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Hybrid Segmentation Method With Confidence Region Detection for Tumor Identification

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ABSTRACT Segmentation methods can mutually exclude the location of the tumor. However, the challenge of complex location or incomplete identification is located in segmentation challenge dataset. Identificationof tumor location is difficult due to the variation of intensities in MRI image. Vairation of intensity extends up to edema. Confidence Region with Contour Detection identifies the variation of intensities and level set algorithm (Region Scale Fitting) is used to delineate among the region of inner and outer of the tumor. Automatic feature selection method is required due to data complexity. An improved Self Organization Feature Map. Method is required. Weighted SOM Map selects a deterministic feature. This feature is one higher trained accuracy feature. When this specific feature is combines with cluster therefore it is known as deterministic feature clustering. This method gives confidence element. Confidence Region with Contour detection is facing the issue due to extended variations of intensities. These intensities are segmented by hybrid SOM Pixel Labelling with Reduce Cluster Membership and Deterministic Feature Clustering. This hyhbrid method segments the complex tumor intensities. This method produces a potential cluster which is achieved through the hybrid of three unsupervised learning techniques. Hybrid cluster method segments the tumor region. Extended intensities are also segmented by this hybrid approach. Above methods are validated on MICCAI BraTs brain tumor dataset, this is a segmentation challenge dataset. Proposed hybrid algorithm is efficient and it's accuracy can be seen with testing parameters like Dice Overlap Index, Jaccard Tanimoto Coefficient Index, Mean Squared Error and Peak Signal to Noise Ratio. Dice OverlapIndex is 98%, Jaccard Index is 96 percent, Mean Squared Error is 0.06 and Peak Signal To Noise ratio is 18db. The performance of the suggested algorithm is compared to other state of the art.

INDEX TERMS Self organization mapping (SOM), KMEAN, Fuzzy C Mean (FCM), features, feature extraction (FE), feature reduction (FR), feature selection (FS), MRI, contour detection, biggest blob area, intensity, hybrid segmentation, confidence region (CR), contour detection (CD).

I. INTRODUCTION

Segmentation of an image gives specific intensity in particular region of image, therefore, segmentation of accurate region of interest is issue with different scenarios. In some MRI images intensities segregate or isolate the boundaries and also the regions. Therefore edge-based segmentation and region-based segmentation is using to separate them.

Magnetic resonance imaging (MRI) is a medical modality which gives image with plentiful information inside the human tissues with views of three dimensions but the issue with them they are low pass image and it is difficult to segment tumor from another cell due to homogeneity. They are taken from different parts of the body like bones, lungs, and brain. We are focusing on MRI of brain so important to know about MRI and its processing. The human body consists of matter called atom and atom is consisting of nuclei, proton, and electron which draw margin inside the human body. The powerful magnetic fields of atom

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are called Nuclear Magnetic Imagining (NMI). A scanner produces magnetic field because protons absorb variable energy and flip their spin when the field has turned off and returned to normal spin called precision. The return of energy-producing radio field which is measured by receiver resulting in an image has been made. Proton in different parts of body return to their normal spin and different rate, scanner can distinguish among different tissues. From the above-obtained image, It is found that the region extraction in MRI image is compromised due to variation of intensities. Tumour intensities variations are visible in none enhancing region whereas enhancing tumour variations are not overcome therefore complete tumour region extraction becomes a challenge.

Cancer is a coherent thing of tumor formation in the human body. Tumor image pertains high dimension of features in an image; therefore, it is difficult to check good features of tumor image. Those features must be reduced with accuracy. This issue and its importance of tumor identification can be seen with this report. The new straits times Malaysia reports cancer that it is second largest disease in Malaysia and 60% people are suffering from later stages. The tumor is ill-defined boundary due to the cancer cells. The brain is important part, because tumor produce, and cancer cell stimulates in the brain portion. MRI is compromising because of many features, data become complex. Therefore, higher dimension features need to reduce to low dimension features. SOFM is a feature selection algorithm. SOFM needs to improve its SOM Map for selection of deterministic feature. Such feature extracts the confidence element.

MRI imaging is examined through the region extraction. MRI is a nosier image. So, it is important to analyze the region extraction [1]. Limitations are also remains in Confidence region Contour Detection. Error in identification should not compromise due to occurrence of extended tumor intensities or extreme variation of intensities. Hence a method requires which can segment such intensities significantly. In the line of above, it is important to identify extreme variation of intensities, highlight the discriminant features for confidence element extraction and segmentation for extreme intensity.

MRI has four sequences of images or they are the appearance of the intensities. Proton weighted densities are named as FLAIR, T1- Weighted, T2-Weighted and T1CE. FLAIR sequences when radiologist needs to suppress the liquid, therefore, it gives illusion of white matter in the middle and gray matter surrounding. T1-weighted suppress the fat, therefore, it has likely illusion of white matter in middle and gray matter in surrounding. In T2-weighted tissues which are Fat and brighter therefore white matter outside and gray inside. T1CE is contrast when T1 pathological tissues demonstrate on leaky vessels and brighter tissues than surrounding. FLAIR, T1, T2, T1Ce are proposed on novel region extraction, confidence element extraction and hybrid segmentation techniques.

II. RELATED WORK

The scope of related work is more focused. Work is emphasized on region extraction, feature selection and segmentation. Firstly, for region extraction, tumor cells are examined then contour is initialized and level set is performed with number of iterations to separate tumor cells and normal cell. Secondly, for complex data set, feature reduction, selection is also important. Thirdly, Hybrid segmentation technique haves been used for segmentation which extract tumor region from input image. The dataset used in this work is MACCAI BRATS brain tumor dataset 2013-2017.

Here, in this study, an improved sobel edge detection algorithm is proposed which draws close contour to extract the accurate region of a brain tumor and accuracy is 35 percent and is determined with Q parameter [1]. In this study, region extraction is important for identification of tumor area. In this study, Image enhancing is performed with de noising, watershedding and visual analysis of the image by connected Component and lastly, the image is evaluated with 42 percent jaccard index(JI) [2]. In this study, FCM is used to enhance the edges of the brain tumor image and enhance edges accuracy is 91 percent, it is calculated with FSCORE [3]. In this study, a multi-level threshold OSTU enhances the image and it is also determining significant intensity point and it assigns them threshold, then image is enhance and region of interest is extracted by the algorithm. Determined Dice overlap index is 93% and Jaccard Index(JI) is 96 percent [4]. In this study, accurate identification of brain tumor is performed through combination of region growing, GLCM feature are extracted and classification is performed through Probabilistic Neural Network (PNN) and accuracy is evaluated through maximum positive model with 76 percent [5]. Region scale fitting (RSF) is improved through edge stop function, It determines the improved edges. With improved edges, the region of interest de noises the noisy region with 92% accuracy through parameter recall [6]. In this study, the hyperintense lesion is dealt with a combination of a Gaussian mixture model, synthetic image and support vector machine [7]. In this study, different modalities have been reviews and it has been found MRI segmentation is more challenging for methods due to low pass and high resolution [8]. In this study, the method detects the inner contour and outer contour; It checks the start point and endpoint of contour. Hence, the background evolves smoothly from the foreground of the image. Performance is evaluated with the 92 Dice overlap Index(DOI) [9]. In this study (Buenestado) [10], the MRI image is segmented through confidence region and confidence region is evaluated with 63 percent of Dice. The confidence region has limitation; it needs improvement for good feature extraction with maximum tumor pixels. In another study, accurate identification of brain tumor is performed through combination of region growing (segmentation), GLCM (feature extraction) and classification (Probabilistic Neural Network). Segmentation is evaluated through 16 dB of Peak Signal to Noise Ratio(PSNR) and Mean Squared Error is 6dB [11].

The feature plays an important role in confidence element extraction. Here in this study [12], feature reduction lessens the dimensions of data based on their accuracy. Gabor and statistical features have been compared. Feature dimension reduction is performed. The selected feature discriminates normal cells against the tumor cells and it helps to segmentation. Discriminant feature classification accuracy is 93 percent. In this study, the multi-kernel selects relevant features from the dataset. Self Organisation Map is improved with its weights therefore it capabilities improve for relevant feature selection. Here classification accuracy is 60 percent [13]. In this study, Self-organization map is improved and it does not need to pre-process. A higher classification accurate feature is selected. Feature classification accuracy is 98% [14]. In this study, the nuclei based neural network classifies the tumor with the help of proposed features. Here, classification accuracy is also 98 percent [15]. In this study, Dataset is extracted using DWT, features are reduced with using PCA and classified through four SVM classifier and classification accuracy is 66.6 percent [16]. In this study, Feature weighted self-organization map is proposed, algorithm performs feature selection, it's initial accuracy of feature classification is 60percent and it is extending [17]. In this stud, predicted pre particle swarm optimization is proposed with single hidden neural network layer and classification accuracy for brain tumor is 97 percent [18].

Segmentation methods mutually exclude the desire object. Different studies are discussed here, In this study, Fuzzy KMEAN is inclusive with a self-organization map and performance is evaluated with testing parameters namely as Jaccard Index(JI) and Dice Overlap Index(DOI). The evaluation percentage is 46 [19]. In this study, a hyper intense MRI image is used, and a small lesion is proposed for clinical application. The method is significant for the visualization of a small lesion of the heterogonous shape of tumor and segmentation accuracy is 96 percent [20].

In this study, segmentation is automatic becomes challenging due to the diverse intensities of the image. but the method is good for segmentation. Methods of a combination of the feature with segmentation are evaluating with the dice index and the evaluation percentage is 70 [20-21]. In this proposed study, a multi-level threshold OSTU enhances the image with determining significant intensity point and assigns them threshold, then using combination they are enhanced by the algorithm (Banerjee, Mitra, & Shankar, 2016) [22]. In this study, SOM performs initial clustering and this initial clustering is inclusive of FKM and average memberships are selecting, hybrid algorithm are giving accuracies for the new biomedical dataset. Soft Computing techniques are also compared with the state of art [4]. This study is based on two phases. In the first phase, the voxel classifier is determined through the Random forest and the second phase is the active contour level set method. With the combination efficient, segmentation is achieved and evaluation with Dice Overlap Index is 90 [23]. In this study, Multi Cascade Neural Network with Conditional Random Field is proposed, it offers performance-oriented segmentation as compared to state of art and segmentation is evaluated with 89 percent of Dice Over Index(DOI) [24]. In the study, image registration is considered to be a faster technique for segmentation as compared to active contour, and, with skull removal image registration performance increases. This study determines the complete enhancement of the tumor shape from a longitudinal analysis of the image. Segmentation accuracy is 93 percent [25]. In this suggested study, the combination of KFCM and HCSD is suggested. KFCM gives tumorous cells as well as none tumorous cells whereas HCSD gives tumorous clusters and technique is evaluated with the Jaccard Index of 90 percent [26]. In this study, a neural network is trained local and global features for segmentation and time cost is also improved with CNN parameters like max pool, max out and learning parameters. Method is evaluated with 75 percent of Dice Index [27]. Moreover in another study With a hybrid of FCM and feature, better segmentation is attained where jaccard index is 23 and dice is 34 [28]. Segmentation through modified FCM is improved with combination of bacterial foraging organization. These segmentation results are good for brain tumor [29].

