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IMAGE & SIGNAL PROCESSING

A Clinical Support System for Brain Tumor Classification Using Soft Computing Techniques

P. Rupa Ezhil Arasi[1] · M. Suganthi[2]

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Abstract

A brain tumor is an accumulation of abnormal cells in human brain. As tumor increases in size, it induces brain damage. Hence it is essential to diagnose the type of brain tumor. The effective modality used for brain tumor diagnose is MRI because of its remarkable image resolution, the speed of acquisition, and high safety profile for patients. The analysis of brain MRI is an important part of patient care and decision. Hence in the proposed Clinical Support System, the brain MRI image is preprocessed using Genetic Optimized Median Filter followed by brain tumor region segmentation using Hierarchical Fuzzy Clustering Algorithm. The features of the tumor region are extracted through GLCM feature extraction method. Lion Optimized Boosting Support Vector machine model is used for further classification of tumor by Brain Tumor Image Segmentation (BraTS) dataset. Hence the proposed clinical support system provides an integrated model for Detection and classification of brain tumor which assists the doctors in appropriate evaluation of tumor.

Keywords Brain tumor · Preprocessing · Segmentation · Genetic optimized median filter · Hierarchical fuzzy clustering · GLCM · Lion optimization technique · Boosting support vector machine

Introduction

Imaging methods are used to diagnose and identify the location of brain tumor. Magnetic resonance imaging (MRI) is the widely employed method for lesion detection [2, 29]. A Clinical Support system enhances the use of MRI in evaluation of brain tumor. Various such systems have two main steps i.e. preprocessing and segmentation which provide remarkable guidance in the automation of brain tumor [10]. In [26], denoising is done using different filters and K-means clustering is used for tumor segmentation. MRIs classification is done by Naïve Bayes Classifier and Support Vector Machine (SVM) so as to provide accurate prediction. Clustering [21] is an Unsupervised learning techniques sufficient for biomedical image segmentation. The tumor is segmented using K-Means clustering algorithm and the abnormalities in the tumor are then detected using morphological operators. Also a results evaluation has been done through detecting tumour cells via k-means clustering and improved results were obtained with the purpose of morphological operators. Fuzzy C Means (FCM) clustering [1] provides optimized cluster centers by working on the pixel positions. The results thus obtained are used for setting up of active edges to be processed by the Level set. This provides satisfactory segmentation accuracy but consumes more time in setting up the values for the initial parameters.

In [35], the segmented portion retrieved using region growing method is used as the basic shape for the level set method. This prevents the user from selecting the region of interest on their own. The main limitation of this work is it deals only with glioma type of tumor. A hybrid intelligent fuzzy Hopfield Neural Network Algorithm [19] based tumor segmentation, region detection and extraction reveals high segmentation accuracy but one major problem is setting the membership

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✉ P. Rupa Ezhil Arasi
rupasharan@gmail.com

M. Suganthi
msuganthib@gmail.com

[1] Department of Computer Science and Engineering, Muthayammal Engineering College, Rasipuram, Namakkal (Dt), Tamilnadu 637 408, India

[2] Department of Electronics and Communication Engineering, Mahendra College of Engineering, Salem (Dt), Tamilnadu 636 106, India

function. The automated system [7] uses Spectral Subtraction De-noising (SSD) for de-noising the noisy image and Kernel Weighted Fuzzy C Means (KWFCM) algorithm for segmenting tumor region from the input brain MRI image. KWFCM segmentation employs a spatial information and membership weighting function of each cluster to present the segmented tissues. In [25] fuzzy filter is used to denoise the image and tumor segmentation is done using conventional FCM algorithm in which the objective function contains a mean field phrase to easily locate the cluster center.

As tumor increases in size, it induces brain damage. Hence it is essential to diagnose the type of brain tumor. The effective modality used for brain tumor diagnose is MRI because of its remarkable image resolution, the speed of acquisition, and high safety profile for patients. The analysis of brain MRI is an important part of patient care and decision. Hence by considering all the above facts a clinical support system to enhance brain tumor detection is presented in this paper. Hence in the proposed Clinical Support System, the brain MRI image is preprocessed using Genetic Optimized Median Filter followed by brain tumor region segmentation using Hierarchical Fuzzy Clustering Algorithm.

The proposed methodology

The proposed model is shown in Figs. 1, 2, 3, 4, 5, 6, 7, 8 and 9. In the proposed model input brain MRI image is de-noised and the tumor region is segmented. The classifier classifies the tumor as benign or malignant based on the features extracted from the region of interest.

