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SEGMENTATION OF BRAIN TUMOUR MR IMAGES IN SOFT COMPUTING TECHNIQUES

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ABSTRACT

The fitness function in Genetic algorithm (GA) based Fuzzy C-Means (FCM) and the morphological operations are widely used to extract tumour from MR medical image segmentation, but suffer uncertainty and vagueness in diagnosis. This paper, concentrates on the foremost and important method of segmentation. It is simple and produces a complete division of the image, when applied to medical image analysis, due to sensitivity to noise and poor detection of thin or low signal to noise ratio structure. The present approach helps to correct some drawbacks, on the initial stage of genetic algorithm and probability-based Fuzzy c-means which are close to the original brain images.

Keywords: *Image, Genetic Algorithm, Segmentation, Brain Image, Probability Based Fuzzy C-Means, Morphological Operations.*

1. INTRODUCTION

Though there is fabulous progress in medical image acquisition devices, they are subject to noise and bias field. There is a possibility for improper acquisition, faulty device or process occurring on the person's habitual movements during the acquisition of images. Thus the artifacts make the segmentation of medical images more challenging. The magnetic resonance (MR) brain image is repeatedly segmented into white matter (WM), gray matter (GM), and cerebral spinal fluid (CSF) and such division is vital in understanding the functioning of the brain, treatment process, and the quantitative analysis. In the medical image processing soft computing is introduced on reason that it is an effective approach to handle uncertainties inherent to the acquired image data. During the past, fuzzy connected approaches to image segmentation, fuzzy clustering methods specific to brain MR image segmentation, and statistical atlases and fuzzy models for object recognition have come in to being. Soft computing approaches include fuzzy logic, neural networks, support vector machines, evolutionary computation, probabilistic approaches, and chaos theory Recently, the initial stage of genetic algorithm and probability-based Fuzzy C-Means are applied to image segmentation. The algorithm proposed in this paper belongs to the category of the hybrid segmentation techniques It is attempting to clarify the embedding approaches with a genetic algorithm probability based Fuzzy C-Means (GAPBFCM). The genetic algorithm combines with a probability of Fuzzy C-Means which enhances the accuracy of the output of brain tumor images. The experimental result demonstrates that the algorithm developed is more efficient and has a reasonable segmentation effect.

2. RELATED WORKS

Parametric entropy puts forward an adaptability to test the pixel scene to the best of suitability.. It endeavored to utilize entropy-based strategies for improving the division process by recognizing the edge required to overcome the problem of the limit esteems prompting the higher closures of the histogram. To take care of this issue and improve the image differentiation a picture division technique, namely perceptual difference model (PDM) is used. The strategy can decide the ideal edge of the Electrical impedance tomography (EIT) picture by limiting the separation of the figured projection of the fragmented image as well as the deliberate projection information so as to; take full utilization of the first projection information as a divisional standard. A Fully Convolutional