In the presence of all-region extraction, feature selection techniques, and segmentation techniques, algorithms need to improve. From the well-defined studies, it is examined, MRI images face the issue of finding a variety of intensities in image, secondly, selection of feature is required due to data complexity issue, thirdly, due extreme intensities variation of tumors, tumor region mix with normal tissues at boundaries of it. If segmentation is improved therefore evaluation parameters show more significant results.

III. SCOPE OF WORK

The main aim of this novel work is to identify the tumor in brain MRI. The work helps to doctor for pre operation decision making. In this work, mostly images are axail, their orientation is Z-axis. Segmentation analysis is performed through features (texture-based, intensity-based, shape-based). On base of image labelling, we can decide, image is tumorous or nontumorous. With this way,it is easy to select the tumorous images from the dataset. Tumorous images are segmented using SOM KMEAN FCM(SOM Pixel Labelling with Reduced Clsuter Memebership). A doctor has clear road map for operation with help of proposed technique. Tagged images are already available in dataset and they have been used for comparison of results. The organization of this paper is as follow. Section IV is explaining the material and also explaining the methods (Region extraction, Feature Selection, Segmentation) for brain tumor analysis. Standard SOM,KMEAN, FCM algorithms have been determined. Section V explains the testing parameters of proposed technique. Section V is core body of paper. Region extraction identifies the tumor edged and boundaries. Feature helps for identification of confidence element in region. SOM provides initial level clustering with initial cluster index

TABLE 1. MACCAI BraTs 2017-2013 dataset.

Categories	patients x sequences x slices)	Total Number of images
HGG	210x4x155(patients x sequences x slices)	130200
LGG	75x4x155(patients x sequences x slices)	46500
Tagged (already segmented)	285 x1 x 155 (patients x sequences x slices))	44175
Subtotal (Validation)	46x1x155(patients x sequences x slices))	28520
Grand total	220875	

and it is helpful to resolve the issue of extreme intensities. Hybrid segmentation produces the significant exclusion of tumor.

IV. MATERIAL AND METHODS

For experimentation, a dataset that has been used is Brats 2013-2017 MACCAI brain tumor dataset. This is published dataset which has been used by different researchers across the world. For detection of tumor, the dataset is consisting of low grades glioma as well as high-grade glioma. Dataset pertains 285 MRI patients known as volume. Their naming convention is like BRATS 17-2013-8-1. This dataset is consisting of images from year 2013 to 2017. In dataset 210 patients are high-grade glioma whereas 75 are low-grade glioma. MRI images sequences are Flair, T1, T1CE, T2. Most images in this dataset are axil orientation where some of orientations are sagittal and coronal. The total number of HGG is 210*155*4=130200 whereas low-grade glioma are 75*155*4= 46500. Tagged images are already segmented images, they have been used to verify proposed segmentation. For every sequence, one tagged image is available for test or validate on the result of segmentation.

A. FEATURE EXTRACTION

In this study features have been extracted which depends upon brain images intensity from sequences of MRI (T1, T2, Flair, and T1CE). Brain scan which includes normal tissues and brain tumor tissues.

In above algorithm, types of feature are intensity-based features, shape-based features, and texture-based features. They have been extracted from every image of dataset. After feature extraction, SVM based model is generated. If their percentage of training accuracy is more than 80 percent they are selected for segmentation. These features are known as deterministic features. With combination of determined features and clustering produces better brain tumor segmentation. In table II, the features with higher accuracy. Table 2 is based on classification accuracy of flair and T1 sequence.

Algorithm 1 Feature Extraction

1. Read dataset
2. Read Volumes
3. Read1:155 input image for every volume
4. Extract 20 features on each image
5. If input image contain tumor
6. Label=1
7. Else
8. Label=0
9. Feat ← 20 Features are texture, intensity and shape based features
10. End
11. End
12. eND

B. REGION EXTRACTION

In this section of method, Tumor region is extracted with intensity adjustment, biggest blob, combination of biggest blobs.

1) INTENSITY ADJUSTMENT

Intensity adjustment is enhanced the tumor region by contrast or brightness adjustment for transformation. Contrast or brightness adjustment boost intensity of image tissues. Thus the intensity of brain tissues edges become more accurately visible. Thresholded intensities are divided in to two classes. One class have tumor intensity whereas other have none tumorous intensities.

$$I = f(x, y) \tag{1}$$

Equation number 1 is an input of image.

$$f(x)\alpha x + \beta \tag{2}$$

In equation 2, α represents tumorous tissue of brain tumor. x is multiply by α, it means that x holds the multiple variations of tumorous tissues for α. β is added to α, it represents whole brain tissue.

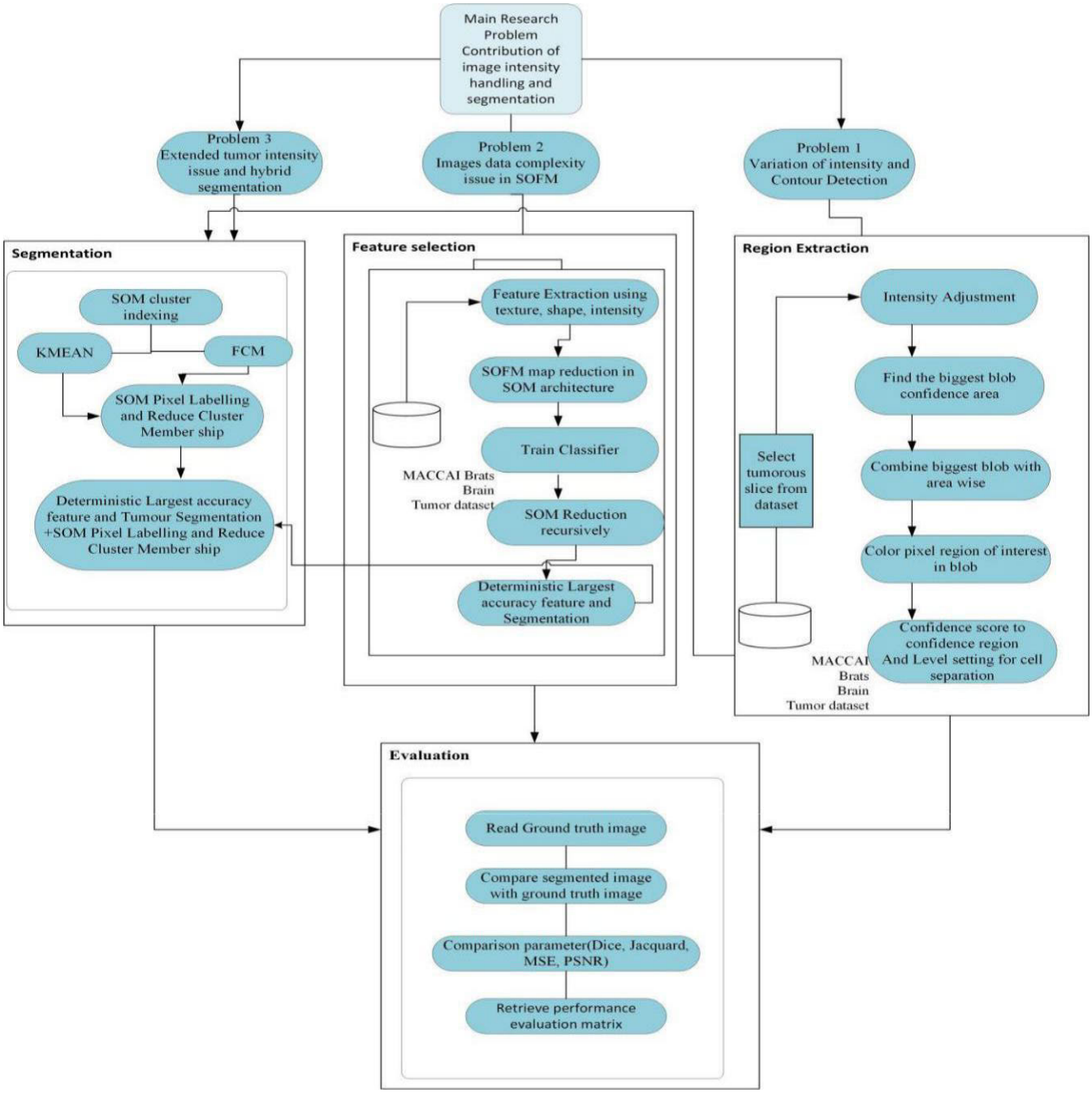


FIGURE 1. Research framework.

Therefore we have adjusted intensities of normal tissues as well as none tumorous tissues.

$$0 < \alpha < 1 \tag{3}$$

α values gives the contrast adjustment, its value exits among 0 to 1.

2) BIGGEST BLOB AREA OF INPUT IMAGE

The input images which are taken from the dataset, they have issue of homogenous intensity region. Homogenous intensity exists where area of tumor and other tissues are mixed in visible slices. Series of steps are taken to separate tumorous tissues from normal tissues. Initially, connected components areas are calculated in homogenous tumorous region. Each connected component region is called bolb. Therefore algorithm scans the region and labels each blob. Scanning is performed on each blob. Each blob is labelled. Biggest blob pixels area is selected from each image.

3) COMBINATION OF BIGGEST BLOBS

In dataset, every patients has 155 images. Tumor is fully visible in only 10 images. But tumor pattern of intensity

TABLE 2. Extracted features training over MACCAI_BraTs images of sequence flair, T1.

Sr-no.	Feature Name	Flair	T1
1	Mean	0.998	0.99
2	range	0.8283	0.9645
3	Area	0.7301	0.6387
4	Perimeter	0.6405	0.4321
5	Kurtosis	0.4373	0.627
6	variance	0.7493	0.9792
7	IDM	0.4863	0.8043
9	contrast	0.661	0.4043
10	Correlation	0.5456	0.5077
11	energy	0.672	0.5157
12	Homogeneity	0.4265	0.3211
13	Root mean square	0.322	0.6086
14	Smoothness	0.5265	0.5265
15	Skewness	0.5495	0.4166
16	Entropy	0.5997	0.5792
17	Ir-regular Feature	0.3936	0.5491
18	Shape index	0.3747	0.4931
19	Shape Circularity	0.6011	0.344
20	pixel orientation	0.5461	0.699

varies from image to image. From image number 65 to 69, tumor homogennous intensity is seen with similar pattern. Intensities are summed. Same process is repeated for image 70 to 74. Homogenous intensities are seen with small variations. Above two patterns of intensities are summed up. One complete region is formed with combination of biggest blobs.

