciences, engineering, and medicine. Therefore, computerized image reconstruction, processing and analysis methods have been developed Magnetic resonance (MR) imaging has several advantages over other medical imaging modalities, including high contrast among different soft tissues, relatively high spatial resolution across the entire field of view and multi-spectral characteristics. Therefore, it has been widely used in quantitative brain imaging studies. Quantitative volumetric measurement and three-dimensional (3D) visualization of brain tissues are helpful for pathological evolution analyses, where image segmentation plays an important role.

The size alterations in brain tissues often accompany various diseases, such as schizophrenia. Thus, estimation of tissue sizes has become an extremely important aspect of treatment which should be accomplished as precisely as possible. This creates the need to properly segment the brain MR images into gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF) and also to identify tumors or lesions, if present.

The main difficulties in brain segmentation are the intensity in homogeneities and noise. In fact, intensity in homogeneities occurs in many real-world images from different modalities [3, 4]. In particular, it is often seen in medical images, such as X-ray radio-graphy/tomography and MR images. For example, the intensity in homogeneity in MR images often appears as an intensity variation across the image, which arises from radio-frequency (RF) coils or acquisition sequences. Thus the resultant intensities of the same tissue vary with the locations in the image. The noise in MR images is Rican distributed and can affect Significantly the performances of Classification methods. The best solutions consist of either filtering the image prior to classification or embedding spatial regularization inside the Classifier itself.

As we know, numerous studies of brain segmentation have been proposed, many of which can be categorized into two classes, region detection methods and boundary detection methods, and their goals are to obtain the region and boundary of the desired objects. Meanwhile, most existing segmentation methods are usually dedicated only for specific objects. Combined with the existing methods and aimed to get better results, it's useful to take soft segmentation methods into account. In soft segmentation, voxels are classified into different classes with various degrees of uncertainty which are given by functions. The larger the value of function for a specific voxel, the larger the possibility that this voxel belongs to that cluster. The fuzzy c-means (FCM) clustering algorithm is soft segmentation method, and it has aroused comprehensive attention. There have been many different families of fuzzy clustering algorithms proposed.

In Ostu's method, it assumes that the image to be threshold contains two classes of pixels foreground and background then calculates the optimum threshold separating those two classes so that their intra-class variance is minimal. As we know, gradient variance is a kind of measurement for the distributed uniformity .Each divided class contains not only interior area but also edge area. In interior area gradient values are smaller; while, in edge area the gradient values are larger.

ISSN: 2277-3754
International Journal of Engineering and Innovative Technology (IJEIT)
Volume 1, Issue 2, February 2012

When the between-cluster variance of two classes is the maximum, the best result of the segmentation will be obtained. Under this enlightening method, a constrained term in FCM will be proposed just modified from Ostu method. In this paper, we will try to develop a new and effective algorithm for segmentation of MRI based on FCM. First we will convert the color model YCbCr modify the objective function of FCM, and then an addition term will be used to constrain the behavior of membership functions. These constrained terms are to take advantage of useful data while overcoming potential difficulties the sum of the mean variance in the region and the reciprocal of the mean gradient along the edge of the region are chosen as an objective function. The minimum of the sum is optimum result. We use the dye applied real MRI data to verify the algorithm and experimental results are good consistent.

II. Color Image Representation

Hardware generally display color via an RGB model. Thus a particular pixel may have associated with it a three dimensional vector which provides respective color intensities, where (0, 0, 0) is a black, (k, k, k) is white, (k, 0, 0) is pure red and so on, here k- is the quantization granularity for each primary (256 is common). This implies a color space of k3 distinct colors (224 if k=256) which not always displays. Most computer displays use 8, 16, or 24 bits per screen pixel. The number of bits per screen pixel determines the display's screen bit depth. The screen bit depth determines the screen color resolution, which is how many distinct colors the display can produce. These images display best on systems with 24-bit color. Color enables us to receive more visual information. While human perceive only few dozens of gray levels, have the ability to distinguish between thousands of colors. Gray scale images do not have enough information to handle some inspection tasks like identification, strong, and process control. In other cases, a solution is possible with the grayscales images, but is greatly simplified by taking into account color information. For example: Images of a pack of crayons in color and gray scale.

