

Available online at www.sciencedirect.com**ScienceDirect**

Procedia Computer Science 79 (2016) 449 – 457

Procedia
Computer Science

7th International Conference on Communication, Computing and Virtualization 2016

TUMOR DETECTION IN BRAIN USING GENETIC ALGORITHM

G Rajesh Chandra ^{*a}, Dr.Kolasani Ramchand H Rao ^b^aResearch Scholar , Dept of Computer Science, Acharya Nagarjuna University , Guntur ,India- 522006^bProfessor, Department of Computer Science ASN Degree College Tenali,

Abstract

Detection of brain tumour is very common fatality in current scenario of health care society. Image segmentation is used to extract the abnormal tumour portion in brain. Brain tumor is an abnormal mass of tissue in which cells grow and multiply uncontrollably, apparently unregulated by mechanisms that control cells. Several techniques have been developed for detection of tumor in brain. Our main concentration is on the techniques which use image segmentation to detect brain tumor. Tumor classification and segmentation from brain computed tomography image data is an important but time consuming task performed by medical experts.

© 2016 The Authors. Published by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Peer-review under responsibility of the Organizing Committee of ICCCV 2016

Keywords: **Keywords :** Brain Tumor, GA, Image Segmentation

INTRODUCTION -Segmentation of medical images is challenging due to poor image contrast and artifacts that result in missing or diffuse tissue boundaries. We present a discrete wavelet based genetic algorithm is proposed to detect the MR brain Images. First, MR images are enhanced using discrete wavelet descriptor, and then genetic

* Corresponding author. .

E-mail address: grajeshchandra@gmail.com

algorithm is applied to detect the tumor pixels. A genetic algorithm is then used in order to determine the best combination of information extracted by the selected criterion. The present approach uses k-Means unsupervised clustering methods into Genetic Algorithms for guiding this last Evolutionary Algorithm in his search for finding the optimal or sub-optimal data partition (Harris and Buxton 1996, Kim et al 2000, Li Zhijun et al 2006) task that as we know, and requires a non-trivial search because of its intrinsic NP-complete nature. To solve this task, the appropriate genetic coding is also discussed since this is a key aspect in the implementation. Our purpose is to demonstrate the efficiency of Genetic Algorithms to automatic and unsupervised image segmentation. Some examples in human MRI brain tumor segmentation are presented and overall results discussed.

Medical imaging is performed in various modalities, such as magnetic resonance imaging (MRI), computed tomography (CT), ultrasound etc. Segmentation is typically performed manually by expert physicians as a part of treatment planning and diagnosis. Due to the increasing amount of available data and the complexity of features of interest, it is becoming essential to develop automated segmentation methods to assist and speed-up image-understanding tasks.

1.1.1 Related Work

Image segmentation is a low-level image processing task that aims at partitioning an image into homogeneous regions. How region homogeneity is defined depends on the application. A great number of segmentation methods are available in the literature to segment images according to various criteria such as grey level, color, or texture (Gonzales and woods 2002). Several automated methods have been developed to process the acquired images and identify features of interest, including intensity-based methods, region-growing methods and deformable contour models. Intensity-based methods identify local features such as edges and texture in order to extract regions of interest. Region-growing methods start from a seed-point on the image and perform the segmentation task by clustering neighborhood pixels using a similarity criterion. Recently, researchers have investigated the application of genetic algorithms into the image segmentation problem (Nordin and Banzhaf 1996, Peng-Yeng 1999 and Ou et al 2004).

