

DETECTION OF MENINGIOMA TISSUE OF TUMOR IN BRAIN USING GENETIC ALGORITHM

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ABSTRACT

National Brain Tumor society of US; a research center established to discover aim proved treatment for brain tumor patients. Meningioma is found to be very dangerous brain tumor disease for humans. These days' brain tumor patients are suffering with high expenditure for diagnosing the conditions of tumors in brain. The chief objective of the work is to find the accurate condition of tumor in brain with low cost. In this thesis, gray scale images are obtained from new MRI scanning image by applying MATLAB. From the obtained images, all histograms and address of image method with LIM dependent Image matching method are generated for diagnosing the exact location of the tumor in Human brain. due to lack of methods, to diagnose the exact position of tumors in Brain, the patients are suffering a lot. With the advent of brain imaging methods, the diagnosis of the diseases is made viable. The analysis of Brain image is possible through many methods like X-Rays, CT scans, PET Images, MRI Images, fMRI Images. MRI and fMRI images provide detailed information of patient's brain and are available in Digital Imaging and Communications in Medicine (DICOM) format. It has contained the detailed data of brain as multimedia images. Meningioma is a Brain tumor that easily damages the brain function and spinal card. This kind of tumors is found in humans due to the radiation effect and genetic disorders of nervous systems. The National Brain Tumor society of US is carrying out a research on meningioma.

INTRODUCTION

The symptoms of Meningioma brain tumor are communication problems, lack of feeling, weakness in arms and legs, Vision problems and Recurrent Headache. This slowly develops into tumor in brain and hence it is very difficult to diagnose its position. In this thesis,, various categories of Mining methods are applied to find this tumor by relating the new brain image with available images. Generally there are different types of brain imaging techniques. The input images are the MRI brain images for this proposed work.Diagnosis of tumor in brain is one of the most common problems in current research. Segmentation of image is the most

common technique applied in image processing to extract the tumor abnormal portion in brain. Tumor in brain is defined as an abnormal tissue part in which bad cell will grow and multiply speedily and wildly. Various categories of techniques have been proposed in the concept of image segmentation for the detection of brain tumor.The objective of this work is to apply methods for the segmentation of image to diagnose tumor in brain. Segmentation and classification of tumor in brain is computed with the data of image tomography, which is a significant concern and time taking consuming performance for many of the experts. Image segmentation process is a tough part of the medical imaging that is due to the poor contrast image and artefacts, which may result in disseminate or

missing boundaries of tissues. This work mostly gives discrete wavelet based on GA to detect the brain MR images. In the first stage the images of MR are enhanced by wavelet discrete descriptor, of which GA was applied in finding the pixel of tumour. GA is used in order to find the good combination of extracted data from the selected criteria. At present this approach will use supervised learning of K-Mean clustering techniques of GA in guiding the Evolutionary algorithm to find and search the sub-optimal or optimal partition of datasets. The major work is to comprehend the requirement of non-trivial process of search based on intrinsic NP-complete process. In solving the problem based on the appropriate coding in genetic algorithm, the basic key process in implementation is discussed. This proposed work demonstrates the effectiveness of GA in automatic and image unsupervised segmentation process. Certain examples in Brain MR Tumor segmentation is presented and results of overall are been discussed. Bio-Medical Imaging has been performed in different modalities, which uses MRI, ultrasound, CT and etc. Segmentation process is typically and manually used by various types of experts and physicians as part of planning in treatment and clinical trial of diagnosis. Based on the rapid amount of increase in available data and the features of complexity in interest features, it is essential for the development of automatic segmentation techniques that speeds up the process

to assist and diagnose the image for better clinical trials.

