



# Patient Specific Brain Tumor Segmentation using Context Sensitive Feature Extraction in MR Images

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**Abstract:** Brain tumor is a serious problem when it is not diagnosed. Different levels of tumors are identified this decade. The severity of tumor can be reduced if it is identified in its early stage. The most important challenge of identifying tumor is its shape and location in the brain tissue. This paper proposes different technique for extracting features for identifying the tumor by reducing the computation time. The identified features are classified using Random Forest classifier. Our proposed framework is experimented on a challenging BRATS 2015 dataset. The investigational results obtained by the proposed method shows better in terms of qualitative metrics such as Dice Score, Positive Predictive Value (PPV) and Sensitivity with a little reduction in computation time when compared to other recent methods.

**Keywords:** Brain Tumor, Segmentation, Glioma, Magnetic Resonance Imaging, Classifiers

## 1. INTRODUCTION

The word 'Gliomas' is termed as the brain tumor disease with the high death rate in the last decade. Generally, the Gliomas is classified as Low Grade Gliomas (LGG) and High Grade Gliomas (HGG) respectively. LGG is less severe than the HGG [1-2]. Most of the tumor patients do not survive even after treatment [3]. Magnetic Resonance Imaging (MRI) is useful to evaluate Gliomas as it provides more detailed information in the brain tissue [1]. The more appropriate segmentation of this tumor is necessary for reviewing its characteristic, for the significance of treatment and also restrict its growth. Even though the physician uses some evaluation and review process over the affected part through manual mechanism, sometimes it leads to error and time-consuming. Therefore, the automatic detection and segmentation techniques have been evolved at different levels to segment the brain tumor.

Generally, the tumors have the specific features such as shape, texture and location where it exists. With the help of that features, it is able to classify the actual tumor part from the brain. The tumor tissues also change the structure of the other normal tissues [4]. There are several methods for brain tumor segmentation. Tumors are identified as abnormal tissues subjected to the constraints of shape and connectivity [5]. Some methods learn

features directly from the input image. For this kind of method, training stage is not necessary. These methods do not follow the traditional model for identifying tumor and use voxels to extract contextual information [6]. Because of this, some voxels in the input image may be misclassified. To overcome this problem, some method used neighborhood information and classified using Conditional Random Field (CRF) [6-9] with some predictions. Some of the frequently used classifiers for brain tumors are such as Support Vector Machine (SVM) and Random Forests (RF) [8-15].

In the recent era, many different techniques are developed for brain tumor segmentation which are all based on first-order and fractals-based texture [8-9, 12, 15], gradients [8-9], brain symmetry [8-9, 13], encoding context [9-10, 15] and physical properties [13]. Even though these techniques exist, still the researches are trying to develop a superior automated technique for segmenting the tumor from the brain.

In this paper, brain tumors are identified by obtaining features directly from the data. Three features are obtained from voxels of MRI data. Initially, Patient specific data are combined to have a single 3-D MRI image for each patient. Then each feature is extracted from all the sub-bands. The features are classified using Random Forest Classifier.



This research work is organized as follows: Section 2 discusses some of the works that are tested on BRATS 2015 dataset and other related works and also explains the overall proposed system architecture, features extraction algorithm and gives a brief explanation of classification using in this method. Section 3 demonstrates the experimental outcomes of the proposed method and its comparison result with the other existed methodology. Section 4 concludes the research work.

## 2. RELATED WORK

A Fully Convolution Network (FCN) architecture using 2D convolutions is developed for brain tumor segmentation [16] which used less memory and faster than other methods. Meier et al. [17] developed the RF classifier to work and train objects for segmenting post-operative brain tumor. Havaei et al. [18] introduced a deep learning model which outperforms other models in BRATS 2013 dataset. This method is further improved by a sequence of models for deep learning by Pereira et al. [19]. They used patch-wise CNN model which became more popular. These deep learning models take more time as it works on 3D data.

