Determination of Gray Matter (GM) and White Matter (WM) Volume in Brain Magnetic Resonance Images (MRI)

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ABSTRACT
In this paper we present a hybrid approach based on combining fuzzy clustering, seed region growing, and Jaccard similarity coefficient algorithms to measure gray (GM) and white matter tissue (WM) volumes from magnetic resonance images (MRIs). The proposed algorithm incorporates intensity and anatomic information for segmenting of MRIs into different tissue classes, especially GM and WM. It starts by partitioning the image into different regions using fuzzy clustering. These regions are fed to seed region growing (SRG) method to isolate the suitable closed region. The seeds of SRG are selected as the output centers of the fuzzy clustering method. To compare the performance of various outputs of seed region technique Jaccard similarity coefficient is used to merge the similar regions in one segment.
The proposed algorithm is applied to challenging applications: gray matter/white matter segmentation in magnetic resonance image (MRI) datasets. The experimental results show that the proposed technique produces accurate and stable results.

General Terms
Image Processing.

Keywords
Fuzzy clustering, seed region growing, performance measure, MRI brain database.

1. INTRODUCTION

Medical imaging includes conventional projection radiography, computed topography (CT), magnetic resonance imaging (MRI) and ultrasound. MRI has several advantages over other imaging techniques enabling it to provide 3D data with high contrasts between soft tissues. However, the amount of data is far too much for manual analysis/interpretation, and this has been one of the biggest obstacles in the effective use of MRI.

The segmentation of region is an important first step for variety of image related applications and visualization tasks. Also, segmentation of medical images is important since it provides assistance for medical doctors to find out the diseases inside the body without the surgery procedure, to reduce the image reading time, to find the location of a lesion and to determine an estimate of the probability of a disease. Segmentation of brain MRIs into different tissue classes, especially gray matter (GM), and white matter (WM), is an important task. Brain MRIs have low contrast between some different tissues. The problem of MRIs is the low contrast between tissues.

Determination of gray matter (GM) volume in brain magnetic resonance images (MRI) has become an important measurement tool for multiple sclerosis (MS) patient monitoring and research. Previously, MS was considered primarily a white matter (WM) disease, with prominent focal regions of demyelination visible by macroscopic examination of the tissue and on MRI. Histological studies of MS brain tissue have shown that MS lesions are also located in the gray matter and that these GM lesions make up a substantial proportion of overall tissue damage due to MS [1,2]. While there are new MRI techniques that allow visualization of cortical lesions, such as fluid-attenuated inversion recovery [3], double inversion recovery [4], averaged high resolution T1-weighted images [5], and phase-sensitive inversion recovery on [6], GM pathology is difficult to measure in vivobecause most GM lesions are not visible on conventional MRI [7]. Measurement of GM volume loss provides an alternative, indirect measure of GM pathology. Previous studies have shown that GM atrophy is detectable at all stages of MS [8, 9, 10, 11] and is correlated with disability[12, 13]. These studies suggest that GM measurements are clinically relevant, provide important insights about disease progression, and may be useful in the evaluation of the efficacy of new therapies.
To measure cross-sectional differences and changes over time in GM volumes, accurate segmentation methods must be used. A variety of different approaches to brain tissue segmentation has been described in the literature. Few algorithms rely solely on image intensity, [14] because these approaches are overly sensitive to image artifacts such as radiofrequencyinhomogeneity, and aliasing, and cannot adequately account for overlapping intensity distributions across structures. Therefore, to improve segmentation accuracy, most tissue segmentation algorithms combine intensity information with other techniques, such as the use of a priori anatomic information [15, 16] or edge information through deformable contours[17,18, 19]. Intensity information is analyzed differently in each approach, including Gaussian mixture models [20, 21, 22, 23], discriminate analysis [24]), k-nearest neighbor classification [25], and fuzzy c-means clustering [26, 27, 28, 29, 30]. The use of multiple images has significant advantages over a single image because the different contrasts can be enhanced between tissues. For example, fluid attenuated inversion recovery (FLAIR) images have desirable contrast between MS lesions and the normal-appearing brain tissue and can be combined with other images to obtain gray/white matter segmentation [31].
In other hand, several algorithms have been proposed such as: C-means [24], fuzzy c-means (FCM) [25], and adaptive fuzzy c-means combined with neutrosophic set [28]. Segmentation is a very large problem; it requires several algorithmic techniques and different computational models, which can be