To improve the image quality we can use any one of the filtering technique (Mostafa et al 2001). Magnetic Resonance (MR) image enhancement are mainly used for reconstruction of missing or corrupted parts of MR images, image de-noising and image resolution enhancement. While using Magnetic Resonance (MR) images resolution enhancement face many problems like Resolution enhancement of MR images (512 x 512 pixels 2 times more), conservation of sharp edges in the image and conservation and highlighting of details. There are two designed and tested methods used for image resolution enhancement: Discrete Fourier Transform (DFT) and Discrete Wavelet Transform (DWT). Recently wavelets have been successfully used in a large number of biomedical applications (Mostafa et al 2001 and Bealy 1992). The multi-resolution framework makes wavelets into very powerful compression and filter tool and the time and frequency localization of wavelets makes it into a powerful tool for feature detection. This chapter, 2D discrete wavelet transform is used for removing noise from MRI brain image. The performance of an Image Denoising System using Discrete Wavelet Transform (DWT) is experimentally analyzed for four levels of DWT decomposition.

Some works have applied genetic algorithms (GA) to image processing and to segmentation particularly. As segmentation can be seen as a process which finds out the optimal regions partition of an image according to a criterion, GA are well adapted to achieve this goal. Indeed, GA is particularly efficient when the search space is really important and when the criterion to optimize is numerically complicated which is always the case in image processing. The main advantages of using GA for segmentation lie in their ability to determine the optimal number of regions of a segmentation result or to choose some features such as the size of the analysis window or some heuristic thresholds. The GA proposed by Holland (1975) is a general-purpose global optimization technique based on randomized search (Franti 2000). They incorporate some aspects of iterative algorithm.

A genetic algorithm is based on the idea that natural evolution is a search process that optimizes the structures it generates. An interesting characteristic of GA is their high efficiency for difficult search problems without being stuck in local extreme. In a GA, a population of individuals, described by some chromosomes, is iteratively updated by applying operators of selection, mutation and crossover to solve the problem. Each individual is evaluated by a fitness function that controls the population evolution in order to optimize it. GA can be used to find out the optimal label of each pixel, to determine the optimal parameters of a segmentation method, or to merge regions of a fine segmentation result. Concerning the fitness function, it can be an unsupervised quantitative measure of a segmentation result or a supervised one using some a priori knowledge. In this chapter, we deal with a general scheme for MRI brain tumor image segmentation that involves a GA. GA is used here as an optimization method for the optimal combination of segmentation results whose quality is quantified through an evaluation criterion. We use a general scheme to define segmentation methods by optimization.

In section 1.2 described image enhancement using discrete wavelet transform, we illustrate the proposed method by defining fitness functions in section 1.3. We use the value of an unsupervised optimization of GA evaluation criterion computed on a segmentation result. We show the efficiency of the proposed method through experimental results on brain tumor images in section 1.4. In section 1.5, we conclude and give some perspectives.

1.2 DISCRETE WAVELET TRANSFORM

An advancement of wavelet theory has taken the interest of researchers in its application to image enhancement which is done by noise removing and edge enhancement. Wavelet basis function enables DWT based filtering procedures to adapt to spatial variations. Wavelets are functions generated from one single function Ψ by dilations and translations. The basic idea of the wavelet transform is to represent any arbitrary function as a superposition of wavelets. Any such superposition decomposes the given function into different scale levels where each level is further decomposed with a resolution adapted to that level.

The DWT is identical to a hierarchical sub band system where the sub bands are logarithmically spaced

in frequency and represent octave-band decomposition. By applying DWT, the image is actually divided i.e., decomposed into four sub bands. These four sub bands arise from separable applications of vertical and horizontal filters. Figure 1.1.(a) shows the sub bands labeled LH1, HL1 and HH1 represent the finest scale wavelet coefficients, i.e., detail images while the sub band LL1 corresponds to coarse level coefficients, i.e., approximation image. Figure 1.1.(b) shows the next coarse level of wavelet coefficients, the sub band LL1 alone is further decomposed and critically sampled.

$$\begin{aligned}
 dw_{ik}^{soft} &= \text{sign}(dw_{ik}) (|dw_{ik}| - \tau) && \text{if } dw_{ik} > \tau \\
 &= 0 && \text{if } dw_{ik} \leq \tau
 \end{aligned}
 \tag{1.1}$$