A. Characterization of Color: Characterization of light is central to the science of color. If the light is achromatic (void of color), its only attribute is its intensity, or amount. Achromatic light is that viewers see on a black and white television set. Gray level refers to a scalar measure of intensity that ranges from black to white. Chromatic light spans the electromagnetic spectrum from approximately 400 to 700 nm. Three basic quantities are used to describe the quality of a chromatic light source:

- Radiance
- Luminance
- Brightness

Radiance. Radiance is the total amount of energy that flows from the light source, and it is usually measured in watt (w)

Luminance. Luminance, measured in lumens (lm), gives a measure of the amount of energy an observer perceives from a light source.

Brightness. Brightness is a subjective descriptor that is practically impossible to measure. It embodies the achromatic notation of intensity and is one of the key factors in describing color sensation. However, there are other models besides RGB for representing colors numerically. For example, a color can be represented by its hue, saturation, and value components (HSV) instead. The various models for color data are called color spaces. Many authors proposed very different color spaces for the task of color modeling. Most commonly used are NRGB (normalized RGB), HIS, HSV (Hue-Saturation-Value), CIEXYZ, YCbCr, YUV.

B. Preprocessing: The input image is a RGB Color image. First step is convert RGB color image into Grayscale scale image. The proposed algorithm is process the grayscale images only. The Captured image has the file format JPEG, JPG, etc. because it provides high compression. So it requires the minimum amount of memory compared with other image file format. It is possible to construct (almost) all visible colors by combining the three primary colors red, green and blue, because the human eye has only three different color receptors, each of them sensible to one of the three colors. Different combinations in the stimulation of the receptors enable the human eye to distinguish approximately 350000 colors. A RGB color image is a multi-spectral image with one band for each color red, green and blue, thus producing a weighted combination of the three primary colors for each pixel. A color image has three channels namely red, green, and blue. To convert the color image as gray, the RGB channels should be extracted and calculated the intensity value using the following formula.

Y=0.299*(red Channel) + 0.587*(red Channel) + 0.114*(blue Channel)

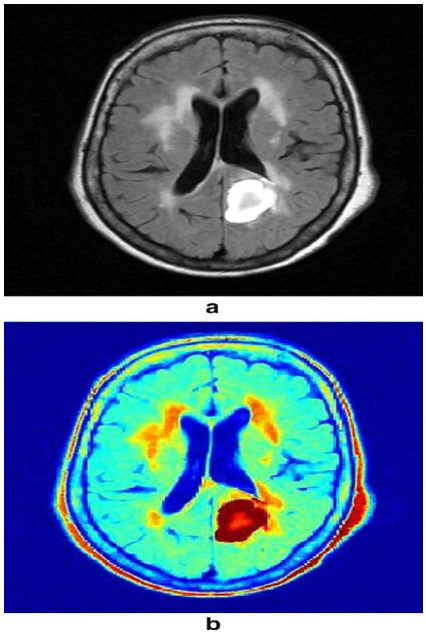

Fig. 1. Original MRI T2-weighted brain Images, (a) gray-level image and (b) Color image

The smoothed RGB image is converted into YCbCr color representation. The Conversion of RGB to YC_bC_r is done by the following formula.

$Y = 0.299R + 0.587G + 0.114 B$

$C_b = -0.169R - 0.331G + 0.500B$

$C_r = 0.500R – 0.419G – 0.081B$

ISSN: 2277-3754
International Journal of Engineering and Innovative Technology (IJEIT)
Volume 1, Issue 2, February 2012

In the YC_bC_r color space, we can regard the Chroma (C_b and C_r) as the functions of the luma (Y): (C_b (Y) and (C_r (Y). Let the transformed chroma be (C'_b (Y) and (C'_r(Y). The skin color model is specified by the centers (denoted as C_b (Y) and C_r(Y) and spread of the cluster denoted as (W_{Cb}(Y) and W_{Cr}(Y) and is used for computing the transformed chroma.