Network (FCN) is proposed for semantic segmentation [1]. The FCN model is trained in an end-to-end style, and is capable to allow input images with distinct sizes for dense output prediction. A hop architecture is also embedded to incorporate semantic information from a deep layer showing differentiation from a shallow layer for pixel wise calculation. A U-Net architecture for lesion segmentation is also suggested [2]. The replica includes encoding as well as decoding paths. Skip-layers are also used to enable every decoding layer to accept inputs from its previous layer as well as its symmetric encoding layer. The network confirmed remarkable performances on numerous biomedical segmentation tasks. Convolutional Neural Networks (CNN) are also considered to measure the quality of an image-segmentation pair [3]. The CNN employed the learned model and also the backpropagation algorithm to perform image segmentation in an iterative procedure. Gossip Networks is proposed to permit the communication between the foreground and background streams. Besides generating segmentation masks from scratch, the associated network was able to improve the outputs produced by other segmentation methods (e.g. U-Net). The present work evaluated the usage of biomedical data sets pertaining to segmentation of skin lesions, teeth, iris, *e.tc.* The developed model outperformed U-Net and U-Net with dilated convolutions (Dilated-Net). Generative adversarial networks (GANs) for skin lesion segmentation were employed [4]. An additional critic deep learning CNN model was formulated, over the segmented FCN network (such as U-Net). The segmented synthesized segmentation masks the critic network synthesized masks from real ground truth (GT). Their work indicated that the incorporation of the critic model with the segmented network showed a better performance. They evaluated the added critic CNN by combining it with the U-Net which outperformed U-Net in a dermofit skin lesion data set. The Skin Net architecture was a modified version of U-Net [5]. It employed dense convolution blocks, instead of convolution layers, in the encoder and decoder paths. It also incorporated dilated convolutions in the lowest encoder layer, in order to better global information. Their study further [6] used the Faster region-based Convolutional neural network (Faster-RCNN) as well as Skin Net for lesion detection and localization. Faster-RCNN was used to create the bounding boxes of the detected lesion regions, which were subsequently cropped for lesion segmentation using SkinNet. Their two-stage system gives an idea on the superior performance for lesion segmentation. Other deep learning networks have also been proposed for lesion segmentation. A multi-scale residual U-Net architecture by way of multi-scale residual connections for lesion segmentation was identified [7]. Their model employed multi-scale residual connections to tackle information loss in the encoding stages in the U-Net. The model is observed to be better than other state-of-the-art networks such as Convolutional-Deconvolutional neural networks [8] for diverse challenging lesion segmentation tasks. Transfer learning based on the pre-trained Fully convolutional networks (FCN) models was performed for multi-class skin lesion segmentation [9]. There are other state-of-the-art hybrid clustering models proposed in recent years for biomedical image segmentation. Genetic Algorithm (GA) and Particle Swarm optimization (PSO) was employed [9] to obtain the initial centroids of the K-Means (KM) clustering model. The K-Means algorithm was subsequently used for the melanoma lesion segmentation. K-Means clustering and ensemble regression were used for skin lesion segmentation [10]. Multiple density clustering algorithms was used to classify the key parameters of the region growing performance for lesion segmentation [11]. An ensemble models for image segmentation was evolved by means of enhanced PSO of clusters which also identified a process using a real-coded variable string length method [12].It takes in to account the images contaminated by noise. The developed model achieved better performances in comparison with those of K-Means(KM), Fuzzy C-Means (FCM) and also several Fuzzy C-Means (FCM) variants. A modified particle swarm optimization (PSO) representation in combination with Kernelized fuzzy entropy clustering (KFEC) was applied for Magnetic Resonance Imaging (MRI) for brain image segmentation [13]. Their particle swarm optimization (PSO) model employed the Halton sequence for population initialization and also an adaptive inertia weight to accelerate convergence. The Kernelized fuzzy entropy clustering (KFEC), incorporated local spatial information and bias correction for particle evaluation. The model outperformed five other competitors in the estimate by means of noisy simulation and real MRI brain images. It is proposed to have an enhanced discrete cosine transformed (DCT)- based nonlocal Fuzzy C-Means (DCT-NLFCM) technique for MRI brain image segmentation. It employed discrete cosine transformed (DCT) domain pre-processed images to attain fast segmentation in comparison by way of other unsupervised discrete cosine transformed (DCT)-based methods. The empirical results indicated that their model was invariant to noise in the midst of superior segmentation performances [14]. A multi-objective spatial fuzzy clustering model was also developed [15] for image segmentation. Non-dominated Sorting Genetic Algorithm-II (NSGA-II) was incorporated through the clustering model to perform image segmentation. The objective function took into account of the intra-cluster fuzzy compactness as well as inter-cluster fuzzy separation derived from non-local spatial information. A cluster validity index was also created to help retrieve the best solution amongst the generated non-dominated individuals. A bacterial foraging evolutionary algorithm was proposed [16] for cell image segmentation. It works on the edge detection model so as to overcome the limitation of the initialization sensitivity of the traditional edge detectors. It considered a bright pixel density map for estimating nutrient concentration. By using synthetic and real cell images, the concerned model achieved an improved segmentation accuracy in comparison with those of several well-known traditional edge detectors such as the active contour model and the canny edge detector. Accomplished nucleus-cytoplasm segmentation for blood cancer detection via a hybrid model of Fuzzy C-Means (FCM) clustering integrated with the Genetic Algorithm (GA) was accomplished [17]. Their fitness took both intra- and inter-cluster variances into account. The hybrid model showed impressive performances and outperformed the state-of-the-art FCM variants for nucleus-cytoplasm segmentation using the Acute Lymphoblastic Leukemia image database 2 (ALL-IDB2). Optic disc (OD) segmentation is used [18] in medical images and applied in a variation model by way of the boundary, shape, and region energies. A sparse coding based technique was initially used to perform optic disc localization. Subsequently, a region of interest was cropped based on the localized disc center and also the surrounding area of Optical disc (OD) in the image. Blood vessel removal was also conducted using morphological operations before segmentation. The Hough transform was conducted to attain the initial boundary information. The three energies involved are the phase-based boundary, Principal Components Analysis (PCA)-based shape and region energies which, were used to enhance the OD segmentation outcome. Parallel algorithm cerebrum MRI image utilizing Rough-fuzzy clustering algorithm was considered by morphological separation of the mis-clustered areas which can unavoidably be framed . A replacement parallel algorithm was designed for clustering based on the model of the neighbor[22]. If two documents are similar, they are considered as neighbors of every other. The new algorithm is known as Parallel K-Means which supported the neighbors (PKBN). It is a parallel sort of Sequential K-Means Based on Neighbors (SKBN). PKBN takes into account for a message-passing multiprocessor system and is implemented on a cluster of Linux workstations. A bottleneck theory and centroid based clustering was also suggested [19]. The clustering method is used in large-scale data analysis. It can enhance the calculation speed by increasing the partition number. The above theory makes a decision of the initial clustering centers. A centroid based clustering-based objective method is proposed to make a decision so as to have the last number of clusters without human intervention.