Image acquisition

Brain tumor images can be obtained through various imaging techniques. Magnetic Resonance Imaging (MRI) captures the pictures of human brain and other organs without causing any damages to the human body. MRI images might be affected by noise and hence this might lead to some incorrectness in the output [31]. Hence the MRI images need to be preprocessed and segmented for further analysis [28].

Preprocessing using genetic optimized median filter

MRI images need to be refined for better understanding by the radiologists. Pre-processing refers to the process of removing the noise and artifacts available in the MRI image [11]. The output of preprocessing stage is the de-noised image with artifacts removed. Noise removal is done using various filters such as Mean filter, Median Filter, Gaussian Filter, Weiner Filter etc. [14]. The type of filter used for de-noising is based upon the nature of noise [13] in the MRI image. In this work Genetic optimized median filter [27] is used for de noising the

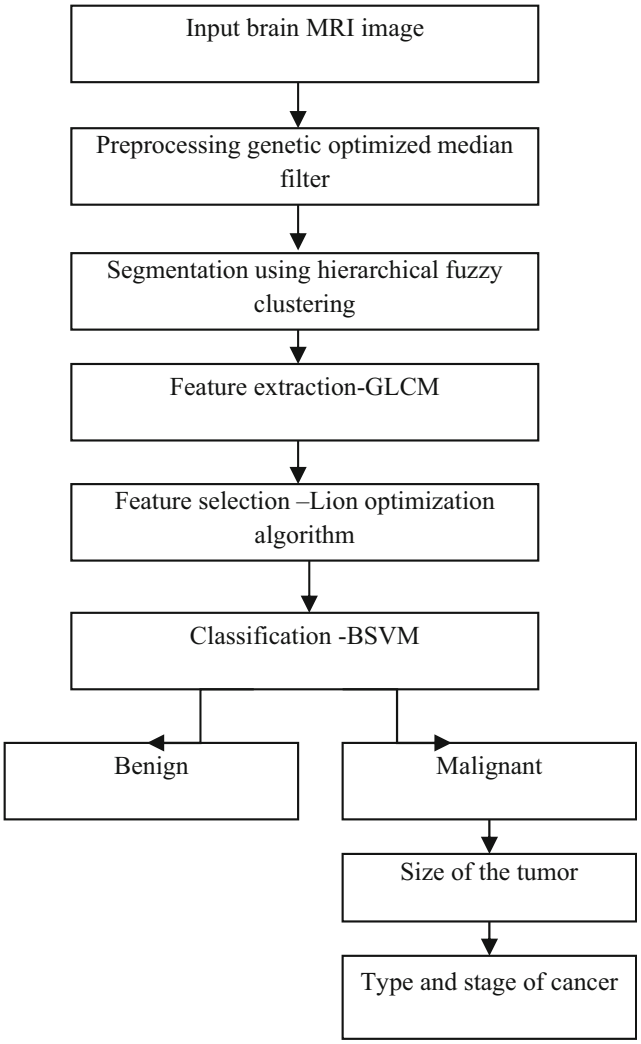

Fig. 1 Functional Diagram of the Proposed System

brain MRI image. This filter operates by selecting a particular vector at each location and then divides the vector into N partitions. Then the suitable filtering operation is applied for the respective partition. Genetic Algorithm is used to find the optimal weighting vector for every partition. This filter operation is applied recursively over the given image to produce the expected image quality. The evaluation function is given as

$$E = \left(P - V.W^T\right)^2 \quad (1)$$

Where E is the total square error, P is the value of uncorrupted pixels and V denotes filtered output vector and W denotes the weighting vector.

Segmentation using hierarchical fuzzy clustering

Brain tumor segmentation is the most important step in differentiating tumor tissues from normal brain tissues. MRI brain

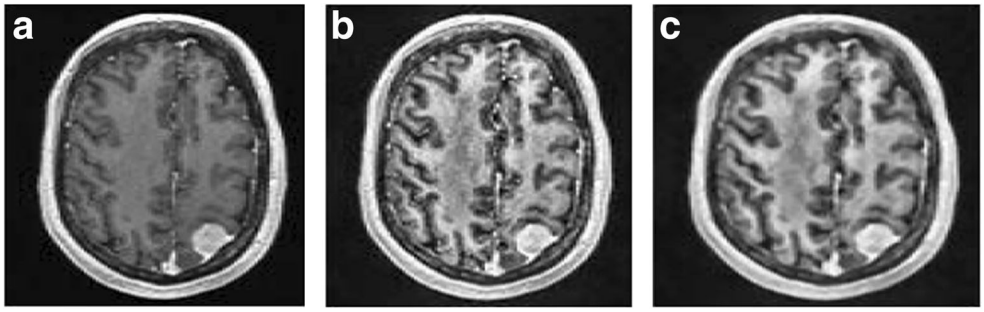

Fig. 2 **a**) Benign sample-Input image **b**) Enhanced image **c**) Genetic Optimized Median Filter output image

