

# Patient-Specific Brain Tumor Segmentation using Hybrid Ensemble Classifier to Extract Deep Features

Divya Mohan<sup>a,c</sup>, V. Ulagamuthalvi<sup>b</sup>, Nisha Joseph<sup>c</sup>, G. Kulanthaivel<sup>d</sup>

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**Abstract:** The abnormal cell development in the Brain is referred to as a tumor. Brain tumors are treated by physicians using radiation and Surgery. The brain tumor is categorized as benign or malignant. The benign tumor can be treated and cured using the appropriate medication suggested. A malignant tumor is an abnormal tissue that affects nearby tissues and can be cured only through proper Surgery by a physician. Manual identification of malignant and benign tumors is a time-consuming and error-prone process. An automatic brain tumor classification technique is proposed to overcome the limitation. An efficient methodology for the detection of brain tumors is done. Initially, the brain MRI image is smoothed and enhanced by a Gaussian filter. Then deep and texture features are extracted. The proposed work uses an ensemble technique using three different classifiers based on Majority Voting Method. The specified method is tested on BRATS 2017 and 2018 datasets. The results are compared with recent methods and prove efficacy.

**Keywords:** tumor, texture, deep features, classifier

## 1. Introduction

Brain tumor must be detected earlier since it is dangerous. After detecting a brain tumor as benign or malignant proper treatment can be given by the physician. The brain tumor is considered dangerous and severe based on the extending capacity of the Brain. Benign tumors are not spread over other tissues, but malignant tumors widen from their normal area. Medications are sufficient for a benign tumor and can be cured easily. However, Surgery is needed for malignant tumors.

Image processing plays a vital role in identifying the type of brain tumor. In the medical field, an MRI image is used to identify the inner structure details of the Brain and the variations in the brain cell. Various researchers in brain tumor segmentation use pre-trained network models for feature extraction and classification. Similarly, handcrafted features are also used for brain tumor segmentation. This paper aims to identify brain tumors with a combination of handcrafted and deep

features. This paper also uses a hybrid classifier approach to improve the accuracy further.

The steps involved in the proposed method are preprocessing, image segmentation, feature extraction, and classification. The basic procedure in preprocessing phase is to develop the brain MRI image quality by reducing the noise and enhancing the image's brightness. Then in feature extraction, Residual Network (ResNet) features, Local Derivative Pattern (LDP) features and Gray Level Co-occurrence Matrix (GLCM) features are used. Finally, an ensemble technique using Random Forest, Support Vector Machine (SVM), and Naïve Bayes (NB) classifier is used to find the type of tumor.

The remaining paper is organized as follows: Section 2 discusses some papers on brain tumor segmentation. Section 3 elaborates on the proposed method with its experiments in Section 4. Section 5 concludes the work with its future scope.

## 2. Related Work

A segmentation method is used for segmenting the tissues in Magnetic Resonance Imaging (MRI) images as tumor and non-tumor [1]. The non-tumor region of the Brain is executed along the tumor region. A modification was recorded as it occurs in the non-tumor region. It is mainly helpful to physicians in identifying the tumor.

A Computer-Aided Design (CAD) based brain tumor segmentation method [2] is proven as one of the efficient techniques for brain tumor segmentation. Local

<sup>a</sup>Research Scholar, Department of Computer Science and Engineering, Sathyabama Institute of Science and Technology, Chennai, India.

Email: divyamohanresearch@gmail.com

<sup>b</sup>Professor, Computer Science, and Engineering, Sathyabama Institute of Science and Technology, Chennai, India. Email:

ulagamuthalvi.cse@sathyabama.ac.in

<sup>c</sup>Assistant Professor, Computer Science, Engineering, SAINTGITS College of Engineering Autonomous, Kerala, India. Email:

nishasjoseph@gmail.com

<sup>d</sup>Professor, NITTTR, Chennai, India. Email: gkveldr@gmail.com

Independent Projection-Based Classification (LIPC) is used to classify the voxel into its corresponding class.

A brain tumor segmentation technique has been implemented using an SVM classifier [3] that uses GLCM for feature extraction. ViswaPriya et al. (2016) introduced a clustering technique for identifying tumors [4]. The input image is smoothed in the preprocessing stage, and the noise is eliminated using the adaptive mean filter. Some morphological processing is also done to identify the tumor.

