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

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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 controled 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 understanding 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.
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 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 \(k^3\) account color information. For example: Images of a pack of Three basic quantities are used to describe the quality of a that ranges from black to white. Chromatic light spans the light source.

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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.

\[
Y = 0.299 \times \text{red Channel} + 0.587 \times \text{red Channel} + 0.114 \times \text{blue Channel}
\]

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.

**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 YCbCr is done by the following formula.

\[
Y = 0.299R + 0.587G + 0.114B \\
C_b = -0.169R - 0.331G + 0.500B \\
C_r = 0.500R - 0.419G - 0.081B
\]
In the YCbcd color space, we can regard the Chroma (Cf and 
Cf) as the functions of the luma (Y): Cf(Y) and 
(Cf(Y). Let the transformed chroma be (Cf(Y) and 
(Cf(Y). The skin 
color model is specified by the centers (denoted as 
Cf(Y) and 
Cf(Y) and spread of the cluster denoted as (W(Cf(Y) and 
W(Cf(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 \( \{x^{(q)}\; q = 1, ..., Q\} \) be a 
set of Q feature vectors. Each feature vector \( x^{(q)} = (x_1^{(q)}, ..., x_{N}^{(q)}) \) has N components. The process of clustering is to assign 
the Q feature vectors into K clusters \( \{c^{(k)}; k = 1, ..., K\} \) 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 
troduced to represent prototypes:

\[
Z_{c^{(k)}} = \prod_{q=1}^{Q} w_{qk} x_{q}^{(q)}, \quad (1)
\]

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

\[
w_{qk} = 1 / D_{qk}, \quad (2)
\]

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 
\( x^{(q)} \) to the cluster \( c^{(k)} \) such that the distance from \( x^{(q)} \) to the 
center of \( c^{(k)} \) 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.

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 \( K_{\text{init}} \) samples as cluster centers.

- Assign all samples to the clusters by minimum distance 
principle.

- Eliminate clusters that contain less than \( n_{\text{min}} \) 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 \( n = 1, \ldots, N \), where the index \( n^{*} \) is for the 
maximum component.

- If there are not enough clusters (\( K_{\text{init}} < K/2 \)) and this is not 
the last iteration, then if \( \sigma_{\text{split}}(k) > \sigma_{\text{split}} \) for any cluster \( k \), split 
that cluster into two.
If this is an even iteration and $K_{\text{init}} > 2K$,

- 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:

$$ J(w_{qk}) = \sum_{k=1}^{K} \sum_{q=1}^{Q} w_{qk} \| x^{(q)} - z^{(k)} \|^2 $$  

$$ \sum_{k=1}^{K} \sum_{q=1}^{Q} w_{qk} = 1 \text{ for each } q $$  

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

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)

$$ \alpha_p^{(t)} = \exp[-(x_p - \mu^{(t)})^2/(2\sigma^2)] / \left( \sum_{m=1}^{M} \exp[-(x_m - \mu^{(t)})^2/(2\sigma^2)] \right) $$

The MFCMs algorithm does the following steps:

- Standardize the Q sample feature vectors and use a large $K_{\text{init}}$.
- Eliminate the prototypes that are closer to other prototype than a distance threshold $D_{\text{thresh}}$, 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 $K_{\text{init}}$ to thin out the prototypes. The default $K_{\text{init}}$ is calculated as:

$$ K_{\text{init}} = \max \{6N + 12\log_2 Q, Q \} $$  

**I)** The Modified Xie-Beni validity $\kappa$ is defined as

$$ \kappa = D_{\text{min}}^2 / \left( \sum_{k=1}^{K} \sigma_k^2 \right) $$  

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.

$$ \sigma_k^2 = \sum_{q \in \text{cluster } k} w_{qk} || x^{(q)} - c^{(k)} ||^2 $$

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

$$ \mu_k^{(t+1)} = \sum_{p=1}^{P} \alpha_p^{(t)} x_p $$  

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

$$ \alpha_p^{(t)} = \exp[-(x_p - \mu^{(t)})^2/(2\sigma^2)] / \left( \sum_{m=1}^{M} \exp[-(x_m - \mu^{(t)})^2/(2\sigma^2)] \right) $$  

$\sigma^2$ 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 $\sigma^2$ 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.

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

**Fig.4. 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**
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.

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