III. CLUSTERING

Clustering is the process of grouping feature vectors into classes in the self-organizing mode. Let $\{\mathbf{x}^{(q)}: q = 1,\ldots,Q\}$ be a set of Q feature vectors. Each feature vector $\mathbf{x}^{(q)} = (x_1^{(q)}, \ldots, x_N^{(q)})$ has N components. The process of clustering is to assign the Q feature vectors into K clusters $\{\mathbf{c}^{(k)}: k = 1, \ldots, K\}$ usually by the minimum distance assignment principle. Choosing the representation of cluster centers (or prototypes) is crucial to the clustering. Feature vectors that are farther away from the cluster center should not have as much weight as those that are close. These more distant feature vectors are outliers usually caused by errors in one or more measurements or a deviation in the processes that formed the object [9].The simplest weighting method is arithmetic averaging. It adds all feature vectors in a cluster and takes the average as prototype. Because of its simplicity, it is still widely used in the clustering initialization. The arithmetic averaging gives the central located feature vectors the same weights as outliers. To lower the influence of the outliers, median vectors are used in some proposed algorithms. To be more immune to outliers and more Representatives, the fuzzy weighted average is introduced to represent prototypes:

$$\mathbf{Z}_n^{(k)} = \Sigma_{\{q:\, q \in k\}} w_{qk} \mathbf{x}^{(q)}_n; \qquad (1)$$

Rather than a Boolean value 1 (true, which means it belongs to the cluster) or 0 (false, does not belong),

A. The weight w_{qk} in equation (1) represent partial membership to a cluster. It is called a fuzzy weight. There are different means to generate fuzzy weights.

B. One way of generating fuzzy weights is the reciprocal of distance

$$w_{qk} = 1/ D_{qk}, \ (w_{qk}= 1 \text{ if } D_{qk} = 0) \qquad (2)$$

It was used in earlier fuzzy clustering algorithms [2]. When the distance between the feature vector and the prototype is large, the weight is small. On the other hand, it is large when the distance is small. Using Gaussian functions to generate fuzzy weights is the most natural way for clustering. It is not only immune to outliers but also provides appropriate weighting for more centrally and densely located vectors. It is used in the fuzzy clustering and fuzzy merging (FCFM) algorithm. In this paper, we implemented the enhanced fuzzy c-means (EFCM) algorithm. The clustering groups a sample set of feature vectors into K clusters via an appropriate similarity (or dissimilarity) criterion (such as distance from the center of the cluster).

A. K-Means Algorithm: The k-means algorithm assigns feature vectors to clusters by the minimum distance assignment principle [5], which assigns a new feature vector $\mathbf{x}^{(q)}$ to the cluster $\mathbf{c}^{(k)}$ such that the distance from $\mathbf{x}^{(q)}$ to the center of $\mathbf{c}^{(k)}$ is the minimum over all K clusters. The basic k-means algorithm is as follows:

- Put the first K feature vectors as initial centers.
- Assign each sample vector to the cluster with minimum distance assignment principle.
- Compute new average as new center for each cluster.
- If any center has changed, then go to step 2, else terminate.

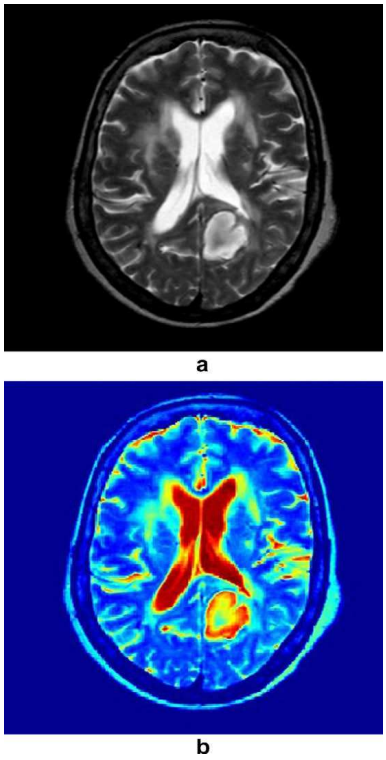

Fig. 2. Original MRI T1-weighted brain images, (a) gray-level image and (b) color image

The advantages of the method are its simplicity, efficiency, and self-organization. It is used as initial process in many other algorithms. The disadvantages are: 1) K must be provided; 2) it is a linearly separating algorithm.

