

Brain Tumor Segmentation Using Fuzzy Otsu Threshold Morphological Algorithm

Wisaeng K. and Sa-ngiamvibool W.

Abstract—This article presents a method of segmentation for brain tumor by Fuzzy Otsu Threshold Morphological (FOTM) algorithm. Due to increases in brain tumors, the numbers of acquired magnetic resonance imaging (MRI) increase accordingly. Therefore, highly accurate algorithms being able to automatically segment and detect brain tumors would have prospective potentials for treatment planning and diagnosis. In order to solve this problem, a novel method for segmentation of brain tumors is proposed by using FOTM algorithm from the most asymmetric parts. In addition, the use of color normalization, noise removal, and intensity bias correction as a preprocessing stage, which, though not common in FOTM algorithms, demonstrated together with data segmentation to be very successful for segmentation of brain tumor in MRI images. The results clearly show that the average accuracy indexes of image gliomas, image meningiomas and image pituitary are 93.77%, 94.32% and 94.37% respectively.

Index Terms—Braintumors, Segmentation, FuzzyOtsu Threshold, Morphological.

I. INTRODUCTION

Nowadays, Magnetic Resonance Imaging (MRI) is most widely used for diagnostics, proper treatment planning and patient follow-up of brain tumors. Therefore, highly accurate segmentation and detection algorithms of brain tumors are substantially important not only for diagnosis and proper treatment planning but also for follow-up and an evaluation. However, it is a challenging task since color, brightness, shape, size and location for each patient highly vary and appear to be extremely differentiated. Several methods such as Thresholding Image Segmentation (TIS), Region-Image Segmentation (RIS), classification (supervised method) and clustering (unsupervised method) have been proposed for segmentation and detection of brain tumors. Below are details of how these methods work to verify the attempts.

Firstly, TIS is the image segmentation algorithm based on a threshold value where an RGB color image is converted into

a8-bit binary image. But the main problem of TIS is that voxels are not considered. This method was presented by Gibbs et al. [1] where the TIS is based on local image properties. However, this method is successful in these cases but it cannot be segmented from the whole image in databases. Moreover, the TIS cannot be used as the first stage of the segmentation processes and requires user interaction.

Secondly, RIS is a traditional image segmentation method which mainly relies on and classified as neighboring pixels within one region that share similar values. The most well-known methods of RIS are Region Growing (RG) method and Watershed Transformation (WT) method. The RG method is the image segmentation algorithms with user interaction. Also, the segmentation of brain tumors in RGB color image by sing RG method was presented by Shin et al. [2]. Several studies have demonstrated that this RG method yielded high performance and spentless computational time for segmentation and detection of brain tumors than other algorithms. For example, in an algorithm presented by Weglinski et al. [3], the segmentation of brain tumors employed the RG method and manual seed point selection. Moreover, the RG method was also applied for the segmentation of brain tumors by Kaus et al. [4]. The adapted version of the RG method by Salman et al. [5] that this algorithm improves the accuracy of brain tumor detection in MRI. Another example is proposed by Rexilius et al. [6]. The authors applied a progressive RG method to seed and fine results of brain tumor regions. Kumar et al. [7] had presented the RG method for brain tumor segmentation tasks after using a dynamic clustering technique with the highest intensity. It was later shown in Zhang et al. [8] that this algorithm was also applied in the brain tumor detection task. Another method of RIS, which was proposed for brain tumor detection, is a WT method. The multi-scale WT algorithm was used for brain tumor detection by Letteber et al. [9]. However, this undesirable algorithm was a semi-automatic detection method and required user interaction to achieve high accuracy detection results. The other algorithm of the WT method presented by Mancas et al. [10] was also used by Cates et al. [11] for brain tumor detection. Their analysis detected failures in the brain tumor segmentation step where MRI images were of low quality. However, the major problem of the WT method is that it can result in an over-segmentation of the image. Therefore, Kong et al. [12] proposed the merging process of over-segmentation tumor by a Fuzzy C-means Clustering (FCM) method. Another improvement in WT results was proposed by Bleau et al. [13]. But, the proposed method was not satisfying.

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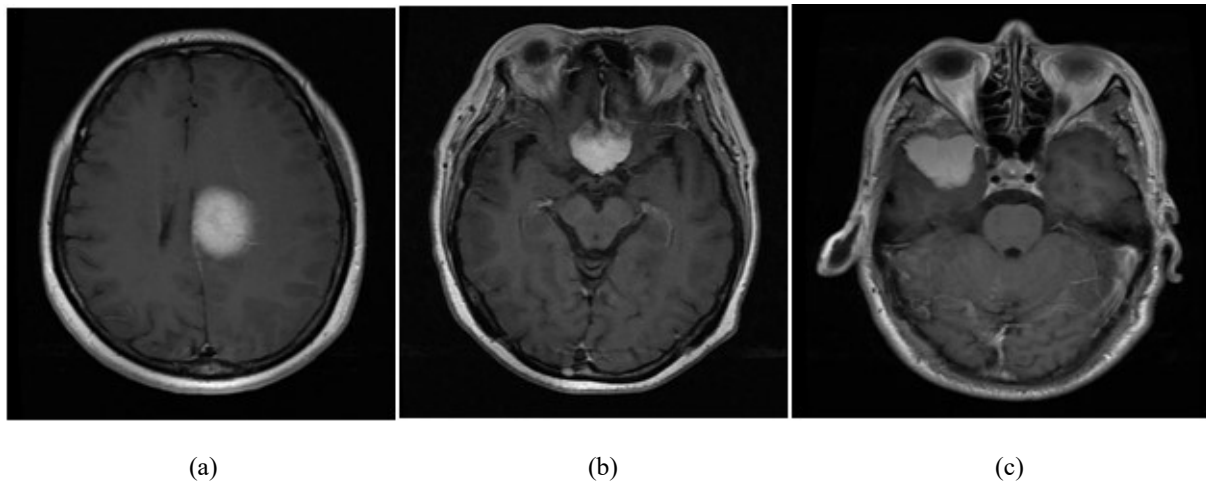


Figure 1. An example of three typical brain tumors: (a) Glioma; (b) Meningioma; and (c) Pituitary tumor.

Finally, several methods similar to FCM in achieving effective results were proposed by Singhai et al. [14]. These methods involve classification (or supervised method) and clustering (or unsupervised method). The classification method requires a dataset to train an algorithm where the dataset consists of training data for manual classification and for representation in feature pixels. While the clustering methods used to select a number of clusters from results without the specified number of clusters. For example, the K-Nearest Neighbors (K-NN) method was adopted for brain tumor detection by Vinitiski et al. [15]. This algorithm is highly sensitive to the noise and intensity in homogeneity of brain tumor lesions. Kaus et al. [16] used a K-NN for brain tumor classification. All pixels were classified into the non-tumors and tumors. Havaei et al. [17] also adopted this method in which a K-NN was combined with conditional random fields.

