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Brain tumors classification based on segmentation techniques and wavelet transform

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Abstract

This paper aims to provide better approaches for segmenting and classifying brain tumours using Magnetic Resonance images (MRI). In this paper, the wavelet features are formed by the transformation of probability density function (PDF) to spectrogram images using Continuous Wavelet Transform (2D-CWT), which is a simple method for extracting features, whereas the Feature extraction methods (PDF and 2D-CWT) are improving the performance. In addition, a morphological operation for segmenting images and a convolutional neural network (CNN) are utilized as a classifier in order to increase the segmentation performance. On the BraTS2019 dataset, the method's performance is assessed in terms of F1-score and tumour region segmentation accuracy. This achieved the greatest results, with accuracy and F1-score of 97.37 % and 97.43 %, respectively.

Keywords: Brain tumor, Magnetic resonance imaging (MRI), Feature extraction, Segmentation, Classification
2020 MSC: 65T60, 92C50

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1 Introduction

Nowadays, the spread of the disease is increasing day by day. Tumors are one of the worst illnesses that may strike any region of the body. The most hazardous sort of fatal tumor is one that affects the brain. Brain tumors are a very serious condition that is difficult to treat and is the leading cause of death. Gliomas are the deadlier form of brain tumor because they originate in the inner region of the brain. Gliomas often spread through a thorough range to inner part of brain and thus, do not always appear on surface of the brain. Low-Grade Gliomas (LGG) and High-Grade Gliomas (HGG) are the two forms of gliomas (HGG) [17, 3].

MRI technology is commonly utilized in order to detect brain tumors and track their growth over time, this form of imaging produces high-quality images. Magnetic resonance imaging (MRI) images are crucial in medical image analysis because they allow for the imaging of various brain areas and hence give extensive information about them [2].

Manual classification of the brain tumor from MRI images with the similar structures or properties is a difficult and complicated procedure which depends upon radiologist's availability and experiences to detect and diagnose the brain tumor accurately. By identifying brain tumor MR images with minimum human skill interference in the linked

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field [12]. Several feature extraction and classification algorithms were used in traditional methods for illness detection and disease classification issues utilizing medical images. The use of deep learning (DL) architecture, specifically the CNN, overcomes that issue to some extent [6].

This paper focuses on brain tumor classification and segmentation. The following is the framework for this study: section 2 delves into related work. The suggested method will be discussed in Section 3. Section 4 discusses the findings of experimentations and performance. Section 5 ends with a conclusion and suggestions for future work.

2 Related works

The methods that have been suggested in earlier researches will be discussed in the subsequent sections. Those approaches diagnose the brain tumours with the use of approaches like the conventional image processing, and ML method based upon the neural networks:

M. Mohammed Thaha et al. [13] suggested Enhanced CNN (ECNN) with the optimization of the loss function by the BAT algorithm for the automatic segmentation approach of an MRI image. The dataset which they used was the Challenge of Brain Tumor Segmentation 2015 dataset (BRATS 2015). Also, the skull stripping and image enhancement algorithms have been utilized for a preprocessing. This model rate reached an accuracy was 92% and a recall of 90%.

R. Thillaikkarasi1 et al. [18] suggested a new M-SVM-based DL method (kernel-based CNN). Pre-processing, image classification, feature extraction, and brain tumor segmentation are all phases of their job. MRI image was smoothed and improved using the Laplacian of Gaussian (LoG) filter approach with the Contrast Limited Adaptive Histogram Equalization (CLAHE), and features were extracted on the basis of tumor shape position, shape, and surface features in the brain, and classify image was performed with the use of the M-SVM based upon chosen features. This method had an accuracy of almost 84%.

Shubhangi Nema et al. [15] proposed a residual cyclic unpaired encoder-decoder network (RescueNet) design network architecture based on mirroring and residual concepts. RescueNet employed the unpaired adversarial training in order to partition the entire tumor, then the core, and improve regions in an MRI image of the brain. Three distinct networks were used to separately train the whole, core, and enhance tumors. The performance of their suggested network has been evaluated using BraTS 2015 and BraTS 2017 brain tumor datasets. On the BraTS 2015 dataset, the DICE value was 0.9401 percent, while on the BraTS 2017 dataset, it was 0.9463 percent.