B. The ISODATA Algorithm: This algorithm is based on the k-means algorithm, and employs processes of eliminating, splitting, and clustering. The algorithm is described as following [8].

- Start with Kinit (initial number of clusters) which is user-given. Assign the first K_{init} samples as cluster centers.
- Assign all samples to the clusters by minimum distance principle.
- Eliminate clusters that contain less than n_{min} feature vectors and reassign those vectors to other clusters to yield K clusters.
- Compute a new cluster center as the average of all feature vectors in each cluster.
- For each *k*th cluster, compute the mean-squared error $\sigma_n^2(k)$ of each *n*th component x_n over that cluster and find the maximum $\sigma_{n^*}^2(k)$ component mean-squared error over within cluster k for over n = 1, …, N, where the index n* is for the maximum component.
- If there are not enough clusters ($K_{init} < K/2$) and this is not the last iteration, then if $\sigma_{max}(k) > \sigma_{split}$ for any cluster k, split that cluster into two.

ISSN: 2277-3754
International Journal of Engineering and Innovative Technology (IJEIT)
Volume 1, Issue 2, February 2012

If this is an even iteration and $K_{init} > 2K$,

- Then compute all distances between cluster centers. Merge the clusters that are close than a given value.

The advantages of the ISODATA are its self-organizing capability, its flexibility in eliminating clusters that are too small, its ability to divide clusters that are too dissimilar, and its ability to merge clusters that are sufficiently similar. Some disadvantages are: 1) multiple parameters must be given by the user, although they are not known a priori; 2) a considerable amount of experimentation may be required to get reasonable values; 3) the clusters are ball shaped as determined by the distance function; 4) the value determined for K depends on the parameters given by the user and is not necessarily the best value; and 5) a cluster average is often not the best prototype for a cluster [9].

C. Fuzzy Clustering Algorithms: Fuzzy clustering plays an important role in solving problems in the areas of pattern recognition and fuzzy model identification. A variety of fuzzy clustering methods have been proposed and most of them are based upon distance criteria [6]. One widely used algorithm is the fuzzy c-means (FCM) algorithm. It uses reciprocal distance to compute fuzzy weights. A more efficient algorithm is the new FCFM. It computes the cluster center using Gaussian weights, uses large initial prototypes, and adds processes of eliminating, clustering and merging. In the following sections we discuss and compare the FCM algorithm and FCFM algorithm. The fuzzy c-means (FCM) algorithm was introduced by J. C. Bezdek [2]. The idea of FCM is using the weights that minimize the total weighted mean-square error:

$$J(w_{qk}, \mathbf{z}^{(k)}) = \Sigma_{(k=1,K)} \Sigma_{(k=1,K)} (w_{qk}) \| \mathbf{x}^{(q)} - \mathbf{z}^{(k)} \|^2 \quad (3)$$

$$\Sigma_{(k=1,K)} (w_{qk}) = 1 \text{ for each } q$$

$$w_{qk} = (1/(D_{qk})^2)^{1/(p-1)} / \Sigma_{(k=1,K)} (1/(D_{qk})^2)^{1/(p-1)}, \; p > 1 \quad (4)$$

The FCM allows each feature vector to belong to every cluster with a fuzzy truth value (between 0 and 1), which is computed using Equation (4). The algorithm assigns a feature vector to a cluster according to the maximum weight of the feature vector over all clusters.

IV. Proposed Algorithm

The MFCMs algorithm [7] uses Gaussian weighted feature vectors to represent the prototypes. The algorithm starts with large numbers of clusters and eliminates clusters by distance or by size so the prototypes are much more representative. The MFCMs algorithm computes fuzzy weights using Equation (10)

$$\alpha_p^{(r)} = \exp[-(\mathbf{x}_p - \boldsymbol{\mu}^{(r)})^2/(2\sigma^2)^{(r)}] / \{ \Sigma_{(m=1,P)} \exp[-(\mathbf{x}_m - \boldsymbol{\mu}^{(r)})^2/(2\sigma^2)^{(r)}] \}$$

The MFCMs algorithm does the following steps:

- Standardize the Q sample feature vectors and use a large K_{init}.
- Eliminate the prototypes that are closer to other prototype than a distance threshold D_{Thresh}, which can be set by a user.
- Apply k-means as the first step to get the prototypes.
- Eliminate small clusters.
- Loop in computing the fuzzy weights and MWFEV (modified weighted fuzzy expected value) for each cluster to obtain the prototype and then assign all of the feature vectors to clusters based on the minimum distance assignment. End the loop when the fuzzy centers do not change.
- Merge clusters.