4) COLOR THE PIXELS IN REGION OF INTEREST, FINAL BIGGEST BLOB

One final biggest blob is defined as the biggest connected component area. Biggest connected component area with higher weights is calculated. Combineation of patterns of blobs are producing maximum tumor pixel area.

RGB colors have been assigned to each biggest blob in combined pixels. Red color is assigned to first pattern, green color is assigned to seacond pattern. These pixels with first and second pattern are highighting confidence score. identified tumor boundary through score visual even small change in tumor region. This region is called confidence region. This confidence core is checked when we compare with ground truth images.

Algorithm 2 Contour-Algorithm()

1. Input image
2. Store input image in array
3. Binarize the input image
4. Label image ← label connected component of binary image
5. Blob measurement = By measure of connected components area wise and centroid wise.
6. All_area= Caculated measure of all individual connected component
7. for k=1 to no. of blobs
8. Display(All_area);
   K=K+1;
   End
9. If number of blobs >0
10. Call function of Extract biggest area()
    A. Sort all areas
    B. Check area is from member of list index
    C. Sort the list and return biggest blolb
    D. Return(biggest_blolb)
    E. end
11.
12. Else
    Close
13. L ← Resultant image of biggest blob store in array
14. Color the pixel of largest blob
15. Add biggest blob to the array
16. Repeat
17. COMBINE BIGGEST BLOBS
18. Evaluate final combined biggest blob through Dice, Jacquard, Mean Squared Error, Peak signal to noise ratio,
19. End

5) CONFIDENCE SCORE TO CONFIDENCE REGION

Confidence score is obtained from biggest blob values. From figure 15, on left hand side histogram of confidence score shows the intensities distribution which was calcualted in above 4 steps of region extraction. From confidence score, confidence region is extracted. In figure 15, histogram shows optimised intensities distribution of image. First step of tranformation is to calculate standard deviation of entire image. Seocnd step is to separating input image into sub images. Each sub image cartesian coordinates of pixel is related to the grey scale pixels. 95 percent confident interval is applied to every sub image. Lastly, image is multithrasholded to handle with target regions. We can see, histogram of confidence region is optimised due to appropriate mechanism. The above process is prorducing confidence region. From figure 15, this work shows complete machanism of tranformation.

The below four picture are with name of Figure 2, Figure 3, and Figure 4, Figure 5 are taken from MACCAI BRATS 2013_2017 brain tumor dataset. Figure 2 is Flair

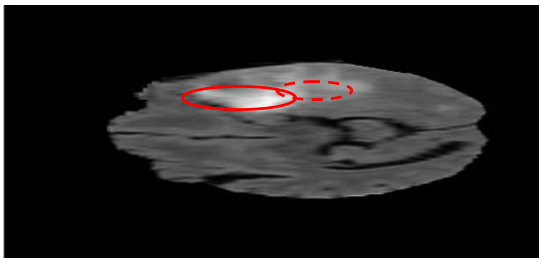


FIGURE 2. T1 sequence original image with a pattern of intensity.

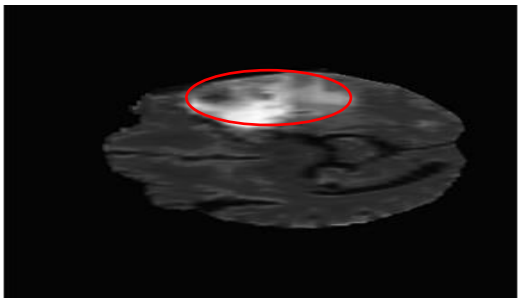


FIGURE 3. Intensity adjustment of one pattern of intensity.

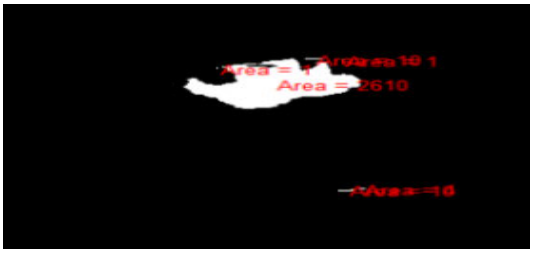


FIGURE 4. Blobs areas from certain intensities.

FIGURE 5. Selected biggest blob.

sequence image. Figure 3 is T1 sequence image, Figure 4 is T2 sequence image, Figure 5 is T1CE sequence image. They show normal tissues and brain tumor on top left with different variations.

C. SOFM REDUCTION ARCHITECTURE AND LABEL MEMBERSHIP

Improved SOFM is working with sequence of steps. First step is random weights assignment. In random weight initialization, weights are assigned for SOM map. For every feature columns, extracted features are trained and their training accuracies are obtained through combination of svm classifiers one by one. Hencce best feature are found. These feature are used for clustering. Next step of SOFM is to find out best match, update neighbour weights..

1) SOM FEATURE MAP REDUCTION IN SOM ARCHITECTURE

Feature extraction has been performed in section number A. Those features are feed to the SOFM algorithm. In SOFM algorithm SOM Map is first and important part which plays

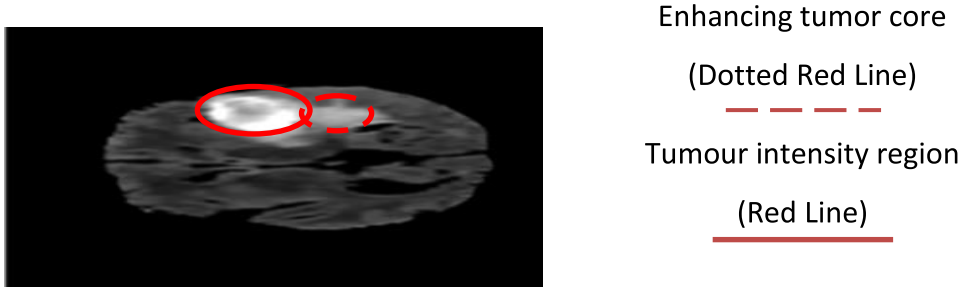


FIGURE 6. Intensity adjust of an image from a particular pattern of intensities they are from 68 towards 74.

Algorithm 3 LEVEL SET ALGORITHM WITH LEVEL SET PARAMETER OVER CONTOUR

MAIN()

1. INPUT BIGGESTBLOLBIMAGE=F(X,Y);
2. DETERMINE PARAMETERS(), THIS FUNCTION DETERMINE PARAMETERS OVER INPUT IMAGE NAMED AS BIGGESTBLOBIMAGE
   - A. CALCULATE MAXROW(IMAGE);
   - B. CALCULATE MINROW(IMAGE);
   - C. CALCULATE MAXCOL(IMAGE);
   - D. CACULATE MINCOL(IMAGE);

   ADJUST 1,2,3,4 ACCORADING TO BIGGESTBLOB BOUNDARY

   LEVELSET(ROWOFMAX,ROWOFMIN,COL.OFMAX, COL.OFMIN)=-2
3. BIGGESTBLOBIMAGE CONVOLVE WITH GAUSSIAN LOW PASS KERNEL
4. U=REGION SCALE FITTING (), THIS FUNCTION GIVES THE INTENSITY FITTING INTO TWO REGIONS. DERIVATE THE IMAGE TO CALCULATE THE STRENGTH OF EDGES
   - A. LOCALIZE THE INNER CONTOUR
   - B. LOCALIZE THE OUTER CONTOUR
   - C. DEFINE INNER AND OUTER INTENSITIES
   - D. DATAFORCE WHICH SEPARATED INNER CONTOUR FROM OUTER CONTOUR
5. RETURN AND DISPLAY THE EDGE DETECTED IMAGE

more important role in feature reduction. Feature reduction and selection is performed in random weight initialisation step. Here classification features accuracy are assigned to their specified features column. Feature column gives list of every feature. In Table 2 feature accuracies are determined determined using seven SVM classifiers accuracies. Those accuraces values are appended in every feature column. Then feature reduction module is called recursively to the features columns. In every call, feature accuracy in column wise are checked. If it is equal or more than 80 percent then feature will be add to matrix otherwise it will be discarded. This process repeats until all of features have not been checked. Therefore best features are selected from the dataset. Feature selection criteria is simple. If feature accuracy is more than 80 percent then they are good feature. If feature accuracy is more than 50 and less than or equal to 80 Then they are average features. If their feature accuracy is less than 50 or equal to 50 then they are bad features. Good features are deterministic features. They are selected. Then rest of SOFM steps are performed.

Algorithm 4 FEATURE REDUCTION

1. LOAD TRAIN DATA SET FROM FEATURE
2. EXTRACTION MODULE
3. LOAD LABEL FOR TARGET TRAIN DATA SET.
4. INITIAL SOM_MAP WHERE ROW=20, COL=20, DATA COL=20, DATA COLUMN IS NUMBER OF FEATURES

   RANDOM WEIGHT INITIALIZATION FUNCTION IS CALLED WHERE PASS STEP 3 ROWS AND COLUMNS TO SOM_MAP
5. TRAIN_CLASSIFIER
6. SOM_REDUCTION
7. SOFM FIND BEST MATCH COMPUTER, NEIGHBOR ARE CALLED
8. END

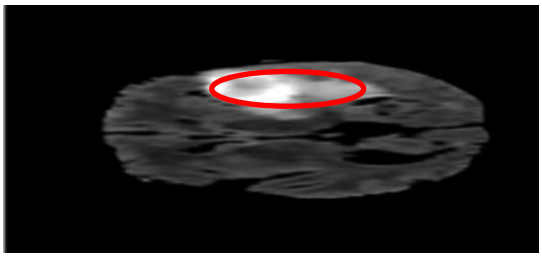
2) REDUCE FEATURE FRO WEIGHTED SOM MAP AND SEGMENTATION

From the best features we have performed max sort and we select the single best feature, this feature is named as deterministic feature. That feature is applied on every single image which gives the best accuracy. This feature highlight region of interest (tumor) in input image. FCM is performed to segment the portion of tumor. FCM defined labels to intensities. Those labels are divided into two classes. Those labels gives tumorous cells as well as none tumorous cells.

SOFM reduce the dimension of data and gives best feature. We can see the performance of best picture in Figure 17 to Figure 17. Figure 16 is input image, Figure 17 shows best feature for confidence extraction and Figure 18 gives confidence extraction element segmentation.