Kamnitsas introduced Ensembles of Multiple Models and Architectures (EMMA) method [20] through aggregation of predictions from various methods. This method solves the problem of sticking particularly to a database. Segmentation of a volume takes less than 30 s but requires 12 GB of GPU memory. A segmentation algorithm [21] is developed to segment different levels of brain tumor on post-contrast T1-weighted MRI based on local texture and abnormality features combined with RF classifier. The drawbacks of these algorithms are that they have less accuracy, efficiency and slow processing of image.

In [22], Harendra et al. framed a new architecture for finding the tumor which inherits the two traditional existing techniques called k-means and Fuzzy C-Means. This work identifies the tumor which existed at the accurate location. Another method [23] derived histograms from each 2D slice of the 3D data [23]. Thresholding and median filtering is applied to the histogram. Then connectivity is identified on the 2D slice and the biggest cluster is selected as tumor region. Finally, the 2D slices are combined to give the segmentation result.

Wei Chen et al. developed a method using super-pixel segmentation for tumor classification [24]. It consisted of three steps: super-pixel segmentation, feature extraction and segmentation model construction. Finally, SVM is used to classify super-pixels in the last step. Another technique is presented for segmentation and classification of brain tumor [25] using cascaded Random Decision Forest (RDF) classifier.

In [26], the Adaptive Pillar K-means Algorithm was used for segmenting the brain which systemized with two-tier architecture for classification purpose. This framework consists of Neural Network (NN) classifier which is used to extract the concrete features using the wavelet process. In [27], eleven layered multi-scale deep 3D Convolution NN is implemented for multi-modal brain dataset for segmenting the tumor. The same process is presented in [28], but the difference is that they have used the FCN with the end-end training methodology for fast training process. The multi-sequence image for brain tumor has some difficulty over the segmentation process. For this issue, Multiple Kernel Learning classifier [29] had been developed to mine the segmented part using some considerable features. Both of these works used the Kernels which is associated with features are allocated the weights which is made as mandatory parameters for their framework.

Likewise, the work done in [27], which uses the multi-modal model and the work done in [30] uses the twenty-two layers CNN with the N41TK methodology to classify the tumor and also correct the bias field distortion. A condition judgment is added in post-processing before threshold processing. The information contained in all modal sequences is used and the difference between them in full.

Even though deep learning models extract deep features which are very useful for classification, the computation time is a big issue. In order to reduce the computational complexity and to increase the efficiency, deep learning models are avoided and Random Forest Classifier is used. Hence the proposed method uses three different features for a single patient by combining multiple sequences into a single sequence.

## 3. SYSTEM ARCHITECTURE OF THE PROPOSED METHODOLOGY

The system architecture of the proposed methodology is discussed in this section. The architecture of the proposed framework is shown in Figure 1.