Mohamed A. Naser et al. [14] proposed a DL strategy combining the tumor segmentation CNN based upon U-net and tumor grading using transfer learning using pre-trained Vgg16 convolution-base and fully connected classifier. This idea shows how MRI scans may be used to offer accurate automated tumor segmentation, identification, and LGG brain tumors' grading utilizing DL and models of transfer learning. The average dice similarity coefficient (DSC) was 0.84, while the method's accuracy was 0.92.

Francisco Javier Daz-Pernas et al [9] proposed a fully automated brain tumor segmentation and classification approach based upon CNN architecture that has been designed for the multi-scale processing for the MRI images, which contain 3 tumor types, which are: glioma, meningioma, and pituitary tumor, with no need to remove parts of the skull or vertebral column in advance. The optimizer was a Stochastic Gradient Descent (SGD). Tumor categorization was a direct result of the segmentation result in their technique. They evaluated their strategy using BRATS 2013. The classification accuracy of their approach was 0.973, and the Dice index was 0.828.

B Kokila1 et al (2021) [10] They suggested a method for classifying brain MRI on many classification tasks that uses a single model rather than a separate model for each classification task. Detecting the tumor and classifying it in terms of grade, kind, and tumor site are all part of this experimental effort in the diagnosis of brain cancers using MRI. For the classification and identification of tumours, a CNN-based multi-task classification was used. By segmenting the brain tumor, a CNN-based model was used to identify the location of the tumor. The total accuracy of this model was 92%. The Dice coefficient was used to assess the tumor identification module. A Dice score of 0.89 was acquired on average.

3 Proposed methodology

The brain tumor MRI image classification based on the CNN and segmentation is discussed in this part. Figure 1 shows the proposed architecture and workflow. Input data, prepared images, image segmentation, feature extraction, and classification were all part of the process. Finally, we evaluate our methodology using a confusion matrix.

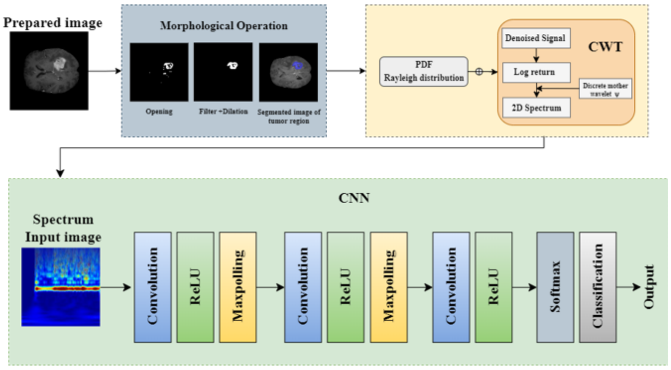


Figure 1: The proposed architecture and workflow (Proposed Method)

3.1 Dataset preparation

The MRI images in the dataset were Prepared; (see Figure 2) as the following:

Figure 2: Data Preparation Steps

3.1.1 Brats dataset

BraTS2019 challenge brain MRI data-set has been utilized to train and test the brain MRI data-sets has been utilized for training as well as testing [4]. Every one of the patients has MRI images in a variety of modalities, (T1, T2, T1ce, and FLAIR (Fluid-attenuated Inversion Recovery)), Figure 3, and segmented ground truth. The data-set includes 335 glioma patients, where 259 of the cases have been HGG cases and the rest of the cases have been 76 LGG cases.