Another classification algorithm, applied for brain tumor detection, is Bayesian Classification (BC) method. Ain et al. [18] applied this BC method for tumors detection in MRI and Wang et al. [19] also attempted this method but further combined the BC method with a three-dimension fluid vector flow. In 1995, Cortes et al. [20] proposed Support Vector Machine (SVM) for training data and classification of tumors in MRI. The advancement of the applied SVM algorithm provided good separates of the feature space of brain tumors and background tasks. A similar algorithm was proposed by Zhang et al. [21], where SVM algorithm and Mathematical Morphology (MM) methods are applied for simple classification of brain tumors parts and error reduction purposes. Whilst several SVM algorithms have been presented, Garcia et al. [22] proposed an Adatron algorithm followed by an SVM algorithm for the classification of tumors in 2D images. Another combination method was proposed by Lee et al. [23], who used MRI images (i.e. T1, T2 and T1C-weighted) for classification of brain tumors by using a combination of SVM and Markov random field (MRF) method. At the same time, Later, Zhang et al. [24] proposed SVM by using maximum likelihood and distance measure for brain tumor segmentation.

Recently, Artificial Intelligence (AI) has been applied for brain tumors. For example, Artificial Neural Networks (ANNs) were widely applied for brain tumors detection task. One of the attempts to detect brain tumors in MRI images by using ANNs was proposed by Clarke [25]. Additionally, Reddick et al. [26] proposed a combining self-organizing map method and a multilayer back-propagation neural network to detect brain tumors in MRI images, especially T1, T2 and PD-weighted images. Moreover, Murugavalli et al. [27] presented a brain tumor classification algorithm based on Hierarchical Self-Organizing Map (HSOM), which is applied for coarse segmentation and fine segmentation by using the FCM method. On the other hand, Havaei et al. [28] proposed the Convolution Neural Networks (CNNs) in the first stage and then used the Dropout algorithm to over-fitting the brain tumor regions in the second step. Collectively, the common characteristics of all the above-described brain tumor classification algorithms is the independent segmentation of single pixels in which pre-processing methods are usually required.

Another brain tumor classification algorithm is based on clustering. The clustering methods involve FCM, k-means clustering, hierarchical clustering, and Gaussian method. For instance, Phillips et al. [29] applied algorithm based on FCM for classification in T1, T2 and PD-weighted images. Additionally, the better brain tumor segmentation results were achieved by Clark et al. [30] who proposed a method combining FCM and standard MRI sequences. Similarly, Zhao et al. [31] presented a clustering algorithm by using Gaussian Mixture Models (GMMs) followed by an active contour method for error boundaries segmentation.

Since the existing detection algorithms for brain tumors are undesirable to rely on different MRI images [32-34], this paper presents a novel method for brain tumor segmentation and detection in MRI images. This proposed method has to be able to classify brain tumor regions without user interaction. This paper is organized as follows. Section 2 describes the materials and preprocessing of the proposed method. This section also includes a brief description of the pre-processing

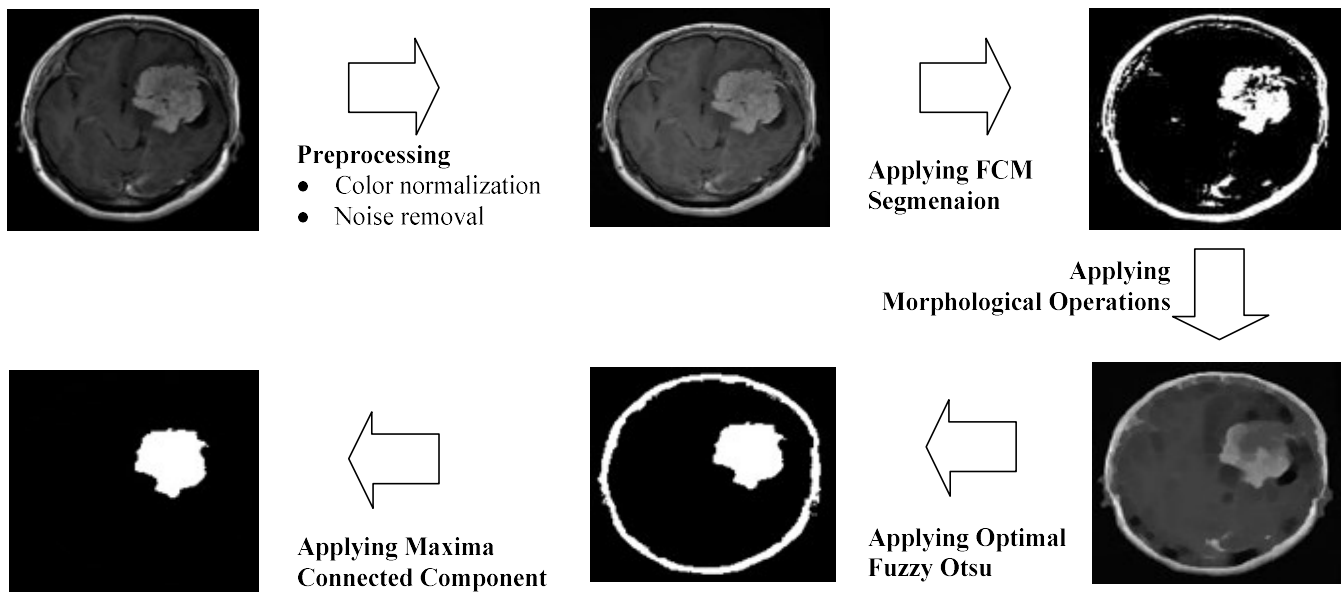


Figure 2. The proposed method for classification of a brain tumor on CE-MRI dataset

of MRI images. Section 3 illustrates the manual segmentation, feature extraction, coarse segmentation, and classification. Sections 4, presents the experimental results of the proposed methods and comparison with other methods. Lastly, Section 5 provides a conclusion of the study and future inquiry.