A genetic algorithm has been developed to identify brain tumors [5]. This method has achieved a precision of 94%. The thresholding technique is applied for segmenting the tumor regions [6]. Then the basic preprocessing, Morphological processing, and thresholding are done to identify the normal and abnormal tissues. A novel algorithm has been developed for identifying brain metastases [7]. This technique uses shape and energy contrast features to identify brain metastases.

A Fully Convolution Network (FCN) architecture using 2D convolutions has been implemented to detect tumors [8]. This method is faster than other methods utilizing fewer resources. A deep learning model was introduced, which segments the tumor more accurately in BRATS 2013 dataset [9]. Patch-wise Convolutional Neural Network (CNN) [10] is used to improve the method developed in [9]. It consumes much time because of processing 3D data.

Kansas has introduced the Ensembles of Multiple Models and Architectures (EMMA) method [11] that combines various methods. The advantage of this method is that it does not depend on a particular database. A segmentation

algorithm [12] has been implemented in multilevel brain tumor segmentation using texture and abnormality features. It used an RF classifier for classification purposes. These two methods have reduced accuracy and efficiency.

In [13], two existing conventional techniques, Fuzzy C-Means, and k-means, are inherited. This method segments tumors more accurately. Another method [14] used the histogram technique to extract features from each 2D slice of the 3D data [2]. Thresholding and median filtering were applied to improve the quality. The connectivity is identified to determine the most significant cluster selected as the tumor region corresponding to each 2D slice. In the end, all the 2D slices are combined to give the segmentation result.

Wei Chen et al. have developed a method using superpixel segmentation for tumor classification [15]. Features are extracted from superpixels, and SVM is used to classify superpixels. Another technique has been presented for segmenting and classifying brain tumors [16] using a cascaded Random Decision Forest (RDF) classifier.

### 3. Methodology

The system architecture of the proposed method is shown in Fig. 1. The proposed work consists of two essential phases: Feature Extraction and Classification. In the Feature extraction phase, features such as ResNet, GLCM, and LDP are extracted. All the extracted features are concatenated and fed as input to the classification phase. In the Classification phase, an ensemble technique using RF, NB, and SVM classifiers is used to identify the brain tumor.

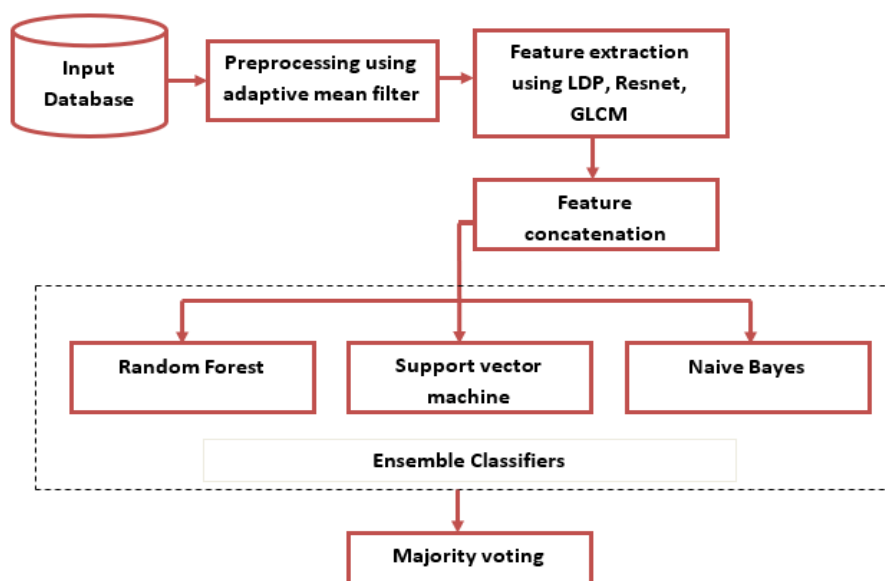


Fig. 1 Proposed System Architecture

### 3.1 Pre-processing

Initially, preprocessing is done to enhance the visualization of the image. Noises are present in the input brain image. The noise is removed using the adaptive median filter to retain the image's fine details. It will increase the accuracy of classification.