3. METHODOLOGY

This section depicts the flow of the complete algorithm for segmentation of a brain MR images utilizing soft computing techniques such as an initial stage of a genetic algorithm along with a probability based Fuzzy C-Means. The image processing primarily comprises three aspects [20]

1. Introduction of the image through optical scanner or via digital photography.
2. Deploying the image which contains data compression, image enhancement.
. 3. Changed image with full information or report based on image analysis.

Image processing has five steps and are given below.

1. Detection the objects that are not visible.

2. Image sharpening and restoration to construct a better image.

3. Image retrieval is to follow for the image of interest.
4. Measurement of objects in an image.
5. Image recognition to differentiate the portion.

The proposed framework comprises preprocessing, the initial stage of the genetic algorithm (EGA), probability based Fuzzy C-Means (PBFCM) and final document with its validation as shown in fig. 1.

4. GENETIC ALGORITHM

Genetic Algorithms (GAs) are adaptive methods which may be utilized to solve over-segmentation, over-lapping and boundary displacement problems. They are based on the genetic processes of biological organisms. Over many generations, natural populations evolve in accordance with the principles of *natural selection and survival of the* "*fittest*", as stated by Charles Darwin in The Origin of Species. By mimicking this process, genetic algorithms are able to "*evolve*" solutions to real-world problems, if they have been suitably encoded. For instance, GAs can be utilized to design bridge structures, for maximum strength/weight ratio, or to resolve the least wasteful design for cutting shapes from cloth. They can likewise be utilized for online process control, for example, in a chemical plant, or else load balancing on a multi-processor personal computer method. During the procreative period of the genetic algorithm (GA), people are preferred from the population. They are recombined, producing offspring so as to have the next generation. Parents are selected randomly from the population using a scheme which favors the ideally fitted individuals. In a generation, good individuals will probably be selected several times. Poor ones may not be able to perform. Their chromosomes are recombined, typically using the mechanisms of crossover and mutation when the two parents are selected. The most basic forms of these operators are as follows.

