Tumor Extraction from MRI images using Dynamic Genetic Algorithm based Image Segmentation and Morphological Operation

Amiya Halder, Anuva Pradhan, Sourjya Kumar Dutta and Pritam Bhattacharya

***Abstract*---Tumor is swelling of the body part, generally without any inflammation that happens due to abnormal growth of cells in that place of the body. Brain tumor is difficult to diagnose at initial stage. The tumor is diagnosed by magnetic resonance imaging (MRI) and depending on it, the tumors are distinguished into different grades of severity. This paper presents a new method to detect and extract tumor from the whole images. This paper proposes a scheme for extracting tumor from MRI based on GA (Genetic Algorithm) based FCM (Fuzzy C-means) clustering and morphological operation. Computer simulations of our algorithm present a considerable improvement over other existing techniques.**

***Index Terms*--- FCM, Genetic Algorithm, Image Segmentation, Morphological operation.**

I. INTRODUCTION

Most of the tumor is two types namely benign and malignant. Malignant tumor is referred to as cancer. Abnormal growth of cell inside brain is called brain tumor. There are two general groups of brain tumor. Primary brain tumor starts in brain and tends to stay there. Secondary brain tumor starts somewhere else in the body but travels to brain. Secondary tumors are more common than primary tumors. The reason for brain tumor is unknown till now. It is considered that probable reasons of brain tumor can be a number of conditions like neurofibromatosis, exposure to chemical vinyl chloride, Epstein-Barr virus and ionizing radiation. The use of mobile phones is also considered as one of the risk factors but there is still no clear evidence. . Meningioma (usually benign), Oligodendrogliomas and astrocytoma such as Glioblastomas are primary tumor commonly found in adults and Medulloblastoma in children. Diagnosis is usually done by medical examination along with MRI. Biopsy is then conducted for confirmation. Tumors are divided into different grades of severity depending on the report obtained from diagnosis. In grade 1, the cells look normal and grow slowly. The cells look slightly abnormal and grow slowly in grade 2. Cell starts to grow actively and look abnormal. They start to grow actively in nearby brain tissue and tend to reoccur. This happens only when it is grade 3 tumor. In grade 4 tumor are most abnormal and fast spreading.

There are various literatures available on the topic of brain tumor detection and extraction on MRI images of brain [1-7]. T. Logeswari and M. Karnan [2] have proposed to use two methods for segmentation, i.e. ACO hybrid with Fuzzy and HSOM hybrid with fuzzy to detect brain tumor. Though the detection is done, still the noise is remaining in the image.

Neda Behzadfar and Hamid Soltanian-Zadeh paper [5] used low pass filtering, Ridler's method, morphological operation and thresholding and lastly region growing methods to extract the brain tumor. But the size of the tumor is not accurate as that were present in original pictures. Sahar Ghanavati et.al [7] has proposed to use multi-modality framework and AdaBoost classifier to detect the tumor. Even if the tumor is detected, it still has noise in it and the accuracy of the detected tumor is not good. It is not like that present in the ground image.

This paper proposed to detect and extract tumor from MRI images using dynamic GA based image segmentation and Morphological operation. This will help in easy detection of tumor and also see the growth and size of the tumor. First, the FCM based GA technique is used to segment the image into F number of clusters [9-17]. The FCM is used because it has better noise removal power. Then the thresholding is applied on segmented images and the region containing the tumor is clearly detected. Finally, morphological operation [8] is used so that only the tumor can be extracted from the whole image while keeping the position, the size and the area intact. The remaining part of the article is arranged as: In Section II, we summarize the proposed method. In Section III, we summarize the an experimental results. We conclude our paper in Section IV.

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II. PROPOSED METHOD

The aim of this paper is to detect and extract tumors from different types of brain tumor images. Therefore, the following methods have been used to cater to the purpose:

- FCM based GA
- Thresholding
- Morphological operations

A. FCM based Genetic Algorithm

The searching capacity of GA is used to appropriately cluster a set of n unlabeled points in N dimensions into F clusters. The GA will help the points found out by the FCM clustering method to converge into a single set of values. The steps for performing the algorithm are given as follows.

