3D Convolutional Neural Network for Brain Tumor Detection

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Abstract

Tumor detection and classification plays a crucial role in medical applications. Magnetic Resonance Imaging is the powerful scan of brain tumor. Segmentation and classification of tumor is done in Magnetic Resonance Imaging (MRI). The MRI of a single patient consists of 4 images of three-dimensional sizes. All the 4 images are integrated to form a single three dimensional image. In the integrated image, the tumor portion is segmented using Grab Cut method. Then features are extracted using 3 Dimensional Convolutional Neural Network (3D CNN) which is specially designed for this research. The deep features thus extracted are classified using multiple classifiers. The proposed method is tested on BRATS 2017 and 2018 challenging datasets. The results are compared with more recent methods.

Keywords. *Convolutional Neural Network, tumor, segmentation*

1. Introduction

One of the most critical tasks in any brain tumor detection system is the isolation of gliomas from healthy brain tissues. The conventional brain tumor detection consists of extraction, segmentation, classification. There are many researches that uses MRI data using its imaging properties. Brain tumor detection has several challenges such as the varying size, location and aging.

The severity of this disease increases gradually. Early detection of this disease may lead to save a life. Hence early detection of brain tumor is done using many image processing methods. The severity of the tumor is divided into two categories such as High-Grade Glioma (HGG) and Low Grade Glioma (LGG) in which the survival rate of HGG is approximately 2 years. So it requires immediate treatment [1]. The rate of growth in LGG is slower compared to that in HGG and can be recovered with proper treatment.

The manual brain tumour segmentation with the help of experts has several difficulties and may not be accurate. The time taken to segment a tumor tissue manually is many times greater than the automatic segmentation of many tissues. Moreover, the tumour structure varies in terms of shape, size and location from each individual patient.The main contributions of this paper include:

Sequence integration is done to reduce the computation and processing burden of further process.

- Grab Cut segmentation is used for segmenting brain tumor.
- 3D CNN is used to extract deep features.Multiple classifiers are used to study the best classifier for this research.

The remaining of this paper is arranged as follows: Section II reviews some most recent literatures based on brain tumor detection using deep learning. Section III elaborates the proposed methodology with all its phases. Section IV demonstrates the proposed method with its experimental results and analysis. Section V concludes the research by giving future scope.

2. Related Works

In this section, some recent researches based on brain tumor detection are discussed. Owing to the drastic growth of deep learning, all the applications use deep learning methodologies. This section discusses some methods of brain tumor detection using deep learning methods. A novel approach has been implemented based on Long Short-Term Memory (LSTM) model using MRI [2]. In [3], triangular fuzzy median filtering has been applied for image enhancement that helps in accurate segmentation based on unsupervised fuzzy set method. Gabor features are extracted and classified using Extreme Learning Machine (ELM) and regression ELM.

A hybrid method using Neutrosophy and CNN (NS-CNN) has been introduced in [4]. It aims to classify tumor region as benign and malignant that is segmented from MRI. A new CNN model named BrainMRNet has been developed in [5]. This architecture is built on attention modules and hypercolumn technique. It also has a residual network. With the help of hypercolumn technique, the features extracted from each layer of the BrainMRNet model are

retained by the array structure in the last layer. The aim is to select the best features among the features maintained in the array.

A fully automatic method has been developed for brain tumor segmentation [6], using U-Net based deep CNN. Another automated method is implemented that easily differentiates cancerous and non-cancerous MRI of the brain [7]. Different techniques have been applied for the segmentation of candidate lesion. Then a features set is chosen for every applicant lesion using shape, texture, and intensity. Support Vector Machine (SVM) classifier is used for classification.

Deep Neural Networks (DNN) based architecture is employed for tumor segmentation in [8]. An improved orthogonal gamma distribution based machine-learning approach [9] is used to analyse the under segment and over segments of the brain tumor regions to detect the abnormality with automatic Region Of Interest (ROI) detection. This method solves the data imbalance due to improper edge matching in the abnormality region by matching the edge coordinates.

A deep learning-based method has been introduced for microscopic brain tumor detection and classification [10]. A 3D CNN architecture is designed to extract brain tumor and extracted tumors are passed to a pre-trained CNN model for feature extraction. The extracted features are transferred to the correlation-based selection method which selects the best features. These selected features are classified using Feed-forward Neural Network (FNN).