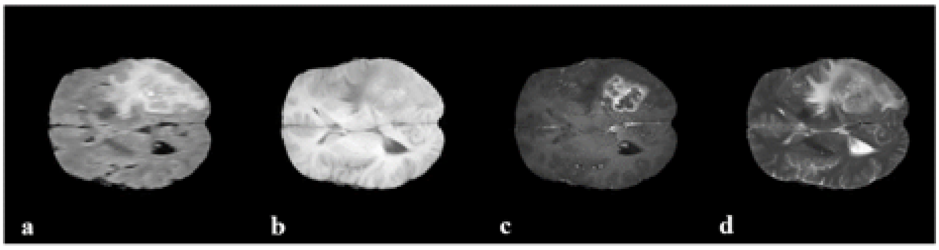


Figure 3: (a) FLAIR (b) T1-w (c) T1-w contrast-enhanced (d) T2-w MRI brain with HGG that have been collected from BraTS 2019 data-set

3.1.2 Preprocessing dataset

Data pre-processing involve the processing of data for the purpose of obtaining data in the needed format i.e., converted from (nii) format into (jpg) image slices format. After that, combine the slice images into an integrated higher-quality image and convert them to Grayscale, Figure 4. Those images are split after that into training and testing datasets. In our proposed method we useT1-weighted contrast-enhanced images (T1ce-weighted).

3.1.3 Data augmentation

Image data augmentation has been utilized for the purpose of increasing training data-set in order to improve model's performance. Since the dataset considered for research is very small, thus, we artificially augment the training images to create a larger dataset to prevent overfitting that can happen in the case where a fully connected layer takes up the majority of the parameters. Overfitting may be reduced by feeding a CNN additional training instance. Commonly, augmented images consisted of rotation, horizontal and vertical translation, and flipping, Figure 5.