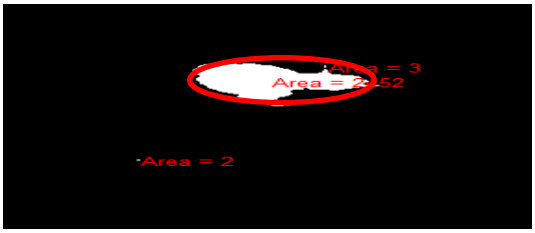
D. SOM KMEAN FCM

With inclusion of SOM to KMEAN then SOM to FCM and their combination solves the issues of variations of intensity during segmentation. Variation intensity issue is resolved



Contrast with intensity adjustment of Slice 65 to 74 (Red Line)

FIGURE 7. Intensity Adjustment of 69 to onward 74.

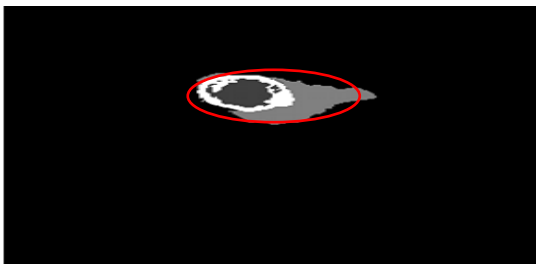


Tumor areas Tumor areas based with connected components (Red Line)

FIGURE 8. Blobs area in slices from 70 to 74.

Combination of biggest areas of weighted connected components from slice 65 to 74

FIGURE 9. Combination biggest blobs from slice 65 to 74.



Ground truth image (Red Line)

FIGURE 10. Ground truth reality image of slice 74.

with complete brain tumor. Their discussion and their hybrid discussion is as followed.

1) KMEAN

KMEAN is a method of clustering in which image is partitioning on basis of n observations. Observation is image; it is divided into K clusters where observation belongs with nearest mean [21]. Therefore Initial values of K centers are adjusted. Algorithm selects K pixels randomly as center of classes. One pixel is assign as center which is close to the class. Distance of one pixel to the center of class I is represented as μ and the relationship can be as followed in equation 4. From the class, center is computed then checks the average of all pixels which belongs to particular class. This work is pre assumed before assignment. Class assignment (Class I) is repeating with p number of steps. This process is iterated whenever difference is not occurred. I difference is occurred then iteration has stopped.

$$\mu^p = \{\mu_1^p, \mu_2^p, \mu_3^p \ldots\ldots \mu_k^p\} \tag{4}$$

$$\mathrm{D1(x, y)} = |\mathrm{I(x, y)} - \mu_1| \tag{5}$$

The FCM implementation consists of different step. It decides the cluster and it also sets the initialization fuzziness param-

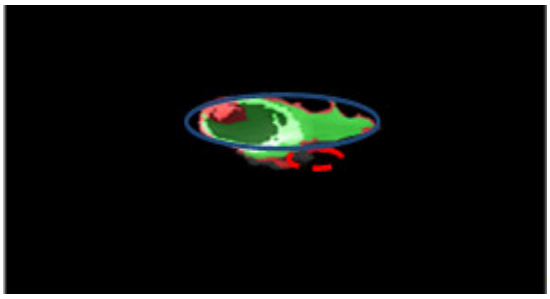


FIGURE 11. Overlap portion of FIGURE. 9 and FIGURE. 10.

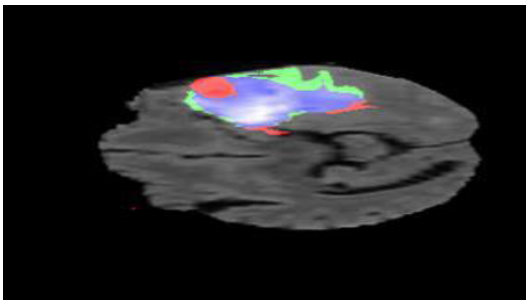


FIGURE 12. The Confidence region of tumour highlight with other cells.

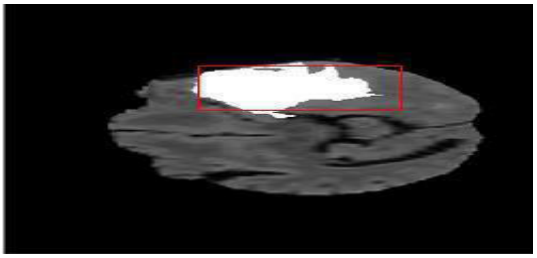


FIGURE 13. Contour drawn around tumour boundaries.

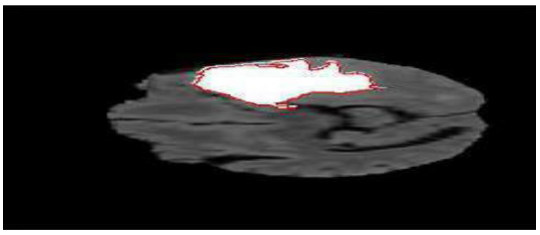


FIGURE 14. Region scale fitting used for the extraction of tumour.

eter. With measure of this parameter, the clusters centers are initialized.

$$\sum_i^n (\mu ik)^2 = (\mu \mathrm{ik})^2 * \mathrm{X_{kj}} / \sum_i^n (\mu \mathrm{ik})^2 \tag{6}$$

μ_{ik} is membership values where Xkj are corresponding data points. In procedure of FCM, next step is to calculate the data points which are associated to each cluster center. It can be seen in equation number 6. Membership of the matrix is updated. It can be seen in equation number 7.

$$\sum_i^n (\mathrm{d}ik) / \sum_i^n (\mathrm{d}jk)^{\mathrm{n}-1} \tag{7}$$

d is the distance of data point from the cluster center. In equation, djk represents the corresponding data point from

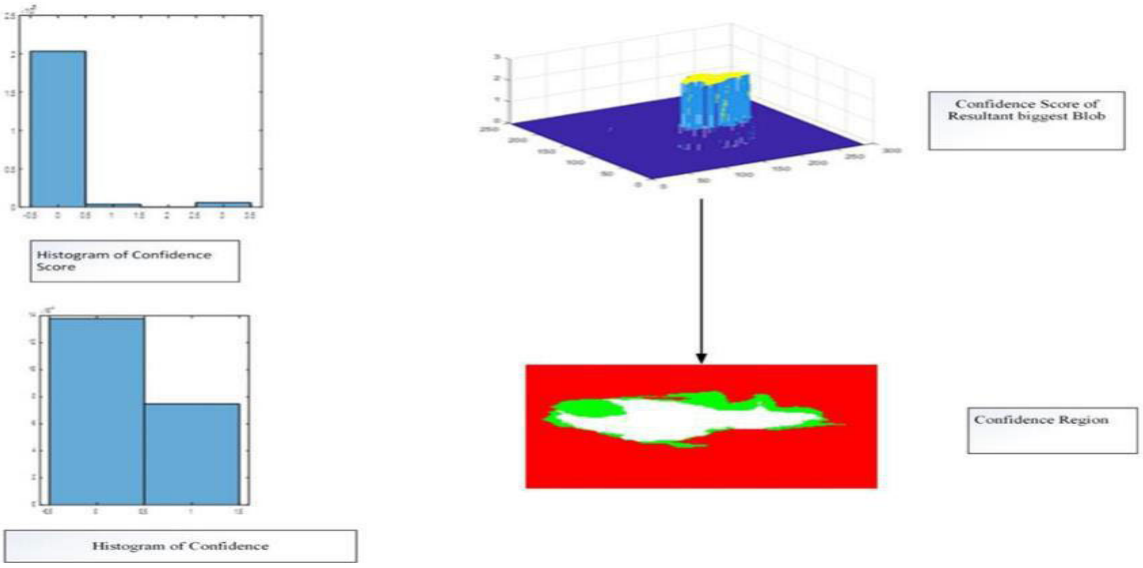


FIGURE 15. Confidence score confidence region.

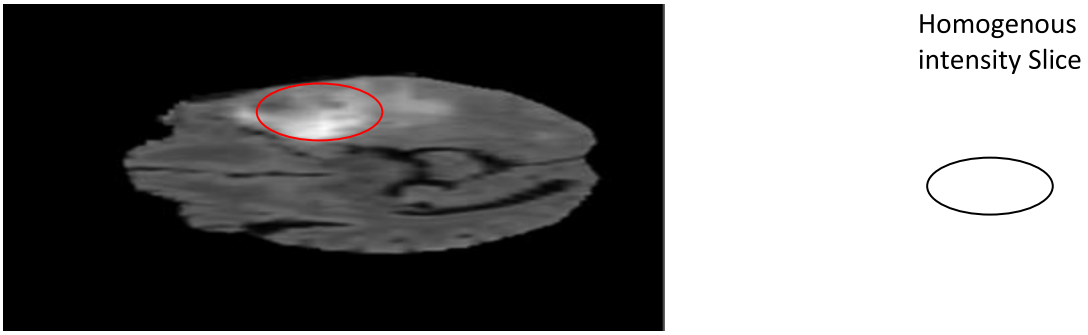


FIGURE 16. Original slice 65 with homogenous intensity.

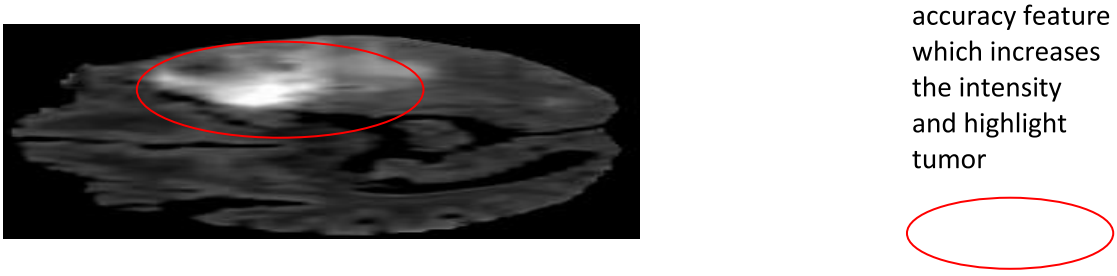


FIGURE 17. With higher accuracy texture feature(MEAN) selection from updated SOFM architecture.

the cluster. Convergence is checked whether the cluster center will not equal to initialization of fuzziness parameter.

This check is performed for optimal cluster centers. In fact this step is validating.