tumor images are inputted as Grayscale images for Brain tumor Segmentation. These grayscale images might have identical portions across various features such as texture, size, shape, location etc. [9]. Segmented Tumor could be either benign or malignant tumor. The benign tumor contains normal tissues where as the malignant tumor contains irregular growth of tissues [22].

Among the various imaging techniques MRI captures the brain tumor images with maximum resolution and high quality [18]. The automatic detection and segmentation of brain tumor from MR image is a challenging task [30]. Brain tumor segmentation techniques rely on variations in the gray level values and the uniqueness among the pixels [8, 24]. Many tumor segmentation methods [15, 20] found in literature are not fully automatic as they require user interaction to place a seed inside the tumor or edema region. But these techniques need to extremely rework the brain atlas to locate the tumors, which typically lead to poor results. Markov Random Field (MRF) [3] provides the parameters for a parametric model that has one term for the probability of each specific voxel being a tumor, and another term relating to the labels for a pair of adjacent voxels. However, the MRF based model has limited region consistency in small neighborhoods because of the computational time.

The fuzzy models [4, 5] uses a thresholding techniques or morphological operations (erosion or dilation) as pre- or post-processing resulting in border enhanced or non-enhanced tumors having very few bright pixels. The most widely used fuzzy clustering algorithm for brain tumor segmentation is Fuzzy C-Means Algorithm (FCM) [16]. Even though FCM is easy to implement its main limitation is that the algorithm requires number of clusters to be initialized in the beginning. So Hierarchical Fuzzy Clustering Algorithm (HFC) is proposed to solve the limitations of FCM. HFC algorithm adopts the agglomerative hierarchical clustering method to locate the more dense data clusters. Then the clusters are analyzed and then merged. As the final step HFC uses the most suitable evaluation function to determine the most optimal cluster.

HFC algorithm is as follows

Step 1

Initialize every pixel as the cluster centroid and.
Set the radius as zero

Step 2

For every centroid determine the K-nearest neighbor and their distances using

$$D_a^2 = \sum_{J=1}^{3} \left(X_{kj} - V_{ij}\right)^2 \quad (2)$$

Where $D^2{}_a$ is the mean square error between X_i and V_j.

Step 3

Group the clusters using

$$T = V * \frac{N_e}{N_e + (A-1) * N_i} \quad (3)$$

Where V is the experience value, N_e is N*k/2 and.
N_i number of distances selected. Obtain the new centroids and new radii of the clusters formed.

Step 4

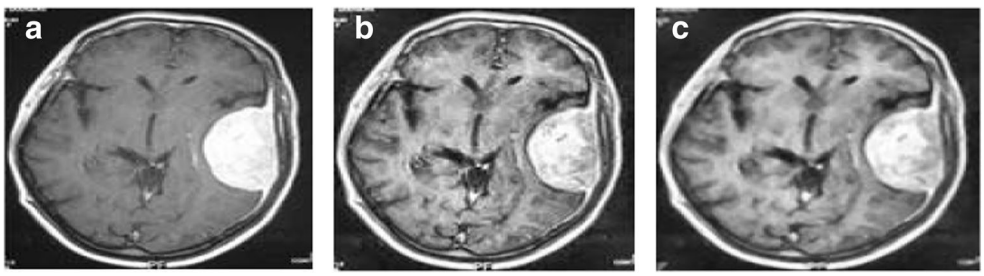

Fig. 3 **a**) Malignant sample-Input image **b**) Enhanced image **c**) Genetic Optimized Median Filter output image

