Segmentation of Brain MRI Images for Tumor extraction by combining C-means clustering and Watershed algorithm with Genetic Algorithm

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Abstract — **Tumor segmentation from MRI data is an important but time consuming manual task performed by medical experts. The research which addresses the diseases of the brain in the field of the vision by computer is one of the challenges in recent times in medicine. Magnetic Resonance Imaging (MRI) is one of the best technologies currently being used for diagnosing brain tumor. In this paper an intelligent system is designed to diagnose brain tumor through MRI using image processing clustering algorithms such as Fuzzy C Means along with Watershed Algorithm and intelligent optimization tools, such as Genetic Algorithm (GA).In proposed work we take any abnormal image of brain tumor and then produce an output which is extracted portion of tumor by applying genetic algorithm with fuzzy C-menas clustering and Watershed algorithm . FCM is superior over different clustering approaches. This combined approach is used to improve segmentation efficiency and obtain higher value of true positive pixels belong to tumorous region. Genetic algorithm is a stochastic global optimization algorithm, their combination can prevent FCM being trapped in local optimum and give more better results in comparison to neural networks.**

Keywords — **Magnetic Resonance Imaging, Brain Image Segmentation,Fuzzy C-Means,Genetic Algorithm, Watershed.**

I. INTRODUCTION

The incidence of brain tumors is increasing rapidly, particularly in the older population than compared with younger population. Brain tumor is a group of abnormal cells that grows inside of the brain or around the brain. Tumors can directly destroy all healthy brain cells. It can also indirectly damage healthy cells by crowding other parts of the brain and causing inflammation, brain swelling and pressure within the skull. MRI is the noninvasive and very much sensitive imaging test of the brain in routine clinical practice. Magnetic resonance imaging (MRI) is a noninvasive medical test that helps physicians diagnose and treat medical conditions [1],[2]. MR imaging uses a powerful magnetic field, radio frequency pulses and a computer to produce detailed pictures of organs, soft tissues, bone and virtually all other internal body structures. It does not use ionizing radiation (x-rays) and MRI provides detailed pictures of brain and nerve tissues in multiple planes without obstruction by overlying bones. It provides clear images of the brainstem and posterior brain, which are difficult to view on a CT scan.

Brain tumor segmentation is a recent research in field of biomedical application. Image segmentation is the process of partitioning an image into different clusters. The goal of image segmentation is a domain independent decomposition of an image into distinct regions such as color, intensity, brightness, textures etc. An important step in segmentation is to extract the region of area in which we are interested in. Clustering is a technique which classifies patterns in such a way that true positive pixels of same group who actually belongs to cancer than false positive pixels who does not belong to tumor belongs to different group. A brain tumor is any intracranial mass created by abnormal and uncontrolled cell division. Tumors can destroy brain cells or damage them indirectly by causing inflammation, compressing other parts of the brain, inducing cerebral edema or by exerting internal pressure as they grow [3]. Brain tumors are classified into:

1. Primary brain tumor.

2. Secondary brain tumor.

An automated diagnosis system for brain tumor detection should consist of multiple phases including noise removal, brain image segmentation and brain tumor extraction. This paper presents a fuzzy clustering approach combined with genetic algorithm and watershed algorithm for brain tumor detection. Our systems extracts tumor by using three phases, pre processing, and genetic algorithm combined with fuzzy clustering means with Watershed algorithm and post processing.

This paper is arranged in four parts. Section 3 explains the proposed method and step by step procedure for automated brain tumor detection and segmentation. Experimental results & their analysis are shown in section 4 and 5 and finally conclusion is explained in section 6 that wraps up whole paper.

II. PREVIOUS WORK

Various segmentation methods have been cited in the literature for improving the segmentation processes and for introducing maximum possible reliability, for example:

Many approaches have been applied to find tumorous part from image. A neural network approach is given in 7 steps of training data (in 2010) [4]. T.LOGESWARI has defined a work on brain tumor detection using soft computing. In this paper, the proposed technique ACO hybrid with Fuzzy and Hybrid Self Organizing Hybrid with Fuzzy describe segmentation consists of two steps [5]. A cellular automata approach is used for radio surgery applications which gave results with far more accuracy than previous results (in 2012) [6]. A CAD approach is also applied to detect tumor which works upon global threshold segmentation is done on the sharpened image to segment the brain tumor [7].