DISCRETE WAVELET TRANSFORM

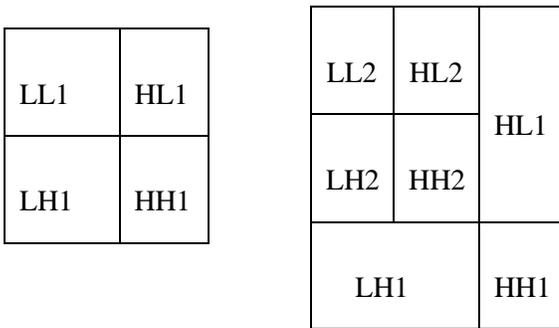
The advancement in the theory of wavelet has taken a key interest in research area for image enhancement related applications that removes noise and enhances the edge contrast of an image.

$$dw^{\text{soft}} = \text{sign}(dw_a)(|dw_a| - a) \quad \text{if } dw_a > a \quad (4.1)$$

$$= 0 \quad \text{if } dw_{ik} \leq a$$

The above Functions based on DWT procedure are used for filtering the variations in spatial. Functions related to Wavelets should be generated based on single based function of 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 identical DWT used for hierarchical sub-band system that uses sub-bands logarithmically which spaces to find the frequency of band-octave decomposition. Based on the DWT application on image and its division i.e the image region is decomposed into 4 sub-bands and each of these sub-bands arises a

separate view of horizontal and vertical application using filters. Figure 4.4(a), uses a sub-band, which are labeled as HL1, LH1 and HH1 that represent the finest wavelet scale coefficients that is Images details of which are based on sub-band LL1 will correspond to a particular course of coefficients level. The image approximation and its Figure 4.4(b) are shown below with its level of coefficient wavelets and the further decomposition of sub-band LL1 from certain critical images of sampled.



A) ONE LEVEL

(B) TWO-LEVEL

Figure 1 Decomposition of Image

A wavelet De-noising based technique relies on certain facts that commonly possess noise and has a structure of fine grained in an image with the DWT scale that is based on decomposition. Thus, mostly image noise tends to represent the wavelet coefficient in a scalar of finer level. This discarding coefficient results in filtering the natural image of noise on the scale of base. The coefficient of this case leads to carry the primary edge of information. The threshold

method of DWT leads to its value of zero coefficients, as if these values are very less and below threshold. These values of coefficients mostly correspond to noise. The corresponding edges relate to the coefficients value on the other hand usually are above the frequency of threshold, DWT inverse of its threshold and of coefficients with its image de-noise. Threshold based wavelet can be estimated with the technique that exploits the performance capabilities for transformation of wavelet using signal de-noising. It also major role in de-noising. 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 in image processing that may cause blur and artefacts. Some of the threshold methods are:

- (i) Hard threshold method
- (ii) Soft threshold method
- (iii) Semi-soft threshold method
- (iv) Quintile threshold method

The proposed brain tumor detection technique (LIM based image matching model) based on Berkeley wavelet

transform (BWT) and support vector machine (SVM) classifier is compared with the ANFIS, Back Propagation, and -NN classifier on the basis of performance measure such as sensitivity, specificity, and accuracy. The detailed analysis of performance measures is shown in Figure 4.12 and, through the performance measure, it is depicted that the performance of the proposed methodology has significantly improved the tumor identification compared with the ANFIS, Back Propagation, and -NN based classification techniques[206].

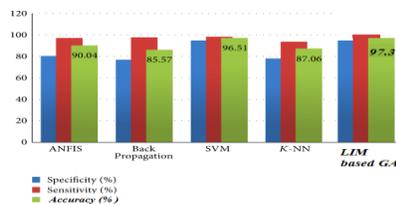


Figure 2: Comparative analysis of classifier

GA FOR IMAGE SEGMENTATION

Genetic Algorithm (GA) is variant type of form to find the local search using the models of different types depending on certain understanding related to evolution. In certain sense, the number of agents who are simultaneously having a certain state of encoding, random performance walk around

the linear space search, which forms a solution of combination related to the combined way of gaining existing solutions over the crossover and then re-adjust the newly generated solution with the combination of existing cross over forms with the refocused and adjusted effort search in gaining the exceptional areas of good location. Certain important measures of choice are to be made based on the genetic method related application that involves the encoding process of population(integer, decimal, binary and etc.), it say mutation of population among, genes, gene to gene mutation etc. Though it is a process to choose the complex in certain situations based on the functional energy and to gain certain hundred and thousands of variable dependencies based on certain parametric features and choices which can yield a new value of optimality on certain variance of variables and concern parameters values.