### 3.2 Feature Extraction

As mentioned, three different features are extracted from the MRI data: ResNet, GLCM, and LDP. All these features are explained in this subsection.

#### 3.2.1 Local Derivative Pattern (LDP)

A local Derivative Pattern is used to extract the deep features using CNN. These features enhance the accuracy of classification efficiently. In the deep learning-based LDP, neighboring values are taken initially, and then equation 1 is applied to find the difference.

$$DLDP = C_p - N_p \quad (1)$$

where  $C_p$  is the value of the center pixel and  $N_p$  is the value of the neighboring pixel. The direction is estimated using the formulas mentioned below.

$$0 \leq IV = 1 \quad \text{if } DLDP1 > 0 \text{ and } DLDP2 > 0 \quad (2)$$

$$0 \leq IV = 2 \quad DLDP1 < 0 \text{ and } DLDP2 < 0 \quad (3)$$

$$0 \leq IV = 3 \quad DLDP1 > 0 \text{ and } DLDP2 < 0 \quad (4)$$

$$0 \leq IV = 4 \quad DLDP1 < 0 \text{ and } DLDP2 > 0 \quad (5)$$

$$PD = \sum_{i=1}^8 IV_i \quad (6)$$

#### 3.2.2 Resnet Feature Extraction

This system uses 194 layers of the residual network. It has three convolutional layers. ResFeatures are extracted from the residual units. The entire shape of the Brain MRI contained within the ROI is extracted as the Residual network features. The deep filter bank produces the residual network outcome. The outcome is of the form  $w \times h \times c$ . Here  $w$  and  $h$  represent the resultant feature vector width and height and  $c$  represents the number of convolutional layer channels. It is expressed as:

$$\begin{aligned} Z_i &= g(y_i) + Fn(y_i, w_i) \\ y_{i+1} &= fn(Z_i) \end{aligned} \quad (7)$$

where the residual function is represented as  $F_n$ , the ReLU function is represented as  $fn$ ,  $w_i$  represents the weight matrix, and the  $i$ -th layer input is represented as  $y_i$ . The  $i$ <sup>th</sup> layer output is represented as  $Z_i$ . The identity value of mapping  $h$  is represented as

$$h(y_i) = y_i \quad (8)$$

The residual function  $F$  is defined in as:

$$F(y_i, w_i) = w_i \cdot \sigma(B(w_i') \cdot \sigma(B(x_i))) \quad (9)$$

#### 3.2.3 Gray-Level Co-occurrence Matrix

The spatial relationship of a pixel is represented using the statistical measure GLCM. The texture of the Brain MRI is calculated using corresponding pixels frequency and spatial relationships among those pixels. Contrast, correlation, energy, homogeneity, kurtosis, and skewness measures are used as features. Detailed information on these features is given below

$$\text{Contrast (C)} = \sum_{t,r=1}^{T,R} |t - r|^2 q(t, r) \quad (10)$$

where  $q(t, r)$  is GLCM,  $t$  &  $r$  are row & column,  $T$  is total rows, and  $R$  is total columns.

$$\text{Correlation (Corr)} = \sum_{t,r=1}^{T,R} ((t - \mu)(r - \mu)q(t, r)) / (\sigma(t) * \sigma(r)) \quad (11)$$

where the mean is  $\mu$ , and the standard deviation is  $\sigma$

$$\text{Energy (E)} = \sum_{t,r=1}^{T,R} q(t, r)^2 \quad (12)$$

$$\text{Homogeneity (H)} = \frac{\sum_{t,r=1}^{T,R} q(t, r)}{1 + |t - r|} \quad (13)$$

$$\text{Kurtosis (K)} = \left\{ \frac{1}{T * R} * \sum_{t=1}^T \sum_{r=1}^R \left( \frac{q(t, r) - \mu}{\sigma^4} \right) \right\} - 3 \quad (14)$$

$$\text{Skewness (S)} = \sqrt{\frac{1}{T * R} * \sum_{t=1}^T \sum_{r=1}^R (q(t, r) - \mu)^3} \quad (15)$$

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**Algorithm 1: Feature Extraction Algorithm**

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**Input:** 3D MR image with dimensions (r,c, l)