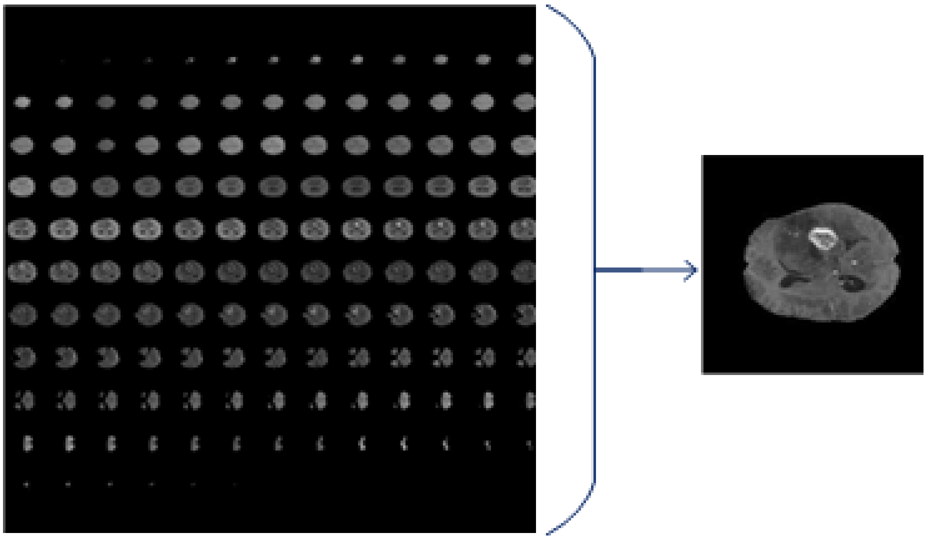


Figure 4: Example of combining the slice images into one image

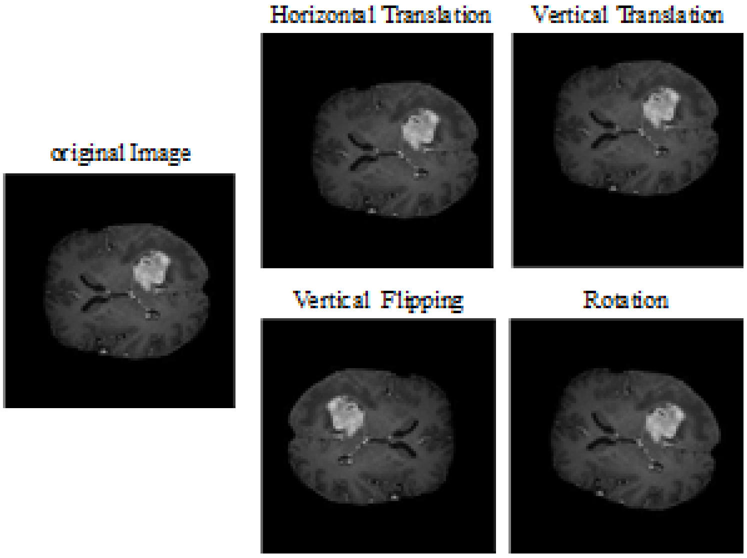


Figure 5: Examples of images after data augmentation

3.2 Segmentation

We performed the morphological operation in our images for segmenting tumor-affected pixels. In this paper, morphological operations applying to eliminate the extra parts in the brain tumor images. The morphological operations for the detection of the tumor regions are clarified as follows:

Grayscale image is transformed into a binary image of black and white (BW), by replacing all input image pixels with a brightness greater than the threshold (T) with the value 1 (white) and all other pixels with the value 0 (black).

$$T(a,b) = \begin{cases} 1, & g(c,d) \geq T \\ 0, & otherwise \end{cases} \tag{1}$$

where T is threshold and $g(c,d)$ is the grayscale image, [8].

Then, the morphological opening is performed to eliminate the details without manipulating the other surfaces:

$$A \odot B = (A \ominus B) \oplus B \tag{2}$$

where, (A) expresses the binary image, and (B) is the structuring element [8].

To make the segmented object look natural, we use a filter to remove small objects. Subsequently, we applied morphological dilating to disappear any gaps:

$$Dilation = (A \oplus B) \tag{3}$$

where, (A) expresses the binary image, and (B) is the structuring element [5].

Finally, the region is selected and segmented by a mask over the original image to display the tumor region segmented image, Figure 6.

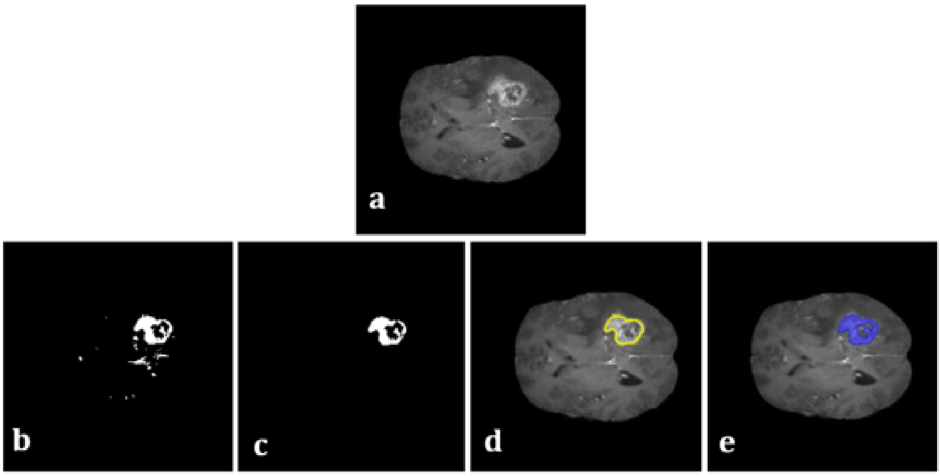


Figure 6: (a) Original MRI, (b) Threshold image, (c) Morphologically processed image, (d) Edge Detection, (e) Segmentation of tumor region

3.3 Proposed feature extraction methods

This section is to understand the performance of the transformation of probability density function (PDF) to spectrogram images with the use of the Continuous Wavelet Transform (CWT) for Feature Extraction.

