International Journal of Scientific Research in Computer Science, Engineering and Information Technology
ISSN : 2456-3307
Available Online at : www.ijsrcseit.com
Volume 10, Issue 7, May-June-2024 | Published Online : 20th June 2024

Tumor Detection Using Genetic Algorithm for Magnetic Resonance Images

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ABSTRACT

Magnetic Resonance Imaging (MRI) is utilized to diagnose or monitor treatments for a diversity of medical conditions, including abnormalities of the brain, tumors in various regions of the physical structure. Brain tumor occurs when abnormal cells form within the brain, which leads to brain cancer. So, brain tumor detection is very important while considering the treatment process. The main thing behind the brain tumor detection is the image segmentation. Segmentation in medical images is more helpful for identification of the diseased portion of the images. The pre-processing stage is the first step of the segmentation process. The images are filtered using median filter which smoothens the overall image and makes that the intensity all over the image is normalized. The skull regions are then removed from the images based on the morphological operations. The optimization methods are employed for exact identification of the tumor portions. A genetic algorithm is used in the optimization process. The performance of the process is measured based on the performance metrics like TP, TN, FP, FN, Precision, Recall, Specificity and Accuracy.

Index Terms- Brain Tumor, Segmentation, Precision, Recall, Specificity, Accuracy.

I. INTRODUCTION

Medical imaging modalities can be used to protect patient's life through an accurate and quick treatment without any side effects. Image segmentation plays a vigorous role in tumor identification and detection. Various techniques for medical image segmentation are available.

Segmentation methods are typically classified into three main categories including manual, semi-automatic and fully automatic based on the degree of required human interaction. In manual brain tumor segmentation, the specialists must know about all the information presented in the brain images. In manual brain tumor segmentation the boundaries of the tumor portion are manually marked and then particular tumor portion is labelled.

Manual segmentation of brain tumor images is a very challenging and time consuming task. But this type of segmentation method can cause human error; also result depends on human to human. So that an automatic and semi- automatic segmentation method is required because it reduces the load on the human observer and accuracy is not affected due to fatigue and large number of images.

Semi-automatic tumor segmentation mainly consists of the user interaction, and software computing. In the semi-automatic brain tumor segmentation methods, the user needs to input some parameters and which is responsible for analyzing the visual details.

Although manual and semi-automatic segmentation by qualified professionals provide better results compared to automatic methods, it has some drawbacks. Manual or semi-automatic segmentation is extremely time-consuming. Another problem with this type of segmentation method is the segmentation results may be varied for different observer. Due to some of the reasons automatic tumor segmentation is now also a challenging task. One of the reasons is, there are several tumor types which differ based on size, tissue homogeneity, tissue composition, shape, and location. In some cases, tumor border with normal tissues cannot be superbly defined with images. The second reason is the partial volume effect (PVE), which means 1 pixel in a brain image may belong to multiple tissue types, in addition to noise due to the MRI acquisition system. So, several segmentation methods and algorithms are continuously proposed and some of them are used to provide better accuracy and computation time.

The foremost purpose of this paper is to develop a work that can accurately classify a tumor from abnormal tissues. The main concept in this work is to locate the tumor position from other items of an MR image by using Thresholding and genetic algorithm. This is used for exact detection of tumor portion and tumor area calculation.

II. PROPOSED WORK

We proposed brain tumor segmentation using thresholding and genetic algorithm for magnetic resonance images. Thresholding is used as a basic segmentation algorithm. A genetic algorithm is used for optimized segmentation result. The block diagram of the proposed work is shown in figure.

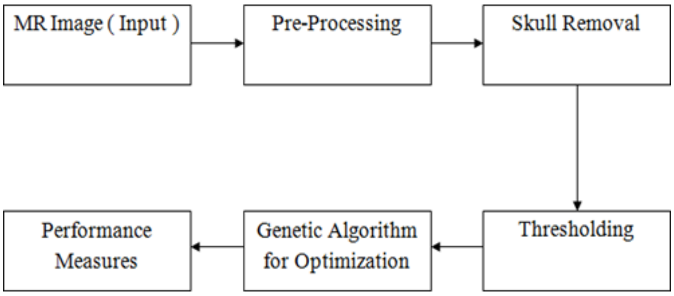


Fig 1: Block Diagram of Proposed work

The input image can be obtained from the DICOM data set. Filtering operation is performed using median filter which is used for removal of noise and preserving the edge information. Skull portion present in the image is removed using morphological operations. Morphological open and close operations are used here for removal of the skull. Thresholding segment the tumor portion of the normal brain tissues. To provide optimized segmentation result genetic algorithm is used. Tumor area is calculated based on the segmented portion. The performance of the algorithm is measured based on the performance metrics like True Positive, True Negative, False Positive, False Negative, Recall, Specificity, Precision and Accuracy.