In Figure 19 is input of original image. Figure 20 produces confidence region extraction score. Tumor and is segmented through SOM KMEAN in Figure 21. Figure 22 produces segmentation of tumor through SOM FCM. Figure 23 is combination of Figure 21 and Figure 22 therefore we have SOM KMEAN FCM (hybrid). Figure 24 is produced through combination of feature extraction (FE). Feature reduction is performed through improved SOM and segmented through FCM. This combination is known as Feature Extraction (FR), Feature reduction (FE) and Fuzzy C Mean (FCM) so we have final combination as FEFRFCM. Figure 25 is combination of Figure 23 and Figure 24. Therefore Final combination is,

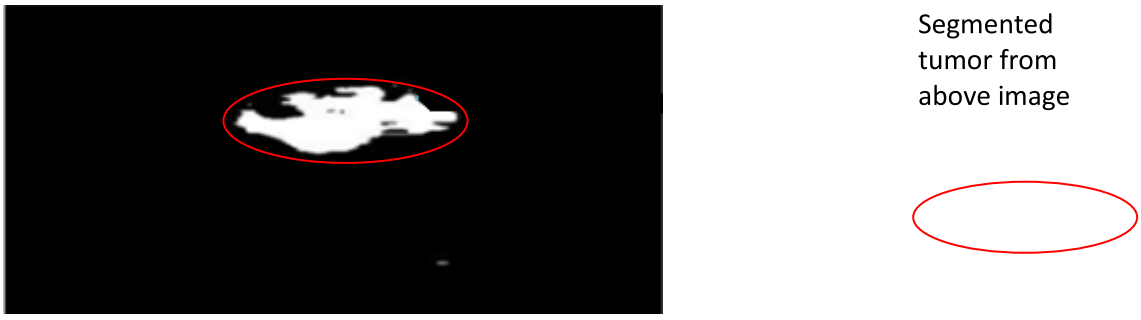


FIGURE 18. Segmentation using FCM on ROI highlighted image.

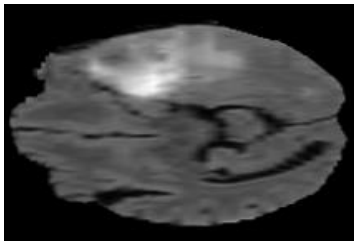


FIGURE 19. Original image.

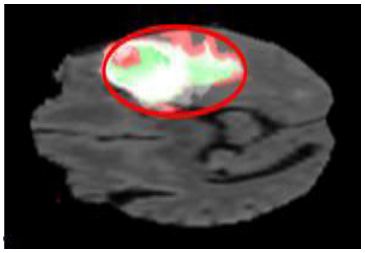


FIGURE 20. Confidence region extraction.

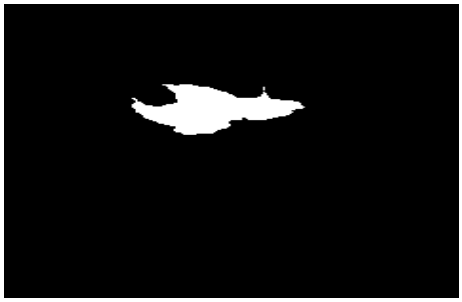


FIGURE 21. SOM KMEAN (SOM Pixel labelling).

FIGURE 22. SOM FCM (SOM member ship reduction).

Algorithm 5 Train Classifier

1. Input train_data2 to the train classifier
2. All of features are stored in column wise col1, col2, col3…col21 where col_1 to col_20 are features and col 21 is label.
3. [col1, col2, col3……..col21] they are picket one by one recursively.
4. Convert col1…col20 array to input table that is called predictor.

Column 1 to column 20 are stored in variable predictor name.

5. Response label variable for label column or col. number 21 is across every feature in input table
6. Predictor name is passed to svm structure of matlab classifier
7. Select col 1 across column 21
8. Apply Kfold for validation
9. Accuracy of validation is also return
10. If col>20
11. Then stop
12. Else go to step 1
13. End

SOM_KMEAM_FCM+FE_FR_FCM. This combination is known as SOM Pixel Labeling with reduced cluster membership and deterministic feature clustering (SPLRCM&DFC). Figure 26 is ground truth image of input image. Algorithm has segmented tumor; tumor size is 22 square mm.

For summarize point of view, Firstly Confidence Region Contour Detection is performed. Secondly SOFM is improved where features have been trained on dataset and their accuracy is retrieved. On base of training accuracies, we have called them good features, average features and best features. One threshold value is settled. On basis of best training feature accuracy, we have selected deterministic feature. This deterministic feature is applied on every image. With good feature the region of interest (ROI) is more highlighting. After this step FCM is applied to segment the

FIGURE 23. Combination of SOM pixel labelling with reduce cluster membership (SOM KMEAN FCM).

Algorithm 6 SOM Reduction()

1. r input column1 to column20 accuracy function is called from train classifier function
2. Feat=[col1.....coln] in Feat accuracy of every column is stored from whole dataset
3. Assign those accuracies to Train_Dataset2
4. Loop 1 to 20 time
   If accuracy of Feat >=80
   new_col ⟵ Append a new column
   And update all accuracies in new_column recursively and it is stored in matrix Featn
5. Check step 4 whenever all of column are not checked and added
6. Largest feat accuracy ← max(Featn) this step returns the highest accurate feature on dataset.
7. End

Algorithm 7 Largest Accuracy Feature and Segmentation

1. Read individual image from dataset
2. T ⟵ t Tumorous image
3. T1 ⟵ t∗x intensity values of largest feature accuracy
4. FCM thrash
5. Display FCM thrash image

FCM thrash()

1. data ← Reshape image intensity into one column
2. Apply Fuzzy c mean on data
3. Store maximum intensity list and define their possible corresponding label
4. If w=0
   Label of data is among 1 to 2 or from low intensity of image to the middle intensities
   Level1=(Label==1), level2=(label==2)
   Else
   Label of data is among 2 to 3 or from middle to high level intensities
   Level2=(Label==2), Level3=(Label==3)
   Both are returned

brain tumor in image. Detail from material and methods in section A, B, C and D, we are concluding: Confidence Region

Algorithm 8 Evaluation

1. T4=READ GROUND TRUTH IMAGE FROM DATASET OF SAME INPUT IMAGE
2. T6=IMREAD FCM THRESHOLDED IMAGE
3. DICE (T4,T6);
4. JACQUARD(T4,T6);
5. MSE(T4,T6);
6. PSNR(T4,T6);

Contour Detection algorithm which identifies the boundaries of tumor tissues of the homogenous intensities. Identification is performed through intensity adjustment, biggest blobs tumor area which highlights tumor and level set algorithm for delineation of tumor boundaries. Deterministic feature clustering gives complete shape of tumor. Last one is hybrid segmentation is shown in Figure 28. Three clusters have particular tumor pixels. Cluster A, D, F are derived through segmentation process and x is showing their members.

FIGURE 24. Segmentation using FCM on ROI highlighted image.

We have proposed Hybrid method of segmentation. SOM Pixel Labelling with reduce cluster membership. It has been achieved through hybrid of SOM KMEAN FCM with Feature slection along FCM. SOM offers initial clustering. It assigns weight to pixel then store their weights to clusters. Best match step is calculated with minimum weight to the pixel. Then neighbor of best match weight have been calculated and their weights are set on base of distance from best match. This process will be repeated until one whole cluster

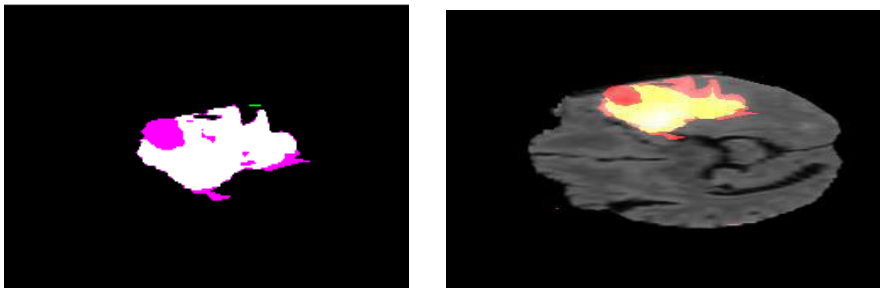


FIGURE 25. Combination of Figure 23 and Figure 24, combination of som pixel labelling with reduce cluster membership and deterministic feature clustering.

Algorithm 9 SOM_KMEAN

1. Input image
2. Divide the image into two columns
3. Take the mean of every row entry
4. Pass this two column image into SOM
5. Define the cluster=3
6. Initialize the number of iterations
7. Assign random weights from among number 2 to 3
8. Loop Number of iterations

Loop through rows of input matrix
Loop for number of input clusters
Assign weights to the input matrix
Calculate best match cluster value
Store it into variable of cluster index
Update weights
End
End
End
Pixel Labelling is performed by KMEAN

1. Reshape cluster index in to number of rows and columns and stores them in variable gray label
2. Three empty segmented cells are created due to storage of cluster values
3. Loop K=1 to cluster = 3 times

Input image is stored to gray color image variable
Check is imposed on same index of gray label and replace on indexed with same intensities of colors of original image
If not cluster index then replace them with 0
Repeat cluster index time
Store in variable segmented image
Store grey color image in to segmented cell cluster by cluster

9. End

Algorithm 10 SOM_FCM

1. MEMBER SHIP OF DATA VALUES ARE REDUCED WITH FCM
2. PASS CLUSTER INDEX RETURNED FROM SOM TO FCM
3. FCM RETURNS CLUSTER CENTER, CLUSTER DATA POINT AND MEMBERSHIPS OF CLUSTERS
4. FIND OUT THE MAXIMUM OF MEMBER SHIP VALUE AND STORE IT INTO INDEX

ASSIGNING PIXEL TO A CLASS WITH SPECIFIC VALUES
IN INDEX 1 MAXIMUM INTENSITY IS STORED
IN INDEX 2, MINIMUM INTENSITY IS STORED
RESHAPE THE REDUCE MEMBERSHIP CLUSTER INDEX MATRIX AND STORED IT IN VARIABLE SOM_FCM

Algorithm 11 Combination of SOM_KMEAN and SOM_FCM

Resize SOM-KMEAN to a specific resolution
Resize SOM-FCM to a specific resolution
Combine both SOM-KMEAN and SOM-FCM
Evaluate with testing parameters (Dice, Jacquard, MSE, PSNR)

index matrix form. KMEAN is doing pixel labeling on cluster index matrix. Pixel labeling has been performed using logical indexing and assignment of clusters to the pixel values. In another case, same SOM cluster index matrix is input to the FCM. FCM has extra membership issue. When SOM is input to the FCM so it membership of cluster reduce and we have achieved good segmentation with optimum reduction of memberships. Therefore KMEAN algorithm greedy nature have been solved with inclusion of SOM. FCM algorithm has also issue of higher membership, they have issue of more memberships and this is minimized with the inclusion of SOM. We have combined their segmentation results. Hence SOM KMEAN FCM is improving segmentation technique and issue of underfitting is also resolved. It has been achieved with the addition of pixels of SOM_KMEAN and SOM_FCM. Hence hybrid is achieved. Hybrid offers good segmentation for extreme intensities of enhancing tumor. It also produces accurate tumor position, this segmentation is confirmed after comparision with tagged images. SOM_KMEAN_FCM(SOM Pixel labelling reduce cluster memeber) is combined with FE FR FCM(Deterministic Feature Clustering) to achieve complete tumor segmentation. The above combination gives three clusters in Figure 28. From hybrid of three clusters a complete segmentaiton solved issue of extreme extended intensities.