(a) One-Level

(b) Two-Level

Fig 1.1 Image decomposition

Wavelet Based Denoising method relies on the fact that noise commonly manifests itself as fine-grained structure in the image and DWT provides a scale based decomposition. Thus, most of the noise tends to be represented by wavelet co-efficient at the finer scales. Discarding these coefficients would result in a natural filtering of the noise on the basis of scale. Because the coefficients at such scales also tend to be the primary carriers of edge information, this method threshold the DWT coefficients to zero if their values are below a threshold. These coefficients are mostly those corresponding to noise. The edge relating coefficients on the other hand, are usually above the threshold. The Inverse DWT of the thresholded coefficients is the denoised image.

Wavelet thresholding is a signal estimation technique that exploits the capabilities of wavelet transform for signal denoising. It removes noise by killing coefficients that are insignificant relative to some threshold, and turns out to be simple and effective, depends heavily on the choice of a thresholding parameter and the choice of this threshold determines, to a great extent the efficacy of denoising. Threshold Selection plays main role in denoising. A small threshold may yield a result close to the input, but the result may still be noisy. A large threshold on the other hand, produces a signal with a large number of zero coefficients. This leads to a smooth signal. Paying too much attention to smoothness, however, destroys details and in image processing may cause blur and artifacts. Some of thresholding methods are: (i) Hard thresholding, (ii) Soft thresholding, (iii) Semi-soft Thresholding and (iv) Quantile thresholding. In our implementation, soft thresholding method is used to analyze the performance of denoising system for DWT decomposition, since soft thresholding results in better denoising performance than other denoising methods.

Soft thresholding leads to less severe distortion of the object of the interest than other thresholding methods. Several approaches have been suggested for setting the threshold for each band of the wavelet

decomposition. A common approach is to compute the sample variance (σ^2) of the coefficients in each band and set the threshold to some multiple of standard deviation (σ) for that band. Thus, to implement a soft threshold of the DWT coefficients for a particular wavelet band, the coefficients of that band should be thresholded. The soft thresholding is generally represented by,

1.3 PROPOSED WORK FLOW

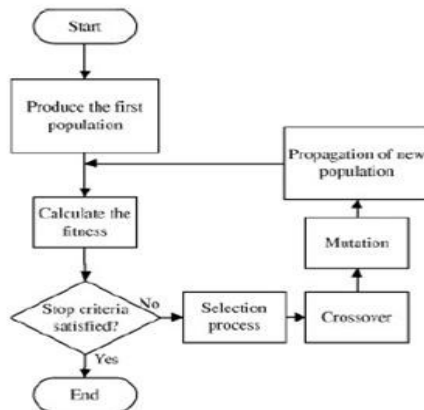


Fig 1.2. Flow for Genetic Algorithm

GENETIC ALGORITHM FOR IMAGE SEGMENTATION

Genetic algorithms determine the optimal value of a criterion by simulating the evolution of a population until survival of best fitted individuals. The survivors are individuals obtained by crossing-over, mutation and selection of individuals from the previous generation. We think that GA is a good candidate to find out the optimal combination of segmentation results for two main reasons. First one is due to the fact that an evaluation criterion is not very easy to differentiate. GA is an optimization method that does not necessitate to differentiate the fitness function but only to evaluate it. Secondly, if the population is important enough considering the size of the search space we have good guarantees that we will reach the optimal value of fitness.

GA is a special form of local search that models our own understanding of evolution. In essence a number of simultaneous agents (the population) each having an encoded state (the chromosome) perform a random walk (mutations) around the search space, while forming new solutions from combinations of existing solutions (crossover) and, thus adjusting and refocusing the efforts of the search on exceptionally good areas once located. A few important choices are made during any application of genetic algorithms, involving how to encode the population (binary, integer, decimal, etc), how to mutate the population (mutate all genes, some genes, etc), how to select the parents for crossovers (roulette wheel, tournament selection), how to perform those crossovers (uniform, single-point), and finally what fitness function to use for evaluation. Though these choices seem complex, in situations where the energy functional has hundreds or even thousands of dependent variables and parameters these few choices can yield nearly optimal values for all variables and parameters concerned.