The Grab cut method [11] is applied for accurate segmentation of actual. The pre-trained VGG-19 model is used to extract deep features which are then concatenated with hand crafted (shape and texture) features through serial based method. These features are optimized and fused feature vector is supplied to classifiers.

An automatic end-to-end method based on Generative Adversarial Nets (GAN) has been implemented for brain tumor segmentation [12]. This method combines the generating model with the discriminant model and takes GAN instead of Conditional Random Fields (CRF) as high-order smoothing method.

The reliability of automated detection and segmentation of grade I and II meningiomas has been investigated using a deep learning model [13] on routine multi-parametric MRI data from diverse scanners including referring institutions. A conditional generative network [14] is designed that learns input distribution by embedding label independence in latent space.

Deep learning procedures combine structural MRI, demographic, neuropsychological, and APOe4 genetic data as input data [15]. An automatic segmentation approach combining Enhanced CNN (ECNN) with Bat algorithm is developed [16]. Bat works on the function loss whereas small kernels characteristics of ECNN allow network with less weight assignment that controls over-fitting.

A deep learning model has been implemented for different brain segmentation. They use hybrid CNN model for the extraction of the local and contextual knowledge of tumors [17]. This method solves the overfitting problem and is passed to FNN for training. A hybrid Self Organizing Map (SOM) pixel labeling has been developed with reduce cluster membership and deterministic feature clustering for brain tumor identification [18]. To segment brain tumor, cluster is obtained using three unsupervised learning techniques.

An automated model based segmentation using Artificial Neural Network (ANN) is presented using MRI data [19]. In this method, ROI is extracted using model-based

segmentation and textural descriptors are obtained. The extracted textural descriptors are recognized through ANN.

A fully automated brain tissue classification method [20] has been developed for normal and abnormal tissues and its associated region from FLuid Attenuated Inversion Recovery (FLAIR) modality of MRI. This method simultaneously detects and segments tumours to pixel-level accuracy. They used region-based features such as statistical, text on histograms, and fractal features.

A novel end-to-end brain tumor segmentation method has been developed using an improved Fully Convolutional Network (FCN) by modifying the U-Net architecture [21]. In this method, an up skip connection is first developed between the encoding and decoding path to enhance information flow. An inception module is adopted in each block to help the network learn richer representations, and an efficient cascade training strategy has been introduced to segment brain tumor sub-regions sequentially. When compared to patch-wise methods, this model automatically generates segmentation maps slice by slice.

An automatic method, named Wide Residual Network & Pyramid Pool Network (WRN-PPNet) [22], which can automatically segment glioma, is presented. Initially, WRN is used to extract features of multimodal brain tumor slices which are proved to have strong expressive ability. Then the global prior representation with different level obtained by PPNet is stacked on the features from WRN. Finally, the scale recovery module is used to produce the pixel-level predictions which have the same size as original inputs.

Patient specific brain tumor segmentation using context sensitive feature extraction in MRI has been implemented in [23]. In this method, a novel sequence integration method is developed which reduces the computation burden of brain tumor detection. Another method has been developed in [24] which use Deep CNN (DCNN) and SVM for feature extraction and classification.

Khan et al. (2020) has implemented multimodal automatic brain tumor classification strategy using deep learning [25],[29]. Linear contrast stretching, deep features extraction using pretrained CNN models, features selection based on correntropy and robust covariant features centered on the partial least square are fused in one matrix[29]. Finally, the fused feature are given to ELM for classification.

Another feature selection approach that selects the best CNN features has been developed in [26],[29]. They used saliency-based approach for tumor detection. Later, the inception CNN model is used to extract the deep features.

3. Proposed Methodology

The proposed system architectures (Level 1 and 2) are shown in Fig 1 and 2. The proposed method consists of four important phases: Sequence Integration, Segmentation, Feature Extraction and Classification.