Hybrid of three cluster is valueable. SOM plays a vital role in solution of extreme intensities. Intensities cause issue of under fitting in suggested technique of region extraction. In hybrid segmentation (SOM Pixel labeling with reduce cluster membership and deterministic feature clustering), SOM is assigning indexes to tumor clusters, limiting memberships and determining the target feature. From figure 18, SOM FCM(maximum values index clsuters) were two clusters and only one cluster is selecting. SOM KMEAN(Pixel labelling) producing three clsuters and one tumorous cluster is selecting. Deterministic Feature clustering producing two clusters and one cluster is selecting. Hence from above three clusters are selecting whereas total number of clusters where seven. These clsuters are tumorous clusters. They are namely as pixel labeling cluster, highest index cluster and deterministic feature cluster. These clusters are combining. Hybrid of cluster solves the issues of extreme intensities. In fact the issue of under fitting is resolved.

V. RESULTS AND DISCUSSION

The results and detail discussion of proposed segmentation algorithm is explained in detail in this section. The implementation of proposed algorithm is done using with core i5 clocked at 3 GHZ with 16 GB RAM using Matlab 2017b. The brain tumor (normal/ abnormal) segmentation of MR image is a complicated process. In this study we have formulated new unsupervised technique for tissues for tissues segmentation in MR brain image. Brain tumor causes gradual damage of other brain tissue and it may fatal if can't treated. Brain tumor tissues segmentation identifies normal tissue and tumor tissues. In order to validated our algorithm, brain tumor detail have been used namely as Brats brain tumor dataset ground truth reality (tagged images). Moreover, the complete enhancing tumor is focused in dataset from multimodal images of Brats MACCAI 2017-2013 dataset. Finally the results of proposed algorithm and ground truth are compared by dice index, Jaccard Tanimoto Coefficient Index (TC) for similarity of shape and for better visualization of tumor MSE and PSNR are tested. In below table 3 testing parameter mathematical formula are given.

A. CONTOUR DETECTION USING BIGGEST BLOB AREA (CONFIDENCE SCORE) WITH SIGNIFICANT CONFIDENCE REGION

Tumor is visible from slice number 65 to 74. Tumor intensities are same from slice 65 to 69 and then 69 to 74. Their intensities are adjusted. This is first step of region extraction. Then, area of connected component (CC) is determined of slice number 65. All CC are assigned specific weights. The weight of biggest connected component is more important. After assignment CC are sorted. we have found biggest component which is called biggest blob. This biggest blob is not giving confidence region of brain tumor. Therefore slice number 65 to 74 biggest blobs are calculated. The combination of biggest blobs gives confidence region because resultant image captures maximum tumor pixels. Result image biggest blob is output variable of region extraction. So contour is drawn around confidence region image with setting of parameter like min col, max col, min row, max row. Level set algorithm is used to delineate the tumor boundary and homogenous tissues issue is resolved with achievement of more than 98 percent of dice similarity index.

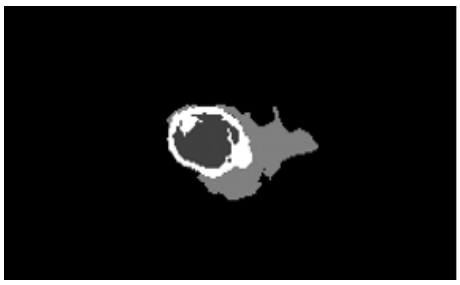


FIGURE 26. Ground truth image.

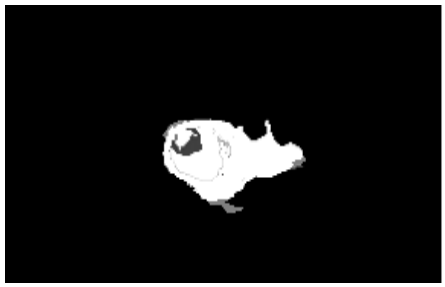


FIGURE 27. Obtained resultant Overlap of above hybrid clustering segmentation with ground truth image.

B. SEGMENTATION OF ABNORMAL TISSUES (COMPLETE TUMOR) OF MULTIMODAL MR IMAGE(BRATS MACCAI DATABASE)

We have extracted region of abnormal tissues of flair, T1, T2, T1Ce sequences using Confidence Region Contour Detection, Deterministic Feature Clustering and Hybrid Segmentation. Three different clusters are combined to segment extreme tumor intensities.

From above discussion, three algorithms are combining. Therefore Resultant Biggest Blob (RBB) giving the confidence score and then it is transformed to confidence region. Confidence region is giving region extraction but still have issue so in further steps region extraction will be input to hybrid segmentation process and in hybrid segmentation all of objectives will combine. We have segmented normal tissues along abnormal tissues with SOM Pixel Labelling with Reduce Cluster Membership and Deterministic Feature Clustering (SPLRCM&DFC) using SOMKMEAN, SOMFCM, FEFRFCM. SOM Pixel labeling is done with SOM KMEAN, It labels pixel and those labels are clustered. Cluster index add pixels. Secondly, Reduce Cluster Membership (RCM) achieve with combination of SOM FCM. RCM reduces the membership of cluster and gives abnormal tissues

TABLE 3. Evaluation metrics.

METRICS	FORMULA	METRICS
JACCARD TANIMOTO COEFFICIENT INDEX (TC) (JI)	J(A,B)=S(A∩B)/S(A∪B) J(A,B)=1-J(A,B)	(VISHNUVARTHANAN ET AL., 2016) (TAN, 2019)
DICE INDEX OVER LAP(DOI)	J(A,B)=2×J(A,B)/1+J(A,B)	(VISHNUVARTHANAN ET AL., 2016) (TAN, 2019)
MEAN SQUARED ERROR (MSE)	$1/mn \sum_{i=0}^{m-1} \sum_{j=0}^{n-1} [A(I,j)-B(I,j)]$	(VISHNUVARTHANAN ET AL., 2016)
PEAK SIGNAL TO NOISE RATIO(PSNR)	10LOG10(MAXI^2/MSE)	(VISHNUVARTHANAN ET AL., 2016)

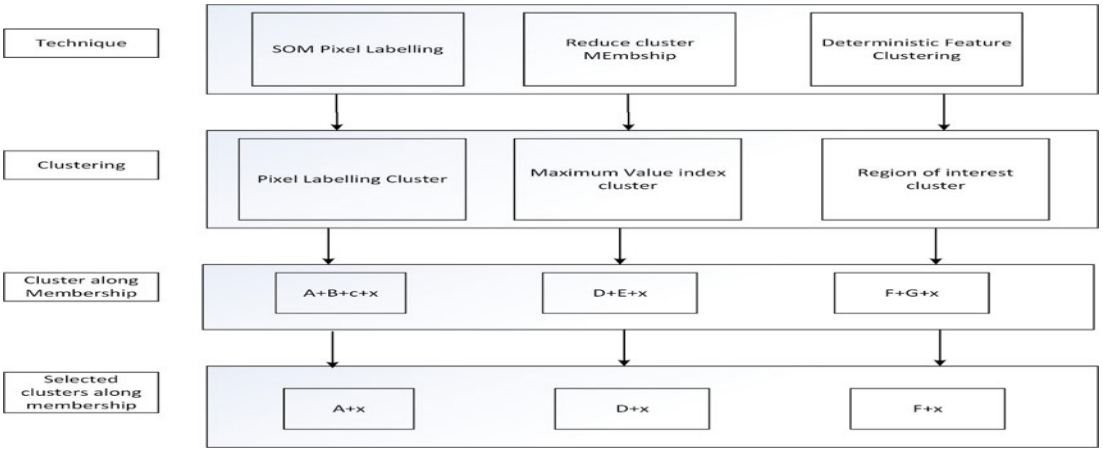


FIGURE 28. Hybrid clustering process.

with tumorous intensities. Maximum value indexes are taken. Other clusters are discarded; it is called Reduce Cluster Membership (RCM). Thirdly, two clusters are combined which are producing region of interest (ROI) and algorithm is known as SPLRCM. FEFRFCM is an combination. It's background philosophy selects best feature of brain tumor image and it is also known as Deterministic Feature Clustering (DFC). Extracted confidence element cluster is segment the tumor. Deterministic Feature Clustering performs better tumor segmentation. Finally, the cluster is named as SPLRCMDFC. Complete tumor shape is segmented with this hybrid.

Performance of algorithm can be seen with following results values. Dice overlap index (DOI) is 0.99, Jaccard Tanimoto Coefficient Index (TC) is 0.94, Mean Squared Error (MSE) is 0.13,Peak Signal to noise ratio(PSNR) is 21.20. The above average value is also look to be high in table 2. Averages of high, low and medium values have been considered.

Due to the extreme variation or expected variations of intensities, it was difficult to segment the enhancing complete tumor and edema (especially T1) and tough task to segment the neighbor pixels of MRI brain tumor. For detail analysis we have not stick to single testing parameter we have tested methodology with Dice overlap index (DOI), Jaccard Tanimoto Coefficient Index (TC), Mean Squared Error (MSE) and Peak Signal To Noise Ratio(PSNR) testing parameters. DOI and JI gives the significance whereas MSE and PSNR produces testing of visualization of brain tumor [19]. Table 4, Table 5 shows result of segmentation using these testing parameters.

In below Figure 29, Figure 30,Figure 31 and Figure 32 graphs are given., they are evaluation of T1 sequence images and they are tested through Dice, JI, PSNR and MSE. Images are segmented through SOM_KMEAN and SOM_FCM. Table 4 and Table 5, High represent maximum efficiency of algorithm. Very high is more than maximum level performance by algorithm. Low values shows the bad evaluation of algorithm whereas middlevalue shows the average the average performance of algorithm. This T1 MRI image sequence is almost equal to evaluation values of Flair, T2 and T1Ce sequences.

