

Brain Tumour Segmentation Using Evolutionary Computation Techniques in MRI Images

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Abstract: Among brain tumours, some of tumours like Malignant brain tumours and gliomas are the most aggressive and common, leading to a very short life expectancy in their highest grade. But the large amount of data produced by MRI images prevents manual segmentation in the available time, restricting the use of specific quantitative measurements in the clinical practice. So, reliable and automatic segmentation methods are required; however, the large spatial and structural variability of brain tumours make automatic segmentation a challenging problem. In this paper, we proposed an automatic segmentation method based on evolutionary computation techniques. An Evolutionary Computation Algorithms (EAs) is an iterative and stochastic process that operates on a set of individuals (population). Each individual represents a potential solution in order to solve the problem. Every individual in the population is provided, by means of a fitness function, a measure of its goodness with respect to the problem under consideration. Among the evolutionary computing techniques, the genetic algorithms (GAs) are the most extended group of methods which represents the application of evolutionary tools. This paper presents a new segmentation approach based on hybridization of the genetic algorithms (GAs) and seed region growing to produce accurate medical image segmentation, and to overcome the over segmentation problem. Pre-processing of medical images is done by seeded region growing algorithm. The method proposed in this paper is promising for detection of stroke.

Keywords: MRI, Image segmentation, Evolutionary Computation Techniques, region growing, genetic algorithms.

I. INTRODUCTION

Gliomas are the brain tumours which are prevalent with the highest mortality rate. These types of tumours are graded into Low Grade Gliomas (LGG) and High-Grade Gliomas (HGG), in which Low Grade Gliomas are being less aggressive and infiltrative than the High Grade. Current treatments for brain tumours include surgery, radiotherapy, chemotherapy or a combination of them. MRI is especially useful to assess gliomas tumours in clinical practice, since it is possible to get MRI sequences providing complementary information.

The accurate segmentation of brain tumor and their intra-tumoural structures is important for treatment planning as well as for follow-up evaluations. Since manual segmentation techniques are time-consuming and are subjected to inter and intra-errors Thus, physicians are usually using rough measures for evaluation. For these reasons, semi-automatic or automatic and accurate methods are required. However, it is a challenging task, since the location, shape and structure of these abnormalities are highly variable. Additionally, the tumor mass

effect may also changes the arrangement of the surrounding normal tissues. Also, MRI images may also present some problems, such as different intensity ranges or intensity inhomogeneity.

In last 20 years, several techniques have been developed to identify brain tumours. But most of techniques have their own limitations. So, none of them has gained wide popularity in the field of brain image segmentation. Some of them are based on clustering, edge detection and basic watershed segmentation. The edge detection technique effectively works on high contrast images. But this method fails in edge detection in low contrast noisy images due to the weak gradient magnitude. Similarly, the clustering-based method like K-means algorithm has a fast speed which allows it to run on large datasets. But, the main disadvantage of this method is that it does not produce same result with each run, because the resulting clusters mainly depend on the initial random assignments. Another method widely used is morphological watershed segmentation, but the major problem with this method is that it produces over segmentation problem. Evolutionary Computation Techniques are powerful methods in medical image segmentation. This paper introduces a combination between GA and seed region growing to overcome the over segmentation problem, improve the quality of image segmentation, and accelerate the search for finding the optima. The region growing is used to extract a complete region. The proposed method consists of four steps: finding the initial population, performing seed region growing, evaluating the fitness function. The proposed computing techniques attempts to find out the optimal centroid for each region for fine segmentation. The chromosome representation includes control genes, gray-levels genes, and x and y-axis values of the gray level. The gray-level genes which have control-genes equal to one and located at (x, y) are centroids of the clusters. Then, the initial population is passed to the seed region growing with initial seed (with location (x, y)). The fitness function is improved by considering the covered and uncovered data for quantitative measure of segmentation result. The proposed method is experimented using different MRI images with weak boundaries to prove its efficiency and applicability. The experimental results show that the proposed technique produces more accurate and stable results compared with other segmentation techniques such as fuzzy c-means and hybrid GA and fuzzy clustering methods.