**Output:** Feature vector – dimension (3, m, n)

**Steps:**

1. For all input MR image
    - 1.1 For each Brain MR image input
      - 1.1.1 Set  $A = I(x, y, z)$ ,
      - 1.1.2 Calculate  $F_1 = Resnet(A_i)$
      - 1.1.3  $F_2 = DLLDP(A_i)$
      - 1.1.4  $F_3 = GLCM(A_i)$
    - 1.2 End
  2. End
  3. Calculate F as a 3D array
- 

Algorithm 1 uses the variables r as the total number of rows and c as the total number of columns. The extracted features related to image A are  $F_1$ ,  $F_2$ , and  $F_3$ , respectively. The features are selected based on their performance. Table 1 presents the feature dimensions used in the algorithm. The dimension of A is the size of the input image. In the BRATS dataset, the image size is

240 x 240 x 155. The extracted features for each feature are concatenated for all sub-bands, i.e., the 3D image is converted to 2D features. Hence, the size of each feature ( $F_1$ ,  $F_2$ , and  $F_3$ ) is 240 x 240. Finally, by concatenating all the features, the vector F is made. Thus the size of the feature F is 3 x 240 x 240.

**Table 1** Dimension

Value	Dimension
<b>A</b>	240x240x155
<b>F<sub>1</sub>, F<sub>2</sub>, F<sub>3</sub></b>	240 x240
<b>F</b>	3x 240 x 240

The concatenated features are classified using the Ensembled classifier.

### 3.3 Classification

The concatenated feature vector of the MRI is fed as input in the classification. RF, SVM, and NB classifiers are used for the classification process. These classifiers' results are combined to form a hybrid ensemble classifier. The advantages of using these three classifiers are:

- RF algorithm is also used to measure the importance of each feature in the prediction. After training, it automatically computes a score for the given features and then scales the results. By feature score, it can be

decided to drop the less-scored features. It is done because the features with low scores do not contribute to classifying the results.

- SVM is the most widely used classifier in many applications.
- NB Classifier works on the principle of the maximum likelihood called the Bayes Theorem. Class conditional independence was assigned by naive to minimize the computation cost. The attributes within the class are independent. The execution, classification, estimation, and prediction steps are performed sequentially. NB overcomes various

limitations, including iteration, computational time, and cost.

### 3.3.1 Hybrid Ensemble Classifier

The proposed hybrid ensemble classifier technique was RF-SVM-NB. The identification of brain tumors is based

on voting. Among three classifiers, at least two ratios, one voting is identified as the corresponding tumor type as benign or malignant.

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#### Algorithm 2: Hybrid ensemble classifier technique

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**Input:** Id from three classifiers Id1, Id2, Id3

**Output:** Brain tumor type

*Steps:*

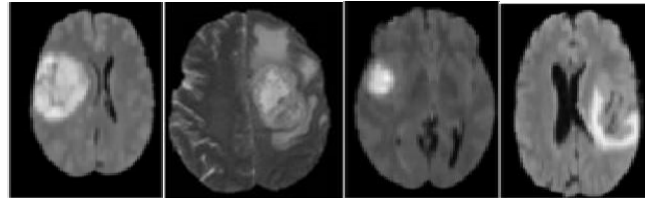
1.     right = 0
2.     left = 0
3.     If Id1 = malignant then  
       right = right + 1
4.     Else  
       left = left + 1
5.     End
6.     If Id2 = malignant then  
       right = right + 1
7.     Else  
       left = left + 1
8.     End
9.     If Id3 = malignant then  
       right = right + 1
10.    Else  
       left = left + 1
11.    End
12.    If right > left, then  
       Type = malignant
13.    Else  
       Type = Benign
14.    End

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## 4. Results and Discussion

The method is tested using two challenging BRATS datasets, such as 2017 and 2018. The BRATS dataset consists of two sets of images(LGG), the Low-Grade Glioma and (HGG) the High-Grade Glioma (HGG) images. They also divided the dataset into training,

testing, and leaderboard datasets. In BRATS 2017, there were 431 cases (both HGG and LGG), among which 285 were used for training and 146 cases in testing [27]. BRATS 2018 dataset contains 285 training images and 191 images for testing a method. Some examples of BRATS 2017 and 2018 are shown in Fig. 2.



