A Novel Method of Multi-Region Tumour segmentation in Brain MRI images Using Grid-based segmentation optimized by Bee swarm intelligence

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**Abstract:** Multi-region Segmentation plays a very important role in various medical image segmentation especially brain tumours detection in MRI images. A novel algorithm for multi-region brain tumour segmentation using grid-based segmentation with bee swarm intelligence and k-means clustering (GIS-BEE-KM) is proposed in this work. The proposed segmentation algorithm will be very effective for grid computing, as it seems to possess specific tasks of image information and detection in order to obtain a detailed and accurate image analysis. Grid-based segmentation decreases overall computation time and reduces the complexity. Various informative region such as ceribro spinal fluid, gray matter and white matter segmented by using proposed algorithm which will be most usefull region to stdy and characterize tumour. Bee swarm optimization used for efficient parameter optimization to improve the accuracy performance.

**Keywords:** MRI Images, Brain tumour segmentation, Bee Swarm Intelligence, Grid Based Segmentation.

1. INTRODUCTION

The segmentation of brain MRI data as normal and abnormal are very important to the affected and unaffected patients [12]. Due to the shortage of radiologists and the large volume of MRI data make such readings labor intensive and cost expensive. This problem leads for an automated system for analyzing and classifying MRI data’s. In dealing with human life, theresults must be very accurate and precise. A robust framework for segmentation of medical images could lead to better tumor detection. Increase the efficiency of detection and as a whole the system will drastically reduce the time and cost to detect tumors.

Image segmentation is a process of splitting a whole image into small segments (pixels or blocks). The main objective of image segmentation is to change the appearance of the image into a suitable form for analysis. It is mainly used to find some objects from images or to find the boundaries. More precisely, image segmentation is the process of assigning a label to every pixel in an image such that pixels with the same label share certain characteristics. Practically image segmentation is widely used in several applications such as video surveillance, Traffic control system, face reorganization and biomedical imaging analysis.

Image segmentation and classification of MRI images plays a huge role in biomedical imaging analysis. MRI images of human organs contains complex structures it’s very difficult to segment the portions accurately. Segmentation of MRI images plays a crucial role in a neuroscience with many applications such as:

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clinical diagnosis of neuron-degenerative and psychiatric disorders, treatment evaluation, and surgical planning. Several techniques are widely used to segment MRI brain images. They can be divided into four groups [1]: region-based techniques, pixel-based classification techniques, threshold-based techniques, and model-based techniques.

Region based segmentation [13] also called as pixel based segmentation because it involves selection of initial seed points. It assumes that different objects are separated by other kind of perceptual boundaries. In these pixels are added to the region based on neighborhood features. Textures are considered as instantiations of underlying stochastic processes and analyzed under the assumptions that stationarity and ergodicity hold.

Threshold based segmentation [14] is the simplest segmentation technique here each pixel is replaced with a black pixel if the intensity (Ii,j) is less than the fixed constant(Threshold value) T and the pixel is replaced with white pixel if the intensity greater than the constant T(Ii,j>T). In automated segmentation algorithms the threshold value is selected based on the following methods they are histogram based, clustering based entropy based, object attributes based, and spatial methods. We can use threshold based segmentation in color picture also, here the threshold value is applied to each RGB components of the picture then the components are combined using AND operation. Threshold based segmentation is very effective when the picture is taken in good lightning condition.

In a pixel based segmentation [15] the pixels are grouped together based on their homogenous region corresponding to an object or an object. In model based segmentation grouping is done based on the shape of an object therefore we can get the information about the probabilistic shape and its variation. When segmenting an image this method is effective only if we use the following methods they are training examples with a common pose, registering probabilistic representation of the variation of the registered samples, and adding information about statistical inference between the model and the image. We can also use active shape models and active appearance model to improve the segmentation quality.