From above figures, the study tests with results of Mean Squared Error in Figure 29, Peak Signal To Noise Ratio in Figure 30, Jaccard Index in Figure 31 and Dice overlap index in Figure 32. These testing parameters are comparing SOM Pixel Labeling versus Reduce Cluster Membership. Figure 31 and Figure 32 gives the analysis of complete

TABLE 4. Performance evaluation of proposed SOM_KMEAN_FCM.

	SOM_KMEAN		SOM_FCM		SOM_KMEAN		SOM_FCM	
	PSNR				MSE			
Vol_1_flair	19.519	Low	19.51	Low	0.05	Low	0.25	**High**
Vol_2_flair	19.265	Low	18.18	Low	0.02	Low	0.2	**High**
Vol_3_flair	19.69	Low	19.68	Low	0.03	Low	0.23	**High**
Vol_4_flair	19.69	Low	20.36	Low	0.04	Low	0.2	**High**
Vol_5_flair	19.34	Low	19.07	Low	0.03	Low	0.24	**High**
Vol_6_flair	19.82	Low	19.82	Low	0.02	Low	0.21	**High**
Vol_7_flair	**26.04**	**High**	26.04	High	0.02	Low	0.29	**High**
Vol_8_flair	**28.08**	**High**	28.08	High	0.02	Low	0.3	**High**
Vol_9_flair	18.62	Low	18.59	Low	0.05	Low	0.26	**High**
Vol_10_flair	18.63	Low	18.61	Low	0.05	Low	0.28	**High**
Vol_1_T1	19.52	Low	19.51	Low	0.034	Low	0.23	**High**
Vol_2_T1	19.26	Low	19.26	Low	0.036	Low	0.17	**High**
Vol_3_T1	19.7	Low	19.69	Low	0.04	Low	0.18	**High**
Vol_5-T1	19.69	Low	20.34	Low	0.036	Low	0.18	**High**
Vol_6_T1	20.36	Low	20.28	Low	0.036	Low	0.17	**High**
Vol_7_T1	19.34	Low	19.31	Low	0.039	Low	0.18	**High**
Vol_8_T1	19.82	Low	19.82	Low	0.025	Low	0.18	**High**
Vol_9_T1	**26.04**	**High**	26.04	High	0.04	Low	0.18	**High**
Vol_10_T1	**28.086**	**High**	28.08	High	0.04	Low	0.19	**High**
Vol_1_T2	19.52	Low	19.51	Low	0.027	Low	0.14	**High**
Vol_2_T2	19.26	Low	19.26	Low	0.05	Low	0.19	**High**
Vol_3_T2	19.7	Low	19.69	Low	0.04	Low	0.15	**High**
Vol_5_T2	19.69	Low	20.34	Low	0.05	Low	0.16	**High**
Vol_6_T2	20.36	Low	20.28	Low	0.05	Low	0.19	**High**
Vol_7_T2	19.34	Low	19.31	Low	0.04	Low	0.22	**High**
Vol_8_T2	19.82	Low	19.82	Low	0.04	Low	0.23	**High**
Vol_9_T2	**26.04**	**High**	**26.04**	**High**	0.04	Low	0.21	**High**
Vol_10_T2	**28.086**	**High**	**28.08**	**High**	0.05	Low	0.2	**High**
Vol_1_T1CE	19.52	Low	19.51	Low	**0.21**	**High**	0.21	**High**
Vol_2_T1CE	19.26	Low	19.26	Low	0.044	Low	0.04	**High**
Vol_3_T1CE	19.7	Low	19.69	Low	**0.19**	**High**	0.19	**High**
Vol_5_T1CE	19.69	Low	20.34	Low	**0.19**	**High**	0.19	**High**
Vol_6_T1CE	20.36	Low	20.28	Low	**0.16**	**High**	0.16	**High**
Vol_7_T1CE	19.34	Low	19.31	Low	**0.17**	**High**	0.17	**High**
Vol_8_T1CE	19.82	Low	19.82	Low	**0.28**	**High**	0.22	**High**
Vol_9_T1CE	**26.04**	**High**	**26.04**	**High**	**0.22**	**High**	0.22	**High**
Vol_10_T1CE	**28.08**	**High**	**28.08**	**High**	0.039	Low	0.04	Low

TABLE 5. Performance evaluation of proposed SOM_KMEAN_FCM.

	SOM_KMEAN			SOM_FCM	SOM_KMEAN		SOM_FCM	
	Dice				Jacquard			
Vol_1_flair	**0.98**	**High**	0.98	**High**	0.97	**High**	**0.96**	**High**
Vol_2_flair	**0.99**	**High**	0.97	**High**	0.99	**High**	**0.94**	**High**
Vol_3_flair	**0.98**	**High**	0.95	**High**	0.97	**High**	0.75	Low
Vol_4_flair	**0.97**	**High**	0.95	**High**	0.95	**High**	0.88	Medium
Vol_5_flair	**0.99**	**High**	0.99	**High**	0.98	**High**	0.8	Medium
Vol_6_flair	**0.99**	**High**	0.98	**High**	0.98	**High**	**0.96**	**High**
Vol_7_flair	**0.99**	**High**	0.98	**High**	0.99	**High**	**0.97**	**High**
Vol_8_flair	**1**	**Very High**	0.991	**High**	1	**Very High**	**0.93**	**High**
Vol_9_flair	**0.99**	**High**	0.99	**High**	0.99	**High**	0.89	Medium
Vol_10_flair	**0.99**	**High**	0.95	**High**	0.99	**High**	**0.95**	**High**
Vol_1_T1	**0.99**	**High**	0.97	**High**	0.99	**High**	**0.95**	**High**
Vol_2_T1	**0.99**	**High**	0.97	**High**	0.99	**High**	**0.95**	**High**
Vol_3_T1	**1**	**Very High**	0.96	**High**	0.99	**High**	**0.94**	**High**
Vol_5-T1	**0.98**	**High**	0.96	**High**	0.96	**High**	**0.93**	**High**
Vol_6_T1	**0.99**	**High**	0.97	**High**	0.99	**High**	**0.96**	**High**
Vol_7_T1	**0.99**	**High**	0.98	**High**	0.97	**High**	**0.97**	**High**
Vol_8_T1	**1**	**Very High**	0.99	**High**	0.99	**High**	**0.984**	**High**
Vol_9_T1	**0.98**	**High**	0.99	**High**	0.97	**High**	**0.98**	**High**
Vol_10_T1	**0.98**	**High**	0.975	**High**	0.97	**High**	**0.95**	**High**
Vol_1_T2	**0.99**	**High**	0.97	**High**	0.99	**High**	**0.95**	**High**
Vol_2_T2	**0.99**	**High**	0.98	**High**	1	**Very High**	**0.95**	**High**
Vol_3_T2	**0.99**	**High**	0.97	**High**	0.98	**High**	**0.93**	**High**
Vol_5_T2	**0.99**	**High**	0.98	**High**	0.99	**High**	**0.96**	**High**
Vol_6_T2	**0.99**	**High**	0.97	**High**	0.99	**High**	**0.95**	**High**
Vol_7_T2	**0.99**	**High**	0.98	**High**	0.98	**High**	**0.97**	**High**
Vol_8_T2	**0.99**	**High**	0.99	**High**	0.98	**High**	**0.98**	**High**
Vol_9_T2	**1**	**Very High**	0.99	**High**	1	**Very High**	**0.98**	**High**
Vol_10_T2	**1**	**Very High**	0.99	**High**	1	**Very High**	**0.99**	**High**
Vol_1_T1CE	**0.97**	**High**	0.97	**High**	0.95	**High**	**0.95**	**High**
Vol_2_T1CE	**0.98**	**High**	0.98	**High**	0.95	**High**	**0.95**	**High**
Vol_3_T1CE	**0.97**	**High**	0.97	**High**	0.94	**High**	**0.93**	**High**
Vol_5_T1CE	**0.96**	**High**	0.96	**High**	0.94	**High**	**0.94**	**High**
Vol_6_T1CE	**0.98**	**High**	0.97	**High**	0.96	**High**	**0.96**	**High**
Vol_7_T1CE	**0.99**	**High**	0.98	**High**	0.97	**High**	**0.97**	**High**
Vol_8_T1CE	**0.99**	**High**	0.99	**High**	0.99	**High**	**0.98**	**High**
Vol_9_T1CE	**0.99**	**High**	0.99	**High**	0.98	**High**	**0.98**	**High**
Vol_10_T1CE	**0.99**	**High**	0.99	**High**	0.99	**High**	**0.99**	**High**

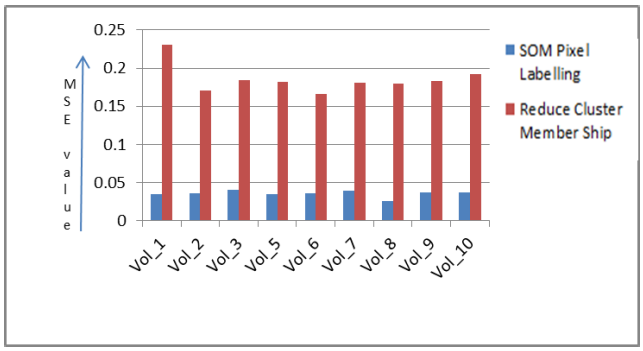


FIGURE 29. MSE for SOM Pixel Labelling of T1 sequence.

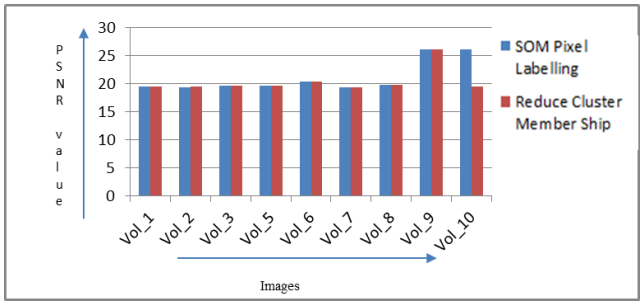


FIGURE 30. PSNR for SOM Pixel Labelling of T1 sequence.

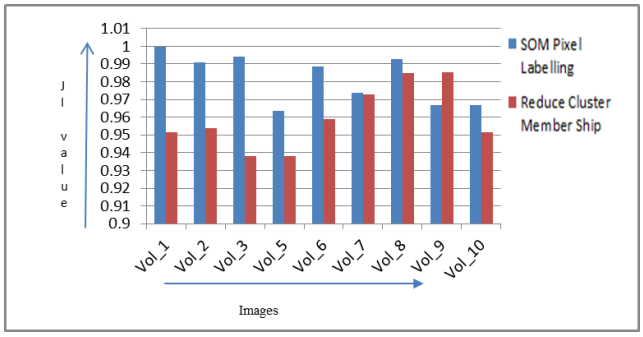


FIGURE 31. JI for SOM KMEAN of T1 sequence.

segmentation of the enhancing tumor core. From Table 4 and Table 5, segmentation similarity measures have been compared among SOM Pixel Labeling (SPL), Reduce cluster membership (RCM), Hybrid of SOM Pixel Labelling with Reduce Cluster Membership (SPLRCM), Hybrid of SOM Pixel Labeling with Reduce cluster membership and deterministic feature clustering (SPLRCM&DFC). The best similarity is achieved when SPLRCM&DFC is compared to ground-truth reality images and hence it shows very high evaluation value.