III. PROPOSED METHODOLOGY

Genetic Algorithm

The word "genetics" is derived from the Greek word "genesis" meaning "to grow" or "to become". Genetic Algorithms (GAs) was invented by John Holland. Holland proposed GA as a heuristic method based on "Survival of the fittest". An implementation of genetic algorithm begins with a population of (typically random) chromosomes. A chromosome is a long, complicated thread of DNA (deoxyribonucleic acid). Hereditary factors that determine particular traits of an individual. Each trait is coded by some combination of DNA (there are four bases, A (Adenine), C (Cytosine), T (Thymine) and G (Guanine). Like an alphabet in a language, meaningful combinations of the bases produce specific instructions to the cell.

GA was discovered as a useful tool for search and optimization problems [8]. FCM clustering degrades the accuracy of image because it takes only pixel attributes and do not consider neighbour pixels but when GA is used in combination with FCM then this approach reduces population size and consider parent neighbour also. As GA is rule based probabilistic approach and always search for global optimum. Once the genetic representation and the fitness function are defined, a GA proceeds to initialize a population of solutions (usually randomly) and then to improve it through repetitive application of the mutation, crossover, inversion and selection operators [9].

Initialization

Initially many individual solutions are (usually) randomly generated to form an initial population. The population size depends on the nature of the problem, but typically contains several hundreds or thousands of possible solutions. Traditionally, the population is generated randomly, allowing the entire range of possible solutions (the search space). Occasionally, the solutions may be "seeded" in areas where optimal solutions are likely to be found.

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Selection

It is the process of choosing two random values from population for next generation. According to Darwin's theory of evolution, the best ones survive to create new off springs. Sum of elements is stored and then cumulative sum of elements is calculated. Choices of values are taken between selected value 0 and 1.

Figure1: Flowchart Representation of Genetic Algorithm

Cross over

Set values as vector containing centroid of clusters. In this paper, crossover value is taken 0.8. We set population as 30 and number of generations as 200. The basic parameter is crossover probability (pc) which describes how often crossover will be performed.

Mutation

Using this operator, it converges to get global minima instead of local minima. The important parameter is mutation probability (pm) which decides how often parts of chromosome will be mutated. If any vector have valueless than equal to 30 then we consider mutation probability as 0.2 if it is between 30 and 50 then we consider it as 0.03 else we consider it as 0.02. The process of one image is shown in figure 1.

FUZZY C MEANS ALGORITHM

The goal of a clustering analysis is to divide a given set of data or objects into a cluster, which represents subsets or a group. The partition should have two properties:

1. Homogeneity inside clusters: the data, which belongs to one cluster, should be as similar as possible.

2. Heterogeneity between the clusters: the data, which belongs to different clusters, should be as different as possible.

The membership functions do not reflect the actual data distribution in the input and the output spaces. They may not be suitable for fuzzy pattern recognition. To build membership functions from the data available, a clustering technique may be used to partition the data, and then produce membership functions from the resulting clustering.