Segmentation of brain tumors from MRI datasets plays a huge role in improved diagnosis, growth rate prediction and treatment planning. Automating segmentation process is very difficult to implement due to the presence of severe partial volume effect and considerable variability in tumor structures, as well as imaging conditions, however, automated and accurate brain tumor segmentation in multimodal MRI volumes is technically challenging due to several reasons. First, the tumor areas are only defined through image intensity profiles that often overlap with adjacent normal tissue due to partial voluming or bias field artifacts [8] . Furthermore, tumors can appear anywhere in the brain, with varying shapes and sizes. Finally, in order to capture rich biological information and better segment each sub-component in brain tumors, it is important to conduct studies on multimodal MRI volumes.

Contour is the boundaries of an object in digital images [8] thus they must be a closed curve. Contour based segmentation is also called as boundary following, contour model is mostly used to extract the boundaries of an object in a digital image. Contour tracing is one of the preprocessing technique used to extract the shape of an object. Contour based segmentation is more effective because contour pixels are generally a small subset of the total number of pixels representing a pattern. Therefore it requires less the time and computation when feature extraction algorithm is applied on the contour instead of on whole image. Contour based segmentation is one of the most efficient preprocessing algorithm in pattern reorganization field.

In this paper we propose an active contour algorithm [8] to detect the tumor region active contour model also called as snakes. An active contour model is used to trace the boundaries of tumor region from noisy 2D images. A snake is an energy minimizing, deformable spline affected by constraint and image forces that pull it towards object contours and internal forces that resist deformation. Snakes will solve the problem only if the approximate shape of the boundary is known. Because of its deformable model it can adapt to difference and noise in stereo matching and motion tracking. Additionally, it can find Illusory contours in the image by ignoring missing boundary information. When compared to other feature extraction techniques snakes have multiple advantages some of the advantages are (i) They can search the minimal states autonomously and adoptively. (ii) External image can force the snake to act upon an instinctive manner. (iii) Snakes can be used to track dynamic objects also.

Active contour models gradually develop an active contour for object boundaries by minimizing an energy functional that derives from image edge or region information. They have been extensively explored in brain tissue segmentation and can create better results than other methods. One difficulty with ACM based methods is to automatically integrate appropriate initial information into the energy functional in order to guide and constraint the contour evolution when segmenting detailed brain tumor substructures.

. Artificial Neural Network [12] is collection of connected nodes called artificial neurons which loosely model the neurons in the biological brain. ANN is not an algorithm but a framework for many different machines having different algorithms works together to process complex data’s. The neural network learn to perform by considering examples without programming for specific task. An artificial neuron can able to receive an input process it can able to transfer the data’s to another neurons. In our proposed method Artificial Neural Network is used to create initial contour of the input MRI image.

Contrast enhancement technique [17] is an image processing technique that improve the perceptibility of an image. Contrast enhancement is performed as contrast stretch and tonal enhancement. Contrast stretch improves contrast level between the adjacent pixels, tonal enhancement improves the brightness between shadow (dark), midtone (grays), or highlight (bright) regions at the expense of the brightness differences in the other regions. In our proposed method the contrast enhancement is used to improve the contrast difference between normal and abnormal region.

# 2 Literature survey

The sensitivity to noise and intensity non-uniformity (INU) artifact and the trapping into local minima and dependency on initial clustering centroids are the most common problems faced when applying fuzzy clustering is applied to segment MRI images. These problems can be addressed using kernelized fuzzy entropy clustering with local spatial information and bias correction (KFECSB) and an improved Particle Swarm Optimization (PSO). PSO-KFECSB[1] algorithm takes advantages of both the excellent feature of LHNPSO algorithm, in optimizing the objective function of kernelized fuzzy entropy clustering with spatial information and bias correction, and the KFECSB gradient method, in speeding up convergence. To make sure that all particles are moving within the searchspace and avoiding divergent behavior, their positions and velocities are limited as follows

where vmax is the largest allowable step size in any dimension; and {xmin, xmax} are the bounds of the search space in each dimension. In image clustering, commonly, vmax is set to 1 and {xmin, xmax} are the minimum and maximum of the feature (intensity or gray value) of the image.