A1. Encoding

Every chromosome is consists of a sequence of F cluster centers. Each cluster center is mapped to G consecutive genes in the chromosome in G dimensional space. For image datasets each gene is an integer representing an intensity value.

A2. Population Initialization

Genetic algorithm needs a population of size S to work on. This population is generated using the FCM clustering method. The FCM method is executed S times to get the population of size S. Each chromosome obtained in S represents the no. of clusters c=F. The membership values of the data points with each cluster center are calculated and clustering operation is carried out. The membership values assigned to the data centers are done on the basis of distance between the data points and its cluster centers. A data point near to a cluster center signifies the membership of that data point to its corresponding center is more. Let X={x_1, x_2, x_3,…….,x_n} be the set of data points and UC={u_1, u_2, u_3, …… , u_c} be the set of centers. Randomly 'c' clusters centers are selected. The fuzzy membership value 'η_{ij}' using:

$$\eta_{ij} = \frac{1}{\sum_{k=1}^{c}\left(\frac{e_{ij}}{e_{ik}}\right)^{\frac{2}{m-1}}} \quad (1)$$

where, $e_{ij} = \| x_i - y_j \|$ and $e_{ik} = \| x_i - y_k \|$

Compute the fuzzy centers 'UCj' using:

$$UC_j = \frac{\sum_{i=1}^{n}\left(\eta_{ij}\right)^m x_i}{\sum_{i=1}^{n}\eta_{ij}}, \quad for\ all\ j = 1,2,3,.....,c \quad (2)$$

The points start to converge gradually while implementing the algorithm.

A3. Fitness Computation

The calculation of fitness consists of two phases. In first phase clustering of data points is done according to the cluster centers which will become chromosome set. The intensity value x_i, i=1,2,….,m×n is assigned to cluster with center y_j, j=1,2,….,F.

$$if\ \| x_i - y_j \| < \| x_i - y_p \|,\ p = 1,2,...F\ and\ \ p \neq F \quad (3)$$

In the next phase, the values of the cluster centers are updated the mean points of respective clusters which are encoded as chromosome.

$$y_i^{/} = \frac{1}{n_i}\sum_{x_j \in C_i} x_j, i = 1,2,....F \quad (4)$$

Where $y_i^{/}$ is new center for cluster C_i.

S is the summation of Euclidean distance of each point from their respective clusters is given by

$$S = \sum_{i=1}^{N} S_i \quad (5)$$

$$S_i = \sum_{x_j \in C_i} \| x_j - y_i \| \quad (6)$$

The fitness function is given by:

$$\omega = \frac{1}{S} \quad (7)$$

A4. Selection

The selection of the best chromosomes in the population is used by Roulette Wheel selection; it is proportional to the fitness of that chromosome. This means the chromosome having the highest fitness has the maximum probability to get selected for the consequent processes.

$$\rho_i = \frac{\omega_i}{\sum_{i=1}^{N} \omega_i} \tag{8}$$

A5. Crossover

The chromosomes are selected through Roulette Wheel selection process, for better improvement of the fitness value the chromosomes perform crossover operation. On the selected pair of chromosomes single point crossover is applied. On the selected pair, a point from the whole length of chromosome *l* is chosen randomly and the whole content beyond that point is interchanged to get the offspring.

A6. Mutation

Chromosomes obtained after crossover undergoes mutation which has a fixed probability μ_m. Here a point in the pair of chromosome is selected randomly and the content of that point is interchanged. The pair will be chosen after the crossover process is completed.

A7. Termination Criterion

The above mentioned four steps, fitness function calculation, roulette wheel selection, crossover and mutation is repeated until it encounters a predefined number of steps. The result of each iteration is updated and saved. At the end of the whole process a chromosome is obtained which will give the best result.