II. MATERIALS AND PREPROCESSING METHODS

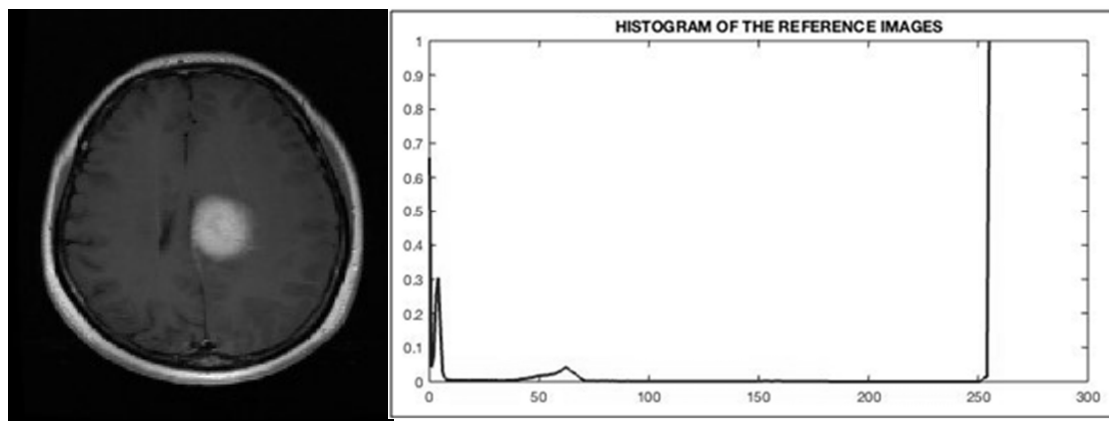
Typically, fully automatic classification and detection of brain tumor applications have been developed by using a publicly CE-MRI available database with a large slice gap. (https://figshare.com/articles/brain_tumor_dataset/1512427). Therefore, the proposed method is based on practical 2D slices MRI images for the clinical systems. The database of the brain T1-weighted CE-MRI database was acquired from Nanfang Hospital, Guangzhou, China, and General Hospital, Tianjin Medical University, China, from 2005 to 2010. The databases contain three types of brain tumors (i.e., 1,426 gliomas, 708 meningiomas and 930 pituitary tumors as illustrated in Fig. 1) from 233 patients with a total of 3,064 slices across the 994 axial images, 1,045 coronal images, and 1,025 sagittal images.

The images have an original resolution of 512×512 in pixels, and the pixel size is 0.49×0.49 mm². The acquired MRI images were resized to 300×300 pixels in JPG format. The overall of the presented algorithm used in this study is illustrated in Fig. 2.

Another challenge to the proposed method resulted from the inconsistencies of the MRI images collected across MRI scanners from myriads of patients at various time feature a wide variety of shapes, sizes, colors, and intensities. The pre-processing stage of MRI image before commencing the classification of brain tumor is, foremost, prerequisite. Referring to the provided image database, one main problem

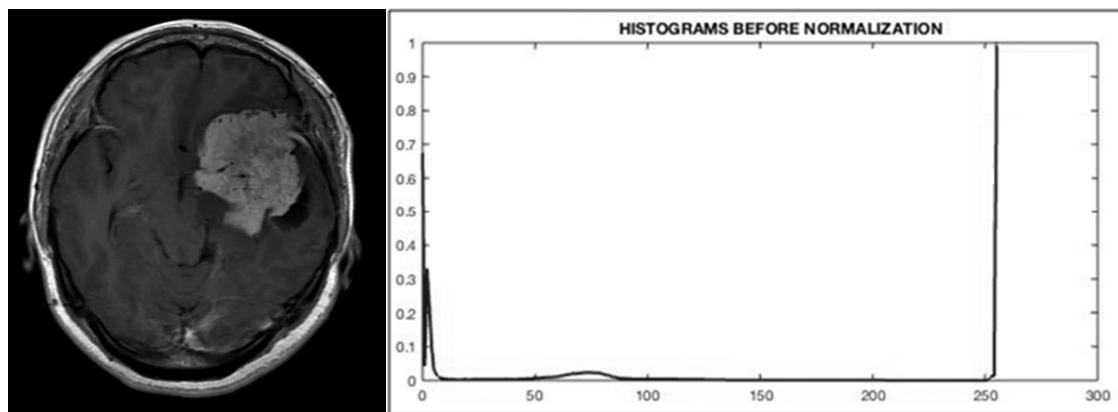
for segmenting brain tumor is that the observed intensity values across MRI images vary greatly, so a normalization preprocessing step is also used in the first step. Here, three experts selected a high-quality image as the reference image. Then a color normalization preprocessing method was also applied by histogram specification (Chen et al. 2019) to modify the values of each image histogram in original MRI image to match the frequency histogram of the reference images and correct field bias so as to bring the optimal value and variance close to 0 and 255 respectively. In this normalization preprocessing includes conversion of the input MRI to grayscale from RGB. Therefore the MRI images are proper grayscale images. The normalization results in MRI images and its histogram are illustrated in Fig. 3.

As evidenced, the color normalization process improves the intensity values and removes the variability in the color on MRI images. While the color normalization stage improves the contrast of MRI images, it also enhances noise or artifacts. These intensities can wrongly be segmented as brain tumor pixels. Normally, the noise in the MRI images is due to the salt and pepper noise. Hence, to remove noise and structures that are not the regions of interest, the median filtering method is one of the pre-processing steps that was adopted for two aims: firstly, for effectively removing noise and preserving edges in the MRI images and secondly, to derive image to be applied in subsequent segmentation for contrast enhancement of MRI images. In this stage, median filtering by using a 3×3 sampling window is applied.



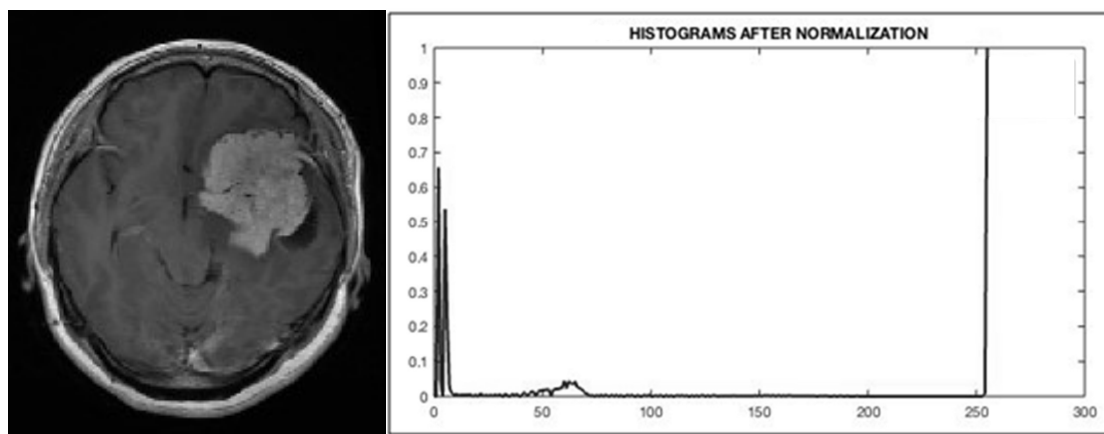
(a)

(b)



(c)

(d)



(e)

(f)

Figure 3. The normalization based on histogram matching: (a) Reference image; (b) Reference image histogram of (a); (c) Original image; (d) Original image histogram of (c); (e) Normalized image; (f) Normalized image histogram of (e).