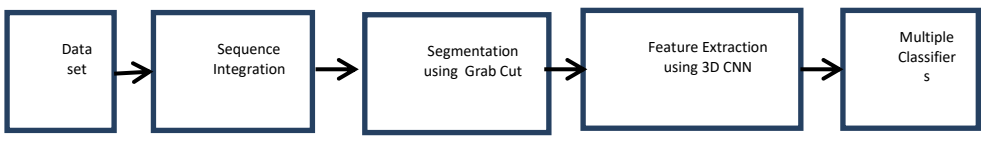

Figure 1 .Proposed System Architecture – Level 1

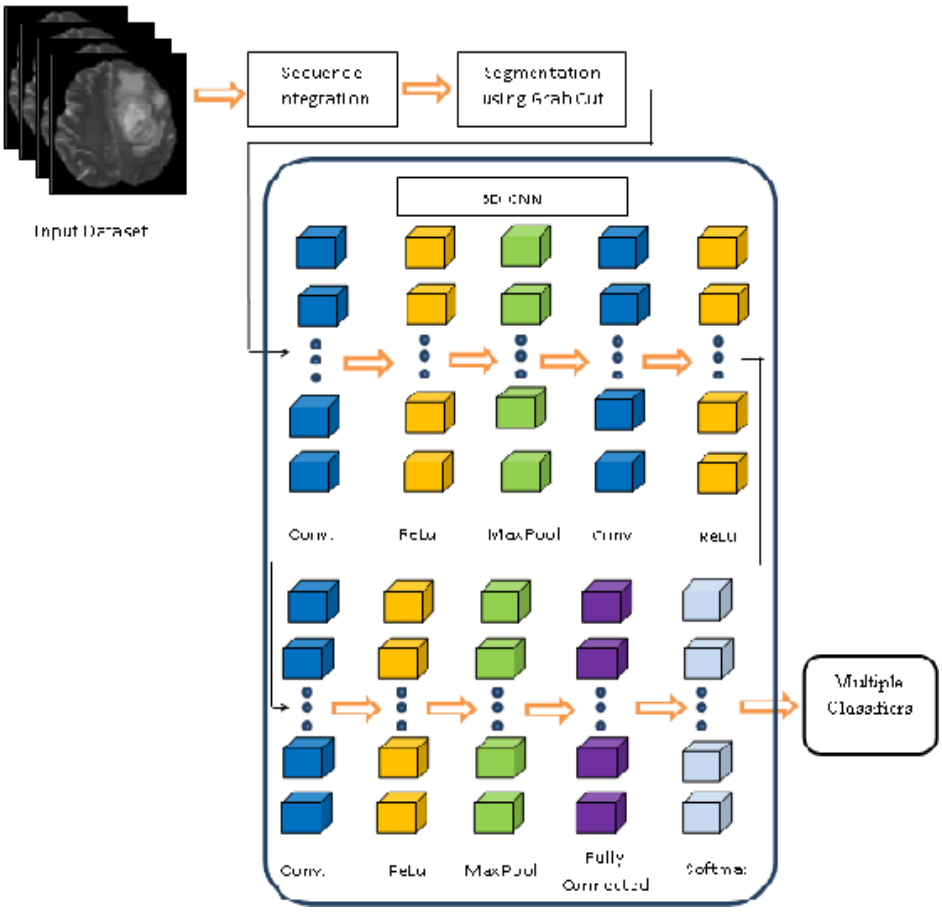

Figure 2. Proposed System Architecture – Level 2.

The MRI of a single patient consists of four 3D data. All the four MRI are combined to form a single MRI in the first phase. From the integrated MRI, tumor portion is segmented using Grab Cut method. As soon as the tumor region is identified, features are extracted using a novel 3D CNN. Finally, the tumors are classified using multiple classifiers.

Sequence Integration

For each patient, 4 MRI sequences are available. 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. The sequence integration method used in this research is based on [23].

For every patient in the database, 4 MRI sequences are available: T1-weighted (T1), T1 with gadolinium enhancing contrast (T1c), T2-weighted (T2) and FLAIR. We assume the entire 4 MRI sequence as a multi-sequence image Ω. It is given as

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

The problem is considered as patient-wise feature extraction problem [23]. 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. Hence, the dimension of MRI data for a single patient is 4 x 240 x 240 x 155. The mean value of each sub-band from each sequence is taken to form a new single 3D data.