The FCFM algorithm uses a relatively large K_{init} to thin out the prototypes. The default K_{init} is calculated as:

$$K_{init} = \max \{6N + 12\log_2 Q, Q\} \quad (6)$$

1) The Modified Xie-Beni validity κ is defined as

$$\kappa = D_{min}^2 / \{\Sigma_{(k=1,K)} \sigma_k^2\} \quad (7)$$

The variance of each cluster is calculated by summing over only the members of each cluster rather than over all Q for each cluster, which contrasts with the original Xie-Beni validity measure.

$$\sigma_k^2 = \Sigma_{\{q:\, q \text{ is in cluster } k\}} w_{qk} \| \mathbf{x}^{(q)} - \mathbf{c}^{(k)} \|^2 \quad (8)$$

To obtain a more typical vector to represent a cluster, the algorithm uses modified weighted fuzzy expected value as the prototypical value:

$$\boldsymbol{\mu}^{(r+1)} = \Sigma_{\{p=1,P\}} \alpha_p^{(r)} \mathbf{x}_p \quad (9)$$

$\boldsymbol{\mu}^{(r+1)}$ is obtained by Picard iterations. The initial value $\mu^{(0)}$ is the arithmetic average of the set of real vectors.

$$\alpha_p^{(r)} = \exp[-(\mathbf{x}_p - \boldsymbol{\mu}^{(r)})^2/(2\sigma^2)^{(r)}] / \{ \Sigma_{(m=1,P)} \exp[-(\mathbf{x}_m - \boldsymbol{\mu}^{(r)})^2/(2\sigma^2)^{(r)}] \} \quad (10)$$

σ^2 is the mean-square error.

The process computes the fuzzy weights and the MWFEV component wisely for each cluster to obtain the cluster center. It also computes the mean-square error σ^2 for each cluster, and then assigns each feature vector to a cluster by the minimum distance assignment principle. For every pair of prototypes, the algorithm computes the distance between them. It finds the pair with shortest distance. If the pair meets the merge criteria, the two clusters are merged into one.

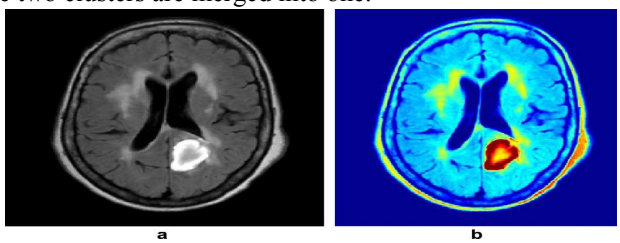

Fig. 3. Original MRI spin-density brain images, (a) gray-level image and (b) Color image

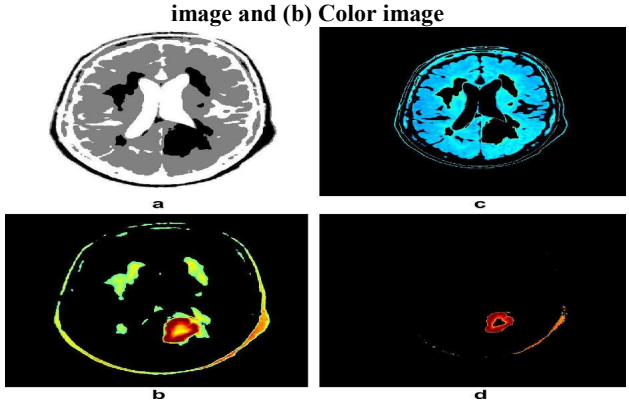

Fig4. Color-based segmentation with K-means clustering process for spin-density brain images (a) image labeled by cluster index, (b) objects in cluster 1, (c) objects in cluster 2 and (d) final segmentation