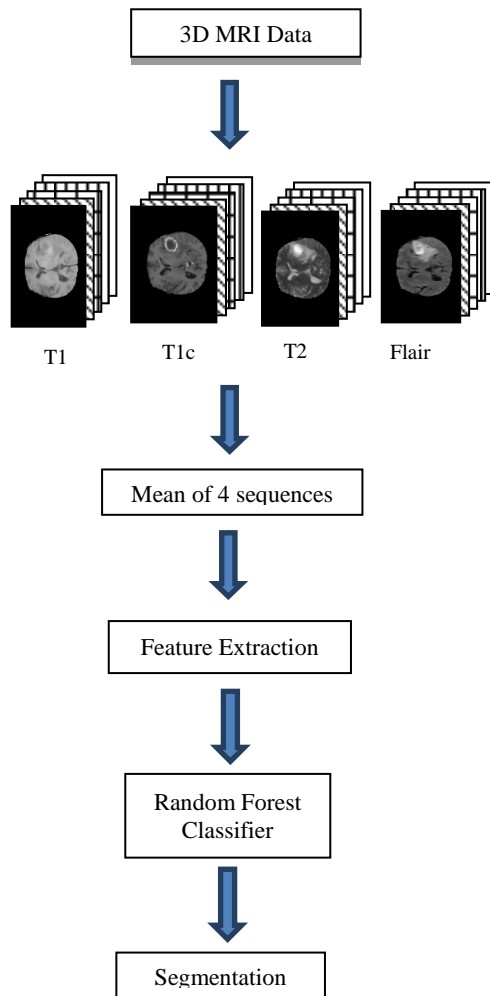


Figure 1. Proposed System

The proposed work consists of two important phases: Feature Extraction and Classification. The newly framed system is tested on the BRATS dataset which consists of 3D datasets. In Feature extraction phase, the significant features are extracted from voxel of the 3D dataset. Each and every MRI sequence of an image is made united to extract the feature. Three features such as Range of Histogram, Center Symmetric Local Binary Pattern (CSLBP) and Mean/Average are extracted from the united sequence. In the Classification phase, Random Forest (RF) classifier is used to identify the 5 different classes/labels which are mentioned in Section 4. The labels obtained by the classification phase are used to segment the tumor.

For each patient, 4 MRI sequences are available which are discussed in the following subsection. By combining all the 4 sequences, single multi sequence image is generated for each patient. As the image has more sub-bands, it contains more pixels. Hence, extracting features from this multi sequence image takes more time. Features from all the sub bands are combined to identify the 5 labels available in the ground-truth. The features extraction algorithm and classification model are discussed in the following subsections.

#### A. Feature Extraction

In this method, 3 different features are extracted from the MRI data: Range of the histogram, Average and Centre Symmetric Local Binary Pattern (CSLBP) based on the statistical data. Based upon the image intensity of the pixel, these features are extracted and made for our study. For a single case, BRATS dataset contain the 4 set of MRI sequence. The features of that 4 MRI sequences are T1-weighted (T1), T1 with gadolinium enhancing contrast (T1c), T2-weighted (T2) and FLAIR. Therefore, these features are combined to form a multi-sequence image and it is represented as  $\Omega$ . The formulation of multi-sequence MRI dataset is given in Equation 1.

$$\Omega = T_1(x, y, z), T_{1c}(x, y, z), T_2(x, y, z), Flair(x, y, z) \quad (1)$$

The problem is considered as patient-wise feature extraction problem. Hence, it paved the way to a hypothesis that it should compute features for every patient. The dimension of each 3D data is 240 x 240 x 155. Then for each sub band, all the 4 sets of MRI sequence image are united to form  $\mathcal{H}$ . The mean value of  $\mathcal{H}$  is calculated for further processing.

Histogram gives the number of bins for all intensity values. The first feature Range of Histogram is calculated as difference between maximum bins Hmax and minimum bins Hmin. CSLBP were developed for region of interest. It aims to create shorter histograms for smaller numbers of LBP labels that are better suited for use in area descriptors. It has been planned for greater stability in flat image regions. In CSLBP, the pixel values with respect to the middle pixel are not symmetrically compared with the opposite pixel.

All the features are extracted from  $\mathcal{H}$  which are named as F1, F2 and F3. These features are selected as these better identifies the features. The dimensions of each step in the feature extraction algorithm of a patient are given in Table 1. The three features are concatenated to form a feature vector and it is classified using RF classifier which is explained in the next subsection. The proposed feature extraction algorithm is structured in the way that is demonstrated below.




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**Algorithm 1: Feature Extraction Algorithm**


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**Input:** 3D MRI data of size (m, n, l)

**Output:** Feature vector of size (3, m, n)

**Steps:**

1. For every 3D MRI data in database

1.1 For each patient

1.1.1 Assume

$\Omega =$

$T_1(x, y, z), T_{1c}(x, y, z), T_2(x, y, z)$  and  $Flair(x, y, z)$ .