II. REGION GROWING

The seeded region growing begins segmenting an image from a set of seeds. Each of these seeds could be a single pixel or a group of pixels, and they can be specified manually by a human operator or automatically by pre-processing steps. These seeds

are then allowed to grow and form regions in a manner to be described below. Finally, the whole procedure finishes when the image is fully partitioned by all the growing regions. Object boundaries are obtained as the boundaries of the final regions. A more precise description of the seeded region growing is as follows. Suppose initially there are N seeds, and they are collected in N sets A_1, A_2, \dots, A_N . Let T be the set of all pixels which are adjacent to at least one of the pixels in A_i 's:

$$T = \{x \notin \bigcup_{i=1}^N A_i \mid \text{nbr}(x) \cap \bigcup_{i=1}^N A_i \neq \emptyset\} \quad (1)$$

where $\text{nbr}(x)$ is the set of all immediate neighbours of pixel x . At each time step, the growing process selects one-pixel x from T and adds it to one of its neighbouring regions; A_i is a neighbouring region of x if $\text{nbr}(x) \cap A_i \neq \emptyset$. This pixel is chosen according to some homogeneity criterion. In the criterion is to choose the pixel whose grey value is closest to the average grey value of one of its neighbouring growing regions, say A_p where $1 \leq p \leq N$. This pixel will then be added to that region, and both T and A_p will be updated. This process continues until all the pixels in the image are allocated to one and only one of the growing regions. The criterion ensures that the grey values for each final region are as homogeneous as possible under the connectivity constraint. The basis of the method is to segment an image of N pixels into regions with respect to a set of seeds using only the initial seed pixels. The initial seed pixel is selected from a pixel with mask 3×3 . These seeds are grown by merging neighbouring 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 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. Since the seed growing is performed only on edge pixels, the amount of data needed to be processed is much reduced, resulting in increased speed.

III. EVOLUTIONARY COMPUTATION TECHNIQUES

Among the evolutionary computation techniques, the genetic algorithms (GAs) are the most extended group of methods which represents the application of evolutionary tools. GAs are efficient, adaptive, and robust search and optimization techniques guided by the principles of evolution and natural genetics and have implicit parallelism. The essential components of GAs are the following:

- 1) Representation strategy is called chromosomes.
- 2) A population of chromosomes encode candidate solutions to the optimization problem.
- 3) Mechanism for evaluating each chromosome (fitness function).
- 4) selection/reproduction procedure.
- 5) genetic operators (crossover, mutation, and elitism).

In the proposed algorithm, chromosomes are represented in binary strings of 0s and 1s and evolved toward better solutions.

A chromosome consists of four parts: control genes, gray-levels genes, and position genes to serve our problem. Usually from a population of randomly generated individuals the evolution starts. The region growing algorithm is used to extract accurate regions for each control gene value to reduce the search space in the whole gray levels image. In each generation, a fitness function is used to evaluate individuals, and reproductive success varies with fitness. The purpose of a fitness function is to provide a meaningful, measurable, and comparable value given a set of genes. If the fitness test takes a long time to perform, then the GA may take a long time to execute. Here, the fitness function is improved in order to reduce the repeated tests.

Fitness Function:

In general, an image can be described by a two-dimensional function $f(x, y)$, where (x, y) denotes the spatial coordinates, and the intensity value at (x, y) is $f(x, y) = [0, 255]$. In a GAs, a population of individuals, described by some chromosomes, is iteratively updated by applying selection, mutation and crossover operators to solve the problem. Each individual is evaluated by the fitness function that controls the population evolution in order to optimize it. Here, we present the most fitness functions that give almost reliable decision.

The new fitness function that works under constraints for cover and uncover data. The proposed fitness function includes two terms: covers and uncovers penalty. The point x called covered point if $x \in S_j$, S_j is a region that contains connected points around the centre j , and x called uncovered if $x \notin U_j$.

$$\text{fitness} = \alpha \sum_{i=1}^n \sum_{j=1}^k \|C_j - R_j(x_i, y_i)\|^2 + UCR \quad (3)$$

where UCR is a penalty for the uncover points.

The Euclidian distance term represents the shortest distances between the centroid c_j , $j = 1, 2, \dots, k$. and all pixels p_i , $i = 1, 2, \dots, N$. of the region R_j . A pixel is selected as a member of region if Euclidian distance of this point is smaller than a prescribed value. Thus, some pixels are still uncovered by regions. UCR is used to represent these pixels. The minimum of the first term is obtained when all pixels fall in regions with the centre c_j . Otherwise the centre of uncovered pixels UCR is obtained by computing the median value of pixels. This value is considered as the centre of the uncover pixels. UCR can be written as:

$$UCR = \alpha \sum_{i=1}^m \|Median - R(x_i, y_i)\|^2.$$

where m is the number of the uncovered points. We provide optimal solutions of fitness function in a limited time by minimizing the value of UCR term.