ISSN: 2277-3754
International Journal of Engineering and Innovative Technology (IJEIT)
Volume 1, Issue 2, February 2012

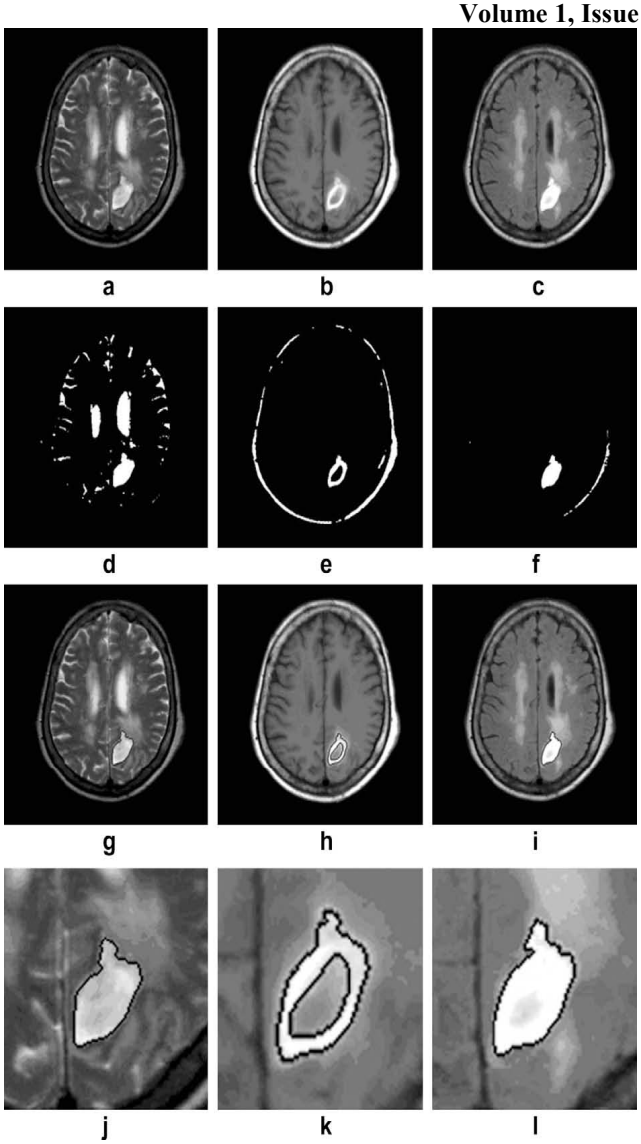

Fig. 7. (a–c) are for original MRI images, (d–f) are after binary images, (g–i) are after Otsu clustering images, and (j–l) are for localized images.

Magnetic resonance (MR) or multi-modality medical images may also require segmentation using a multi-dimensional feature space with multiple parameters of interest. Images can be segmented by pixel classification through clustering of all features of interest. The number of clusters in the multi-dimensional feature space thus represents the number of classes in the image. As the image is classified into cluster classes, segmented regions are obtained by checking the neighborhood pixels for the same class label. However, clustering may produce disjoint regions with holes or regions with a single pixel. After the image data are clustered and pixels are classified, a post- processing algorithm such as region growing, pixel connectivity or rule-based algorithm is usually applied to obtain the final segmented regions. The following tests show how to use color-converted segmentation with K-means clustering to track tumor from an MRI brain image (288 288) which is stained with lesion as shown in Fig. 1a. First converts the original gray-level image into YCbCr color space image as shown in Fig. 1b, where the YCbCr space consists of a luminosity layer 'L*', chromaticity-layer 'a*' indicating where color falls along the red– green axis, and chromaticity-layer 'b*' indicating where the color falls along the blue–yellow axis. All of the color information is in the 'a*' and 'b*' layers. The difference between two colors can be measured by using the Euclidean distance metric. Then classify the colors in 'YCbCr *' space using MFC-means clustering. MFC means clustering treats each object as having a location in space. It finds partitions such that objects within each cluster are as close to each other as possible, and as far from objects in other clusters as possible. MFC -means clustering requires specifying the number of clusters to be partitioned and a distance metric to quantify how close two objects are to each other. Since the color information exists in the 'YCbCr' space, the objects are pixels with 'Cb and 'Cr*' values. Use MFC means to cluster the objects into three clusters using the Euclidean distance metric. and then labels every pixel in the image using the results from MFC -means, as Fig. 2a shown is the image labeled by cluster index. Using pixel labels, we can separate objects in the brain image by color, which will result in three images, as Fig. 2b shown are objects in cluster 1, objects in cluster 2, and the final segmentation, respectively. From the final segmentation result shown, the brain regions related to the white matter, cerebrospinal fluid in the sulci, ventricles and a tumor (in the right half of the image) can be seen in the segmented image obtained using color-converted segmentation with MFC -means clustering Figs. 1 and 2 shown. To prove the proposed method is best on accuracy and computing time, we also used another method [44], ''Brain Tumor Segmentation Based on Otsu Clustering with Multi-threshold Method", for the comparison. Fig. 5a–c are for original MRI images, (d–f) are after binary images, (g–i) are after Otsu clustering images. Fig. 5 are gray level images without color-converted segmentation. The results show their accuracy and computing time are 96% and 10 min. So, the proposed method saves lots computing time and has the best accuracy.