In Bounding box and Image-specific Fine-tuning-based Segmentation framework [2] CNN takes content of a bounding box of one instance as input and gives a binary segmentation for that instance. In the testing stage, the user provides a bounding box, and BIFSeg extracts the region inside the bounding box and feeds it into the pre-trained CNN with a forward pass to obtain an initial segmentation. This is based on the fact that CNNs are designed and trained to learn some common features, such as saliency, contrast and hyper-intensity, across different objects, which helps to generalize to unseen objects. Then unsupervised (without additional user interactions) or supervised (with user-provided scribbles) image-specific fine tuning is used to further refine the segmentation. This is because there is likely a mismatch between the common features learned from the training set and those in (previously unseen) test objects. Therefore, fine-tuning is used to leverage image specific features and make our CNNs adaptive to a specific test image for better segmentation. This framework is general, flexible and can handle both 2D and 3D segmentations with few assumptions of network structures

Brain tumor segmentation using CNN in MRI Images [3] uses bias field distortion to alter the images. This makes the intensity of the same tissues to vary across the image. N4ITK method is used to correct the intensity variation of tissues, to make the contrast and intensity ranges more similar across patients and acquisitions, we apply intensity normalization method is applied on each sequence. In this intensity normalization method, a set of intensity landmarks are learned for each sequence from the training set. After normalizing the MRI images, the mean intensity value and standard deviation across all training patches extracted for each sequence are calculated. CNN were used to achieve some breakthrough results and win well-known contests. The application of convolutional layers consists in convolving a signal or an image with kernels to obtain feature maps. So, a unit in a feature map is connected to the previous layer through the weights of the kernels. The weights of the kernels are adapted during the training phase by back propagation, in order to enhance certain characteristics of the input. Some small clusters may be erroneously classified as tumor. To deal with that, we impose volumetric constrains by removing clusters in the segmentation obtained by the CNN that are smaller than a predefined threshold

In Automatic segmentation of MR brain images with a convolutional neural network method [4] segment MRI images into number of tissue classes using convolutional network. To ensure that the method obtains accurate segmentation details as well as spatial consistency, the network uses multiple patch sizes and multiple convolution kernel sizes to acquire multi-scale information about each voxel. This method is not dependent on explicit features, but learns to recognize the information that is important for the classification based on training data. Rectified linear units are used for all nodes because of their speed in training CNNs. Drop-out is used on the fully connected layers to decrease the effect of over fitting on the training set. Mini-batch learning and RMSprop are used to train the network and cross-entropy is used as cost function to optimize the weights and biases

MRI brain tumor segmentation based on texture features and kernel sparse coding [5] uses four steps to segment MR Images. First, the MRIs are pre-processed to reduce noise, enhance contrast and correct the intensity non-uniformity. Then sparse coding is performed on the first order and second order statistical eigenvector extracted from original MRIs which is a patch of 3 × 3 around the voxel. The kernel dictionary learning is used to extract the non-linear features to construct two adaptive dictionaries for healthy and pathologically tissues respectively. A kernel-clustering algorithm based on dictionary learning is developed to code the voxels, then the linear discrimination method is used to classify the target pixels. In the end, the flood-fill operation is used to improve the segmentation quality.

The process of manually generating precise segmentations of brain tumors from magnetic resonance images (MRI) is time-consuming and error-prone. To address this issue, Potential Field Segmentation   
(PFS) algorithm [6], and propose the use of ensemble approaches that combine the results generated by PFS and other methods to achieve a fused segmentation. For the PFS method, Potential Field Clustering algorithm is used, which is based on an analogy with the concept of potential field in Physics. The intensity of a pixel in an MRI as a “mass” that creates a potential field. Specifically, for each pixel in the MRI, the potential field is computed and, if smaller than an adaptive potential threshold, the pixel is associated with the tumor region. This “small potential” segmentation criterion is intuitively valid because tumor pixels have larger “mass” and thus the potential of surrounding regions is also much larger than in other regions of smaller or no “mass”.