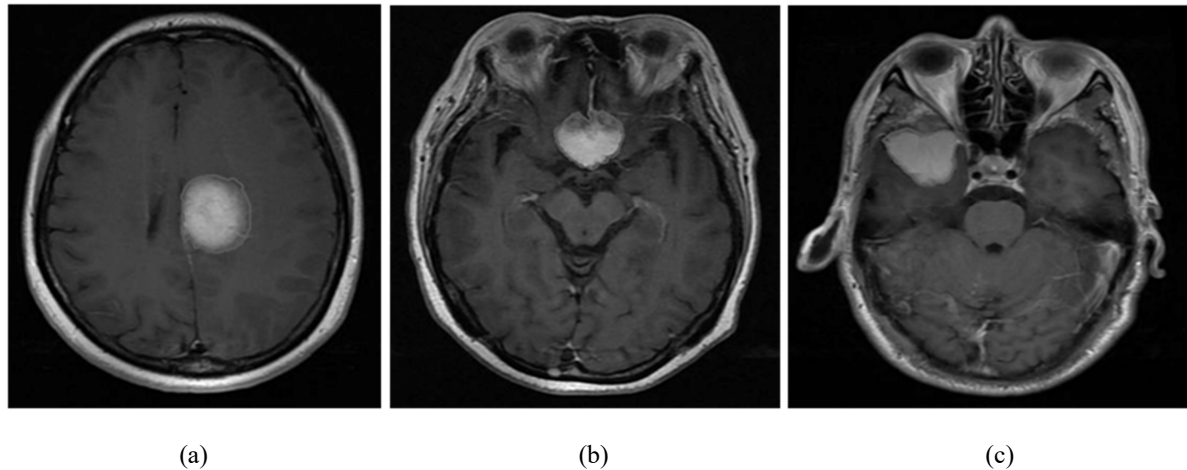


Figure 4. Manual segmentation of three typical brain tumors: (a) Glioma; (b) Meningioma; and (c) Pituitary tumor.

III. THE SEGMENTATION

The segmentation is a process of dimensionality reduction of raw data and defined as locating brain tumor pixels in MRI image [35,36]. In the process of segmentation in image processing, there are also a variety of algorithms proposed. The proposed technique divided those algorithms into three major processes. One process is the manual segmentation method. Another process is the coarse segmentation method. This method locates the brain tumor area while preserving the edges features. This process is typically an iterative algorithm that involves several parameters. The last one is a classification method based on mathematical morphology and optimal Otsu's thresholding, aiming to segment and classify brain tumor regions in MRI images. The following are the processes of the proposed algorithm.

A. Manual Segmentations

Manual segmentations of brain tumors from MRI images are a challenging and time-consuming task. Also, the manual segmentation of the tumor sub-regions is done by three experts. Three examples are showed in Fig.4.

B. Coarse Segmentations

The FCM algorithm has been a very important tool for image segmentation in clustering ROI in an image [Shamsi et al. 2012]. Let the data set of FCM features to be clustered as X . The set of $X = \{x_1, x_2, \dots, x_N\}$, $x_i \in R^f$, where the parameter of N is the number of FCM features and f denotes the dimension of features vector. The formulation of the FCM method optimization is defined by using Eq. [1].

$$\text{Minimize } J_m(U, W) \equiv \sum_{j=1}^C \sum_{i=1}^N (u_{ij})^m d_{ij}^2 \quad (1)$$

where U and W are the variables whole optimal values are being sought, N denotes the total number of data items in X , C is the number of clusters assumed to exist in X with $2 \leq c \leq n$, u_{ij} is the degree value of the membership function of feature vector of the i^{th} feature belonging to the j^{th} cluster, d_{ij} describes the distance measure between feature vector from X_i and cluster center W_j . The formulation of the FCM method focuses on minimizing J_m subject to the following constraint on U is defined as Eq. (2).

$$u_{ij} \in [0, 1], i = 1, \dots, N, \text{ and } j = 1, \dots, C \quad (2)$$

$$\sum_{j=1}^C u_{ij} = 1, i = 1, \dots, N \quad (3)$$

$$0 < \sum_{i=1}^N u_{ij} < N, j = 1, \dots, C \quad (4)$$

From the results of Eq. (1), we reduce preliminarily as long as the separation between clusters is height. The FCM method starts with a set of initial cluster centers. Then it iterates the two updating Eq. (5) and (6) at the i^{th} iteration until the cluster centers are stable in Eq. (1) converges to a local minimum.

$$\mu_{ij}^{(i)} = \frac{1}{\sum_{l=1}^C \left(\frac{d_{ij}}{d_{il}} \right)^{\frac{2}{m-1}}}, i = 1, \dots, N, j, l = 1, \dots, C \quad (5)$$

$$W_j^{(i)} = \frac{\sum_{i=1}^N (\mu_{ij}^{(i-1)})^m x_i}{\sum_{i=1}^N (\mu_{ij}^{(i-1)})^m}, j = 1, \dots, C \quad (6)$$