sequential or parallel using processor elements (PE), cellular automata or neural networks. There are a few widely available and commonly used brain tissue segmentation methods that use both intensity and a priori anatomic information. These algorithms, such as the segmentation tool in SPM on, [20] and FAST in FSL [32], have been designed for general use, and therefore, are not necessarily optimized for specific pulse sequences or for application to images from patients with a specific disease. For example, the use of such general programs to segment MR images of MS patients often results in misclassification of MS lesions as gray matter due to overlapping intensities, which then requires time-consuming manual editing and introduces operator variability into the measurements [33]. To overcome these methods [20, 24, 25, 27, 32, 33], some recent results of fuzzy algorithms for improving automatic MRI image segmentation have been presented in [27-29].

These methods are also prone to classification errors due to partial volume effects between MS lesions and normal tissue. Furthermore, for retrospective image analysis, where image data may not have been acquired using optimal sequences for use with one of the widely available segmentation tools, a customized segmentation method may be required to obtain the most accurate results.

In this paper, we present an approach based on combining fuzzy c-mean clustering, seed region growing, and Jaccard similarity coefficient [33] to determine GM and WM tissues in brain MRIs. This approach begins by partitioning the given image into several regions. The seed region growing method is applied to the image using the centers of these regions as initial seeds (if this center is not in image, a quite neighbor point to this center is selected as initial seed). Then the Jaccard similarity coefficient is used to perform a suitable merging which produces the final segmentation. The proposed method are evaluated and compared with the existing methods by applying them on simulated volumetric MRI datasets.

The rest of the paper is organized as follows. The MRI segmentation problem is discussed in section 2. The proposed method is described in section 3. In Section 4, the experimental results are presented. Our conclusion is presented in section 5.

2. THE MRI SEGMENTATION PROBLEM

The basic idea of image segmentation can be described as follows. Suppose that $X= \{x_1, x_2,..., x_n\}$ is a given set of data and P is a uniformity set of predicates. We aim to obtain a partition of the data into disjoint nonempty groups $X= \{v_1, v_2...v_k\}$ subject to the following conditions:

1. $\bigcup_{i=1}^{k} v_i = X$
2. $v_i \bigcap v_j = \phi$, i≠j
3. $P(v_i) = TRUE, i = 1,2,..,k$
4. $P(v_i \bigcup v_j) = FALSE, i = j$

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

Our study is related to 3D-model from MRI and simulated brain database of McGill University [48]. MRI has several advantages over other imaging techniques enabling it to provide 3-dimensional data with high contrast between soft tissues. However, the amount of data is far too much for manual analysis/interpretation, and this has been one of the biggest obstacles in the effective use of MRI. Segmentation of MR images into different tissue classes, especially gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF), is an important task.

MR image segmentation involves the separation of image pixels into regions comprising different tissue types. All MR images are affected by random noise. The noise comes from the stray current in the detector coil due to the fluctuating magnetic fields arising from random ionic currents in the body, or the thermal fluctuations in the detector coil itself, more discussion can be seen in [23]. When the level of noise is significant in an MR image, tissues that are similar in contrast could not be delineated effectively, causing error in tissue segmentation. Then more sophisticated techniques would be needed to reconstruct the 3D image from incomplete information [35-39], where a 3D image can be obtained from many consecutive 2D slices.

3. THE PROPOSED ALGORITHM DESCRIPTION

The objective of image segmentation is to divide an image into meaningful regions. Errors made at this stage would affect all higher level activities. In an ideally segmented image, each region should be homogeneous with respect to some criteria such as gray level, color or texture, and adjacent regions should have significantly different characteristics or feature. In MRI segmentation, accurate segmentation of white matter (WM) and gray matter (GM) is critically important in understanding structural changes associated with central nervous system diseases such as multiple sclerosis and Alzheimer's disease, and also the normal aging process [40]. Measures of change in WM and GM volume are suggested to be important indicators of atrophy or disease progression. In many situations, it is not easy to determine if a voxel should belong to WM or GM. This is because the features used to determine homogeneity may not have sharp transitions at region boundaries. To alleviate this situation, we propose an approach based on fuzzy set and seed region growing concepts into the segmentation process. If the memberships are taken into account while computing properties of regions, we obtain more accurate estimates of region properties. Our segmentation strategy will use the FCM for finding optimum seed as a pre-segmentation tool, seed region growing algorithm will operate on this seed to obtain close regions, and then refine the results using the performance measure. We use Jaccard similarity coefficient [33] as performance measure to compare the performance of various outputs of the seed region growing method. The proposed algorithm is described in Fig 1. The advantage of the proposed approach is that it combines the advantages of both methods: the FCM pre-segmentation is rough but quick, and the seed region growing needs only the initial seed point to produce the final, fast, highly accurate and smooth segmentation.