Two-Pathway CNNs [7] exploit both local features of an image, as well as the larger context simultaneously. The Two-Pathway Group CNN architecture was based on the pathway convolutional network, which consisted of dense blocks with layers that use the stack of all previous layers as input, alternated with transition blocks consisting of an 1x1 convolutional layer and 2x2-strided average pooling. Two-Pathway Group convolutional neural networks architecture consist of two parallel streams of CNN. Stream-I, convolutional neural networks with smaller receptive fields (7x7 or 5x5) and stream II that consist of larger receptive fields (13x13, 15x15 or 17x17). In this two convolutional neural networks streams as the local CNN pathway and the global CNN pathway, respectively. Two-Pathway Group convolutional neural networks is able to predict the label of pixel by using visal detail of the pixel through local CNN pathway and larger context of the pixel through global CNN pathway. The motivation of using two-pathway CNN is to utilize the local as well as context information of the image to reach precise segmentation. As in Two-pathway group CNN, we have two different streams of CNNs (local pathway CNN and global pathway CNN), we have performed concatenation of both CNN at second-last layer. The concatenationed features set is finely fed to the output layer.

In random forests and active contour model for the automated segmentation [8], the segmentation problem as a hybrid problem with tissue voxel classification and tissue boundary contour evolution. Specifically, with the input of multimodal volumetric MRI datasets, the method is carried out in two stages: (1) Multiscale feature representations adapted specifically to the task of brain tumor segmentation are learned directly from MRI volumes to fully capture both local and contextual image information across MRI modalities. These task-adapted feature representations are provided as the input to the subsequent voxel classification. Each sub-component in brain tumors are inferred using ccRFs in the representation learning scheme which take into account both the local details of the brain tumors and their larger context. Specifically, ccRFs employs a concatenated and connected structure to produce a hierarchy of tissue probability maps for each tissue type by voxel-wise classification. At the end of the forest ensemble, ccRFs will generate highly accurate soft segmentation maps by assigning the tissue label with the largest fused probability at each voxel within MRI volumes.(2) The ccRFs output may be not satisfying the local dependencies of labels, which is one common problem with many learning based methods. In order to refine the tissue labels, ccRFs is further combined with mpAC model that imposes contour evolution on the voxel classification and produces the final hard segmentation labels. After training each stage of the flowchart offline and achieving the optimum values of the parameters, the system can be deployed for automatic brain tumor segmentation tasks.

The basic idea of MAS[9] is to register and fuse label information from multiple normal brain atlases to a new brain image for segmentation. However, most of them are developed for normal brain images, and tumor brain images usually pose a great challenge for them. This is because tumors cause difficulties in registration of normal brain atlases to the tumor brain image. To address this challenge, in the first step of our MAS framework, a new low-rank method is used to get the recovered image of normal-looking brain from the MR tumor brain image based on the information of normal brain atlases. Different from conventional low-rank methods that produce the recovered image with distorted normal brain regions, our low-rank method harnesses a spatial constraint to get the recovered image with preserved normal brain regions. Then in the second step, normal brain atlases can be registered to the recovered image without influence from tumors. These two steps are iteratively proceeded until convergence, for obtaining the final segmentation of the tumor brain image. During the iteration, both the recovered image and the registration of normal brain atlases to the recovered image are gradually refined.

The LIPC [10] method consists of four major steps, preprocessing, feature extraction, tumor segmentation using the LIPC method, and post processing. This method treats tumor segmentation as a classification problem. Additionally, the local independent projection-based classification (LIPC) method is used to classify each voxel into different classes. A novel classification framework is derived by introducing the local independent projection into the classical classification model. Locality is important in the calculation of local independent projections for LIPC. Locality is also considered in determining whether local anchor embedding is more applicable in solving linear projection weights compared with other coding methods. Moreover, LIPC considers the data distribution of different classes by learning a softmax regression model, which can further improve classification performance

# 3 Proposed System

**3.1 Block digarm**

Figure 1. demonstrates the block diagram of proposed brain tumor system. First step in the proposed methodology is to collect all MRI images and corresponding mask for training purpose. This MRI image set have tumor and tumor less image. After collecting all MRI and corresponding mask images we have to do some preprocessing steps to enhance quality of the MRI image. Contract enhancement is applied to each MRI images before going to feature extraction. This preprocessing step enhance fine details of MRI images. Further, Region of Interest (ROI) of MRI image is obtained from vertical and horizontal histogram. Following to that we crop the corresponding pixels from the mask image also. The K-mean clustering is applied to the entire ROI. Clustering alludes to the way toward gathering tests so the examples are comparative inside each gathering k-means clustering regards each question as having an area in space. It discovers segments to such an extent that items inside each bunch are as near one another as could be expected under the circumstances, and as a long way from articles in different groups as would be prudent. K-means clustering requires the quantity of groups to be divided and a separation metric to evaluate how close two articles are to one another. In image examination, clustering can be utilized to discover gatherings of pixels with comparable dark levels, hues or nearby surfaces with the end goal to find the different areas in the image. So, tumor