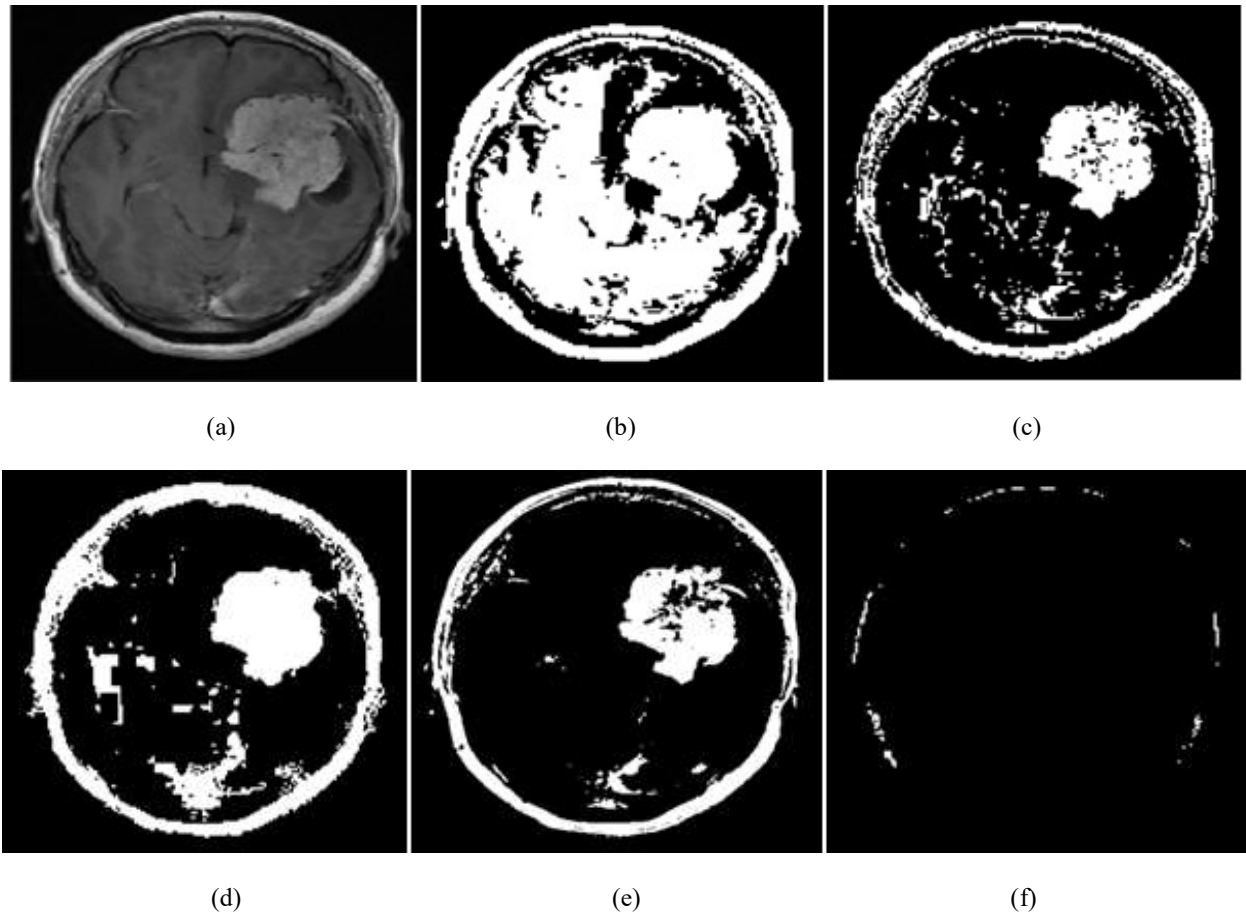


Figure 5. Segmentation of brain tumor by FCM algorithm: (a) Pre-processed image; (b) Results of brain with a number of cluster = 2; (c) Cluster = 4; (d) Cluster = 6; (e) Cluster = 8; (f) Cluster = 12.

The complete method consists of the following:

Step 1: Set values for $c=2$ (number of clusters is chosen by testing algorithm, $m=2$ (fuzzification parameter $m=2$ in all examples); initialize the fuzzy membership matrix.

Step 2: Compute the c fuzzy partition matrix $U^{(0)}$ by using Eq. (5) and (7).

$$\text{If } d_{ij} = 0 \text{ then } \mu_{ij} = 1 \text{ and } \mu_{ij} = 0 \text{ for } i \neq j \text{ (7)}$$

Step 3: Increase t by one. Re-compute the new cluster center matrix $W^{(t)}$ by using (6).

Step 4: Update the new membership matrix $U^{(t)}$ by using Eq. (5) and (7).

Step 5: If $\|U^{(t)} - U^{(t-1)}\| < \epsilon$, stop; (If termination condition not achieved), otherwise go to step 3.

The result from the FCM method is a list of cluster centered and m membership-grades for each pixel, where m is the number of desired clusters. To determine the suitable value of m , we tried values ranging from 2 to 12. In our experiment, the estimated time taken for running the whole process for

each MRI image with number of cluster = 2, 4, 6, 8 and 12. With number of cluster equal 8, the SE, SP and AC are 80.12% and 79.40% and 79.24%, respectively. The results of images using $m = 2$ through cluster = 8 are illustrated in Figure 5.

IV. THE CLASSIFICATION

The results of FCM method are assigned to classification by using optimal Otsu thresholding method [37]. Otsu method is very popular thresholding method based on the principle that involves the gray-level for which the between-class variance or within class variance. For the MRI image, let the pixels of a given picture be represented in L gray levels $[0,1,2,\dots,L-1]$. At each gray level, the number of pixels at level i is denoted by n_i and the total number of pixels by $N = n_0 + n_1 + \dots + n_{L-1}$. In order to simplify the discussions, the gray level histogram is normalized and regarded as a probability distribution by Eq. (8).

$$p_i = \frac{n_i}{N}, p_i \geq 0, \sum_{i=0}^{L-1} p_i = 1 \tag{8}$$

Now suppose that the foreground class C_0 (C_0 is the pixels with levels $[0, \dots, t]$) corresponds to the background region in the MRI image, and the object region belong to the background class C_1 (C_1 denotes the pixels with levels $[t+1, \dots, L-1]$). Then the probabilities of class C_0 and C_1 are given by Eq. (9) and (10), respectively.

$$\omega_0 = P(C_0) = \sum_{i=0}^s \sum_{j=0}^t p_{ij} = \omega_0(s, t) \quad (9)$$

$$\omega_1 = P(C_1) = \sum_{i=s+1}^{L-1} \sum_{j=t+1}^{L-1} p_{ij} = \omega_1(s, t) \quad (10)$$

Correspondingly, the non-brain tumor (background) mean and brain tumor (object) mean of gray level value of pixels are given by Eq. (11) and (12).

$$\mu_0 = (\mu_{0i}, \mu_{0j})^T = \left(\sum_{i=0}^s \sum_{j=0}^t \frac{ip_{ij}}{\omega_0}, \sum_{i=0}^s \sum_{j=0}^t \frac{jp_{ij}}{\omega_0} \right)^T \quad (11)$$

$$\mu_1 = (\mu_{1i}, \mu_{1j})^T = \left(\sum_{i=s+1}^{L-1} \sum_{j=t+1}^{L-1} \frac{ip_{ij}}{\omega_1}, \sum_{i=s+1}^{L-1} \sum_{j=t+1}^{L-1} \frac{jp_{ij}}{\omega_1} \right)^T \quad (12)$$

The whole gray level image and the total mean vector of the histogram is calculated by using Eq. (13).

$$\mu_T = (\mu_{Ti}, \mu_{Tj})^T = \left(\sum_{i=0}^{L-1} \sum_{j=0}^{L-1} ip_{ij}, \sum_{i=0}^{L-1} \sum_{j=0}^{L-1} jp_{ij} \right)^T \quad (13)$$

The non-brain tumor variance and brain tumor variance of gray level value of pixels is calculated by using Eq. (14) and (15), respectively.

$$\sigma_0^2 = \sum_{i=0}^t (i - \mu_0)^2 P(i|C_0) = \sum_{i=0}^t (i - \mu_0)^2 p_i / \omega_0 \quad (14)$$

$$\sigma_1^2 = \sum_{i=t+1}^{L-1} (i - \mu_1)^2 P(i|C_1) = \sum_{i=t+1}^{L-1} (i - \mu_1)^2 p_i / \omega_0 \quad (15)$$

Since the variance σ_ω^2 is the weighted sum of group. The optimal threshold value t^* is the threshold value with minimum the within class variance σ_ω^2 by using Eq. (16).

$$\sigma_\omega^2 = \omega_0(t) * \sigma_0^2(t) + \omega_1(t) * \sigma_1^2(t) \quad (16)$$

where $\omega_0(t) = \sum_{i=1}^t P(i)$, $\omega_1(t) = \sum_{i=t+1}^L P(i)$,
 $\mu_0(t) = \sum_{i=1}^t i * P(i) / \omega_0(t)$, $\mu_1(t) = \sum_{i=t+1}^L i * P(i) / \omega_1(t)$,
 $\sigma_0^2(t) = \sum_{i=1}^t (i - \mu_0(t))^2 * P(i) / \omega_0(t)$, and
 $\sigma_1^2(t) = \sum_{i=t+1}^L (i - \mu_1(t))^2 * P(i) / \omega_1(t)$,

The between-class variance is calculated using Eq. (17).

