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Utilizing Deeplabv3+ architecture for precise and automated segmentation of brain tumors in MRI imaging

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ABSTRACT

Magnetic resonance imaging (MRI) plays a critical role in brain tumor diagnosis. However, manual segmentation takes too much time, is subjective, and may lead to inconsistencies in interpretation among different observers. An automatic framework for brain tumor segmentation (BraTS) based on image preprocessing and a semantic segmentation network named DeepLabv3+ is proposed in this paper. First, MRI images are converted into a specific fixed size, after which high-pass filtering is used to emphasize the borders of the tumors and contrast-limited adaptive histogram equalization (CLAHE) is employed to enhance the local contrast. Then, the obtained preprocessed images are fed into the DeepLabv3+ model that implements multi-scale feature extraction and atrous convolution to precisely delineate the boundaries of complicated tumor areas. The proposed model is evaluated on the BraTS 2020 dataset. Results of the experiment prove the efficiency of the proposed framework, as its accuracy reached 99.79%, sensitivity 99.19%, specificity 99.78%, and precision 99.02%. Using the DeepLabv3+ architecture along with image preprocessing, the use of deep learning in the model becomes possible.

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1. INTRODUCTION

A brain tumor can be described as an abnormality in the formation of cells taking place in the brain. Some of the factors which might increase the possibility of getting a brain tumor include exposure to radiation and the presence of a brain tumor in the family [1]. Although there have been many efforts in the area of research on brain tumor segmentation (BraTS), it is still not satisfactory in terms of diagnosing the patients [2]. Meningiomas, gliomas, and glioblastomas are the common types of tumors found in adults [3]. The most frequent way of treating brain tumors is surgery; nevertheless, radiation therapy and chemotherapy are some of the other methods that can be adopted to stop the growth of the tumor [4]. In order to visualize different areas of the brain, multiple slices of the magnetic resonance imaging (MRI) must be taken. An expert radiologist will conduct an extensive analysis of the scanned images of the patient's body, after which

they will separate all the problematic areas. It is the job of the radiologist to manually segment the images, which is not only tedious but also very variable both inter-rater and intra-rater [5].

In addition, manual segmentation is a time-consuming process. Consequently, qualitative assessment or visual inspection is the sole method that may be used for manual segmentation [6]. Through quantitative analysis of the cells that are affected, it is possible to get information on the progression of the sickness, its features, and the effects it has on the particular anatomical structure. Additionally, in order to effectively segment lesions, it is required to take into account a wide variety of imaging modalities, each of which illustrates a distinct contrast [7]. By using neural networks, deep learning models, on the other hand, are able to learn and identify traits on their own without any training or instruction [8]. When it comes to integrating the whole detection process in an automated way, this is the ultimate goal [9]. As a consequence of its ability to analyze huge volumes of sophisticated data, such as medical imaging, in an efficient way and consistently discover patterns that are symptomatic of diseases, deep learning networks have gained a great deal of popularity in the area of medical diagnostics [10].

Among all medical imaging modalities, MRI is considered to be of great importance in the detection and treatment of brain tumors. An enhanced convolutional neural network (CNN) has been proposed by Ranjbarzadeh *et al*. [11] for achieving the objective of creating an automatic and robust segmentation of brain tumors with the help of four brain tumor images. The improved chimp optimization algorithm (IChOA) is employed for the tuning of weight and bias parameters of the CNN model. In the first step, all four images have been normalized to identify the location of the brain tumor that already exists. Afterward, each object that exists in the binary image and extract 17 features from it [11].

Optimized spiking neural systems aimed at enhancing the threshold segmentation of brain tumor images have been described by Dong *et al.* [12]. A threshold segmentation technique for brain tumor images using the optimized numerical spiking neural systems along with adaptable multi-mutation operators (ONSNPSamos) has been suggested. To be more precise, an ONSNPSamo system using a multi-mutation approach is illustrated to make a balance between exploration and exploitation abilities [12]. Asl *et al.* [13] suggested a novel approach for the automatic segmentation of brain tumors that makes use of hybrid filters and makes use of three-dimensional medical images. In order to do semantic segmentation, the UNet model is used. This guarantees that there are no tumor spots that have been missed for detection, and it also assures that the images of the tumor volume are provided in two dimensions [13].

The proposed advanced fusion of Transformer and UNet is presented by Zhang *et al.* [14] propose the idea of reevaluating the core components of the architecture, that include the encoder, the bottleneck, and some of the skip connections. First of all, the traditional CNN module inside the encoder should be replaced by CNN-transformer module that allows extracting deep spatial relationships of the input images. Such a layer helps to highlight semantic elements extracted from the encoder route output [14]. Alwadee *et al.* [15] proposed the lightweight 3D attention UNet with parallel convolutions (LATUP-Net). In this study, the use of a deep learning model for image segmentation is presented based on DeepLabV3+.