Grab Cut Segmentation

Initially, RGB sequence integrated image is converted into a grayscale image. Then Grab cut method is applied for gliomas segmentation [11]. Next, seed point is set as a threshold between 0 and 180. The seed points grow by adopting the neighboring pixel values in which the value of threshold is similar to primary seed point. For subsequent iterations, similar pixels are grouped and act as seed point. This process is repeated until similar pixels are grouped at a specified threshold level.

3D CNN Feature Extraction

A new 3D CNN is proposed in this work for brain tumor detection and classification. Using 3D CNN, features are extracted from the segmented tumor region. A detailed architecture of the proposed 3D CNN is illustrated in Figure. 3.

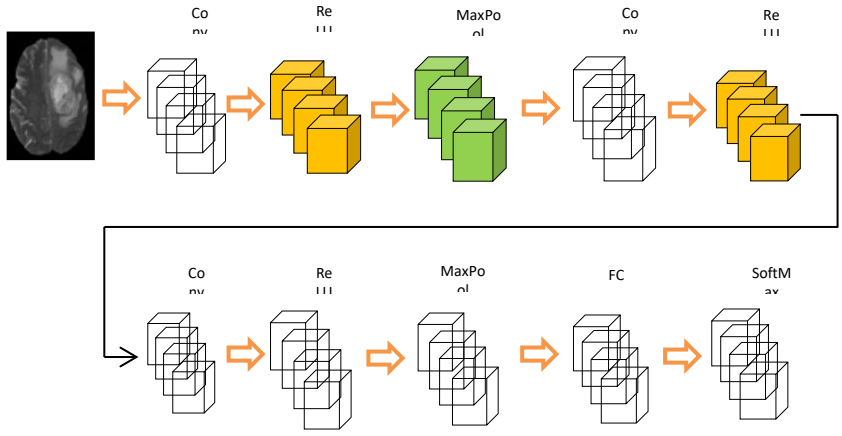

Figure 3. Proposed 3D CNN Architecture

Here, the extracted tumor affected area from the input image is applied to the precise classifier in the next steps. The layer details are shown in Table 1.

Table 1. Architecture of 3D CNN

Layer Type	Dimension	# Filters
Conv.	3x3x3	64
Relu.	-	-
Max-pool	1x2x2	-
Conv.	3x3x3	128
Relu.	-	-
Conv.	3x3x3	512
Relu.	-	-
Max-pool	2x2x2	-
FC	1x1x4096	-

The 3D CNN consists of 3 convolutional layers, 3 Rectified Linear Units (ReLU), 2 Maximum Pooling layers, 1 Fully Connected (FC) Layer and 1 SoftMax Layer. The convolution filters are of size 3 x 3 x 3 with stride [1 1] and padding [1 1 1 1]. The 3D CNN is trained with 100 epochs, mini-batch size of 32 with learning rate of 0.001.

Classification

Segmented images are obtained using the Grab cut algorithm. Then deep learning features are extracted from all segmented images using 3D CNN. These images are supplied to multiple classifiers such as K-Nearest Neighbor (KNN), Random Forest (RF), Naïve Bayes (NB) and Support Vector Machine (SVM) for the classification. These classifiers separate gliomas and healthy images.

4. Experimental Results

The proposed method is tested on two BRATS Challenge datasets including 2017, 2018. In 2017 dataset, there are 431 cases (both HGG and LGG), among which 285 are used for training and 146 cases in testing [27]. Training samples of BRATS 2018 contain 285 cases. Testing samples include 191 cases. The training and testing details of these dataset are shown in Table 2.

Table 2. Details of Dataset

Dataset	Training		Testing	
	HGG	LGG	HGG	LGG
2017	210	75	73	73
2018	210	75	95	96

Some examples of BRATS 2017 and 2018 are shown in Figure 4.