In general, a GA contains a fixed-size population of potential solutions over the search space. These potential solutions of the search space are encoded as binary or floating-point strings and called the individuals or chromosomes. This formulation can

capture the intuition of segmenting an image; it is difficult to solve due to two reasons: first, the proper number of regions is not known beforehand

IV. PROPOSED ALGORITHM

The figure below gives the overall diagram of the proposed algorithm. The figure shows that input of algorithm is only given image. The different steps of proposed algorithm are

Input: image to be segmented

Step 1: Read the image.

Step 2: Find the initial population

Generate randomly chromLen of binary digits to be Control Genes of the current chromosome.

Select randomly chromLen of pixels to be Gray-levels Genes of the current chromosome. can be stated as follows:

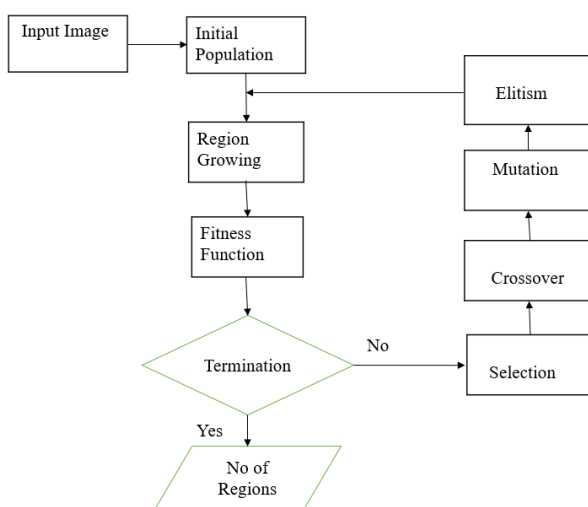


Fig.1: Proposed Algorithm

Get the X-Axis values and Y-Axis values and add them to the current chromosome.

end for

Step 3: Evaluate the initial population for $i = 1$ to popsize

Find the Control Genes of the current chromosome with value "1" and the corresponding gray level value to be the centroids the regions.

For each centroid apply the seed region growing to get the region.

Find the required uncovered pixels.

Applying the fitness function for evaluating the current chromosome.

end for.

Let current population is the initial population.

Step 4: Repeat the following steps while number of generation is less than maxGen.

Keep the best chromosome of current population and its fitness.

Select the mating pool (the parents of the next population) using Tournament algorithm.

Crossover the mating pool to generate the offsprings.

Mutation the offsprings to generate the new population.

Evaluate the new population as in step 3.

Keep the best chromosome of new population and its fitness.

Apply the Elitism.

Let current population is the new population.

Step 5: Output the following:

The best chromosome of current population and its fitness.

Initial Population: A GA requires a population of potential solutions to be initialized at the beginning of the GA process. In this approach, we randomly select a set of gray levels from the image as the initial parametric genes and their given x and y axis values.

Selection: The selection/reproduction process copies the individual strings into a uncertain new population, the mating pool, for genetic operations. The number of copies individually received in the next generation is usually taken to be directly proportional to its fitness value; thereby mimicking the natural selection procedure. This scheme is commonly known as the proportional selection scheme.

Crossover: The main purpose of crossover is to exchange information between randomly selected parent chromosomes by recombining parts of their genetic information. The common crossover techniques are two-point crossover, multiple-point crossover, shuffle-exchange crossover, and uniform crossover

Mutation: Mutation is the process by which a random alteration in the genetic structure of the chromosome takes place. The main objective is to introduce genetic diversity into the population. Mutating a binary gene involves simple negation of the bit, while that for real coded genes is defined in a variety of ways.