$$\sigma_B^2(t) = \sigma^2 - \sigma_\omega^2(t) \quad (17)$$

where σ^2 is the total variance and μ the total mean of the MRI image, respectively. Considering Fig. 6(a), the input image is segmenting by using FCM algorithm, as showed in Fig. 6(b). Of the two features, namely, background and brain tumor region) are presents in Fig. 6(b), only one of the brain tumor pixels can be seen in its entirety and will segment this pixel. The brain tumor pixels to be detected differ greatly in contrast to the non-brain tumor image. However, the main problem of incorrect segmentation of brain tumor was caused by losing too much of brain tumor pixels from binary image classification process. In this case, the proposed method may segment the wrong brain tumor regions. Therefore, a morphological image processing method based on dilation is used to the resulting mask to separate pixels connected by thin area. Let A and B be the two images as sets in Z^2 , the dilation of A by B, denoted as $A \oplus B$, is represented by using the following Eq. (18).

$$A \oplus B = \left\{ z \left| \left(\hat{B} \right)_z \cap A \neq \emptyset \right. \right\} \quad (18)$$

This equation is based on \hat{B} about its origin and translating the reflection by z. The dilation of A by B then is the set of all displacements. Based on this interpretation, Eq. (18) can be written equivalently as Eq. (19).

$$A \oplus B = \left\{ z \left| \left[\left(\hat{B} \right)_z \cap A \right] \subseteq A \right. \right\} \quad (19)$$

One of the simplest systems of dilation is for bridging gaps. Fig. 6(b) shows the brain tumor with broken regions. Fig. 6(c) illustrated the result of dilating the input image with a structuring element of 6 is used for repairing the gaps. In this step, the optimal Otsu's method value of 0.58 is used resulting in Fig. 6(c), and new binary image is obtained, as showed in Fig. 6(d). The gaps were bridged, is that the morphological image processing method resulted directly in a binary image. However, this method fails in an extremes case for example in Fig. 6(d), when the edge of the image is a large bright structure. First, an area of brain tumor by the values of V, is used to the obtained maxima connected components and remove false positive values. The function is calculated by Eq. (20).

$$V = \frac{4\pi(A)}{(P)^2} \quad (20)$$

where A is the number of regions in the brain tumor pixels and P is the total number of regions around the boundary of tumor region. All connected components with a pixel smaller than 2800 pixel are removed (Fig. 6(e)). Meanwhile, candidates within the region of brain tumor are removed and superimposed in original image is shown in Fig. 6(f). This is a

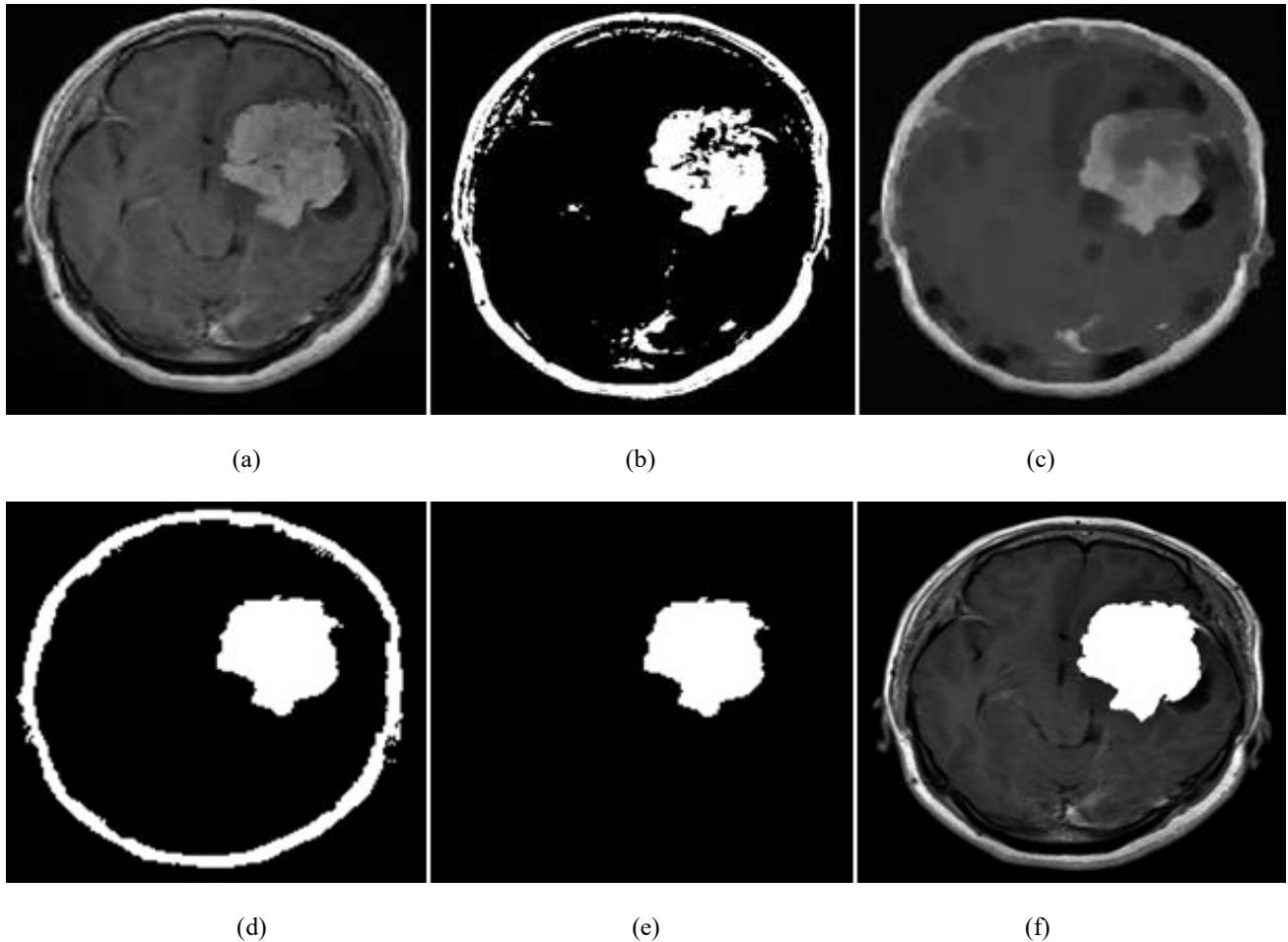


Figure 6. Segmentation of brain tumor: (a) Brain tumor in pre-processed image; (b) Results of brain tumor segmentation by FCM algorithm with the number of cluster = 8; (c) Result of reconstruction by using morphological method; (d) Binaty image by an optimal Otsu method with $t = 0.58$; (e) Final candidates by removing small regions and candidates inside brain tumor; (f) Superimposed on the original image.

big improvement. Strengths of the proposed algorithm include its simple classification method based on optimal Otsu thresholding method, robustness with respect to different tumors type and its efficiency of computation time.