The proposed algorithm consists of three procedures as:

- FCM algorithm for finding optimum seed;
- Seed region growing to isolate suitable regions;
- Performance measure procedure for merging regions and extracting the final segmentation.

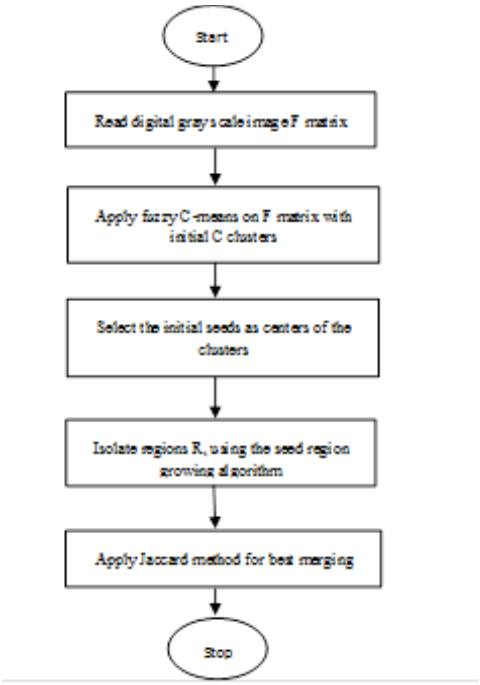


Fig 1: The steps of the proposed method.

3.1 The fuzzy c-means

Fuzzy c-means clustering (FCM) is a data clustering algorithm in which each data point belongs to a cluster to determine a degree specified by its membership grade [41-43]. Bezdek [41] proposed this algorithm as an alternative to earlier *k*-means clustering. FCM partitions a collection of N vector $x_i,\ i=1,\ldots,N$ into C fuzzy groups, and finds a cluster centre in each group such that an objective function of a dissimilarity measure is minimized. The major difference between FCM and *k*-means is that FCM employs fuzzy partitioning such that a given data point can belong to several groups with the degree of belongingness specified by membership grades between 0 and 1. In FCM, the membership matrix $U = [u_{ij}]$ is allowed to have not only 0 and 1 but also the elements with any values between 0 and 1. This matrix satisfies the constraints:

$$\sum_{i=1}^{C} u_{ij} = 1, \quad \forall j = 1,\ldots,N; \quad 0 \le u_{ij} \le 1,$$

$$\sum_{j=1}^{N} u_{ij} > 0, \quad \forall i; \qquad (1)$$

The objective function of FCM can be formulated as follows:

$$J_m = \sum_{i=1}^{C}\sum_{j=1}^{N} u_{ij}^{m} \left\| x_j - c_i \right\|^2$$

Where C is the number of clusters; c_i is the cluster centre of fufuzzy group i, and the parameter m is a weighting exponent on each fuzzy membership Fuzzy partitioning is carried out through an iterative optimization of the objective function shown above, updating of membership u_{ij} and the cluster centres c_i by:

$$c_i = \frac{\sum_{j=1}^{N} u_{ij}^{m} x_j}{\sum_{j=1}^{N} u_{ij}^{m}} \qquad (2)$$

$$u_{ij} = \frac{1}{\sum_{k=1}^{C} \left(\frac{\left\| x_j - c_i \right\|}{\left\| x_j - c_k \right\|} \right)^{2/(m-1)}} \qquad (3)$$

The FCM clustering algorithm is composed of the following steps:

Algorithm 1: FCM clustering

Step 1: **Fix** $c, t_{\max}, m > 1$ and $\varepsilon > 0$ for some positive constant.

Step 2: **Initialize** the memberships u_{ij}^{0}.