Clustering is a process to obtain a partition P of a set E of N objects X_i (i=1, 2,…, N), using the resemblance or dissemblance measure, such as a distance measure d. A partition P is a set of disjoint subsets of E and the element Ps of P is called cluster and the centers of the clusters are called Centroid or prototypes. Many techniques have been developed for clustering data. In this report c-means clustering is used. It's a simple unsupervised learning method which can be used for data grouping or classification when the number of the clusters is known. It consists of the following steps.
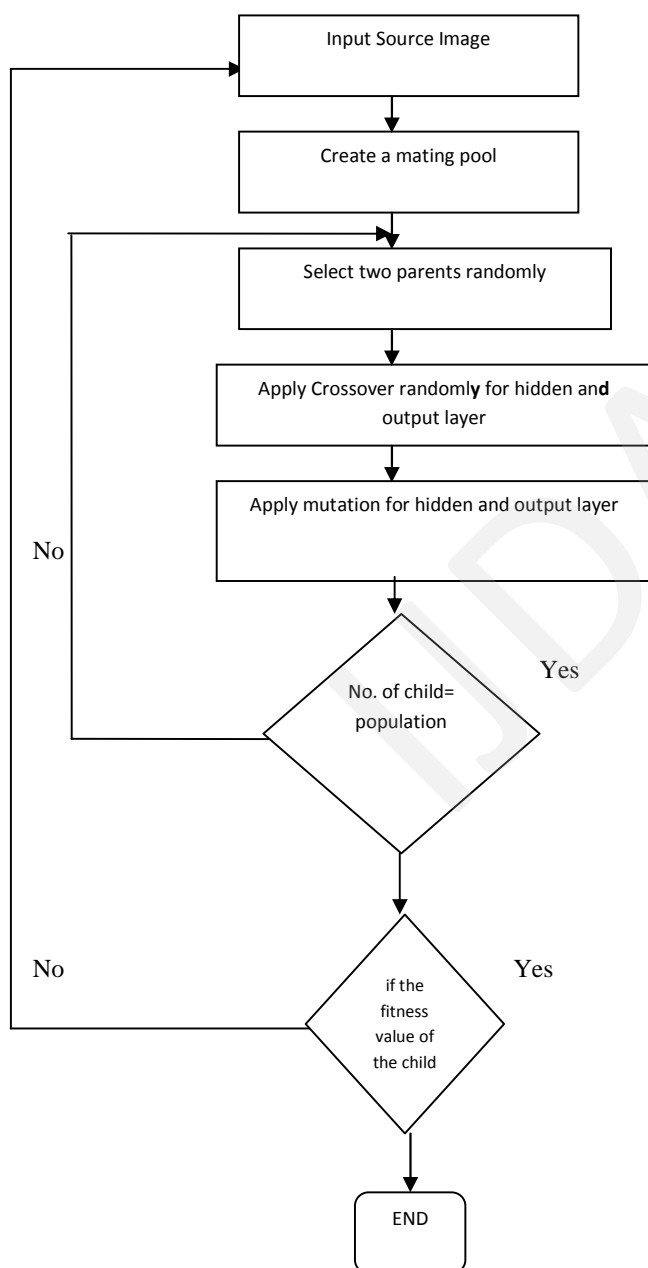
Step 1:

Choose the number of clusters - K

IJDACR
ISSN: 2319-4863

IJDACR
International Journal Of Digital Application & Contemporary Research

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Step 2:

 Set initial centers of clusters c1, c2… ck;

Step 3:

Classify each vector x [x , x ,....x] T into the closest centre ci by Euclidean distance measure ||xi-ci ||=min || xi - ci||

Step 4:

 Recomputed the estimates for the cluster centers ci Let ci = [ci1 ,ci2 ,....cin] T cim be computed by,

$$cim = \frac{\Sigma xli \in Cluster(Ixlim)}{Ni}$$

Where, Ni is the number of vectors in the i-th cluster.

Step 5:

 If none of the cluster centers (ci =1, 2,…, k) changes in step 4 stop; otherwise go to step 3.

Marker Controlled Watershed Segmentation Algorithm

Segmentation using the watershed transforms works well if you can identify, or mark, foreground objects and background locations. The gradient magnitude of the primary segmentation is obtained by applying the Sobel operator. The Canny edge detector was also experimented on, but it was found that the results obtained by both methods are comparable. Hence, we decided on the Sobel filter as the canny edge detector has higher complexity. In addition, the Sobel filter has the advantage of providing both a differencing and smoothing effect. Marker-controlled watershed segmentation follows this basic procedure:

1. Compute a segmentation function. This is an image whose dark regions are the objects we are trying to segment.

2. Compute foreground markers. These are connected blobs of pixels within each of the objects.

3. Compute background markers. These are pixels that are not part of any object.

4. Modify the segmentation function so that it only has minima at the foreground and background marker locations.

5. Compute the watershed transform of the modified segmentation function.

Fig 2. Shows the Flowchart of proposed Methodology

1. Convert the image to Grayscale.
2. Perform the image enhancement using preprocessing Tools to Normalize the Image.

3. Initialize the population respective to the Genetic algorithm.
4. Perform the Image Segmentation using Fuzzy C Means.
5. Define the initial Fitness Function.
6. For i=1 to Maximum Iteration . [Repeat Steps 6 to 11]
7. Perform the Selection of Selection on this Training Dataset.
8. Perform the Crossover on selected parents and generate the next level child.
9. Perform the Mutation to neglect the values that does not support fitness function.
10. Recombine the generated child with existing population to generate new Population Set.
11. Apply the Fuzzy C Means on this new population Set.
12. Generate the Mean of this Image
13. Compare the image pixel with this obtained clustered Threshold value, and derive the result image.
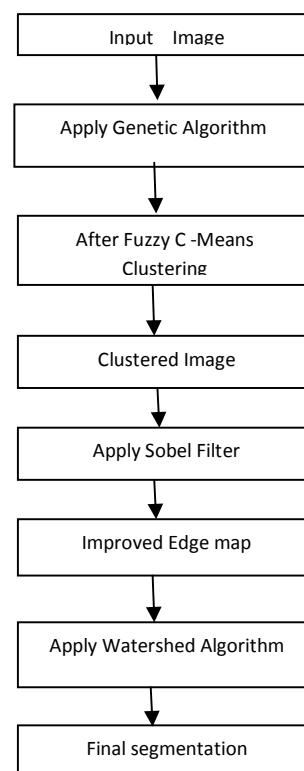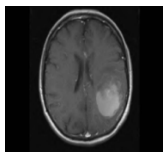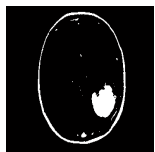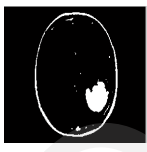
Present the tumor detected image.
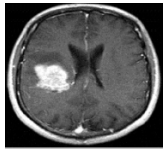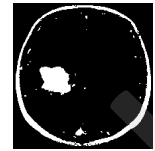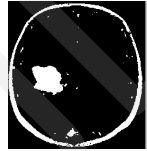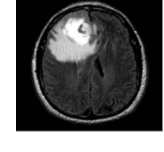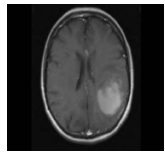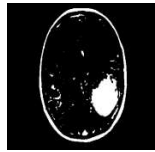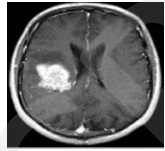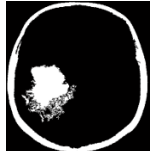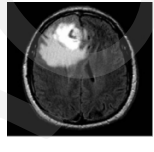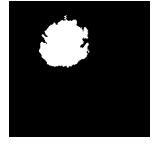

Fig.2 Flowchart of Proposed Methodology

IV. EXPERIMENTAL RESULTS

We applied our proposed methodology of C-Means clustering and optimization techniques integrated with watershed algorithm to MR brain tumor images of the head and obtained segmented region of tumor of them. We evaluated the performance of our proposed methodology by comparing it with conservative watershed algorithm and Fuzzy c-means. The use of Fuzzy C-means clustering with optimization techniques before applying marker controlled watershed segmentation algorithm has achieved the objective of reducing the problem of over-segmentation when applied to MR brain images. The segmentation results are displayed below in Fig 3(a) and (b).

Input Image	After Fuzzy C-means clustering	Final segmentation

(a)

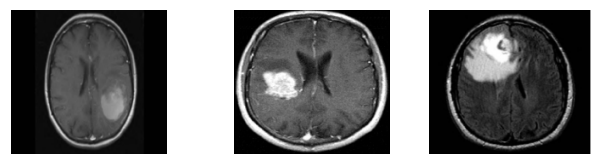| Input Image	After Fuzzy C-means clustering with optimization techniques	Final segmentation

(b)

Fig 3. Segmentation Result By using Traditional

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Table 1
Comparison of segmentation Results of Traditional Fuzzy C-means and Optimization Techniques with Fuzzy C-means

S.No.	Test image	Tumor Area by using Traditional Fuzzy C means	Tumor Area By using Optimization Techniques with Fuzzy C-means
1	A	11954	13986
2	B	4350	4763
3	C	18563	44374

V. Conclusion

The result shown above in graphical & tabular form, it is concluded that, the level of segmentation in clustering algorithm in case of optimizing it through genetic algorithm is much better than that in traditional clustering algorithm.

By calculating area of tumorous region in magnetic resonance imaging data, the results shows that the segmented tumor area in case of traditional fuzzy c-means clustering with watershed transform become evanesce from the corners.

While, in our proposed methodology, that is, in case when we optimize fuzzy c-means clustering with a well known artificial intelligence called genetic algorithm, the output tumor region is extracted well from corners as well, and we get a sharp results from our simulation instruction set.

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