V. CONCLUSION

We have proposed a realization of tumor tracking method of MRI brain image using color-converted segmentation with Modified fuzzy C-means clustering technique. A preliminary evaluation on MRI brain image shows encouraging results. Color-converted Segmentation with MFC-means clustering algorithm for tracking objects in medical images is performed to be very promising for MRI applications. The brain regions related to a tumor or lesion can be exactly separated from the colored image. This proposed method will be able to help pathologists distinguish exactly lesion size and region.

REFERENCES

[1] A. Rangarajan, I.T. Hsiao, G. Gindi, a Bayesian joint mixture framework for the integration of anatomical in functional image reconstruction, J. Math. Imaging Vis. 12 (2000) 199–217.

[2] F.M. Enzinger, S.W. Weiss, Malignant vascular tumors, in: F.M.Enzinger, S.W. Weiss (Eds.), Soft Tissue Tumors, third ed., Mosby, St. Louis, MO, 1995, pp. 655–677.

ISSN: 2277-3754
International Journal of Engineering and Innovative Technology (IJEIT)
Volume 1, Issue 2, February 2012

[3] L.V.D. Hauwe, F. Ramon, Lymphatic tumors, in: A.M. De Schepper (Ed.), Imaging of Soft Tumors, second ed., Springer, Heidelberg, 2001, pp. 246–254.

[4] K.Y. Tu, T.B. Chen, H.H.S. Lu, R.S. Liu, K.L. Chen, C.M. Chen, J.C. Chen, Empirical studies of cross-reference maximum likelihood estimate reconstruction for positron emission tomography, Biomed. Eng. – Appl. Basis Commun. 13 (1) (2001) 1–7.

[5] C.M. Kao, X. Pan, C.T. Chen, W.H. Wong, Image restoration and reconstruction with a Bayesian approach, Med. Phys. 25 (5) (1998)600–613.

[6] G.N. Hounsfield, Computerized transverse axial scanning tomography: Part 1, description of the system, Br. J. Radiol. 46 (1973) 1016–1022.

[7] B. Lipinski, H. Herzog, E.R. Kops, W. Oberschelp, H.W. Muller-Gartner, Expectation maximization reconstruction of positron emission tomography images using anatomical magnetic resonance information, IEEE Trans. Med. Imaging 16 (2) (1997) 129–136.

[8] A. Bazille, M.A. Guttman, E.R. Mcveigh, E.A. Zerhouni, Impact of semiautomated versus manual image segmentation errors on myocardial strain calculation by magnetic resonance tagging, invest. Radiol. 29 (4) (1994) 427–433.

[9] H. Anger, Use of gamma-ray pinhole camera for vivo studies, Nature 170 (1952) 200–204.

[10] X. Ouyang, W.H. Wang, V.E. Johnson, X. Hu, C.T. Chen, Incorporation of correlated structural images in PET image reconstruction, IEEE Trans. Med. Imaging 13 (2) (1994) 627–640.