B. Thresholding

Finally, the best chromosomes set that is obtained is used as the centers points of the cluster, and get final segmented image. After that the thresholding is applied on the segmented image to generate a binary image having two values 0 and 255. A value γ is chosen and every pixel that has intensity value less than γ is made 0 otherwise 255. This operation helps in identifying the region that contains tumor and also helps in extracting it. Hence a binary image *I* is constructed, where g is original image and γ is threshold value.

$$I(n) = \begin{cases} 0 & if\ g(n) \le \gamma \\ 1 & if\ g(n) > \gamma \end{cases} \tag{9}$$

C. Morphological Operation

Any shape and morphology feature related operation of images, mostly morphological operation is used. In this paper, the unwanted non-tumor portions of the MRI images are removing by morphological operations. For this purpose, we apply morphological opening operation. Dilation and erosion are combined together to form the opening operations. The dilation, erosion and opening operation are given by:

$$Dilation: D(f,g) = f \oplus g = \bigcup_{\alpha \in g} (f + \alpha) \tag{10}$$

$$Erosion: E(f,g) = f \Theta(-g) = \bigcap_{\alpha \in g} (f - \alpha) \tag{11}$$

$$Opening: O(f,g) = f^{\circ} g = D(E(f,g)g) \tag{12}$$

After performing these steps two other steps are conducted. They are to determine the connected components then computing area of each component and then removing the small objects. The overview of the method is given in Fig.1.

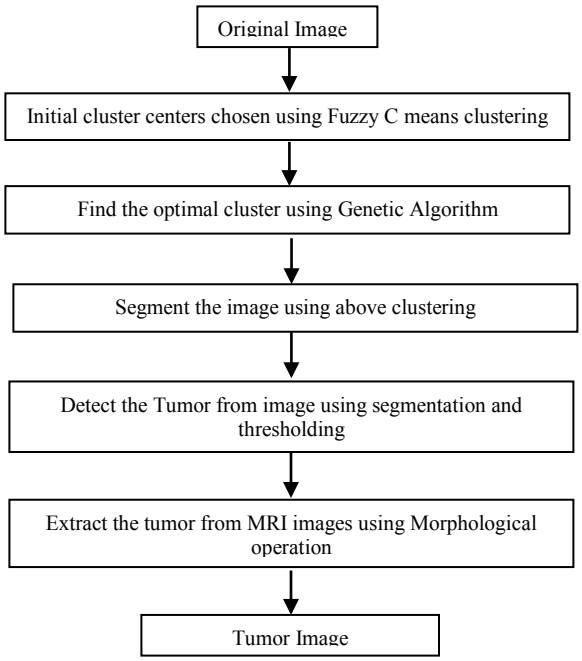

Fig. 1. Block diagram of the proposed method

III. EXPERIMENTAL RESULTS

Extensive experiments are performed on a variety of standard tumor affected T2 weighted MRI images with distinctly different features and different sizes. The outcome of the different MRI images using proposed method is shown in Fig.2. Fig.2 (b), (e), (i), (l), (o) are shown the extracted tumor from original images using our proposed method and Fig.2 (c), (f), (j), (m), (p) are also shown the original image where tumor is detected and it is identified by red color. Our proposed scheme gives better results than K-means and KFCM [6]. The performance of each of the algorithms is evaluated by the number of missed alarms (MA), false alarms (FA) and overall errors (OE). From this result, it is shown that the accuracy of the proposed method is better than the K-means and KMCM (in Fig.3 and Fig.4). Overall error and accuracy is calculated from the given equation:

$$Overall\ error = FA + MA \tag{14}$$

$$and \qquad Accuracy = 1 - \frac{Overall\ error}{Total\ \ pixel} \times 100 \tag{15}$$