A. Input Image

The DICOM data set is used for getting the input brain magnetic resonance images with tumor and without tumor. Digital Imaging and Communications in Medicine (DICOM) is a standard for handling, storing, printing and transmitting information in medical imaging. DICOM consists of 50 images that contain brain tumor and 50 images that does not contain tumor.

B. PreProcessing

Image Pre-Processing stage is the most significant step before applying the segmentation algorithm. Pre-Processing removes the noise and high frequency artifact present in the image. The input image is resized to [256,256] to obtain a common size image. If the input image is RGB then RGB to grey level conversion is performed for obtaining grey scale image. Noise present in the image is removed using median filter. It is a non-linear filter used for preserving edges. Median filtering works by moving pixel by pixel through the image, replacing each value with the median value of neighboring pixel. Median filtering is performed better than linear filtering for removing noise in the presence of edges [10].

C. Skull Removal

A Skull portion of the brain image does not contain any useful information for tumor segmentation. But, this unwanted portion increases the processing time. So, skull portions can be removed using morphological operations. Morphological open and close operations are used in this paper. Structuring element is important while considering any morphological operation. Morphological operations probe an image with a small shape or template called a structuring element. The structuring element is positioned at all possible locations in the image. The output of morphological operation is a binary image in which the pixel has a non-zero value only if the test is successful at that location in the input image.

D. Thresholding

The Threshold based method is simple and effective segmentation method by comparing their intensities with one or more thresholds. It is used to segment the foreground from background. The Maximal value of the skull removed image is used as a threshold value. Thresholding creates binary images from grey-level ones by turning all pixels below the threshold to zero and all pixels above that threshold to one. Threshold image is given as a input for the optimization process.

E. Genetic Algorithm

Evolutionary algorithm is used to generate the optimized results. Genetic algorithms belong to the larger class of Evolutionary Algorithm (EA) which generate optimized solutions using techniques inspired by natural evolution, such as inheritance, mutation, selection and crossover.

Fitness Function Based On Fisher Criterion

The fisher criterion measures the distance between all the classes and the divergence within the members of each class. Thus, it reflects the classification accuracy under the absence of classifiers. Let d be the number of considered feature elements, w = (w1, w2,......,wd) be the feature-weight vector, where wi ∣ i= 1 to dreflects the importance of the ith feature.According to GA’ sterminology, a wis an individual required to be evaluated in this work. The evolution task is performed based on fisher criterion. Accordingly, the fitness of individuals is computed in the following manner. Let X i,j = (x1i,j , x2i,j , , xdi,j) be the full feature vector of the jth example of the ith class, nibe the number of examples of the ith class, C be the number of classes, m be the mean of feature vector of all training samples.

The average weighted distance between all the training examples and the corresponding class mean calculated using the following formula.

$$S_w = \sum_{i=1}^{C} \frac{1}{n_i} \sum_{j=1}^{n_i} \sum_{k=1}^{d} w_k \left(x_k^{i,j} - m_k^{i} \right)^2$$

And the weighted distance between classes can be calculated using following formula.

$$S_B = \sum_{i=1}^{C} \sum_{k=1}^{d} w_k \left(m_k^{i} - m_k \right)^2$$

Finally the fisher criterion can be formulated as maximizing SB and minimizing SW simultaneously. Thus, the fitness function for evaluating w is designed as

$$f(w) = \frac{S_W}{S_B}$$

The optimal w is taken as the one that minimizes the above function. Then, select the features whose weight in the optimal w is larger than a threshold. The flowchart of the FIG algorithm is shown in Fig 2.

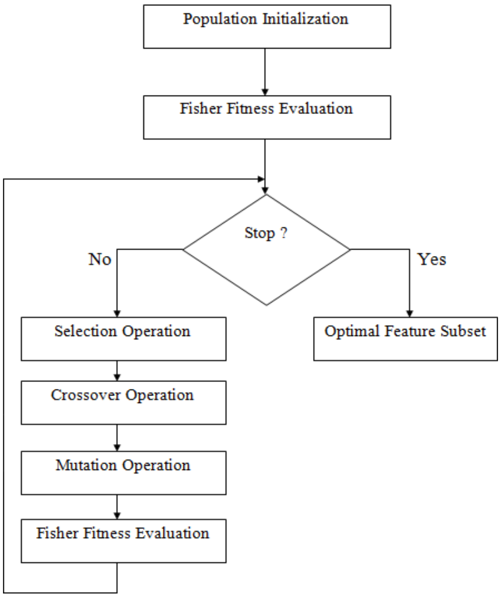


Fig 2: Flowchart of the FIG algorithm

The various stages involved in genetic algorithm are described below.