Step 3: **For** $t = 1,2,\ldots,t_{\max}$ **do**

(a) **Update** all prototype c_i^t with Eq. (2);

(b) **Update** all memberships u_{ij}^t with Eq. (3);

(c) **Compute** $E^t = \max_{i,j} \left| u_{ij}^t - u_{ij}^{t-1} \right|$, if $E^t \le \varepsilon$, stop;

End;

3.2 Seed region growing

These seeds positions (*pixel_x, pixel_y)* are grown by merging neighboring pixels whose properties are most similar to the premerged region. Typically, the homogeneity criterion is defined as the difference between the intensity of the candidate pixel and the average intensity of the premerged region. If the homogeneity criterion (threshold T) is satisfied, the candidate pixel (*p*) will be merged to the premerged region. The procedure is iterative: at each step, a pixel is merged according to the homogeneity criterion (under threshold T). This process is repeated until no more pixels are assigned to the region [43]. Since we only perform the seed growing on edge pixels, the amount of data needed to be processed is much reduced, resulting in increased speed.

Algorithm 2: seed region growing

Output X_{seed} of $m \times n$

Input X_i of $m \times n$

Label initial seed point (*pixel_x, pixel_y).*
Put neighbors of seed points (the initial T).
Seed region growing:
function X_{seed} = region growing(X_i , *pixel_x, pixel_y,*T, *m, n*)
While X_i is not empty **do**
Remove first pixel *p* from the X_i.
Test the neighbors of this point:
If all neighbors of *p* which are already labeled (other than boundary label)

have the same label **then**
Set *p* to this label.
Update running mean of corresponding region.
Add neighbors of which are neither already set nor already in the X_i to the X_{seed} according to their value
else
Flag *p* with the boundary label.
EndIf
End While
End;

3.3 Performance measures

To compare the performance of various outputs of seed region growing technique, several methods such as: Jaccard similarity coefficient [33], Dice similarity coefficient [44], Sensitivity and specificity [45] are used. In this section, we use Jaccard similarity coefficient method which almost gives
good stable results. We compute different coefficients reflecting how well two segmented regions match. According to the Jaccard similarity coefficient *JSC* is formulated as:

$$JSC = Card(R_1 \cap R_2) / Card(R_1 \cup R2) \quad (4)$$

Where R_1 is the automatically segmented region, R_2 is the correspondent region of the manually segmented image, and Card(*X*) denotes the number of voxels in the region *X*. A *JSC* of 1.0 represents perfect overlap, wheras an index of 0.0 represents no overlap. *JSC* values of 1.0 are desired. According to Zijdenbos' statement [47] *JSC*>0.70 indicates excellent agreement. In this case two regions can be merged into one segment.

Algorithm 3: Jaccard similarity
Input $R_l; l = 1,2,3,.....,C$
For i=1 to k
For j=2 to k
Compute $Card(R_l \cap R_k)$
Compute $Card(R_l \cup R_k)$
Compute *JSC*
If *JSC*<=0.70 then
$R_l = R_l \cup R_k)$
EndIf
End For
End For
End;

4. EXPERIMENTAL RESULTS

The experiments were performed with several data sets using MATLAB. We used a high-resolution T1-weighted MR phantom with slice thickness of 1mm, different noise and different intensity inhomogeneities, obtained from the classical simulated brain database of McGill University Brain Web[48]. The advantages of using digital phantoms rather than real image data for validating segmentation methods include prior knowledge of the true tissue types and control over image parameters such as modality, slice thickness, noise, and intensity inhomogeneities.

The quality of the segmentation algorithm is of vital importance to the segmentation process. The comparison score *S* for each algorithm can be found in Zanaty et al.[49- 51] , and defined as:

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

where*A* represents the set of pixels belonging to a class as found by a particular method and A_{ref} represents the reference cluster pixels.

4.1 Experiments on MRIs

The original image size is 129×129 pixels, as shown in Fig 2 obtained from the classical simulated brain. We apply our technique to segment generated at various noise levels (0%, 1%, 3%, 5%, 7%, and 9%) and spatial intensity non-uniformity (RF) levels (0%, 20%, and 40%). We generate various inhomogeneities and boundary weakness by controlling noise and RF respectively. t is set to be 20 for all following tests .