4.1 CROSSOVER

The crossover cuts the chromosome strings at some randomly chosen position, to produce "*head*" and "*tail*" segments. To produce two new full-length chromosomes the tail segments are then swapped. Each of the two offsprings inherit some genes from each parent. This is known as single point crossover. Crossover is not generally applied to all pairs of individuals chosen for mating. A random choice is made, where the likelihood of crossover is typically between 0.6 and 1.0. Simply by duplicating the parents, if crossover is not applied offspring are produced. This gives each individual a chance of passing on its genes without the disruption of crossover as shown below.

4.2 MUTATION

Mutation applies to each child individually after crossover. It by chance modify each gene by means of a small probability (typically 0.001). The traditional view is that crossover is an important techniques for rapidly exploring a search space. Mutation provides a small amount of random search, and helps ensure that no point in the search space has a zero probability of being examined as shown below.

5. PROBABILITY

Frequently two or more events are grouped so as to make it. capable of standing for use in set theoretic operations. Take for granted a sample space S along with two events A and B:

- Complement A (also A0): all elements of S that are not in A;
- Subset A ⊆ B: all elements of A are also in elements of B;
- Union A ∪ B: all elements of S that are in A or B;
- Intersection A ∩ B: all elements of S that are in A and B. If A plus B are two events, subsequently the conditional probability of B given A is: PROBABILITY=A+B/2

6. FUZZY C-MEANS (FCM) ALGORITHM

FCM is one of the most popular fuzzy clustering techniques in seventies [21] and eventua/lly modified [22] in 1981. It is an unsupervised method of analyzing the data which do not force an object to belong to a specific subject. This allows to have a data point so as to take membership between 0 and 1 and it belongs to all groups of the cluster. Class Center is used in membership function for which data close to that class is having more relationship.[23,24] The FCM makes use of prior information in segmentation. The FCM algorithm consists of the following steps:

Let X = {x1, x2, x3 ..., xn} be the set of data points and V = {v1, v2, v3 ..., vc} be the set of centers.

1) Randomly select 'c' cluster centers.

2) Estimate the fuzzy membership 'μij' using in below equ.1.

$$K=1$$

$$\mu_{ij}=1/\Sigma(d_{ij}/d_{ik})^{(2/m-1)} \qquad (1)$$

3) Work out the fuzzy centers 'vj ' using in below

equ.2

$$V_j = \left(\sum_{I=1}^{n} (\mu_{ij})^{n} x_i / \sum_{I=1}^{n} (\mu_{ij})^{m} \right), \forall j = 1,2, \ldots c \qquad (2)$$

4) Repeat step 1) and 2) until the minimum 'J' value is achieved or $||U(k+1) - U(k)|| < \beta$.

Where,

k refers the iteration step.

β refers the termination criterion between 0 and 1.

$U = (\mu_{ij})n*c$' is the fuzzy membership matrix.

J refers the objective function.

After performing FCM clustering, each pixel is assigned to the cluster for which its membership value is maximized. As high as 989 images based on the intensity distribution were obtained using the histogram of the image. The threshold value is calculated by taking the mean of a maximum of cluster as 1 and minimum of cluster as 2 or maximum of cluster as 2 and minimum of cluster as 3. This technique of threshold variety takes into account of the intensity distribution of the image. This choice helps in obtaining optimumthreshold values for different images obtained under dissimilar conditions. The yield of this stage is a binary image (Bi).

7. EXPERIMENTAL ANALYSIS

This work mainly focuses on the identification of brain tumor in an efficient Fig.2. MR Brain images collected from a local Scan centre and utilized for this study manner with a lesser rate of similarity by using soft computing System so that surgeon can have a clear knowledge about the tumor and its location in the brain. The brain tumor location can be spotted by applying our proposed algorithm using Matlab Simulator. A GUI (Graphical User Interface) is created to make the system user