The assessment of PDF of intensity values plays a significant role in medical image analysis. The PDF assessment methods have the feature of most in their application. In this step, we applied Rayleigh distribution. The Rayleigh distribution in probability theory and statistics is a continuous probability distribution for nonnegative-valued random variables. This distribution is commonly employed in medical imaging-magnetic resonance imaging (MRI). When applying the PDF, the intensity of pixels increases and the image domain converts to a 1D vector. So, it makes image features more suitable for other steps, as the following formulated:

$$P(I)_{Rayleigh} = I(x,y)\sigma^2 exp(\frac{I(x,y)^2}{\sigma^2}) \tag{4}$$

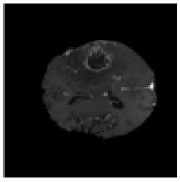
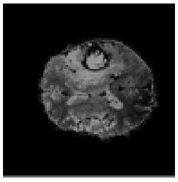
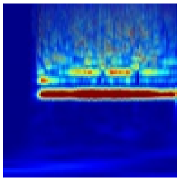
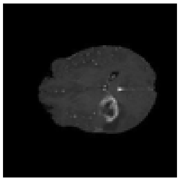
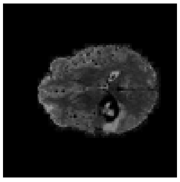
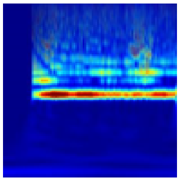
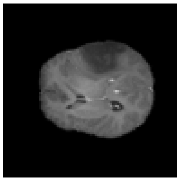
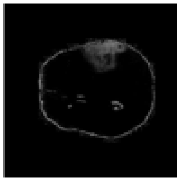
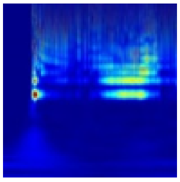
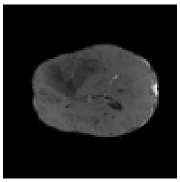
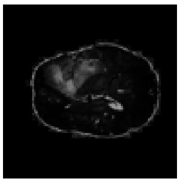
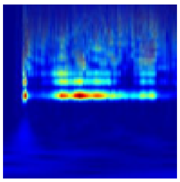
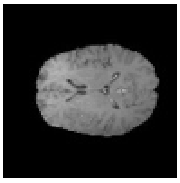
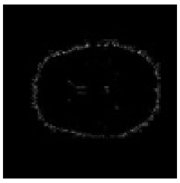
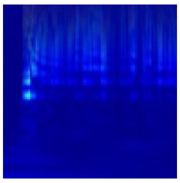
where, $I(x,y)$ is an image, and $\sigma > 0$ is the scale parameter of the distribution.

After that, the transformation of a 1D vector after PDF is applied to a 2D matrix, which is then represented as a spectrogram image using the CWT, See Table 1. The CWT produces a wavelet feature whose spectrogram image dimension is (227 × 227) to be used as inputs to CNN for classification.

$$CWT_{\psi(t,s} = \int_{-\infty}^{\infty} \frac{1}{s^n}\psi * (\frac{\tau - t}{s})X(\tau)d\tau \tag{5}$$

where: τ- translation parameter, s- scale (or dilation) parameter and $\psi(t)$ is called the mother wavelet, [11].

Table 1: Example results of the transformation of PDF to spectrogram image using CWT

Image Type	Original images	PDF images	CWT images
HGG			
			
LGG			
			
Normal (No Tumor)			

The 2D-CWT transform may be applied to a whole image without the requirement for single-pixel linearization for regions of interest. Another advantage is that regions of interest do not need to be identified in advance.

For another, it considers the connection between pixels and the detection of changes in pixels, which can lower the detection error rate. The CWT is used in the various images. Also extracted are the changing features in high-frequency zones. As previously mentioned, the (227 × 227) images are then produced by recreating each layer's high-frequency and low-frequency sub-bands. Finally, the final change detection result is achieved, and it is used as input to CNN for classification.

3.4 Classification using CNN

Using the classification approaches, brain MRI images are classified into (1-HGG or 2-LGG) cases. The network used in this paper is the standard CNN, standard CNNs often include convolutional, max-pooling layers and limited number of fully-connected layers, besides input and output layers.

CNN model involves three convolutional with size 3×3 filters of all convolutional with the support of 3 channel tensors and Rectified Linear Unit (ReLU) is used as an activation function. Following each of these convolution layers is max-pooling, with a pool size of (2, 2), as shown in Figure 7.