Figure 33 and Figure 34 shows comparison of propose method with bench mark. Evaluation parameters are Dice and Jacquard. In Figure 35, graph is showing a comparison drawn on four proposed techniques of segmentation which are SOM Pixel Labeling (SPL), Reduce Cluster Membership (RCM), Deterministic Feature with Clustering (DFC), Hybrid of

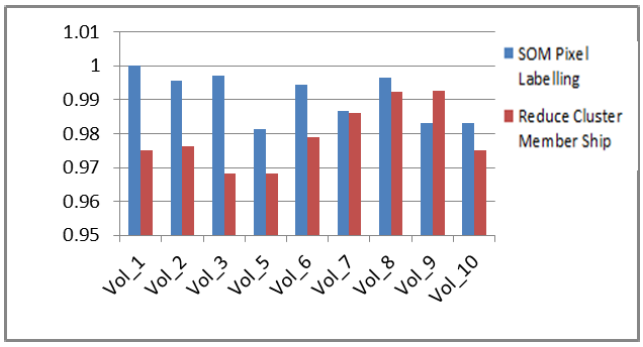


FIGURE 32. Dice for SOM Pixel Labelling of T1.

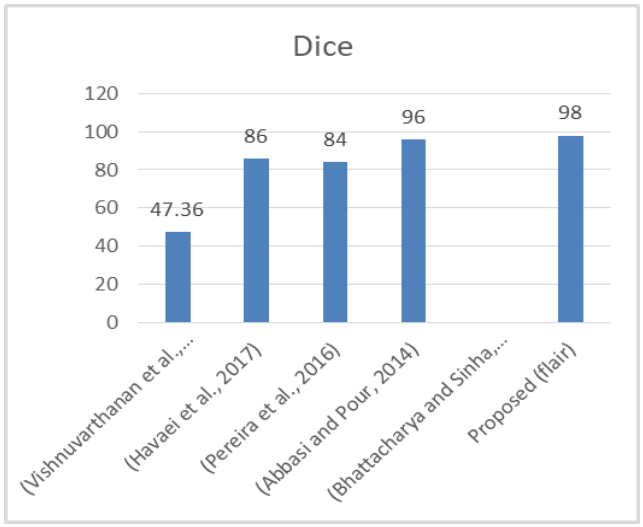


FIGURE 33. Overall comparison of Dice values with an Approximation.

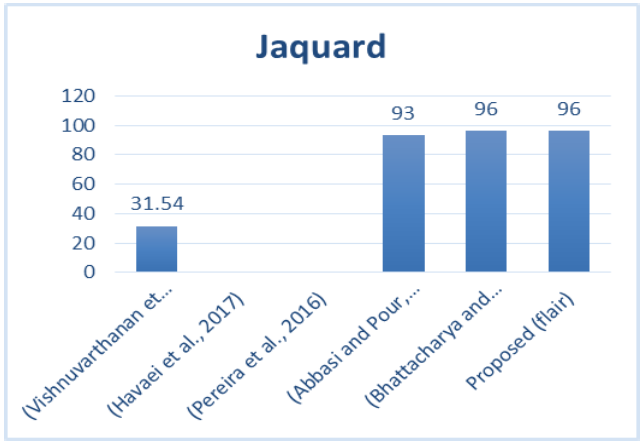


FIGURE 34. Overall comparison of Jacquard values with an Approximation.

SOM Pixel Labelling with Reduce Cluster Membership and Deterministic Feature with Clustering (SPLRCM&DFC). Hybrid has the capacity to produce performance-oriented segmentation.

TABLE 6. SOM_KMEAN_FCM+SOM_FE_FCM(jacquard).

Vol_no.	SOM_KMEAN	SOM_ FCM	FE_ FR_FCM	SOM_KMEAN_FM+FR_FCM
Vol_1-5	0.91	0.95	0.99	0.97
Vol_5	0.92	0.93	0.94	0.94
Vol_6	0.92	0.93	0.93	0.94
Vol_15	0.96	0.91	0.96	0.95
Vol_29	0.83	0.91	0.91	0.95

TABLE 7. SOM_KMEAN_FCM+SOM_FE_FCM(DICE).

VOLUME NO.	SOM_KMEAN	SOM_ FCM	FE_ FR_FCM	SOM_KMEAN_FM +FR_FCM
VOL_1-5	0.95	0.99	0.99	0.984
VOL_5	0.96	0.96	0.96	0.967
VOL_6	0.96	0.96	0.96	0.972
VOL_15	0.90	0.98	1.00	0.972
VOL_29	0.98	0.96	1.00	0.975

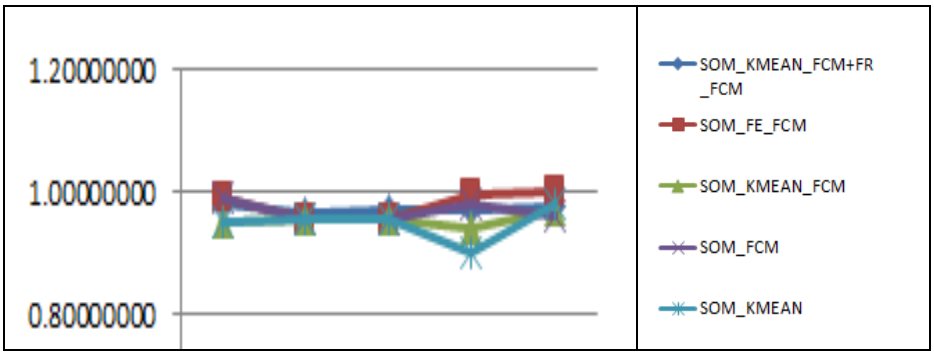


FIGURE 35. Jacquard of segmentation through the addition of Hybrid SOM Pixel Labelling with reduce cluster membership and deterministic features.

Tables 6 and 7 show the performance of the proposed segmentation using DOI and JI. In addition, Figure 35 and Figure 36 gives the comparison among all suggest methods namely SPL, RCM, DFC and SPLRCM&DFC Their performance of clustering the extreme intensity can be seen on the scale of graph.

C. RE CAPITULATION

The Figure 33 and Figure 34 also give comparison of proposed algorithm with bench mark. Proposed algorithm (SPLRCM&DFC) is compared with existing methods such as self-organization mapping and Fuzzy KMEAN (SOM FKM), Deep learning neural network along with features (DNN+Faatures), Deep learning neural network along with classifiers (DNN and Classifier), Hybrid (KFCM and HCSD) and Local binary pattern along with GLCM (LBP+GLCM). The final results of the proposed method are, average dice overlap index (DICE) similarity of the complete tumour is 0.99, Jaccard Tanimoto Coefficient Index (TC) is 0.95, Peak signal to noise ratio (PSNR) is 21.20 and Mean Squared Error (MSE) is 0.13. It is observed that better JI,

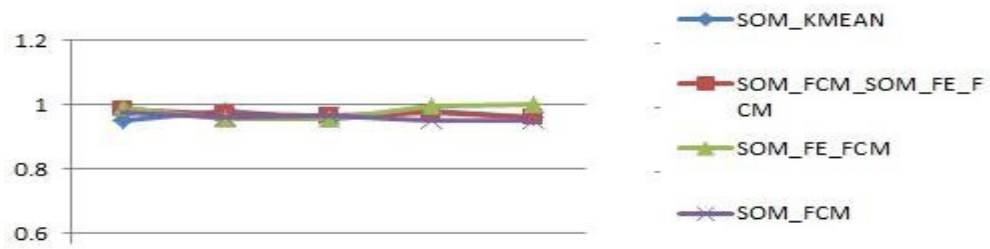


FIGURE 36. Dice of segmentation through addition of SOM_KMEAN_FCM+FE_FR_FCM.

DOI, MSE are achieved. These values are better than combination of DNN+Feature, CNN+Kernel, LBP+GLCM, KFCM+HCSD methods. So, proposed method resolves the issue of enhancing tumour for homogenous tumour, data set complexity issue and extreme variations of intensity.

From Table 6, Table 7 are showing testing results. They are obtained using Jaccard Tanimoto Coefficient Index (TC). In figure 35, hybrid segmentation shows graph of all techniques such as SOM_KMEAN_FCM (SPLRCM), FE_FR_FCM (DFC) and hybrid SOM_KMEAN_FCM+FE_FR_FCM (SPLRCM&DFC). They are testing results on volume 1, volume 5, volume 6, volume 15 and volume 21.

The graph in figure 36 shows segmentation evaluation using Dice and Jaccard Tanimoto Coefficient Index (TC). Four important segmentation proposed methods are shown over here. There are SPL (SOM_KMEAN), RCM(SOMFCM), DFC(FEFRFCM) and SPLRCM&DFC. Their result can be seen on five volumes. Red line is seeming to more good and this line reflects DFC in Figure 36 and Figure 37.

VI. CONCLUSION

A novel hybrid segmentation technique is proposed. we conclude step wise so firstly the Resultant Biggest Blob(RBB) is determined for Confidence Region on MRI image and further accurate localization of tumor performed with Contour Detection algorithm has been generated. CRCD delineates for identification of the tumor cells and normal cells are separated from tumorous cells. Moreover, the results of confidence Region methods are segmented through also proposed hybrid segmentation technique such as SOM Pixel Labelling with Reduce Cluster Membership and Deterministic Feature Clustering (SPLRCM). From second flow, deterministic feature selection method is proposed for good features. Highly accurate feature in dataset produces good region of interest. Good feature are applied on image and feature based segmentation is achieved with combination of FCM for complete tumor detection therefore this flow is known as Deterministic Feature Clustering (DFC). At end both flows (SPLRCM+DFC) are combined. Better segmentation results are achieved with this combination. They are as compared to benchmark studies. Experimental evaluation shows the promise in results. Results have been evaluated using four testing parameters like Dice overlap Index (DOI Jaccard Tanimoto Coefficient Index (TC), Mean Squared Error (MSE) and Peak Signal to Noise Ratio (PSNR). In future we are planning to compare our segmentation results with low grade glioma (LGG) images. Future direction is to define some method with deep learning neural network. We will compare our current results with new one. Because every algorithm has its own benefits and limitations.

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