V. THE EXPERIMENTS AND RESULTS

In this section, the experimental dataset, algorithm evaluation and performance on the proposed methods were proposed. Also the comparisons of the proposed method to the other algorithm, quantitative and experimental results obtained from the application of brain tumor segmentation and classification were proposed.

A. Experimental Dataset

Brain tumor images are preferred to be used in this study, due to poor quality image compared to MRI. The MRI image data set has been chosen from Nanfang Hospital, Guaungzhou, China, and General Hospital, Tianjing Medical University, China. The data set used for the evaluation of the proposed method contains 1,426 gliomas, 708 meningiomas, and 930 pituitary tumors. The original size of the images was 512×512 and then it resized to 300×300 pixels in JPG format to get

better quality. The data set is created by the proposed application. This data set is enough since the created application is an MRI image analysis.

B. Algorithm Evaluation

Brain tumor segmentation methods are usually evaluated by the sensitivity (SN), specificity (SE), and accuracy (ACC), is defined as Eq. (21), (22), and (23), respectively. Sensitivity also used an evaluation the classification application. It can represent as the percentage of true positives which are correctly classified pixels.

$$\text{Sensitivity} = \frac{TP}{TP + FN} * 100 \quad (21)$$

where TP “True Positive” represents the MRI images that were classified and that they have brain tumor pixels and FN “False Negative” is the MRI image that were classified, and they have no tumor. Specificity is the parameter was used for application evaluation in the scope of all positive detection. It can be defined as Eq. (22).

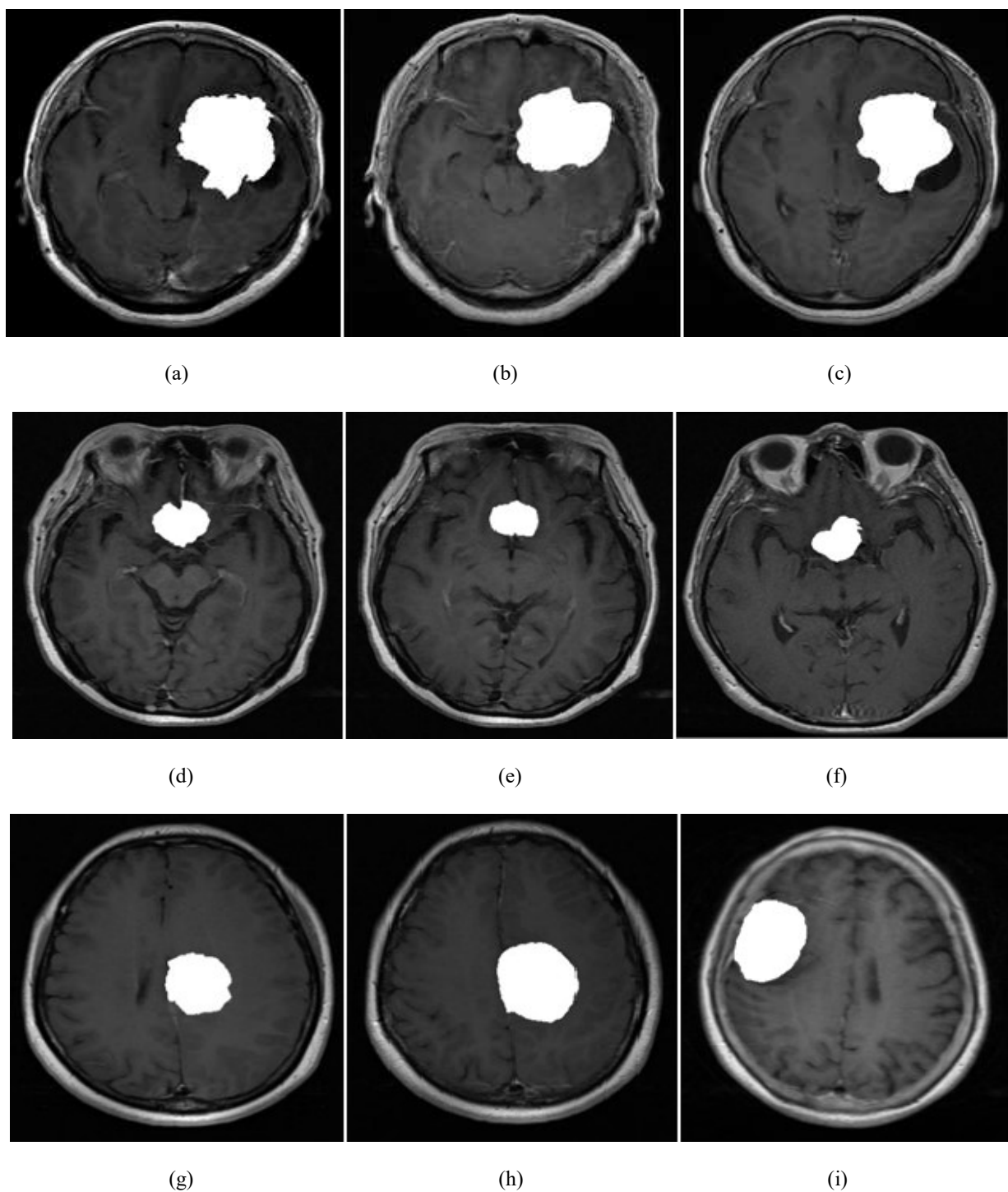


Figure 7. Visual results of classification with three categories of brain tumors: (a)-(c)classification results for the image glioma; (d)-(f) Results of brain tumor classificationwiththe image pituitary; (g)-(i) Classification results for the iage meningioma.

TABLE I
RESULTS ON PITUITARY BRAIN TUMOR CLASSIFICATION BY THE PROPOSED METHOD.

Algorithms	Sensitivity (%)	Specificity (%)	Accuracy (%)
Fuzzy C-mean+Otsu method	75.45	78.12	77.20
Fuzzy C-mean+Morphological+Otsu method	94.50	94.28	94.37

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}} * 100 \tag{22}$$

where TN represent for “True Negative” are the MRI images that have no brain tumor pixels and they were classified correctly, and FP represents for “False Positive” are the images that were not classified and they have brain tumor pixels. Accuracy is the total percentage of correctly classified brain tumor. It can be defined as Eq. (23).

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{FP} + \text{TN} + \text{FN}} * 100 \tag{23}$$

C. Performance on the Proposed Methods

In order to verify the effectiveness of the presented methods used, the fuzzy Otsu threshold morphological algorithms were compared experimentally. Whilst the algorithm performance of the quality score can be calculated by three evaluation criteria: SE, SP, and ACC ranging from 0 to 100, the performance of fuzzy C-mean clustering (FCM) and FOTM, is compared. Each of the image preprocessing methods was used to conduct a comparison of the proposed method. The comparison results of FCM and FOTM are illustrated in Table 1.