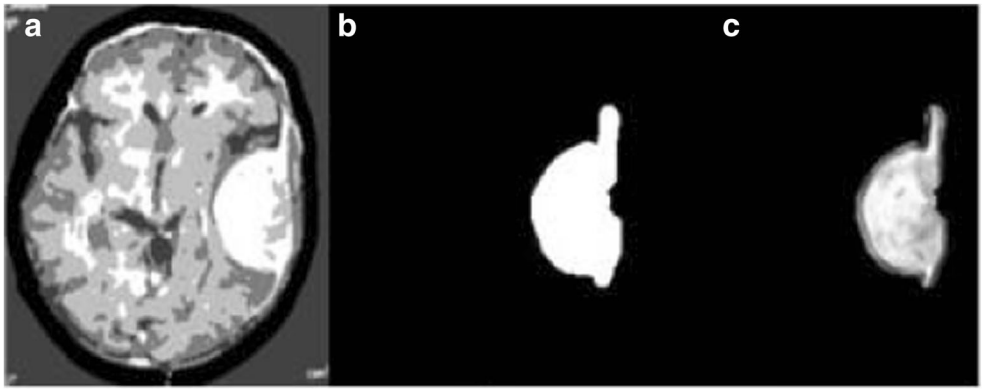

Fig. 4 **a**) Clustered benign image **b**) Segmented tumor **c**) Refined tumor image

Determine the effectiveness of the clusters formed using the following equations

$$W(C) = \sum_{i=1}^{C}\sum_{k=1}^{N} U_{ik}^{m} d_{ik}^{2} \quad (4)$$

$$B(C) = N^{*}\min_{j\neq k}\left|\left|V_j - V_k\right|\right|^2 \quad (5)$$

$$S = W(C)/B(C) \quad (6)$$

Where U belongs to the fuzzy membership value and m denotes the fuzzification parameter (m = 2), d denotes the distance between the centriod (V) and cluster points.

Step 5

Repeat the step 6. Determine the number of clusters formed if it is equal to the threshold go to.

Step 6 otherwise repeat step 2

Step 6 the cluster with minimum optimum value is considered to be the optimal cluster

Feature extraction using GLCM

Feature extraction is a technique that derives a set of new features from the existing features through some functional mapping. Texture features are obtained from the statistical distribution of predicted combinations of intensities at specified positions relative to each other in the image. Based on the number of intensity points in each combination, statistics are classified into first-order, second-order and higher-order statistics. The Gray Level Co-ocurrence Matrix (GLCM) method is a way of deriving second order statistical texture features from the segmented tumor image [12]. The number of rows and columns in a GLCM matrix is equal to the number of gray levels, G, in the image. The following equations are used to calculate the texture features.

$$\text{Mean} = \frac{1}{n}\sum_{i=1}^{n} x \quad (7)$$

$$\text{Standard Deviation} = \sqrt{\frac{1}{n-1}\sum_{i=1}^{n}\left(x-\bar{x}\right)^2} \quad (8)$$

$$\text{Entropy} = -\sum_i\sum_j P(i,j)\ln P(i,j) \quad (9)$$

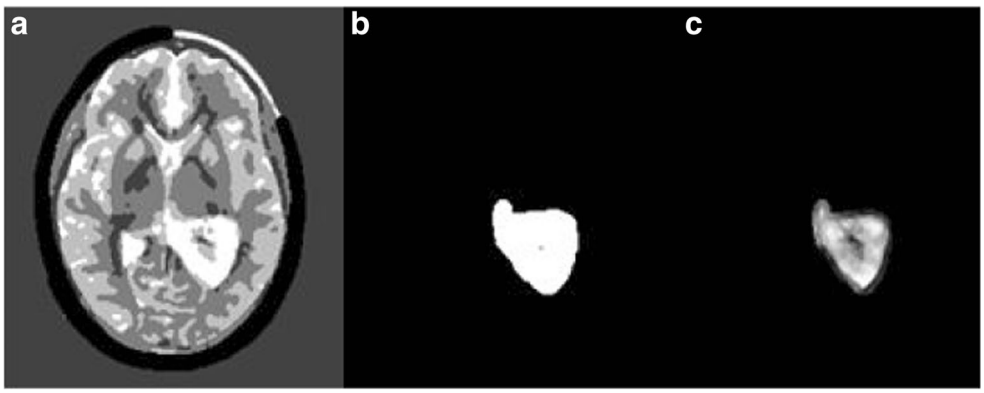

Fig. 5 **a**) Clustered malignant image **b**) Segmented tumor **c**) Refined tumor image