Figure 1. block diagram of proposed system

cells in MRI image has similar gray levels and local textures pattern. There by we can segment corresponding tumor cells. After extracting this clusters, we find gray level co-occurrence image,then we split the segmented image and corresponding mask into n x n overlapping blocks for feature extraction. A measurable strategy for inspecting texture that considers the spatial relationship of pixels is the gray-level co-occurrence matrix (GLCM), otherwise called the gray-level spatial reliance matrix is utilized for feature extraction of tumor cells from MRI images. The GLCM capacities portray the texture of an image by computing how frequently matches of pixels with particular qualities and in a predetermined spatial relationship happen in an image, making a GLCM, and after that separating factual measures from this matrix.

GLCM gives a few parameters, for example, contrast, correlation, homogeneity, vitality of each block. After calculating the GLCM of each block, feature vector is formed with GLCM features, mean ,variance and corresponding pixels. This feature vector and center pixels of block of corresponding mask image is set as input and target of the classification neural network respectively. For training, feature vector and corresponding target pixels of all MRI and correspond mask image is calculated. Finally, we created trained neural network which outputs the detected tumor region.

After training next step is testing with trained Neural network. All preprocessing step and Region of Interest is applied to the testing image. After that, the feature vector of all block of MRI image for detecting tumor is given as input to the trained neural network. Its output is the detected tumor mask. After finding this mask we find the shape of the tumor by using active contour method. Finally, we get the detected tumor region in the MRI image. Finally, performance parameter is calculated to analysis the performance of the proposed system when compared to other state of art.

**3.2 Pre processing**

Preprocessingisimportant step because the input image should be in standard format for processing and also it improve the quality of an image before processing into an application. An efficient denoising and an improved enhancement technique is required to protect the edges and contour information of medical images. Contrast enhancement is a process of removing noises and highlight the features of an image. It uses a small neighborhood of a pixel in an input image to get a new brightness value in the output image. There by it alter the contrast level to improved one.

**3.3 Region of Interest**

In MRI image Region of interest extraction is important because of information about brain image is located in one region. So we didn’t need to process the entire image for further analysis. A portion of an image in which you want to filter or to perform some operation is called as Region of interest. You can create ROIs of many shapes using the high-level ROI functions, such as draw circle or draw polygon.

Then ROI (Region of Interest) is obtained as show in figure 2. To find the ROI horizontal and vertical histogram of image is calculated. Horizontal and vertical count is used to crop the image to obtain region of interest.Then crop the MRI image into corresponding Ix and Iy value obtained from horizontal and vertical histogram respectively.

**3.3 K-Means clustering**

K-Means clustering is a vector quantization algorithm. It aims to partition n observations into k clusters in which each observation belongs to the cluster with the nearest mean. Let us consider x1,x2….xn be the dataset where each observation is a d-dimensional real vector k-means clustering aims to partition the n observations into k (≤ n) sets S = {S1, S2, …, Sk} so as to minimize the within-cluster sum of squares. Formally, the objective is to find:



Figure 2. ROI extraction from MRI image

(1)

Where μi is the mean of points in Si

This is equivalent to minimizing the pairwise squared deviations of points in the same cluster:

(2)

The equivalence can be deduced from identity

(3)

Because the total variance is constant, this is also equivalent to maximizing the sum of squared deviations between points in different clusters (between-cluster sum of squares, BCSS), which follows easily from the law of total variance.