After the pooling layer, fully connected layers were used as a dense layer. In this layer, we utilized the softmax function as an activation function where the total number of nodes are two. Table 2, shows the proposed CNN architecture model.

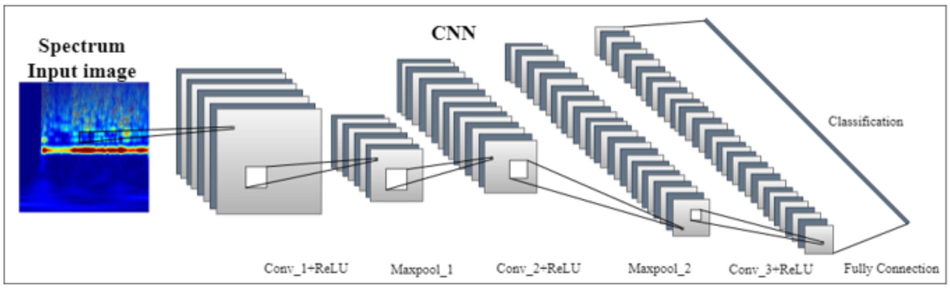
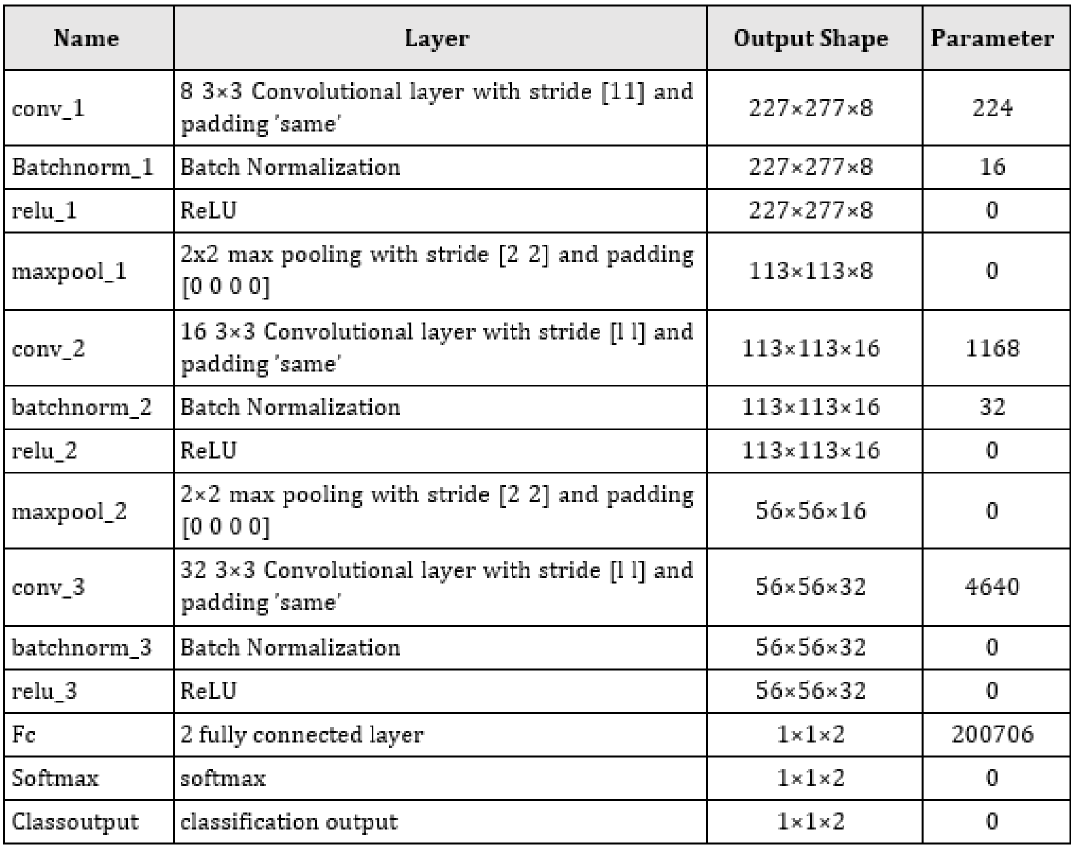