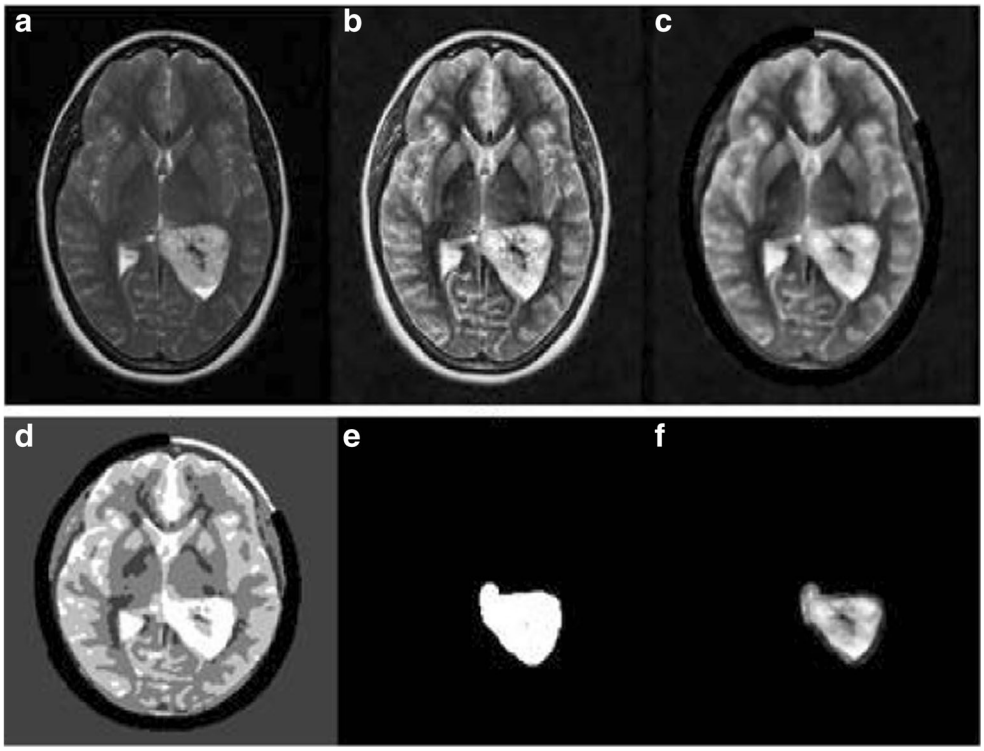

Fig. 6 **a**) input image **b**) Enhancement **c**) Genetic Optimized Median Filter Output **d**) Clustered image **e**) Segmented tumor **f**) Refined tumor image

$$\text{RMS} = \sqrt{\frac{1}{N}\sum_{n-1}^{N} x_n^2} \tag{10}$$

$$\text{Variance} = \sum_{i=0}^{G-1}\sum_{i=0}^{G-1}(i-\delta)^2 P(i,j) \tag{11}$$

$$\text{Smoothness} = 1-\frac{1}{1+\sigma^2} \tag{12}$$

$$\text{Kurtosis} = \sum_{i=0}^{n-1}(i-\mu)^4 P(i) \tag{13}$$

$$\text{Skewness} = \sum_{i=0}^{n-1}(i-\mu)^3 P(i) \tag{14}$$

$$\text{IDM} = \sum_{i=0}^{G-1}\sum_{i=0}^{G-1}\frac{1}{1+(i-j)^2}P(i,j) \tag{15}$$

$$\text{Contrast} = \sum_{i,j=1}^{n-1} P_{i,j}(i-j)^2 \tag{16}$$

$$\text{Correlation} = \frac{\sum_i\sum_j\{ijP(i,j)\}-\propto_i\propto_j}{P_iP_j} \tag{17}$$