K -means algorithm consists of two separate phases. In the first phase it calculates the k centroid and in the second phase it takes each point to the cluster which has nearest centroid from the respective data point. There are different methods to define the distance of the nearest centroid and one of the most used methods is Euclidean distance. Once the grouping is done it recalculate the new centroid of each cluster and based on that centroid, a new Euclidean distance is calculated between each center and each data point and assigns the points in the cluster which have minimum Euclidean distance. Each cluster in the partition is defined by its member objects and by its centroid. The centroid for each cluster is the point to which the sum of distances from all the objects in that cluster is minimized. So K -means is an iterative algorithm in which it minimizes the sum of distances from each object to its cluster centroid, over all clusters. Let us consider an image with resolution of x×y and the image has to be cluster into k number of cluster. Let p(x, y)be an input pixels to be cluster and ck be the cluster centers. The algorithm for k-means13 clustering is following as:  
1. Initialize number of cluster k and centre.  
2. For each pixel of an image, calculate the Euclidean distance d, between the center and each pixel of an image  
using the relation given below.

(4)

4. After all pixels have been assigned, recalculate new position of the centre using the relation given below.

(5)

5. Repeat the process until it satisfies the tolerance or error value.

6. Reshape the cluster pixels into image.

Although k-means has the great advantage of being easy to implement, it has some drawbacks. The quality of the final clustering results is depends on the arbitrary selection of initial centroid. So if the initial centroid is randomly chosen, it will get different result for different initial centers. So the initial center will be carefully chosen so that we get our desire segmentation. And also computational complexity is another term which we need to consider while designing the K -means clustering. It relies on the number of data elements, number of clusters and number of iteration. By using above clustering algorithm, we get three clusters. From that we extract third cluster because this cluster contains more detals about the tumor.

3.4 Feature Extraction:

Feature extraction is a process of reducing amount of resources required from available resources to process a data. Analyzing large data requires more memory and large computation time and also it reduce the performance of the classifier algorithm. So feature extraction algorithms used to constructing the variable combinations that requires to produce the desired accuracy. For our proposed method GLCM is used find feature vector. in addition to that variance and mean is also used. This features is used to distinguish normal and abnormal brain tumors.

3.5.1 GLCM:

MRI image composed of several pixels and each pixels having their own intensity level. Grey Level Co-occurrence matrix is a method of tabulating the pixels with different intensity level. It is the most classical second-order statistical method for texture analysis. Texture analysis differentiate the normal and abnormal brain tissues. GLCM improves the accuracy level by choosing effective quantitative level for early diagnosis. In the first step, the first-order statistical textural analysis-features information of the MRI image was extracted and frequencies of gray level at a random image positions were measured without considering neighbor pixels. In the second step, the second-order textural analysis-features were extracted by considering neighbor pixels The statistical features were extracted using GLCM, also known gray-level spatial dependence matrix (GLSDM). GLSDM is an approach that describes the spatial relation between pixels of various gray-level values. Gray-level co-occurrence matrix (GLCM) is 2D histogram in which (p,q)th elements is the frequency of event p occurs with q. It is a function of distance S=1, angle at 0 ˚ (horizontal), 45˚ (with the positive diagonal), 90 ˚ (vertical) and 135 ˚ (negative diagonal) and gray scales p and q, and calculates how often a pixel with intensity p, occurs in relation with another pixel q at a certain distance S and orientation. In GLCM method, gray-level co-occurrence matrix has the textural features such as contrast, correlation, energy, homogeneity, entropy and variance were obtained from block nxn size image. The textural features extracted are listed below

1. Contrast (CONT):

(6)

1. Energy (COR):

(7)

1. Correlation (COR):

(8)

1. Homogeneity (HOM):

(9)

1. Entropy (ENT) :

(10)

1. **Homogeneity:**

Homogeneity passes the value that calculates the tightness of distribution of the elements in the GLCM to the GLCM diagonal [19]. For diagonal GLCM its value is 1 and its range is [0, 1].Opposite of contrast weight is homogeneity weight values, with weight decreases exponentially loose from the diagonal. The weight employed in contrast is (i, -j) ^2 and in homogeneity, it is the homogeneity is given as:

(11)

**3.5 Active Contour Model**

An active contour model is used to trace the boundaries of tumor region from MRI images. An active contour model is also called as snakes. A snake is an energy minimizing, deformable spline affected by constraint and image forces that pull it towards object contours and internal forces that resist deformation. Snakes will solve the problem only if the approximate shape of the boundary is known. Because of its deformable model it can adapt to difference and noise in stereo matching and motion tracking. Additionally, it can find Illusory contours in the image by ignoring missing boundary information. Energy function of a snake is defined as [18].