Execution of the genetic algorithm is carried out in four steps:

1. Definition of the genotype, initial population (segmentation results) and computation of the fitness function (evaluation criterion) of each individual.
 - Genotype: the K-means segmentation result of an image S_1 is considered as an individual described by the class of each pixel.
 - Initial population: a set of individuals characterized by their genotypes. It is composed of the segmentation results to combine.
 - Fitness function: this function enables us to quantify the fitness of an individual to the environment by considering its genotype.

The fitness computation process consists of two phases. In the first phase, the clusters are formed according to the centers encoded in the chromosome under consideration. This is done by assigning each point $x_i, i=1,2,\dots,n$ to one of the clusters C_j with centre z_j such that

$$|X_i - Z_j| < |X_i - Z_p|, p = 1,2,\dots,K, p \neq j \tag{1.2}$$

All ties are resolved arbitrarily. After the clustering is done, the cluster centres encoded in the chromosome are replaced by the mean points of the respective clusters. In other words, for cluster C_i , the new centre z_i^* is computed as

$$Z_i^* = \frac{1}{n_i} \sum_{x \in C_i} X_i, i=1,2,\dots,K \tag{1.3}$$

These z_i^* s now replace the previous z_i s in the chromosome. Subsequently, the clustering metric M is computed as follows:

$$M = \sum_{i=1}^K M_i \tag{1.4}$$

$$M_i = \sum_{x_i \in C_i} \|X_j - Z_i\| \tag{1.5}$$

The fitness function is defined as $f=1/M$, so that maximization of the fitness function leads to minimization of M .

2. Selection of individuals

The selection process selects chromosomes from the mating pool directed by the survival of the fittest concept of natural genetic systems. In the proportional selection strategy adopted in this article, a chromosome is assigned a number of copies, which is proportional to its fitness in the population, which then goes into the mating pool for further genetic operations. Roulette wheel selection is one common technique that implements the proportional selection strategy.

3. Mutation and Cross-over of individuals

Individual mutation: individual's genes are modified for better adaptation in the environment. We use the non-uniform mutation process which randomly selects one chromosome x_i , and sets it as equal to a non-uniform random number:

$$\begin{aligned} x_i + (b_i - x_i)f(G) & \text{ if } r_1 < 0.5 \\ x_i - (x_i - a_i)f(G) & \text{ if } r_1 \geq 0.5 \end{aligned} \quad (1.6)$$

$$f(G) = (r_2(1 - G/G_{\max}))^b \quad (1.7)$$

r_1, r_2 : numbers in the interval $[0, 1]$

a_i, b_i : lower and upper bound of chromosome x_i

G : the current generation

G_{\max} : the maximum number of generations

b : a shape parameter

Crossover is a probabilistic process that exchanges information between two parent chromosomes for generating two child chromosomes we use the arithmetic crossover which produces two complementary linear combinations of the parents

$$\begin{aligned} X' &= aX + (1 - a)Y \\ Y' &= (1 - a)X + aY \end{aligned} \quad (1.8)$$

where

X, Y : genotype of parents

a : a number in the interval $[0, 1]$

X', Y' : genotype of the linear combinations of the parents

4. Evaluation of individual /Termination criterion

This criterion allows stopping the evolution of the population. We can consider the stability of the fitness function $f=1/M$ of the evaluation criterion of the population or set a maximal number of iterations ($G_{\max}=1000$: the maximum number of generations).