$$\text{Energy} = \sum_{i=1}^{m}\sum_{j=1}^{n}|C(i,j)| \tag{18}$$

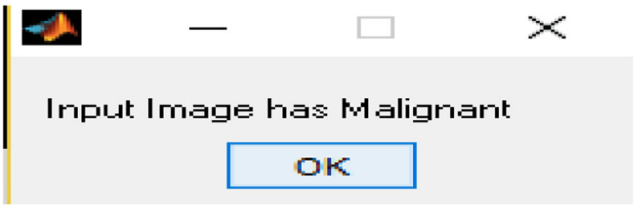

Fig. 7 BSVM output

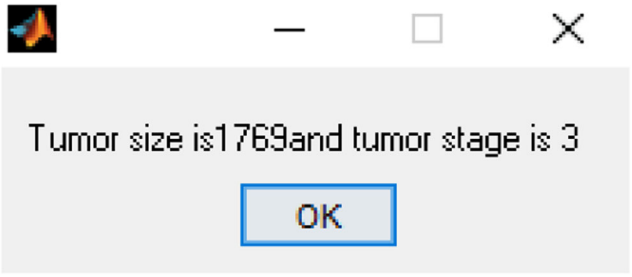

Fig. 8 Size and stage of cancer

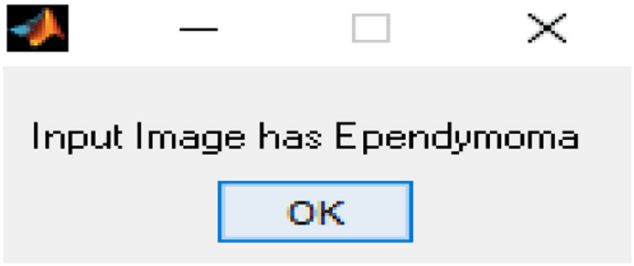

Fig. 9 Type of cancer

$$\text{Homogeneity} = \sum_i \sum_j \frac{P(i,j)}{1+|i+j|} \tag{19}$$

Feature selection using lion optimization technique

Due to the availability of huge volume of data, selection of relevant data and elimination of irrelevant data has gained most importance in the field of machine learning. Feature selection is aimed at selecting the required features based on the predefined criteria thus reducing the dimensionality of available data [34]. Hence Feature selection has a significant impact on classification accuracy, predictive accuracy of algorithms etc. The real time applications had to deal with many complex problems. The dimensionality and the volume of data increases rapidly as the complexity of the problem grow. Meta heuristic search techniques such as Genetic Algorithm, Ant Colony Optimization, Particle Swarm Optimization, Bee Optimization Algorithm, Cat swam algorithm etc. have been used to find out the solution of complex problems [34]. In this paper Lion Optimization algorithm based on Lion's behavior is used for feature selection. The Lion Optimization technique is explained in the following steps.

Step1-. Make the following assumptions

a. Npopl- initial species of Lions
b. %NMD-percentage of Nomad Lions selected from the initial species of Lions
c. %LP- the non nomad lions are grouped into subsets called as Lion Prides
d. %SF-indicates the percentage of female lions in the pride and the remaining are male lions
e. Pride Territory-Group of best visited position by each member

Step2-. the algorithm is as follows

a. the randomly selected female lion goes for hunting
b. The remaining females moves to various positions within the territory
c. The male lions too roam within the territory
d. The female lions mate with the male lions
e. The young lions are separated from their Lion pride once they grow
f. Nomad lions moves within the territory to find a better place
g. If the position of the nomad lion is better than the resident lion then the nomad lion replaces the position of the resident lion.
h. Female lions move in between prides and become resident
i. The weakest lions strives hunger and then dies

Step3-. the above process is repeated until the optimal solution is obtained.

Classification using boosting support vector machine

Classification is the method which assigns a class to the given test sample based on the knowledge obtained by the classifier during training. In this work Support vector machine integrated with boosting algorithm is used to classify the brain tumor images as benign or malignant. The search process is optimized using Lion Optimization technique. The main advantage of BSVM algorithm is that the algorithm performs well when trained with large and high dimension data set and the complexity of the algorithm does not increases when training time is decreased [6, 32]. The BSVM's hypothesis is given as

$$H(X) \leftarrow WSVM(S, D, \text{Kernel}, C \text{ or } V) \tag{20}$$

The structure of BSVM is similar to that of Adaboost. In the case of BSVM the output hypothesis is expressed as hyperplane in feature space. The calculations of coefficients do vary with the Adaboost algorithm. The coefficients are chosen in such a way that it minimizes the training error. The BSVM algorithm stops when the error of the classifier [17, 23] cannot be further decreased.

Determining size and stage of the tumor

The output tumor image of the BSVM algorithm is further analyzed for its size and stage of cancer as follows.

Stage 0-If the size of the tumor is very minimum then it is concluded to be edema.
Stage 1- If the size of the tumor is less than 0.5 mm/in. then it is considered to be benign tumor.
Stage 2-If the tumor size varies between 1 and 4 mm/in. it is categorized as necrosis and may contain many abnormal cells. Astrocytoma, Ependyoma is of this type.

Table 1 Performance of Genetic optimized median filter technique

S.NO	Filtering method	Parameters					
		MSE	PSNR	CNR	IQI	MAE	SSIM
1	Genetic median filter	8.6449	38.625	109.25	0.7029	20.783	0.9883

Stage 3- If the tumor size varies between 5 and 10 mm/in. they can be either Anapalstic Astrocytoma, Anaplastic Ependyoma. This type of tumor might contain many dividing or dead cells

Stage 4- The tumor size might be greater than 10 mm/in.. They are mainly called as Glioblastoma. These tumors might contain dividing cells or dead tissues or blood vessels.