[11] Y.S. Akgul, C. Kambhamettu, M. Stone, Extraction and tracking of the tongue surface from ultrasound image sequences, in: Proceedings of the IEEE Computer Vision Pattern Recognition, Santa Barbara, CA,1998, pp. 298–303.

[12] U.R. Abeyratne, A.P. Petropulu, J.M. Reid, on modeling the tissue response from ultrasonic B-scan images, IEEE Trans. Med. Imaging 1 (2) (1996) 479–490.

[13] T.L. Faber, E.M. Stokely, Orientation of 3D structures in medical images, IEEE Trans. Pattern Anal. Mach. Intell. 2 (2) (1980) 127–135.

[14] G.J. Grewera, J.K. Udupa, Shape based interpolation of multidimensional grey-level images, IEEE Trans. Med. Imaging 15 (6) (1996) 881–892.

[15] F.S. Cohen, G. Georgiou, E. Halpern, WOLD decomposition of the backscatter echo in ultrasound images of soft tissue organs, IEEE Trans. Ultrason., Ferroelect. Freq. Contr. 1 (2) (1997) 460–472.

[16] K.D. Donohue, F. Forsberg, C.W. Piccoli, B.B. Goldberg, Classification of breast masses with ultrasonic scattering structure templates, IEEE Trans. Ultrason., Ferroelect. Freq. Contr. 1 (2) (1999) 300–310.

[17] G. Georgiou, F.S. Cohen, Statistical characterization of diffuse scattering in ultrasound images, IEEE Trans. Ultrason., Ferroelect. Freq. Contr. 1 (2) (1998) 57–64.

[18] T. Taxt, A. Lundervold, Multispectral analysis of the brain using magnetic resonance imaging, IEEE Trans. Med. Imaging 13 (1994) 440–470.

[19] L. Liberman, E.A. Morris, C.L. Benton, A.F. Abramson, D.D. Dershaw, Probably benign lesions at breast magnetic resonance imaging: preliminary experience in high-risk women, Cancer 98 (2) (2003).377–388.

[20] M.N. Ahmed, S.M.N. Mohamed, A.A. Farag, T. Moriarty, A modified fuzzy c -means algorithm for bias field estimation and segmentation of MRI data, IEEE Trans. Med. Imaging 21 (2002) 193–199.

[21] R.T. Constable, R.M. Henkelman, Contrast, resolution and detectability in MR imaging, J. Comput. Assist. Tomogr. 15 (1991).297–303.

[22] I. Bloch, H. Maˆıtre, M. Anvari, Fuzzy adjacency between image objects, Int. J. Uncertainty Fuzziness Knowledge-Based Syst. 5 (6) (1997) 615–653.

[23] I. Bloch, on fuzzy distances and their use in image processing under imprecision, Pattern Recognit. 32 (11) (1999) 1873–1895.

[24] I. Bloch, Fuzzy relative position between objects in image processing: a morphological approach, IEEE Trans. Pattern Anal. Mach. Intell. 21 (7) (1999) 657–664.

[25] M.N. Ahmed, S.M.N. Mohamed, A.A. Farag, T. Moriarty, A modified fuzzy c-means algorithm for bias field estimation and segmentation of MRI data, IEEE Trans. Med. Imaging 21 (2002) 193–199.

[26] S. Ardekani, H. Kangarloo, U. Sinha, Region based fuzzy clustering for automated brain segmentation, in: EMBS/BMES Conference Proceedings of the Second Joint 2, 2002, pp. 1041–1042.

[27] X. Wang, J. Keller, P. Gader, Using spatial relationships as features in object recognition, in: Proceedings of the Annual Meeting of the North American Fuzzy Information Processing Society NAFIPS 1997, Syracuse, NY, USA, 1997, pp. 160–165.

[28] T. Géraud, I. Bloch, H. Maître, Atlas-guided recognition of cerebral structures in MRI using fusion of fuzzy structural information, in: CIMAF'99 Symposium on Artificial Intelligence, La Havana, Cuba, 1999, pp. 99–106.

[29] I. Bloch, T. Géraud, H. Maˆıtre, Representation and fusion of heterogeneous fuzzy information in the 3D space for model-based structural recognition—application to 3D brain imaging, Artif. Intell.148 (2003) 141–175.