i). Initial population

The size of the population is considered first and then a method by which individuals are chosen is considered. All the individuals in each generation construct the population. Each individual is encoded as a binary string, which is thought to be the individual's chromosome. An individual in the FIG algorithm is a feature-weight vector.

ii). Selection Operator

This operator used for selecting the parent individuals to producing offsprings for the next generation. Here roulette wheel selection technique is used. The probability of selecting an individual is calculated as

$$P(C_i) = f(C_i) / \sum_{K=1}^{M} f(C_k)$$

Where Ci is the chromosome of the ith individual in the population, f(Ci) is the fitness value corresponding to Ci ,and M is the number of individuals in the population.

iii). Crossover Operator

Crossover is the operation of replacing some of the genes in one parent by the corresponding genes of another. Let Pcbe the probability of crossover. Initially, a large Pc is used to strengthen the search ability. Formally, Pc0be the initial crossover probability, g be the number of generation; Ciand Cjbe the chromosomes of parent individuals, then Pcis adjusted by

$$pc = \begin{cases} \dfrac{pc_0}{\log_{10}(g+1)} & , f_{max} \geq \overline{f} \\ pc_0 & , f_{max} < \overline{f} \end{cases}$$

$$f_{max} = \max(f(C_i), f(C_j))$$

$$\overline{f} = \frac{1}{M} \sum_{i=1}^{M} f(C_i)$$

iv). Mutation Operator:

Mutation is performed by inversing one bit in each part of an individual's chromosome to create a child. The chromosomes of individuals to be different from their parent individuals due to mutation. Each part of the chromosome is corresponding with a type of features, and the mutation probability is also adjusted adaptively. The adaptive equation is

$$pm = \begin{cases} \dfrac{pm_0}{\log_{10}(g+1)} & , f \geq \overline{f} \\ pm_0 & , f < \overline{f} \end{cases}$$

Where Pm0 is the initial mutation probability.

f is the fitness of the individual mutated.

g is the number of generations.

v). Termination:

The algorithm is terminated when it converges or the predefined maximum number of generations is reached. The condition used to evaluate whether the algorithm converge is: The difference between the maximum fitness values of adjacent two generations does not exceed an infinitesimal after m generations.

F. Tumor Area Calculation:

Area of an image is the total number of pixels present in the area which can be calculated in the length units by multiplying the number of pixels with the dimension of one pixel. To calculate the number of pixels in the segmented image the function regionprops() is used.

G. Performance Measures:

The performance of the process is measured based on accuracy. Accuracy is the weighted arithmetic mean of precision and inverse precision. True positive value refers to the correctly identified images. True negative value refers to the correctly rejected images. False positive value refers to the incorrectly identified images. False negative value refers to the incorrectly rejected images.

Precision measures the degree to which repeated measurements under unchanged conditions show the same result.

$$\text{Precision} = \frac{TP}{(TP + FP)}$$

Recall or Sensitivity is the ability of a test to correctly identify those with the disease.

$$\text{Recall} = \frac{TP}{(TP + FN)}$$

Specificity is the ability of the test to correctly identify those without disease.

$$\text{Specificity} = \frac{TN}{(TN + FP)}$$

Accuracy measure the degree of closeness to which tumor is detected.

$$\text{Accuracy} = \frac{(TP + TN)}{(TP + TN + FP + FN)}$$

III. EXPERIMENTAL RESULTS

Brain image contains tumor portion is analyzed first. After genetic optimization detected tumor portion is specified as a red color region.

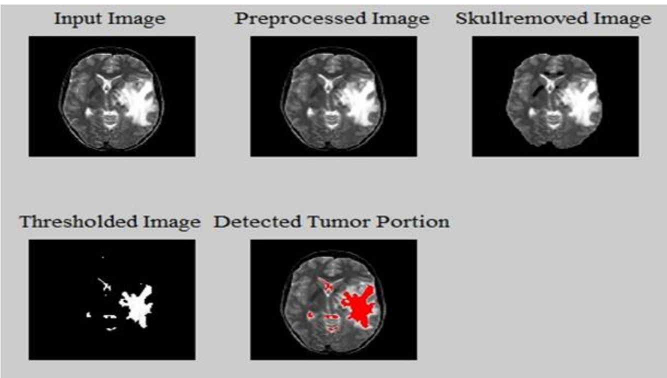
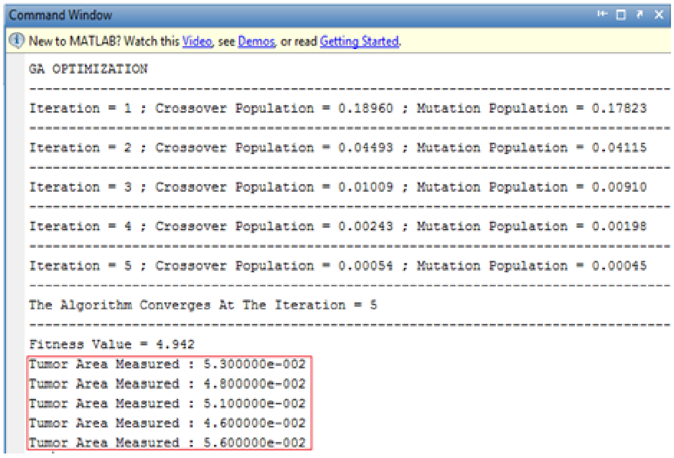