Results and discussion

The input images are obtained from the databases BraTS 2015. The proposed system is implemented in MATLAB and the images from these databases are tested. Preprocessing of input MRI images is done using Genetic Optimized Median Filter and the results are tabulated. The method is detailed in [33], and it won the 2nd place of MICCAI 2015 BraTS Challenge is adapted to deal with tumor classification. The proposed work is implemented via the use of the MATLAB software. In the proposed work Benign- 75/65 (training/testing) and Malignant −75/65(training/testing) are used for implementation (Tables 1, 2, 3, 4, 5 and 6).

The performance of Genetic Median Filter is evaluated by computing the following measures

$$\mathrm{MSE} = \frac{1}{\mathrm{MN}}\sum_{i=1}^{M}\sum_{j=1}^{N}\left(\left(\mathrm{x(i,\,j)}-\mathrm{y(i,\,j)}\right)\right)^2 \tag{21}$$

$$\mathrm{PSNR} = 10\log_{10}\frac{\left(2^{\mathrm{n}}-1\right)^2}{\sqrt{\mathrm{MSE}}} \tag{22}$$

$$CNR = \frac{(S_A - S_B)}{\sigma_\circ} \tag{23}$$

$$MAE = \frac{1}{MN}\sum_{i=1}^{M}\sum_{J=1}^{N}|x(i,j)-y(i,j)| \tag{24}$$

$$\mathrm{IQI} = \frac{4*\sigma_{xy}*\overline{x}*\overline{y}}{\left(\sigma_x^2+\sigma_y^2\right)*\left(\overline{x}^{\,2}*\overline{y}^{\,2}\right)} \tag{25}$$

$$\overline{x} = \frac{1}{N}\sum_{i=1}^{N}x_i \tag{26}$$

$$\overline{y} = \frac{1}{N}\sum_{i=1}^{N}y_i \tag{27}$$

$$\sigma_x^2 = \frac{1}{N-1}\sum_{i=1}^{N}\left(x_i-\overline{x}\right)^2 \tag{28}$$

$$\sigma_y^2 = \frac{1}{N-1}\sum_{i=1}^{N}\left(y_i-\overline{y}\right)^2 \tag{29}$$

$$\sigma_{xy} = \frac{1}{N-1}\sum_{i=1}^{N}\left(x_i-\overline{x}\right)\left(x_i-\overline{x}\right) \tag{30}$$

$$\mathrm{SSIM} = \frac{\left(2*\overline{x}*\overline{y}+c1\right)\left(2*\sigma_{xy}+c2\right)}{\left(\sigma_x^2+\sigma_y^2+c2\right)\left(\overline{x}^{\,2}+\overline{y}^{\,2}+c1\right)} \tag{31}$$

Where x (i,j) is original image, Y (i,j) is modified image, (i,j) is the pixel position of M*N image, S_x & S_y are signals. The tumor region is segmented using HFC algorithm. The performance of HFC segmentation technique is evaluated using the following equations.

$$\mathrm{Accuracy} = \frac{\mathrm{TP}+\mathrm{TN}}{\mathrm{TP}+\mathrm{TN}+\mathrm{FP}+\mathrm{FN}} \tag{32}$$

Table 2 Performance of Hierarchical fuzzy clustering segmentation techniques

S.NO	Segmentation method	Parameters						
		TP	TN	FP	FN	Accuracy	Precision	Recall
1	Hierarchical fuzzy clustering	0.912	0.881	0.114	0.061	0.9633	0.9090	0.9199

Table 3 Estimated value of features extracted

S. No	Features	Estimated values	
		Benign	Malignant
Texture Features			
1	Autocorrelation	2.1278965	1.658822
2	Contrast	5.5873508	3.05282687
3	Correlation 1	−1.81445557	−1.40214076
4	Correlation 2	−1.815455	−1.4023214
5	Cluster Prominence	1.736881828	5.8935271
6	Cluster shade	−8.2426809	4.746544
7	Dissimilarity	2.07550868	4.889368
8	Energy	1.4496425	3.1561318
9	Entropy	6.59570	8.0904307
10	Homogeneity 1	6.87671	2.8958974
11	Homogeneity 2	3.282538	0.00108
12	Maximum probability	1.9649516	3.91372
13	Sum of squares	2.457686	1.18058005
14	Sum average	2.925469	2.6248085
15	Sum variance	8.3572013	6.7088876
16	Sum entropy	3.615927	4.451079
17	Difference variance	5.58735	3.0528268
18	Difference entropy	3.75035338	4.5878274
19	Information measure of correlation1	−4.7363829	−4.8882927
20	Information measure of correlation2	5.27254730	5.8944478
21	maximal correlation coefficient	0.87654	0.9978
22	Inverse difference	0.090747651	0.0886576
23	Inverse difference normalized	0.090837348	0.081184812
24	Inverse difference moment normalized	0.098636392	0.093325278
Shape features			
25	Area	800	3407
26	Equivalent diameter	31.91	66.12
27	Solidity	0.95579	0.99899
28	Perimeter	108.22	270.3
Intensity features			
29	Intensity	0.219585	0.19091
30	Mean	−0.12391	0.07654
31	Variance	0.018765	0.008865
32	Kurtosis	0.10067	0.09871