(13)

Where *v*(*s*) is the contour of the snake, *Eint* is the internal  
deformation energy that characterizes the contour as:

(14)

Where α and β are weighting parameters, vʹ(s) and vʺ(s) are the first and second derivatives of the contour with respect to v(s).

The external energy function *Eext* is derived from the image id defined as

(15)

Where P denotes scalar potential function

With the calculus of variations, the contour *v*(*s*) which minimizes the energy *E* needs to satisfy the Euler-Lagrange equation as:

(16)

where ∇ is the gradient operator, and vʹ (s) is a fourth derivatives of the contour function vʺ(s).

**3.7 Artificial Neural Network:**

In this paper Artificial neural network is used to find the tumor region in MRI images by comparing original images with masked image. Artificial Neural Network is similar to the biological neural network it has different elements they are operated in parallel. Each elements in the network called as neurons. ANN will discharge energy to the next element only if the  
sum of multiplication of weights and inputs plus bias  
at the node is positive, otherwise it doesn’t discharge energy to the next elements. In ANN all the nodes are inter connected with the adjacent nodes. Input to a node is the weighted sum of the output of all the nodes in which it is connected. That is the output value is the non-linear function of the input valve. The multiplicative weighing factor between the input and output node (i, j respectively) is called the weight Wj.

ANN is a non-linear and the adoptive system that learns to perform functions from data. ANN is said to be adaptive because it can change its parameters when the parameters of the system changes in its training phase. After training the parameters of the network are fixed then this network is used to solve the problems. There are two modes of operation one is feed forward mode and another one is back propagation mode. In this paper the implemented ANN has one input and one output layer with one or two hidden layers. In back propagation method every time the output is compared with the target and the error is computed. The weight of the ANN is adjusted to reduce the error every time the weight changes the neural model get closer to the targeted output.

**4 Experimental Results And Discussion**

In this section, we analyze the effect of key components and the performance of the proposed method. Also, we compare our method with the state of the art using the same database, including also methods ----------learning for brain tumor segmentation. Further, It gives brief explanation about how our proposed method works. The proposed algorithm is simulated in the MATLAB2017a version in an I5 system with 4GB RAM. Real-time brain images used for the proposed algorithm to validate the performance. Brain MRI images which is used for the proposed method can be shown in **figure 6**. To avoid the computational complexity the images are down sampled by a factor of 2. The computation time of the algorithm is directly proportional to the resolution of the image. For sensitivity analysis of our algorithm, we have used mask images which are obtained from the database which is used for testing.

First step is selecting training image dataset. In proposed work Preprocessing step such as contrast enhancement is applied to MRI dataset. Then ROI (Region of Interest) is obtained as show in figure 2. To find the ROI, horizontal and vertical histogram of image is calculated. Then crop the MRI image into corresponding Ix and Iy value obtained from horizontal and vertical histogram respectively. After that we find the ROI gray cooccurance matrix for MRI. This gives the texture details of tumor cells. Following by, we split the graycomatrix into 3x3 blocks. The GLCM features such as correlation, energy, homogeneity, contrast, mean , variance is calculated for each block. Then feature vector is formed with this parameters, and vector array of pixels. After that for training with neural network, target is set mask image. The neural network is trained with feature vector and target pixels. After training,we want do evaluate the system with test MRI image. During testing phase also some preproessing step and feature extraction as in training process is applied. After feature extraction , this feature vector is given as input to the trained neural network. This results the detected mask region of tumor in the test MRI image. Then, we find active contour with test MRI image and detected mask. This gives accurate boundary of tumor cells in the MRI image. Finally we identified the morphology of the detected tumor.