The genetic algorithm execution is carried out in four steps:

Genotype definition, 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.
- Fitness function: it enables to quantify the fitness of an individual to the environment by considering ones genotype.

2. Selection of individuals

The selection process chooses chromosomes from the mating pool directed by the endurance of the fittest theory of natural genetic systems. In the proportional selection approach embraced in this work, a chromosome is allocated to a number of copies that is proportional to its fitness in the population, which then goes into the mating pool for advance genetic processes. Roulette wheel selection is one of the common methods that apply the proportional selection strategy.

3. Mutation and Cross-over of individuals

Individual mutation: Individual's genes are customized for better adaptation to the environment. The used non-uniform mutation

process that randomly selects one chromosome x_i , and sets it as equal to a non-uniform random number:

$$x_i + (b_i - x_i)f(G) \quad \text{if } r_1 < 0.5 \tag{4.2}$$

$$x_i - (x_i - a_i)f(G) \quad \text{if } r_1 \geq 0.5 \tag{4.3}$$

$$f(G) = (r_2(1 - G/G_{max}))^b \tag{4.4}$$

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 and the use of arithmetic crossover produces two complementary linear combinations of the parents

$$X' = aX + (1 - a)Y \tag{4.5}$$

$$Y' = (1 - a)X + aY \tag{4.6}$$

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. The stability of the fitness function $f=1/M$ of the evaluation criterion of the population or set a maximal number of iterations (Gmax=1000: the maximum number of generations) is considered.

Table 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(Minutes)	Accuracy
P1-4 Years/male	438	4	300	1.223e-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

The focus on the interest of soft threshold method DWT for enhancement and Segmentation of image in genetic algorithms is shown its kind in various approaches and are applied for either level of gray or resonance magnetic images. The method of development will use GA that has the ability to optimize and solve problems of space large search. The methods developed are integrated with a knowledge of prior from the ground

local truth, if they are available, the method of developed will achieve value of SNR ranging from 22 to 46 with an accuracy value of segmentation of 85% to 98% in tumour detection of pixels from truth ground. To overcome the problems in detection of meningioma in brain this method is developed using LIM based image mining for better detection and performance. When the particular concept is applied then first of all, the new image information like the patient's sex, age is required. Then the selection of exact dataset from the 6 types of datasets has to be carried out. Then the gray scale image of a patient can be generated from the DICOM file of a patient, then the black and white histograms of new image is generated and similarly the black and white histograms of all datasets can be obtained. Then the address of new image can be created and so for all images in dataset. Then the address of new image can be matched with existing dataset's all images. If any matches are found among new image and existing image then the existing image then automatically be selected. Once there is availability background information of existing image the identification of the position of new image is easily possible and that leads to the easy identification of the patient condition.

CONCLUSION

In this work if the number of similarities in between new image and existing images are zero means brain condition is good. If the number of similarities are high means that patient have Meningioma tumour in brain, the focus is on the interest of soft threshold DWT for enhancement and Segmentation of image in genetic algorithms showed of its kind in various approaches and is applied for either level of gray or resonance magnetic images. The method of development uses GA, which has the ability to optimize and solve problems

of space large search. The methods developed are integrated with the knowledge of prior, from the ground local truth, if they are available, the method developed achieves value of SNR ranging from 22 to 46 with an accuracy value of segmentation of 85% to 98% in tumor detection of pixels from truth ground. In this chapter the representation for creation of new dataset and identified the similarities between new image with existing images and generation of a gray scale image from DICOM format's MRI image files and after then create the different types of histograms of new image and generates the address of images are explained..