Table 4 Performance comparison of Feature Subset selection

Feature set	Specificity (%)	Sensitivity (%)	Overall Accuracy (%)
Texture	82	88	93.33
Shape	72	85	93.81
Intensity	70	84	92.78
Texture +Shape	89	91	97.22
Texture +Intensity	90	92	96.88
Shape +Intensity	91	90	97.43
Texture+Shape +Intensity	95	94	97.55

Table 5 Performance of the Classifier

Classes	No. of data for training/ testing	No.of correctly classified data for BSVM			Percentage of correct classification		
		Without optimal feature subset generation	With optimal feature subset generation	With optimal feature subset generation using BSVM	Without optimal feature subset generation	With optimal feature subset generation	With optimal feature subset generation using BSVM
Benign	75/65	58	61	63	89.23	93.84	96.92
Malignant	75/65	60	62	64	92.3	95.38	98.46
Average					90.765	94.61	97.69

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \tag{33}$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}} \tag{34}$$

Where TP is true positive, TN is true negative, FP is false Positive and FN is false negative.

GLCM algorithm is used to extract the required features from the tumor region for further classification. The extracted features are listed as follows.

The subset of required features is formed from extracted features using Lion Optimization Technique. The features with greatest accuracy are chosen for classification for tumor image.

Specificity, Sensitivity and Accuracy are calculated as follows

$$\text{Senistivity} = \frac{\text{TP}}{\text{TP} + \text{FN}} * 100\% \tag{35}$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}} * 100\% \tag{36}$$

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{FN} + \text{TN} + \text{FP}} * 100\% \tag{37}$$

The tumor classification is done using Boosting Support Vector machine classifier. The tumor is classified as either benign or malignant. In the case of malignancy size of the tumor, type of cancer and stage of cancer are determined further. The performance of the classifier is tabulated as follows.

The proposed work classifies the tumor image with 97.69% accuracy. The classification accuracies obtained using various methods are tabulated below.

Conclusion

The proposed clinical support system for brain tumor detection and classification has been tested using images from the BraTS database. Hence in the proposed Clinical Support System, the brain MRI image is preprocessed using Genetic Optimized Median Filter followed by brain tumor region segmentation using Hierarchical Fuzzy Clustering Algorithm. The features of the tumor regions are extracted through GLCM feature extraction method. Lion Optimized Boosting Support Vector machine model is used for further classification of tumor. From the results it is evident that the proposed system classifies the tumor with 97.69% accuracy. The main advantage of the proposed system is that it also analyzes the size of the tumor, determines the types and stages of the cancer.

Table 6 Performance of the Proposed System based on Classification Accuracy

Author	Techniques used					Classification accuracy (%)
	Denoising	Segmentation	Feature extraction	Feature selection	Classifier	
El-Dishan et al. [6]	–	–	HAAR wavelet transform	Principal Component Analysis (PCA)	Artificial Neural Network (ANN)	97
Madhes waran et al. [17]	ORNRAD Filter	Penalized Fuzzy C means clustering	GSDM and Tamura Method	Joint Entropy	SVM-ANOVA	97.09
Nazir et al. [17]	Denoising Filtering	–	Colour Moment extraction	–	Feed Forward Artificial Neural Network (ANN)	97.65
Proposed work	Genetic Median Filter	Hierachical Fuzzy clustering	GLCM and gabor feature	Lion Optimization	BSVM	97.69

Compliance with ethical standards

Conflict of interest We(Authors and Co-Authors) have no conflicts of Interests. The Paper is not submitted to any other Journals.

Ethical approval (Involving human participants and/or animals) This article does not contain any studies involving human participants or animals performed by any of the authors.

Informed consent The article does not use any animal or human participants. So, it is not applicable.

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