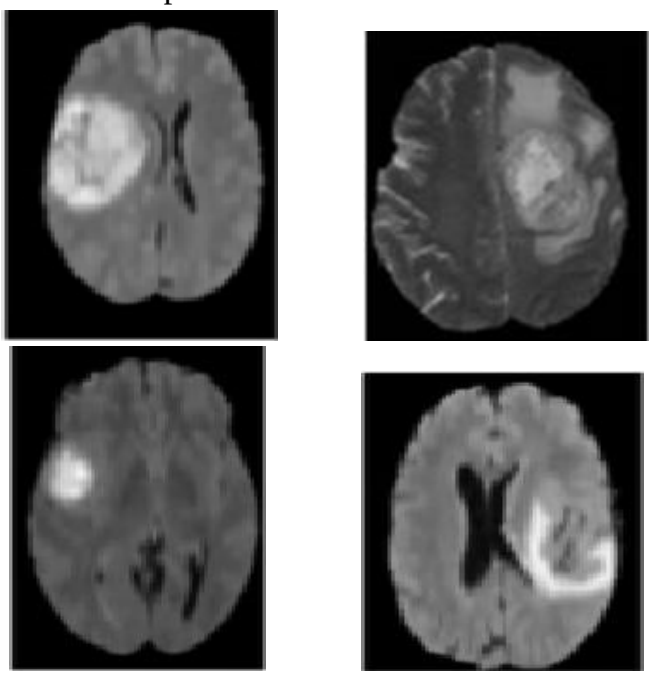

Figure 4. Examples of BRATS Dataset

Performance Measures

To analyze the performance of the tumor segmentation methods, accuracy, Positive Predictive Value (PPV), Dice Similarity Coefficient (DSC), Jaccard Index (JI), Sensitivity and Specificity are used. If TP denotes True Positive (tumor regions that are identified as tumor), FP denotes, False Positive (non-tumor regions that are identified as tumor), TN dentoes True Negative (tumor regions that are identified as non-tumor) and FN denotes False Negative (tumor regions that are identified as non- tumor), then the above-mentioned metrics are defined in Table 3.

Table 3. Performance Measures

Measure	Formula
Accuracy	$Ac_r = \frac{T_p + T_n}{T_p + T_n + F_p + F_n} \times 100$
Positive Predictive Value (PPV)	$PPV = \frac{TP}{TP + FP}$
Sensitivity	$Sensitivity = \frac{TP}{TP + FN}$
Specificity	$\text{Specificity} = \frac{\text{TN}}{(\text{FP} + \text{TN})}$
DSC	$DSC = \frac{2 \times TP}{FP + (2 \times TP) + FN}$
JI	$JI = \frac{TP}{TP + FP + FN}$

The accuracy gives the correct classification of brain tumor. The PPV is the portion of extracted illustrations that are related to locate. The sensitivity is the portion of related illustrations that are extracted in relation to the uncertainty. Specificity measures the proportion of negatives which are correctly identified. DSC 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. The Jaccard Index is calculated as the amount of the intersection of the brain tumor and non-brain tumor pixels divided by the amount of their combination.

Results

The Grab cut segmentation results in BRATS 2017 dataset are shown in Figure 5.