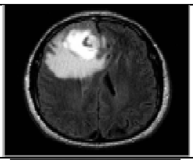
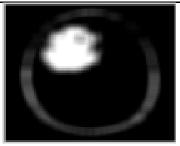
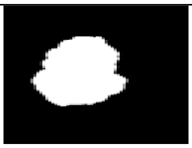
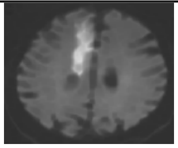
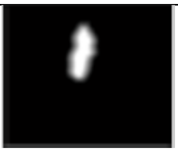
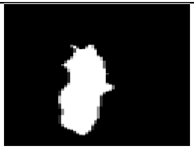
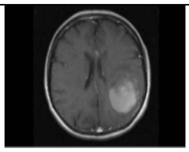
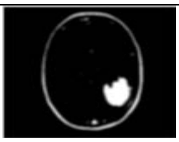
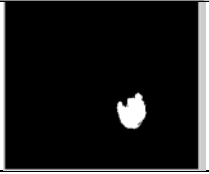
friendly. In this design there is genetic algorithm and also combination of probability

$$J(A,B) = \frac{S(A \cap B)}{S(A \cup B)} \qquad (3)$$

and could be converted to Dice overlap score by

$$J(A,B) = 2 \frac{J(A,B)}{1+J(A,B)} \qquad (4)$$

Based on Fuzzy C-Means predict the brain tumor Results and discussion images show the final detected a portion of brain MR images.

SNO	INPUT IMAGES	PRE-PROCESSED IMAGES	GROUND TRUTH IMAGES	SEGMENTED IMAGES
I1				
I2				
I3				

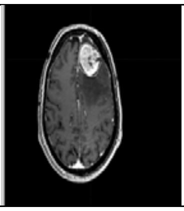
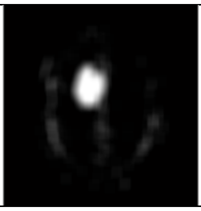
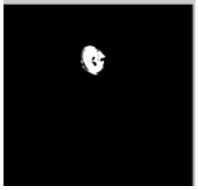
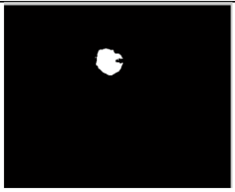
I4				

Fig.2. MR Brain Images Collected From A Local Scan Centre And Utilized For This Study.

In Fig.2 the first column represents the input images of the various real time MR images. The second column represents the pre-processed images. In this Gaussian filter is used as it is a linear filter. Here, in the medical images it is usually used to blur or reduce the noise. The main reason for using a Gaussian filter is it to remove noise keep the edges relatively sharp and also to make it faster than other filter through multiplication and addition The third column of the image refers to the ground truth images. Here, white pixel for I1 image is 6.43mm, I2 image is 3.28mm, I3 image is 1.67mm and I4 image is 1.40 mm . The fourth column stands for the segmented image of the enhanced probability based Fuzzy C –means and active contour. Here, the number of white pixels of I1 image is 6.21mm, I2 image is 3.10mm, I3 image is1.57mm and I4 image is 1.28mm. Thus, white pixel of the segmented image is compared with the manually segmented ground truth image. It indicate that the error rate of number of pixels of I1 image is 0.22mm, I2 image is 0.18mm, I3 image is 0.1mm and I4 image is 0.12mm. Usually there is variation in pixels since the brain tumor originates with the white matter and exhibit irregular growth patterns along with the white matter fiber as a result of the irregular boundaries. Since the average error of white pixels is 0.1mm and also the difference of pixel values under 0.2mm very closely matches with the ground truth image across all grades, leading to more accurate method of brain tumour segmentation *i.e.,* Enhanced probability based Fuzzy C- Means and Active Contour are a to be better than the other algorithms .

7.1. Performance Measures Sensitivity

Sensitivity represents the medical test being used to correctly identify the clinical issue of the patients which is mathematically, expressed as:

$$\text{Sensitivity}=\frac{\text{Number of true positive}}{\text{Number of true positive + Number of false Negative}} \qquad (5)$$

SPECIFICITY

In diagnosing the disease specificity is used which relates to the test's ability to reject healthy patients without a condition. Specificity of a test is the proportion of healthy patients known not to have the disease, who will test negative Mathematically, It is given as:

$$\text{Specificity}=\frac{\text{Number of true negative}}{\text{Number of true negative + Number of false positive}} \qquad (6)$$

ACCURACY

An *accuracy* is directly concerned with the factual results such as true positives and true negatives among the total number of case Milieu lucid is composed by means of semantics, which is referred as "*Accuracy*". It is expressed as:.