1.1.2 For each subband k in  $\Omega$ ,

1.1.2.1

$\mathcal{H}_k(x, y) =$

$T_1(x, y, z_k), T_{1c}(x, y, z_k), T_2(x, y, z_k), Flair(x, y, z_k)$

1.1.2.2 For every pixel i in  $\mathcal{H}$

$\mathcal{T}_i = \mathcal{H}_k(x_i, y_i)$

$A_i = \text{mean}(\mathcal{T}_i)$

End

1.1.3 Compute  $F_1 = H_{max}(A_i) - H_{min}(A_i)$

where  $H(A_i)$  is intensity bins of the histogram

1.1.4  $F_2 = \text{cslbp}(A_i)$

1.1.5  $F_3 = \text{mean}(A_i)$

End

End

2. Compute F as 3D array of 3 subbands

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In the Algorithm 1, m, n and l are the dimension of the input MRI data. Among them, m and n are the total number of rows and columns respectively and l indicates the total number of subbands.

TABLE 1 DIMENSION OF EACH VALUE USED IN THE FEATURE EXTRACTION ALGORITHM

Value	Dimension
$\mathcal{H}$	4 x 240 x 240 x 155
$\mathcal{T}$	240 x 240
$\mathbf{A}$	240 x 240 x 155
$\mathbf{F}_1, \mathbf{F}_2, \mathbf{F}_3$	240 x 240
$\mathbf{F}$	3 x 240 x 240

### B. Classification

The extracted features in the previous subsection are classified by this phase. For the classification process, Random Forest (RF) classifier is used. Here we have used the 10-fold cross validation. Since the feature vector is three dimensional, features from each dimension are combined to get the classification label.

The feature vector obtained from the Algorithm 1.1 looks like

$$\mathbf{F} = [\mathbf{F}_1 \ \mathbf{F}_2 \ \mathbf{F}_3] \quad (2)$$

For classification, features from each dimension is obtained by

$$\vec{f} = \{F_1(i, j) \ F_2(i, j) \ F_3(i, j)\} \quad (3)$$

## 4. EXPERIMENTAL RESULTS

The proposed method is tested using BRATS 2015 dataset. It consists of 3 subsets: Training, Testing and Leader board dataset. Among these subsets, the training dataset is publicly available to all. The training dataset consists of 220 HGG cases, out of which 146 are training and 74 are test cases. The size of the input 3D image is mentioned in the previous subsection. The training dataset images contain ground truth values within it. The annotated 5 labels are: 1 - necrosis, 2 - edema, 3 - non-enhancing tumor, 4 - enhancing tumor and 0 - everything else. The evaluation is performed for the enhancing tumor (only the enhancing tumor region considered positive, everything else considered negative), the core (necrosis, enhancing tumor and non-enhancing tumor taken together as the positive class), and the complete tumor (all tumor structures lumped together as the positive class).

Brain tumor segmentation is considered as a multi-class classification problem in this research as it contains 5 classes. However, in brain tumor, the classes are imbalanced. So, we used all samples from the abovementioned classes and randomly sampled from the other. Figure 2 shows the input slices of 4 MRI sequence of a particular patient. In Figure 3, the proposed algorithm results are represented with corresponding to the ground-truth images.

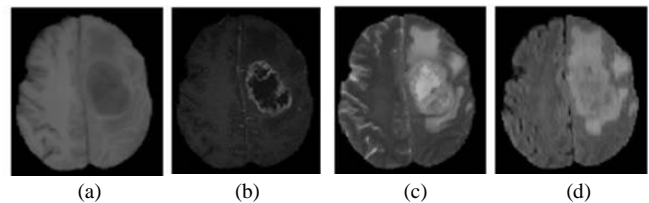


Figure 2. Input images (a) T1 (b) T1c (c) T2 (d) Flair weighted image

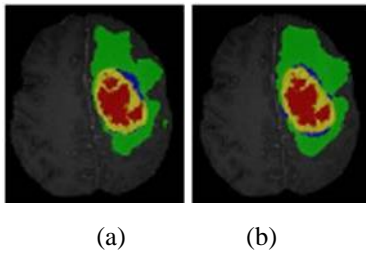


Figure 3. (a) Ground truth of T1c image (b) Segmentation result of the proposed method

From the above Figure 3, the red coloration is meant for the necrotic; the yellow is for enhancing tumor region, blue to indicate the non-enhancing tumor and green to represent the edema of the brain. It is also inferred that the segmented region obtained from the proposed method matches the same angle or structure or location of the ground-truth region.