To analysis the performance of the proposed method different state of art method is used. Different paramters which are used to analysis the performance is given below. Here the test image is compared with reference images of the subject for each class. For analyzing the algorithm performance, we have used the number of images with different classes. For performance metrics, we have used seven standard performance metrics. For the performance analysis fist, we have to catch out specificity analysis with respect to the ground truth image depend on True-positive (*tp*) pixels, True-negative pixels (*tn*), False-positive pixels (*fp*), and False-negative pixels (*fn*). True-positive pixels (*tp*) are correctly detected pixels by the algorithm of the moving object. By using sensitivity values, we can find out the following parameters.

The relevant pixels of the detected object can be found out by using sensitivity. Irrelevant pixels can be determined by using precision, the formula for precision and sensitivity and other measures are is given below.

**Accuracy:**

**Sensitivity:**

**Specificity:**

**Precision:**

Sample MRI and corresponding mask images used for training is shown in below figure.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **MRI image** |  |  |  |  |
| **Mask** |  |  |  |  |

Figure 3. Some of the MRI images and corresponding masks used for training

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Contrast | Energy | Correlation | Homogeneity | Mean | Variance | Block vector | | | | | | | | | Target Pixels |
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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Contrast | Energy | Correlation | Homogeneity | Mean | Variance |  |  |  |  |  |  |  |  |  | Target |
| 1.33 | 0.11 | 0 | 0.62 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 |
| 1.33 | 0.11 | 0 | 0.62 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 |
| 1.33 | 0.11 | 0 | 0.62 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 |
| 1.33 | 0.11 | 0 | 0.62 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 |
| 1.33 | 0.11 | 0 | 0.62 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 |
| 0.63 | 0.22 | 0.62 | 0.77 | 3.33 | 12.25 | 8 | 8 | 1 | 1 | 1 | 1 | 1 | 1 | 8 | 1 |
| 0.63 | 0.22 | 0.62 | 0.77 | 3.33 | 12.25 | 8 | 1 | 1 | 1 | 1 | 1 | 1 | 8 | 8 | 1 |
| 2.04 | 0.25 | -0.24 | 0.5 | 2.55 | 9.52 | 1 | 1 | 1 | 1 | 1 | 1 | 8 | 8 | 1 | 1 |
| 2.5 | 0.28 | -0.39 | 0.5 | 1.77 | 5.44 | 1 | 1 | 1 | 1 | 1 | 1 | 8 | 1 | 1 | 1 |
| 1.56 | 0.22 | 2.60E-17 | 0.61 | 3.33 | 12.25 | 1 | 1 | 8 | 1 | 1 | 8 | 1 | 1 | 8 | 1 |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Input image | output | Ground Truth | accuracy | Sensitivity | Specificity | Precision | F1\_score |
| FCM |  |  |  | 0.9585 | 0.9584 | 0.9745 | 0.9999 | 0.9787 |
| K-Means |  |  | 0.9614 | 0.9612 | 0.9831 | 0.9999 | 0.9802 |
| GIS-BEE-KM(Proposed) |  |  | 0.9712 | 0.9656 | 0.9900 | 0.9999 | 0.9888 |

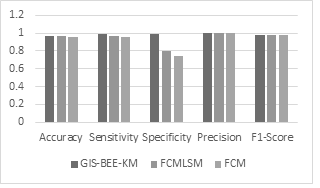
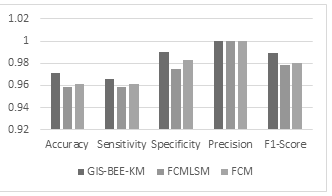


Fig.10. Various performance metrics for Image-1

Fig.11. Various performance metrics for Image-2

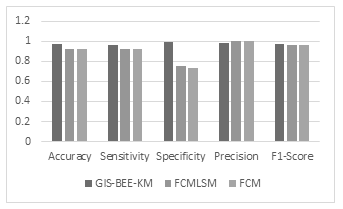


Fig.12. Various performance metrics for Image-3

**Conclusion:**

In this paper, GIS-BEE-KM implemented and validated with different brain MRI images with different sizes and characteristics. From experimental results, it is clear that the accuracy of the work is improved when compared to the existing work. In this work, performance has been evaluated with different methods such as FCM, FCMLSM etc. By using the proposed method, we have improved the sensitivity analysis performance by a factor of 1.5%.

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