1.4 EXPERIMENTAL RESULTS

Proposed system shows the results of two types of experiments. First, System uses soft thresholding based DWT for denoising MR images. Fig1.3(a) shows the original MR image without denoising and Fig1.3 (b) shows the enhanced image for single level of decomposition. Moreover, magnetic resonance images are lesser noise densities corrupted images, single level of DWT decomposition is sufficient for this type of images. During the decomposition $\sigma = 5$, $SNR = 43.5$ and $\sigma = 50$, $SNR = 20.3$, while σ value increases value of SNR will be reduced gradually.

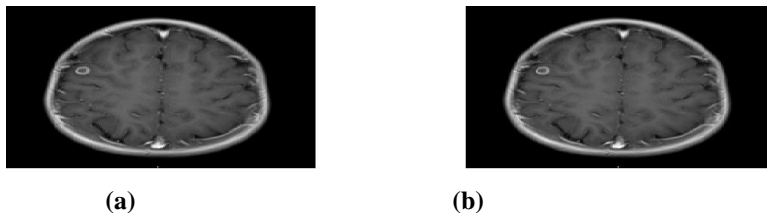


Fig 1.3 (a) original T2 weighted MRI brain tumor image(before denoising), Figure 1.3 (b) Enhanced image using DWT algorithm (soft thresholding)

Second, we present some genetic segmentation results of human MR brain tumor T1 and T2 weighted and PD modality of images. For all the following experimental results, we set the value of the selection probability to 8%, the crossing-over probability to 60% and the mutation probability to 5%. This method has been tested with more than 100 real MRI images. There are two aspects to check whether the proposed segmentation algorithm has to be used in real time clinical applications: accuracy and reliability. The segmentation results of the wavelet based genetic algorithm are shown in Figure 1.4. The computation time, accuracy and their corresponding iterations are shown in Table 1.1. Figure 1.4.a-d shows segmented images using the K-means algorithm with mean and variance as attributes with different numbers of clusters (NC) 2, 3, 6, 9, which constitutes the initial population for the GA.

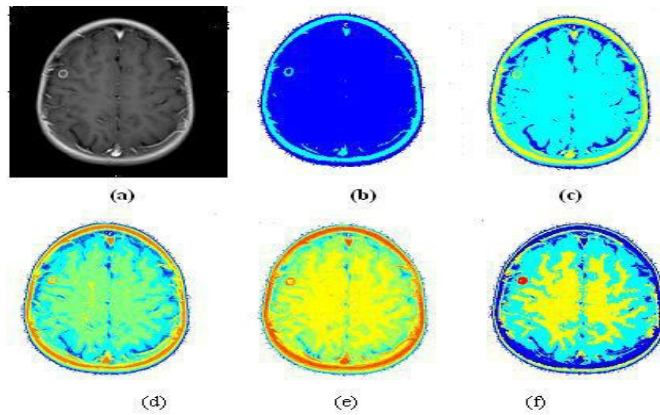


Fig 1.4 (a) Enhanced T2 weighted MRI brain tumor image, (b-e) is segmented image using wavelet based GA algorithm with NC=2,3,6,9 (Number of cluster) and (f) is a resultant segmented image with four cluster (white matter, gray matter, CSF and tumor(red)).

In this case, the genotype of an individual is a vector of size 262144 (the size of each image is 512 x 512 pixels). A gene corresponds to the label of each pixel in the considered segmentation result. Figure 1.3.e shows the final segmented result. The importance in this experiment point is that we did not specify the number of clusters we wanted. It has been automatically determined (NC=4).