Table 2 shows the application performance and we can come to several conclusions. Above all, for FCM and FOTM, the proposed a new image processing method (FOTM) achieved is 94.37% as the average accuracy after testing and better performance than FCM method. The performance is a good balance between SE and SP values in both cases. Additionally, the proposed FOTM has an advance over FCM as it gives flexibility for a case of small region segmentation, which makes them encouraging. Therefore, we choose the brain tumor segmentation system through FCM by the use of optimal Otus’s threshold method and image mathematical method which promotes the increase of the accurate result. This, in turn, allows us to begin a quantitative comparison between pixel-based brain tumor segmentation with merely FCM for segmenting brain tumors and such classification with FOTM algorithms. The classification of tumors along with three typical brain tumors and the different classification performance criteria is shown in Table 2–4. The accuracy values show that on average 94.37% of tumor classification. The average computing time per image is 14 seconds, where 80% of the times are consumed by the brain tumor segmentation and classification. Therefore, the experimental results show that the proposed method in this application was suitable and efficient enough to classify the brain tumor images. To show experimental results, three classification examples for the three types of brain tumors are illustrated in Fig. 7

D. Results Comparison with Other Algorithms

Many studies have been developed for the purpose of brain tumor segmentation and classification. Therefore, we compare the result with seven brain tumor classification algorithms, already presented in this study, namely, D. Kumar and A. Halder [6], M. Letteboer, et al. [9], M. Mancas

and B. Gosselin [10], Ain et al., [18], J. G. Zhang, et al., [21], W. Reddick, et al., [26], and X. Chen, et al., [32]. To compare the proposed algorithms with the other algorithm for brain tumor segmentation, the results of all algorithms are summarized in Table 5. Compared with them, the proposed algorithms were unable to reach the top brain tumor classification results with 94.37%, but it still reached comparative results with other algorithms described in this study. For example, X. Chen, et al., [32] showed good accuracy values in classifying the brain tumor with accuracy of 94.13%, while M. Letteboer, et al. [9] showed a performance in classifying the brain tumor with average accuracy of 93.50%. On the other hand, the proposed application by using histogram model adaptation [6], show a performance in detecting the brain tumor with lower accuracy of 73.00%. The unsuccessful classification of brain tumor in MRI image shows the failure of the algorithm in case of a small amount of tumor regions.

TABLE II
RESULTS ON GLIOMAS CLASSIFICATION BY THE PROPOSED METHOD.
(N = 1,456)

Image gliomas	Sensitivity (%)	Specificity (%)	Accuracy (%)
Tumor 1	93.19	92.08	92.74
Tumor 2	94.92	94.56	94.18
Tumor 3	92.23	92.40	92.36
Tumor 4	91.78	92.03	92.02
Tumor 5	93.46	93.12	93.24
Tumor 6	94.13	94.24	94.10
Tumor 7	94.44	94.38	94.29
Tumor 8	94.26	94.18	94.10
.	.	.	.
.	.	.	.
Tumor 1,425	93.19	93.23	93.20
Tumor 1,426	94.40	94.12	94.36
Average	93.92	93.86	93.77

TABLE III
RESULTS ON MENINGIOMAS CLASSIFICATION BY THE PROPOSED METHOD.
(N = 708)

Image gliomas	Sensitivity (%)	Specificity (%)	Accuracy (%)
Tumor 1	94.88	94.76	94.72
Tumor 2	94.19	94.27	94.22
Tumor 3	93.89	93.76	93.72
Tumor 4	94.79	94.10	94.52
Tumor 5	93.93	94.11	94.08
Tumor 6	94.22	93.86	94.10
Tumor 7	93.96	93.72	93.80
Tumor 8	94.25	94.22	94.24
.	.	.	.
.	.	.	.
Tumor 707	94.10	94.38	94.25
Tumor 708	93.89	93.91	93.90
Average	94.26	94.37	94.32

TABLE V
RESULTS ON BRAIN TUMOR CLASSIFICATION BY THE PROPOSED METHOD WITH OTHER METHODS

Authors	Paper title	Methods	Accuracy (%)
D. Kumar and A. Halder [6]	Multispectral brain tumor segmentation based on histogram model adaptation	Histogram model adaptation	73.00
M. Letteboer, et al. [9]	Segmentation of tumors in magnetic resonance brain images using an interactive multiscale watershed algorithm	An interactive multiscale watershed algorithm	93.50
M. Mancas and B. Gosselin [10]	Toward an automatic tumor segmentation using iterative watersheds	Iterative watersheds segmentation	95.00
Ain et al., [18]	Bayesian classification using DCT features for brain tumor detection	Naïve bayes classification, K-means clustering and boundary detection techniques.	99.00
J. G. Zhang, et al., [21]	Tumor segmentation from magnetic resonance imaging by learning via one-class support vector machine	One-class support vector machine	87.00
W. Reddick, et al., [26]	Automated segmentation and classification of multispectral magnetic resonance images of brain using artificial neural networks	Artificial neural networks	87.00
X. Chen, et al., [32]	Automatic histogram specification for Glioma grading using multicenter data	Histogram specification	94.13
Proposed Method	Brain Tumor Segmentation Using Fuzzy Otsu Threshold Morphological Algorithm	Fuzzy C-mean clustering, Otsu method and Morphological Algorithm	94.37

TABLE IV
RESULTS ON PITUITARY CLASSIFICATION BY THE PROPOSED METHOD
(N = 930)

Image gliomas	Sensitivity (%)	Specificity (%)	Accuracy (%)
Tumor 1	93.97	93.89	93.92
Tumor 2	94.47	94.39	94.42
Tumor 3	94.29	94.30	94.29
Tumor 4	93.88	93.98	93.89
Tumor 5	94.45	94.35	94.40
Tumor 6	94.77	94.89	94.80
Tumor 7	93.90	93.49	93.58
Tumor 8	94.19	94.50	94.38
.	.	.	.
.	.	.	.
.	.	.	.
Tumor 929	93.88	93.50	93.76
Tumor 930	94.77	94.80	94.68
Average	94.50	94.28	94.37

VI. CONCLUSIONS

In this article, a segmentation and classification algorithm for the problem of brain tumors is presented. The MRI images also provide a fundamental feature for detecting brain tumor disease. The process of segmenting brain tumor aims only to correctly segment the intensity of the brain tumor pixels. For example, brain tumor segmentation is generally performed based on histogram model adaptation, an interactive multi scale watershed algorithm, watersheds segmentation, Naïve Bayes classification, K-means clustering, ANNs, and SVM. In this study, two chosen methods for brain tumor segmentation, namely FCM and FOTM, were used to compare the algorithm performance of the brain tumor classification with a publicly

available data set. Among all methods, FOTM achieved an overall generalization and SE of 94.50%, SP of 94.28%, and ACC of 94.37%. On the other hand, the brain tumor classification developed by the only method, namely, FCM, showed an overall accuracy of 75.45% with 78.12% SE and 77.20% SP. There has been a big improvement. Strengths of the proposed algorithm include its simple classification method, robustness with respect to different tumors type and its efficiency of computation time. For future inquiry, classifying the brain tumor by using machine learning algorithms such as k-Nearest Neighbors, Decision Trees, and SVM should be further investigated.

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