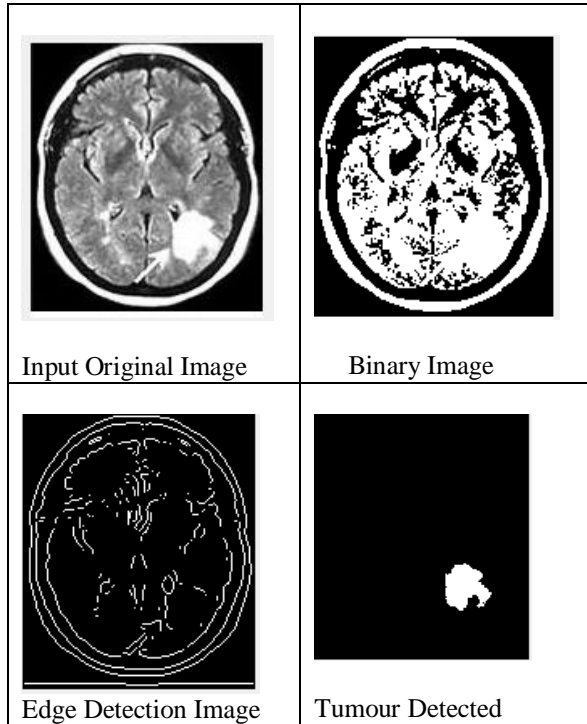
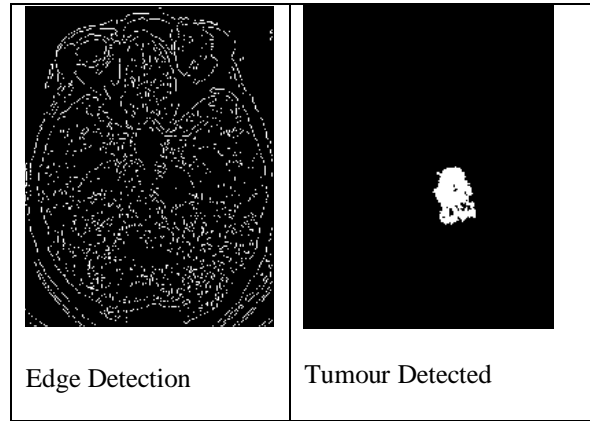
Elitism: This step keeps the best chromosome from destroying. In this step, if the best chromosome of the previous population is suitable than the best chromosome of the current population then we exchange them. Then we replace the worst chromosome of the current population with the best chromosome of the previous population. If the best chromosome of the previous population is not fitter than the best chromosome of the current population then we replace the worst chromosome of the current population with the best chromosome of previous population.

V. EXPERIMENTAL RESULTS AND DISCUSSION

Seeded Region growing algorithm was implemented on different MRI brain images after pre-processing. Experimental results that are obtained after implementation of seeded region growing algorithm are as shown below.

The experimental results from the proposed method show that this method gives more stable and more accurate results in complex medical image structures even with varying

chromosome parameters like PS, MG, and CL. the average of the runs for GA produces keys that are at a very similar level of correctness are interesting to note, yet the GA with the proposed fitness function significantly scoring the higher fitness levels. The proposed approach has a major improvement of the original GA in three aspects



- (1) It does not require a prior number of image regions, however it can adaptively and effectively controls the segmentation quality.
- (2) The chromosome structure is revised from the original image and condition of the fitness is Convinced.
- (3) Three revised genetic operations along with region growing method are presented to make the proposed algorithm computation-efficient.

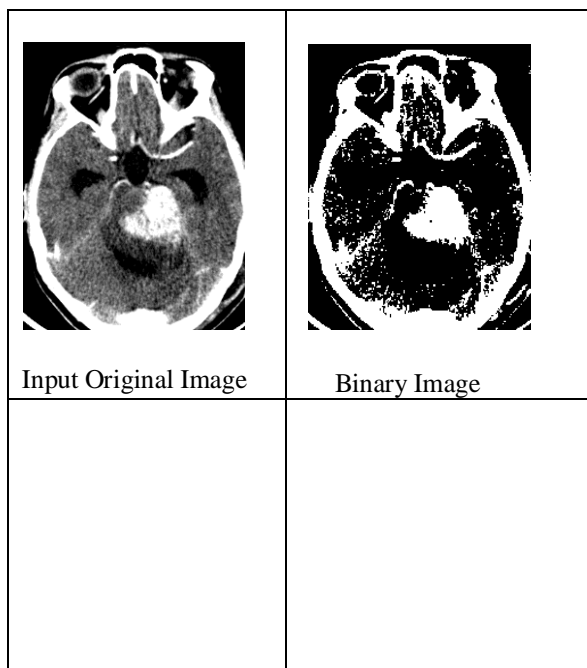
VI. CONCLUSION

A new approach for automatic segmentation that has been presented in this paper could improve medical images segmentation. The proposed method combines seed region growing and the GA algorithms process to overcome their limitations such as: the consumed time for the search space and the accuracy of image segmentation

The method begins with optimising the parameters of input image segmentation algorithms to find: a best way to represent the chromosomes, a fitness function that is a good measure of image segmentation quality and the best way to reduce the time consumed. These improvements are included in algorithm to present automatic, stable and accurate medical image segmentation.

VII. REFERENCES

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