Table 1 shows the score *S* of WM using our technique at various noise and RF levels. These results show that our algorithm is very robust to noise and intensity; homogeneities and inhomogeneities.The best *S* is achieved for low noise and low RF, for which values of *S* are higher than 0.97.

Table 1. The score S of WM

Noise/RF	0	20%	40%
0%	0.98	0.97	0.95
1%	0.97	0.97	0.95
3%	0.95	0.96	0.94
5%	0.95	0.94	0.92
7%	0.93	0.92	0.90
9%	0.91	0.87	0.87

4.2 Comparative results

In this section, we compare the performance of our technique with two recent methods: Del-Fresno et al. [52] and Yu et al. [53] techniques which gave good results in brain segmentation. The segmentation results of these algorithms are presented in Figs 3a,3b,and 3c respectively. The performance of each segmentation method on this dataset is reported in Table 2.
Table 2 shows the S of WM using different techniques for the Brain data. In this Table, we compare between our method, Del-Fresno et al. [52] and Yu et al. [53] techniques. In particular, although the segmentation quality logically deteriorates in the presence of noise and variations in intensity, the robustness of the present technique is highly satisfactory compared with the results of other segmentation techniques [52, 53].

Table 2. The S for WM using the Brain Web [24].

Noise	**3%**		**9%**	
RF	0%	40%	0%	40%
Our method	0.95	0.94	0.91	0.87
Del-Fresno et al.[3]	0.94	0.89	0.91	0.87
Yu et al.[6]	0.90	0.90	0.88	0.88

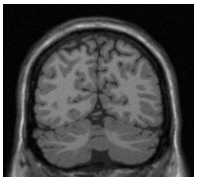
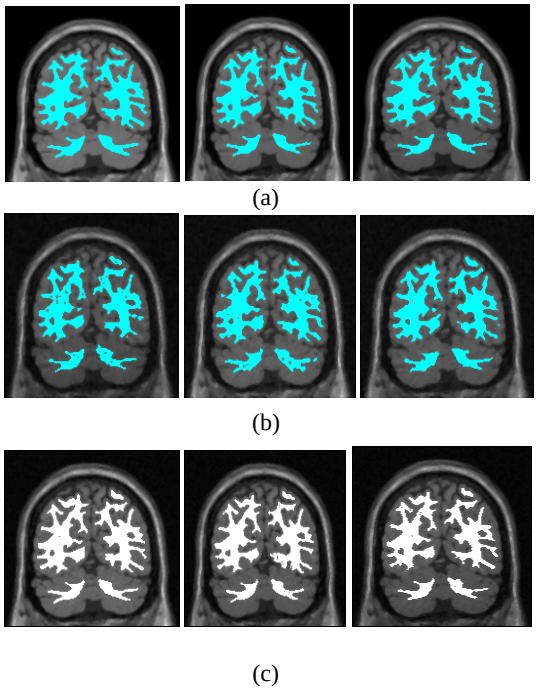


Fig 2: Test image is original slice#62.



(a)

(b)

(c)

Fig 3: Segmentation of WM at noise levels 1%, 5% and 9% respectively.(a) The proposed method, (b) Del-Fresno et al.[52], (c)Yu et al [53].

5. CONCLUSION

In this paper, we have presented an approach which integrates three existing methods: fuzzy clustering, seed region growing, and Jaccard similarity coefficient. The first two methods have a common advantage: they have no constraints or hypothesis on topology, which may change during convergence. The third method is used to determine the similar ones. An initial partitioning of the image into primitive regions has been performed by applying a fuzzy clustering on the image. This initial partition is the input to a computationally efficient seed region that produces the suitable segmentation. The Jaccard similarity coefficient is used to perform a suitable merging of regions which produces the final segmentation. It is observed that the proposed methods have shown higher robustness in discrimination of regions because of the low signal/noise ratio characterizing most of medical images data.

By comparing the proposed methods with Del-Fresno et al. [52] and Yu et al. [53] methods, it is clear that our algorithms can estimate the correct tissues WM and GM much more accurately than the established algorithms. Although, the accuracy of WM and GM clusters are varied according to noise factor, but we have shown that the proposed method gives good accuracy than Del-Fresno et al. [52] and Yu et al. [53] techniques with high noise level.

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

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