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

TP=True positive is indicates true condition.

TN=True negative is one that doesn’t detect the condition is not true.

FP= False positive is one that detects the condition is not true.

FN= False negative is one that doesn’t detect the condition is true

Table 1: Comparison of Jaccard Index (Similarity)

IMG	FCM	EPBFCM	GAPBFCM
I1	0.8738	0.9268	0.9866
I2	0.7896	0.8881	0.9229
I3	0.8534	0.9440	0.9878
I4	0.7724	0.8789	0.9203
AVG	0.8223	0.90945	0.9544

Outcome in segmentation overlapping ,over-segmentation,and boundary displacement in brain tumor is assessed using Jaccard Index (J), Dice verlap (D) and Accuracy. The Jaccard index, also known as the Jaccard similarity coefficient by Paul Jaccard, is a statistical tool used for comparingthe similarity and diversity of sample se ts. Jaccard Index (J) of two sets A and B is given in equ4

Table2: Comparison of Dice Overlap

IMG	FCM	EPBFCM	IGAPBFCM
I1	0.7759	0.8636	0.9736
I2	0.6524	0.7988	0.8570
I3	0.7444	0.8940	0.9760
I4	0.6292	07840	0.8524
AVG	0.6997	0.8353	0.9147

In Table 1, Jaccard index expresses the high similarity and its 0.91 which is near to one. Jaccard index has a value in the range of 0 to 1. The above table indicates the comparison of Fuzzy C-Means, and Enhanced Probability based Fuzzy C-Means of Jaccard Index. Table 2 describes the Dice overlapping segmentation which outperforms disjoint segment in the low false alarm rate to concentrate on the boundary of the segments. The Dice overlap is defined as 2* Jaccard index divided by 1+Jaccard index. Here Jaccard index is used for evaluating the similarity. The Dice overlap is high.

Table 3: Comparison of Accuracy

IMG	FCM	EPBFCM	GAPBFCM
I1	90.35	91.46	97.36
I2	94.18	95.05	96.97
I3	81.29	97.16	97.20
I4	86.41	96.79	96.83
AVG	88.05	95.11	97.09

In Table 3, the accuracy is defined as the condition in which the result is true *i.e.*, as simple as freedom from error or the defected portion of an object. The Tables 1,2 and 3 are based on the initialization of genetic algorithm and enhanced probability based fuzzy c-means. On comparing the overall performance, of genetic algorithm probability based Fuzzy C-Means (GAPBFCM) are observed to be better than the fuzzy c-means threshold and fuzzy c-means. The overall accuracy of ay Fuzzy C-Means is 88.05%, a Fuzzy C-Means threshold is 93.34% , probability based Fuzzy C-Means is 95.11%. and initializing genetic algorithm and probability based Fuzzy C-Means is 97.09%.

8 CONCLUSION

The method developed is compared to Fuzzy C-Means (FCM), probability based Fuzzy C-Means (PBFCM) and Inilised Genetic algorithm based probability based Fuzzy C-Means (IGAPBFCM) with their Dice overlap and the Jaccard coefficients With the comparisons of these algorithms, the method now proposed performs very well with the highest coefficients values. It eliminates the drawbacks of over segmentation, over-lapping and boundary displacement Due to these advantages, IGAPBFCM showed enhanced algorithm for segmenting MR brain images. A fair conclusions can be drawn from the results reported in this paper that 1. The IGAPBFCM is superior to other Fuzzy C-Means algorithms. Also, the performance is significantly higher than other C-Means. 2. IGAPBFCM appears to be a soft computing algorithm. 3. The indices such as dice, jaccard based on the theory of IGAPBFCM provide good quantitative measures.

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