**Fig. 2** Examples of BRATS Dataset

#### 4.1 Performance Measures

To analyze the performance of the proposed method, accuracy, sensitivity, and Specificity are used. If  $T_p$  represents True-Positive,  $F_p$  is the False-Positive,  $T_n$  is the True- Negative, and  $F_n$  is the False-Negative, the above metrics are defined as follows.

$$Accuracy = \frac{(T_p+T_n)}{(T_p+T_n+F_p+F_n)} \times 100 \quad (16)$$

$$Sensitivity = \frac{T_p}{T_p+F_n} \quad (17)$$

$$Dice\ Score = \frac{2 \times T_p}{F_p+(2 \times T_p)+F_n} \quad (18)$$

#### 4.2 Results

The results of the method tested on BRATS 2017 and 2018 datasets are given in Table 2. The proposed method is also tested with individual classifiers such as RF, NB, and SVM without a majority voting method.

**Table 2** Results

Measure	Classifier	BRATS 2017	BRATS 2018
Accuracy	RF	96	97
	NB	94.8	95
	SVM	96	97
	Hybrid Ensemble	98.3	99
Sensitivity	RF	97	98
	NB	98	98.5
	SVM	98	99
	Hybrid Ensemble	99	99
Dice Score	RF	98	98
	NB	98	98.6
	SVM	98	99
	Hybrid Ensemble	99	99

Table 2 shows that the accuracy, sensitivity, and dice score obtained by the proposed method using the SVM classifier is better than other individual classifiers. The accuracy obtained by individual classifiers ranges from 94 – 97%. However, the accuracy of the hybrid ensemble classifier ranges from 98-99%. The sensitivity and dice score obtained by the hybrid ensemble classifier is 99% for both datasets, which is also more remarkable than the

sensitivity and dice score obtained by individual classifiers. The hybrid ensemble classifier outperforms all the individual classifiers in all the measured metrics.

#### 4.3 Comparison of Proposed Method with Recent Methods

From Section 4.2, it is analyzed that the hybrid ensemble classifier obtained satisfactory results when compared to all other classifiers. Hence the results obtained by the

hybrid ensemble classifier are compared with some current methods [17 - 22]. Tables 3, 4, and 5 present the

dice score, accuracy, and sensitivity proposed algorithm, tested using BRATS 2017 and 2018 datasets.

**Table 3** Accuracy

Method	BRATS 2017	BRATS 2018
Rehman et al. [17]	96.97	92.67
Khan et al. [18]	96.9	92.5
Sharif et al. [19]	96.9	92.5
Saba et al. [20]	-	99
Amin et al. [21]	-	98
Aboussaleh et al. [22]	98	-
<b>Proposed Method</b>	98.3	99

**Table 4** Dice Score Comparison of Proposed Method with Recent Methods on BRATS 2017 and 2018 datasets

Method	BRATS 2017	BRATS 2018
Saba et al. [20]	99	-
Amin et al. [21]	-	99
Ranjbarzadeh et al. [23]	-	92.03
Liu et al. [24]	89.28	-
Wang et al. [25]	87	-
Myronenko et al. [26]	-	81
Nema et al. [27]	-	94
<b>Proposed Method</b>	99	99

**Table 5** Sensitivity

Method	BRATS 2017	BRATS 2018
Saba et al. [20]	99	-
Amin et al. [21]	-	98
Aboussaleh et al. [22]	99	-
Ranjbarzadeh et al. [23]	-	97.12
<b>Proposed Method</b>	99	99

Table 3 shows that the accuracy obtained by all other methods on both datasets is less than 98%. However, the proposed method achieved a higher accuracy, more than 98%, on both datasets. Table 4 implies that Saba et al.'s and Amin et al.'s methods achieve the highest dice score of 99%, whereas other methods achieve significantly fewer dice scores. The proposed method reaches this maximum on both datasets. From Table 5, the inference obtained is that the sensitivity obtained by the proposed method also reaches its maximum obtained by other methods.

## 5. Conclusion

Healthcare applications are the most widely used in all parts of the world. One among them is brain tumor identification and segmentation. This paper proposed to use of handcrafted and deep features for feature extraction. Then three different classifiers are combined to form a hybrid ensemble classifier. The proposed method is tested on BRATS 2017 and 2018 datasets. The proposed method achieves a higher accuracy of 99% with 99% sensitivity and dice score. This method can also be tested on recent datasets such as BRATS 2019 and 2020.

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