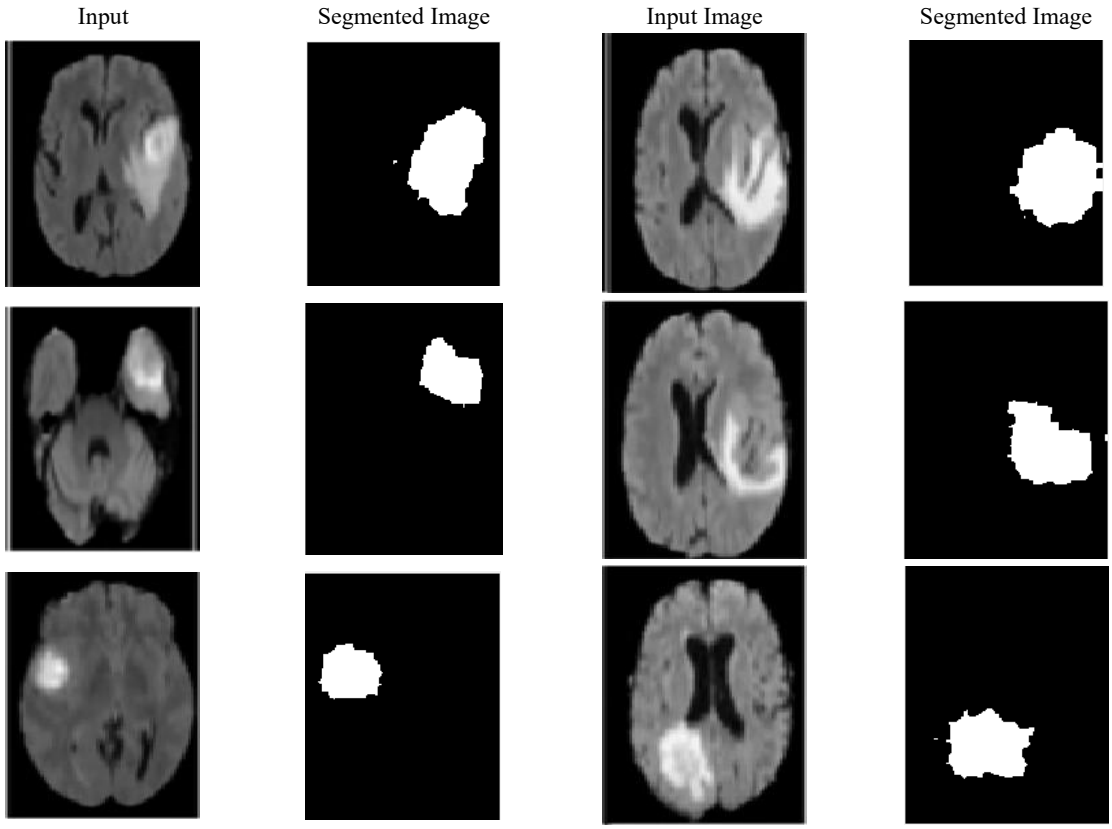

Figure 5. Input and Segmented Image Results of BRATS 2017 dataset

From Fig. 5, it is observed that the Grab cut method segments the tumor more approximately. Table 4 shows the results obtained by the proposed method in BRATS 2017 and 2018 datasets.

Table 4. Results obtained by the Proposed Method for BRATS 2017 and 2018 Datasets

Classifier	BRATS Dataset	Accuracy	PPV	Sensitivity	Specificity	DSC	JI
KNN	2017	98	98	98	97	98	98
	2018	97.1	97.34	96.8	96	97	96.65
RF	2017	97.7	98.23	97.89	97	95	97.6
	2018	97.79	96.87	96.2	96	96	97.67
NB	2017	97.65	97.84	95.23	98	98	96.39
	2018	96.76	96.42	96.57	97	98	96.9
SVM	2017	**98.7**	**99**	**99**	**99**	**98**	**98**
	2018	**98.54**	**98**	**99**	**99**	**98**	**99**

From Table 4, it is observed that the proposed achieves above 98% accuracy, PPV, sensitivity, specificity, DSC and JI for BRATS 2017 and 2018 datasets. When classifiers are compared, the proposed method with SVM classifier achieves 98.7% accuracy, whereas KNN obtains 98%, RF obtains 97.7%, NB obtains 97.65% accuracy for BRATS 2017 dataset. Similarly, SVM classifier obtains 98.54% accuracy for BRATS 2018 dataset which is greater than other classifiers. Hence, the proposed method suggests using SVM as classifier. The results obtained by the proposed method with SVM classifier is used for comparison.

Comparison with Recent Methods

The proposed method is compared with recent methods [2, 3, 17, 20] that are discussed in Section II. Table 5 compares of accuracy obtained by the proposed method with recent methods.

Table 5 Accuracy Comparison of Proposed Method with Other Methods

Method	Year	BRATS Dataset	Accuracy
Amin et al. [2]	2019	2018	98
Rehman et al. [10]	2020	2017	96.97
		2018	92.67
Khan et al. [25]	2020	2017	96.9
		2018	92.5
Sharif et al. [26]	2020	2017	96.9
		2018	92.5
Proposed Method		2017	98.7
		2018	98.54

From Table 5, it is observed that the proposed method achieves 98.7% accuracy for BRATS 2017 dataset which is higher than other methods. Amin et al. [2] method obtained 98% accuracy for BRATS 2018 dataset. Table 6 compares sensitivity, specificity, DSC, JI and PPV obtained by the proposed method with other methods.