Fig 3. Tumor Image Result

And the area of the tumor is also calculated. Genetic algorithm results such as number of iterations, mutation and crossover population, fitness value, tumor area measured is displayed in the command window.

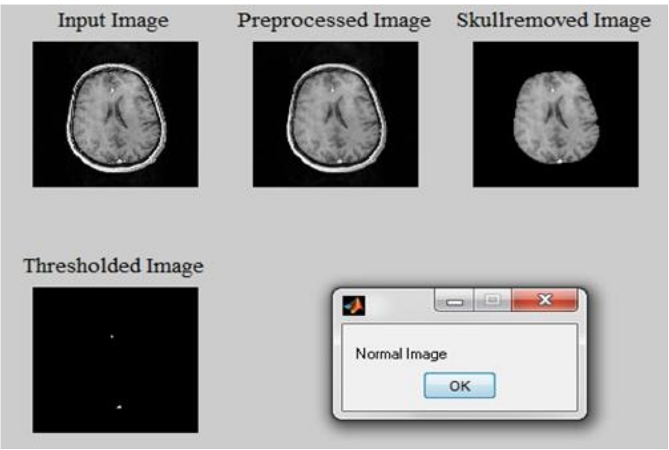


New to MATLAB? Watch this Video, see Demos, or read Getting Started.

```
GA OPTIMIZATION
----------------------------------------------------------------------------------
Iteration = 1 ; Crossover Population = 0.18960 ; Mutation Population = 0.17823
----------------------------------------------------------------------------------
Iteration = 2 ; Crossover Population = 0.04493 ; Mutation Population = 0.04115
----------------------------------------------------------------------------------
Iteration = 3 ; Crossover Population = 0.01009 ; Mutation Population = 0.00910
----------------------------------------------------------------------------------
Iteration = 4 ; Crossover Population = 0.00243 ; Mutation Population = 0.00198
----------------------------------------------------------------------------------
Iteration = 5 ; Crossover Population = 0.00054 ; Mutation Population = 0.00045
----------------------------------------------------------------------------------
The Algorithm Converges At The Iteration = 5
----------------------------------------------------------------------------------
Fitness Value = 4.942
Tumor Area Measured : 5.300000e-002
Tumor Area Measured : 4.800000e-002
Tumor Area Measured : 5.100000e-002
Tumor Area Measured : 4.600000e-002
Tumor Area Measured : 5.600000e-002
```

Fig 4: Genetic Optimization and Tumor Area Result

Brain image does not contain tumor is displayed with a normal image message box. skull regions in the images were removed based on morphological operations. Thresholding operations were employed to segment the tumor portions of the image. The GA was used to obtain an optimized segmentation result. From the solutions obtained the images were optimized and the tumor portions were identified. The performance measures of the process were estimated.

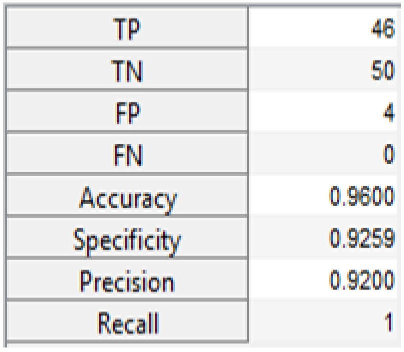


Normal Image

Fig 5: Normal Image Result

The performance measures obtained from this process are displayed in the following table. This table contains the information such as True positive, True Negative, False Positive, False Negative, Precision, Recall, Specificity, and Accuracy. This algorithm provides better accuracy compared to the K-means integrated with Fuzzy C means algorithm which provide 90.5 % accuracy but the genetic algorithm provide 96% accuracy.

Table 1: Performance Measures



TP	46
TN	50
FP	4
FN	0
Accuracy	0.9600
Specificity	0.9259
Precision	0.9200
Recall	1

CONCLUSION

Brain diseases are evolutionary in nature, their detection and treatment will also progress based on the dynamic nature of the disease. The input MRI was filtered using median filter. The skull regions in the images were removed based on morphological operations. Thresholding operations were employed to segment the tumor portions of the image. The GA was used to obtain an optimized segmentation result. From the solutions obtained the images were optimized and the tumor portions were identified. The performance measures of the process were estimated.

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