Table 1.1 Comparison between genetic algorithms with ground truth

Patient (P)	Ground truth tumor size	Pop. size	Max.No iteration	Stability of fitness	Tumor volume	Execution time (Minute)	Accuracy
P1-4 yrs/male	438	4	300	1.213e-10	412	5	94.1
		5	350	1.201e-10	423	7	96.5
		6	410	1.195e-10	425	8	97.03
		7	450	1.192e-10	429	10	97.94
P4-58 yrs/male	2678	4	300	5.337e-09	2240	5	83.64
		5	350	5.162e-09	2483	8	92.71
		6	410	5.051e-09	2512	8	93.8
		7	450	4.008e-09	2604	11	97.23

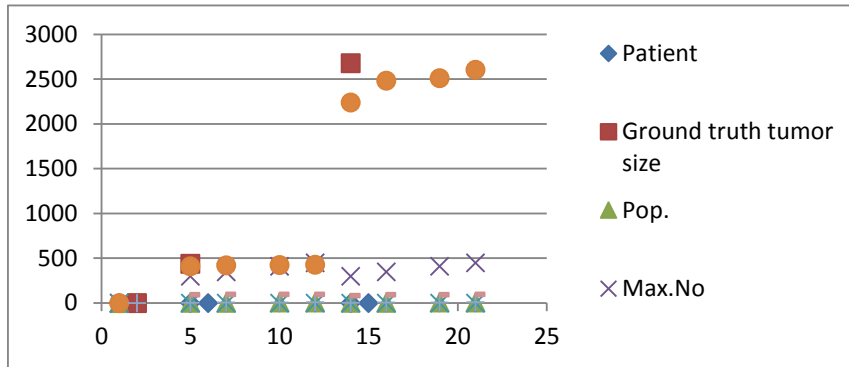


Fig 1.5 Comparative graphs with stability value

1.5 CONCLUSION

In this paper we focused on the interest of soft thresholding DWT for enhancement and genetic algorithms for image segmentation. We showed that this kind of approach can be applied either for grey-level magnetic resonance images. The developed method uses the ability of GA to solve optimization problems with a large search space (label of each pixel of an image). The developed method can also integrate some a prior knowledge (such as a local ground truth) if it is available. The developed method achieved SNR value from 20 to 44 and segmentation accuracy from 82 percent to 97 percent of detected tumor pixels based on ground truth.

References

1. Chang-Tsun Li and Randy Chiao (2003), 'Multiresolution genetic clustering algorithm for texture segmentation', Image and Vision Computing, Vol. 21, pp. 955 - 966.
2. Kim E.Y., Park S.H. and Kim H.J. (2000), 'A genetic algorithm-based segmentation of Markov random field modeled images', Signal Processing Letters, IEEE, Digital Object Identifier 10.1109/97.873564. Vol. 7, No. 11, pp. 301- 315.
3. Minglun Gong and Yee-Hong Yang (2001), 'Genetic-based multiresolution color image segmentation', Vision Interface, pp. 141–148.
4. Nordin P. and Banzhaf W. (1996), 'Programmatic compression of images and sound', In Genetic Programming 1996, Proceedings of the First Annual Conference, Koza J. R. Editors, MIT Press, pp. 345-350.
5. Ou Y., Cheng W. and Han Ferng-ching (2004), 'Based on genetic algorithm fuzzy c- means clustering algorithm', Journal of Chongqing University, Vol. 27 No. 6, pp. 89 - 92.
6. Philippe Andrey (1999), 'Genetic algorithms applied to image segmentation' Image and Vision Computing, Vol. 17, pp.175- 187.



Gogineni.Rajesh Chandra is born in 1981 at coastal Andhra Pradesh, India. I am graduated from Acharya Nagarjuna University and post graduated from JNTU A University. Now I am a part time research scholar of Acharya Nagarjuna University under guidance of Dr.K.Ramchand H Rao and working as an Asst Professor in the Department of ECM , K L University



Dr.Kolasani Ramchand H Rao graduated from Gulbarga University and received his doctoral Degree from Acharya nagarjuna University. And he is working as Professor in Computer Science & Engg at ASN Women's Engineering College ,Tenali,Guntur(Dt),Andhra pradesh and presently under his guidance 8 members are doing their doctoral degree in Acharya Nagarjuna University. He has published 20 research papers in IEEE & ACM Conferences ,