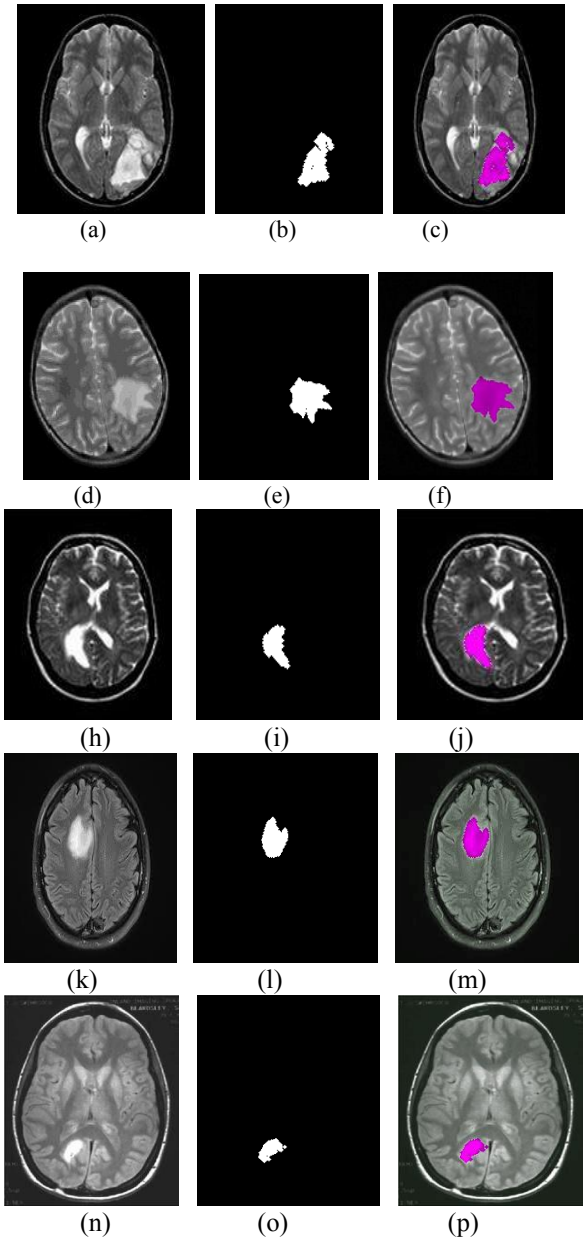

Fig. 2. Output of the five different MRI images: (a), (d), (h), (k), (n) Original Image (b), (e), (i), (l), (o) extract tumor from original images using proposed method (c), (f), (j), (m), (p) shown the original image where tumor is situated.

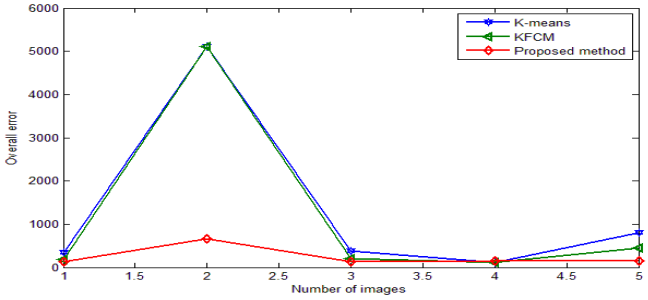

Fig. 3. Overall error measure using K-means , KFCM and Proposed Method.

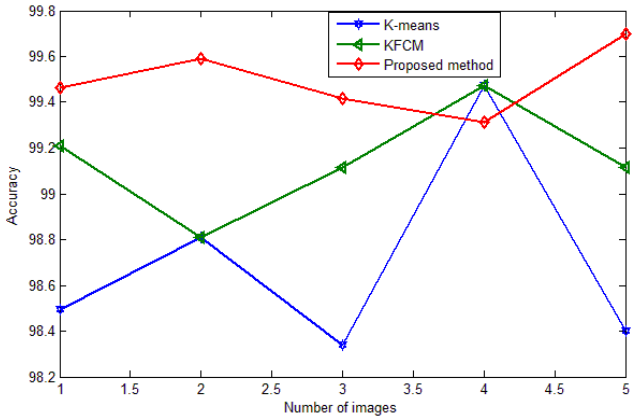

Fig. 4. Accuracy measure using K-means, KFCM and Proposed Method.

IV. CONCLUSIONS

The proposed methodology presents a new method to detect and extract tumor from a MRI of brain images. This proposed method does not need any previous information for segmentation. This detection technique established the advantage and more steady than other tumor detection techniques. In future, this method needs to be improved more for real time applications.

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