Figure 7: CNN Architecture

Table 2: CNN Architecture



Name	Layer	Output Shape	Parameter
conv_1	8 3×3 Convolutional layer with stride [11] and padding 'same'	227×277×8	224
Batchnorm_1	Batch Normalization	227×277×8	16
relu_1	ReLU	227×277×8	0
maxpool_1	2x2 max pooling with stride [2 2] and padding [0 0 0 0]	113×113×8	0
conv_2	16 3×3 Convolutional layer with stride [l l] and padding 'same'	113×113×16	1168
batchnorm_2	Batch Normalization	113×113×16	32
relu_2	ReLU	113×113×16	0
maxpool_2	2×2 max pooling with stride [2 2] and padding [0 0 0 0]	56×56×16	0
conv_3	32 3×3 Convolutional layer with stride [l l] and padding 'same'	56×56×32	4640
batchnorm_3	Batch Normalization	56×56×32	0
relu_3	ReLU	56×56×32	0
Fc	2 fully connected layer	1×1×2	200706
Softmax	softmax	1×1×2	0
Classoutput	classification output	1×1×2	0

4 Results and discussion

In this section, the performance of our suggested approach has been evaluated based upon the segmenting of tumors on the MRI images. The suggested approach was compared to other methods' accuracy and F1-score. In the present study, a set of images from 152 Patients was utilized and those images are divided to 2 groups (1-HGG) and (2-LGG). These images are separated into (25%) that were utilized for testing data, and (75%) have been employed for the training.

For training, Training options include minibatch size = 16 images per iteration, maxepochs = 10 with step 7, and an initial learning rate= 0.001. The size of the input image is 227 × 227. Furthermore, as previously mentioned, we augmented the training set.

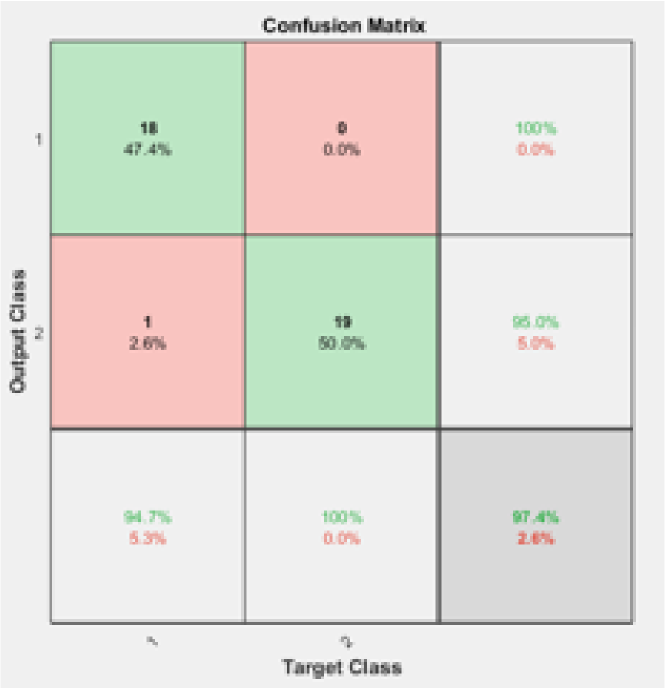
Figure 8, illustrates confusion matrix for suggested method, consisting of TP, FP, TN, and FN. From confusion matrix, performance evaluation accuracy, precision, F-score, and recall are calculated:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{6}$$