For analyzing the performance of the proposed system, Dice Score (DSC), Positive Predictive Value (PPV) and Sensitivity measures are used. These evaluation metrics were computed by the organizers of the challenge Dice Score finds matches between the segmented region and ground-truth image. It finds how much similarity existed when the segmented region is overlapped with the ground-truth image. To find the percentage of the overlapped region of the ground-truth and segmented region, PPV is used. Sensitivity gives the percentage of overlapped region between the obtained segmented result and the ground truth with regard to the ground truth region.

The above discussed measures are formulated below.

$$DiceScore = \frac{2 \times TruePositive}{FalsePositive + (2 \times TruePositive) + FalseNegative} \quad (4)$$

$$PPV = \frac{TruePositive}{FalsePositive + TruePositive} \quad (5)$$

$$Sensitivity = \frac{TruePositive}{FalseNegative + TruePositive} \quad (6)$$

The proposed method is compared with Shreyas et al [16], Pereira et al. [19], Wang al. [30] and Konstantinos et al. [27] methods and the comparison is shown in Table 2 and 3.

TABLE 2. DSC AND PPV COMPARISON OF THE PROPOSED METHOD WITH OTHER METHODS

Methods/ Measure	DSC			PPV		
	Complete	Core	Enhanced	Complete	Core	Enhanced
<b>Proposed Method</b>	0.89	0.79	0.74	0.9	0.88	0.66
<b>Shreyas et al.</b>	0.83	0.75	0.72	0.79	0.74	0.76
<b>Pereira et al.</b>	0.88	0.76	0.73	0.91	0.90	0.72
<b>Wang et al.</b>	0.84	0.79	0.75	0.88	0.86	0.70
<b>Konstantinos et al.</b>	0.85	0.67	0.63	0.85	0.86	0.63

TABLE 3. SENSITIVITY COMPARISON OF THE PROPOSED METHOD WITH RECENT METHODS

Methods	Sensitivity		
	Complete	Core	Enhanced
<b>Proposed Method</b>	0.92	0.8	0.82
<b>Shreyas et al.</b>	0.89	0.78	0.73
<b>Pereira et al.</b>	0.86	0.74	0.81
<b>Wang et al.</b>	0.82	0.75	0.86
<b>Konstantinos et al.</b>	0.88	0.60	0.67

The qualitative result obtained from the Table 2 and Table 3, compares the result of proposed method with DSC, PPV and sensitivity and it is found that the proposed method outperforms the existing methods. Table 4 shows the computation time of the proposed method and the recent methods.

TABLE 4 COMPUTATION TIME COMPARISON OF THE PROPOSED METHOD WITH OTHER METHODS

Method	Computation Environment	Computation Time (seconds)
<b>Pereira et al.</b>	Quadro K4000 GPU	18000
<b>Shreyas et al.</b>	Quadro K4000 GPU	976
<b>Weng et al.</b>	Intel Core i7 2.8 GHz machine with a GPU NVIDIA GeForce GTX 1050	8400
<b>Proposed Method</b>	Intel Core i5 – 1.70GHz machine	724

From Table 4, it is studied that the proposed method segments the whole training set of BRATS 2015 dataset, in about 724 seconds. Pereira et al.'s method segments the same training set in 18000 seconds. The proposed method also works faster than Shreyas et al. method [16] and Wang et al method [30]. In medical imaging, the volume of data is more when compared to other data.



Therefore, the computational processing time is more for the existing system. From the Table 4, it is inferred that the proposed architecture has high computational time over the existing techniques.

## 5. CONCLUSIONS

Segmenting different levels of brain tumor in a huge volume of 3D MRI data is very challenging. As the multi sequence 3D MRI data has more pixels, processing them takes more time. But in medical imaging, any processing should take less time. The proposed method combines the different MRI sequence of a single patient to a single MRI data. Three features are extracted from each level of the MRI data and given to Random Forest classifier. This method reduces the computation time with good Dice Score, PPV and sensitivity when compared to other recent methods

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