Table 6. Comparison of Proposed Method with Recent Methods

Method	Year	BRATS Dataset	Sensitivity	Specificity	DSC	JI	PPV
Amin et al. [2]	2019	2018	98	99	99	97	99
Saba et al. [11]	2020	2017	99	-	99	-	-
Proposed Method		2017	99	99	99	98	98
		2018	98	99	99	98	99

From Table 6, it is noted that the proposed method achieves approximately 99% results which is not greater than other methods for both BRATS 2017 and 2018 datasets. Figure 6 compares the accuracy obtained by the proposed method with the recent methods.

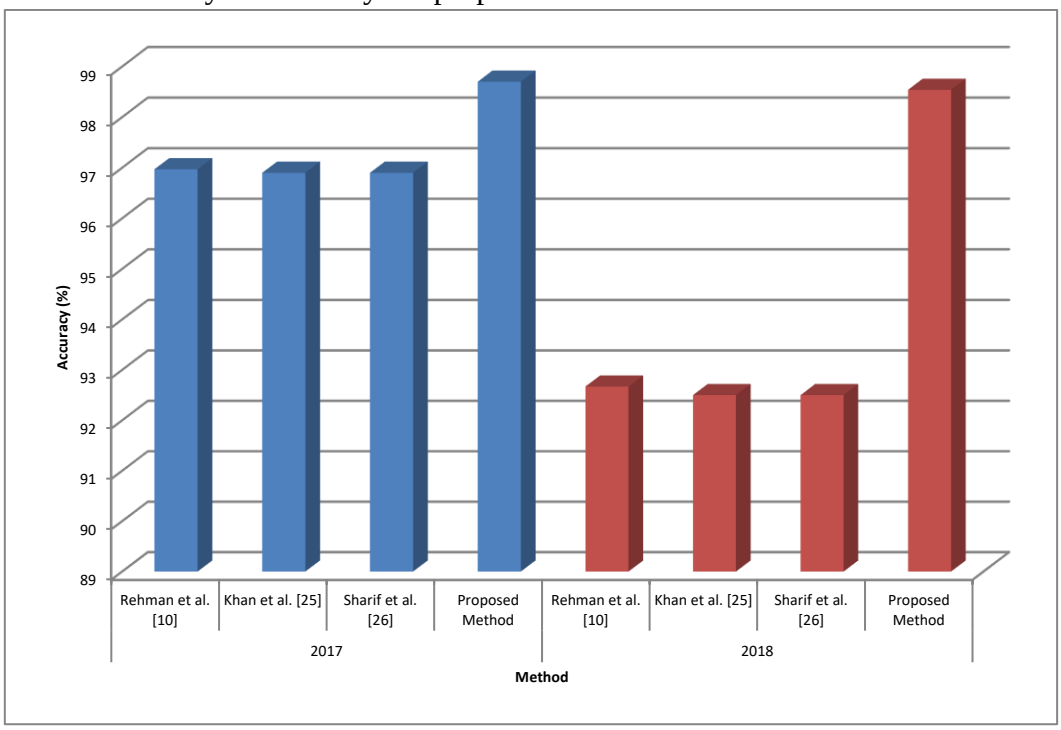

Figure 6. Accuracy Comparison of Proposed Method with Recent Methods

The presented approach is assessed by using MATLAB 2018b, Intel Core i7 2.8 GHz machine with a GPU NVIDIA GeForce GTX 1050. The computation time of the proposed method is mentioned in Table 7.

Table 7. Computation Time of the Proposed Method

BRATS Dataset	Training (s)	Testing (s)
2017	764	0.001156
2018	795	0.002146

The computation time for training is approximately 785 seconds for both datasets. For testing, it is merely 0.0015 seconds for both datasets.

5. Conclusion

There are several medical applications. One among them is brain tumor detection. This paper designs a 3D CNN for deep feature extraction. It integrates all the 4 sequences of a patient to a single sequence. Tumors are segmented using Grab Cut method and features are extracted using 3D CNN. Finally, tumors are classified using multiple classifiers. The proposed method is experimented on BRATS 2017 and 2018 datasets. It achieves 98.7% accuracy on BRATS 2017 dataset and 98.54% accuracy with 98% sensitivity in BRATS 2018 dataset. The results are higher than the results obtained by other methods. In future, the proposed method can be tested on recent BRATS datasets. Also, gliomas can be further classified into necrosis, edema, non-enhancing tumor and enhancing tumor.

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