$$Precision = \frac{TP}{TP + FP} \tag{7}$$

$$Recall = \frac{TP}{TP + FN} \tag{8}$$

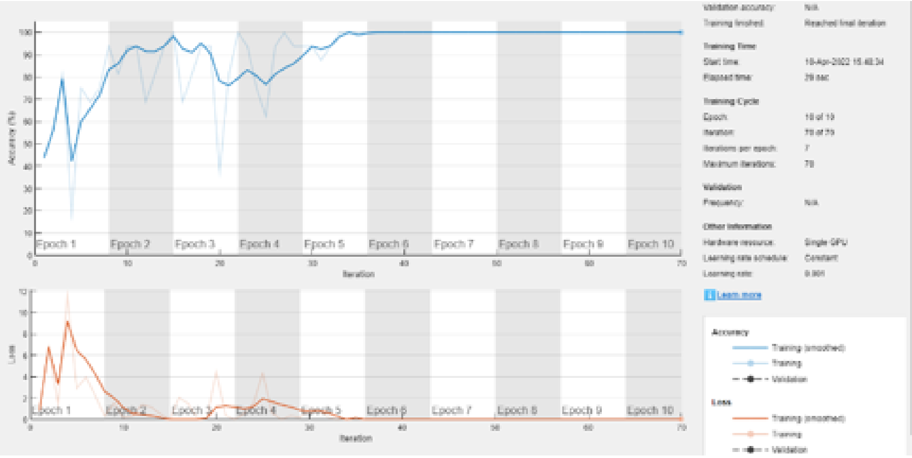
$$F1 - score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \tag{9}$$



18 47.4%	0 0.0%	100% 0.0%
1 2.6%	19 50.0%	95.0% 5.0%
94.7% 5.3%	100% 0.0%	97.4% 2.6%

Figure 8: The proposed method confusion matrix

The proposed method's accuracy rate in this paper is 97.37%, the precision of 97.5%, recall of 97.36%, and F1-score of 97.43%. The performance analysis up to epoch 10 and the loss rate is shown in Figure 9.



Validation accuracy: N/A
Training finished: Reached final iteration

Training Time
Start time: 18-Apr-2022 15:48:34
Elapsed time: 29 sec

Training Cycle
Epoch: 10 of 10
Iteration: 70 of 70
Iterations per epoch: 7
Maximum iterations: 70

Validation
Frequency: N/A

Other Information
Hardware resource: Single GPU
Learning rate schedule: Constant
Learning rate: 0.001

Figure 9: Analysis of accuracy and loss rate of our method

Table 3, shows a comparison with state-of-the-art approaches. On the BraTS dataset, we compare the result of our method with state-of-the-art approaches to confirm its efficacy and resilience. The findings show that our method framework performs better with state-of-the-art approaches. Our method has the greatest average accuracy of 97.37% among the many approaches.

Table 3: methods comparison

Methodology	Accuracy (%)	F1-score (%)
Akila Gurunathan et al [7]	95.3	95.6
Gokay Karayegen et al [1]	95.7	93.0
V.V.S. Sasank, et al [16]	95.56	96.875
Proposed Method	**97.3684**	**97.4342**

The benefits of our proposed method are that the proposed model not just to uses low contrast MRI images to segment the whole brain tumor, but it may also save the lives of patients. This model uses CWT and PDF features for tumor detection as a wavelet feature that doesn't take time to perform.

5 Conclusion

In this paper, CNNs are proposed to determine whether the tumor is HGG or LGG with feature extraction in the form of spectrogram wavelet features. A morphological segmentation procedure, which involves opening followed by dilation of the tumor brain images, is also used to identify the affected pixels. Then, the features are extracted by PDF, which focuses on the increasing intensity of the pixels, and then converted into a spectrogram using CWT which is considered a Simple way to extract features. This method improves performance. The MRI images have been obtained from the BraTS2019 dataset. The efficiency of this approach has been analyzed concerning F1-score, recall, precision, and accuracy. The suggested segmentation of brain tumors achieved 97.36% of the average rate of classification accuracy, with 97.43% F1-score, 97.37% recall, and 97.5% precision. In addition, the findings show that the proposed method outperforms the competition. We find that our method produced higher accuracy with a lower error rate. Our method has diagnostic significance in brain tumor diagnosis for patients.

For future work, we can increase the number of the dataset and extended it to many classes about brain tumors like glioma, meningioma, and pituitary, and also detect abnormalities in the brain.

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