In this work, employ a specialized filter to enhance the visibility of tumors within the images, facilitating easier identification. Secondly, use contrast-limited adaptive histogram equalization (CLAHE) in order to increase the clarity of images, especially in problematic places. By using the opportunities provided by the DeepLabv3+ neural network, the problem of tumor localization can be given to this artificial intelligence computer network. DeepLabv3+ has already proven its ability to find tumors in many cases because of being fed with lots of different examples. This method has been tested extensively on a variety of brain MRIs and has produced good results. The following are the main contributions of the suggested method:

i) The primary goal of the presented approach is to use the benefits of the DeepLabv3+ neural network in order to increase the precision of BraTS in MRI images. Using the abilities of semantic segmentation of DeepLabv3+, it will be possible to detect tumors with greater accuracy.
ii) Using DeepLabv3+ in the BraTS process will allow creating an efficient and effective automated system, which can perform identification of tumors without any manual interventions.
iii) Testing the capabilities of DeepLabv3+ on various MRI images will help to show the versatility of the approach and its usefulness in practice.

The paper is structured as follows: section 2 gives the research methodology for deep learning with emphasis on brain tumor classification. In section 3, numerical results are presented, along with a discussion of the performance achieved by the investigated deep learning algorithms. Finally, section 4 serves as the conclusion of the paper.

2. PROPOSED METHOD

During the training phase, the images from the training database go through several pre-processing stages to make them of higher quality and uniformity. Such pre-processing includes the resizing of the

images, application of the edge-sharpening technique, and CLAHE to improve the image contrast. Such processed images, together with the resized masks, are then processed through a chain of other pre-processing stages or initial models' predictions before the training of the DeepLabV3+ model. It is important because it allows training the model on high-quality data and, thus, obtaining accurate segmentation results. In the testing phase, the images from the testing database are pre-processed in the same way as in the training phase. Such pre-processed images are then tested by means of the trained DeepLabV3+ model. Figure 1 shows the workflow for the proposed model. It is divided into two main parts: the training process and the testing process.

In the training process, images and their corresponding masks from the training database undergo several steps. The images are rescaled, sharpened along edges, and enhanced by CLAHE. The preprocessed images are then subjected to the cascade and input to the DeepLabV3+ network. On the other hand, the masks are rescaled and preprocessed just like the images to make sure that they fit well with the preprocessed images. The testing stage uses the remaining 30% of the dataset from the testing database. The same preprocessing is conducted on the testing images as is done to the training images for consistency. The preprocessed images are fed into the trained DeepLabV3+ network, and segmented images are generated. The segmented images are then analyzed using performance metrics.

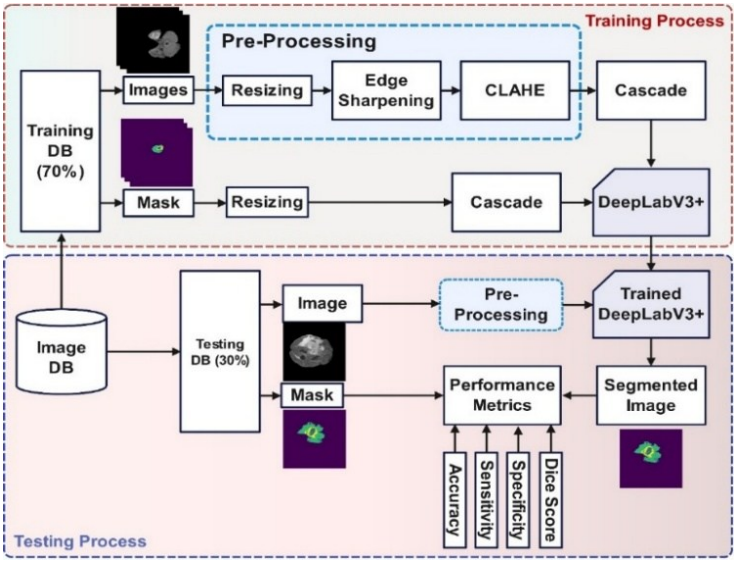

Figure 1. Block diagram of proposed method

2.1. Image preprocessing

MRI image processing for the detection and segmentation of brain tumors plays an important role in the proper diagnosis and treatment of the disease [16]–[18]. Preprocessing of MRI images is a technique that assists in improving image quality. It reduces artifacts and increases contrast for proper segmentation of the tumor.

2.2. Edge sharpening

A high-pass filter is the name of an image processing filter. It sharpens the edges in an image by amplifying the higher frequency content and suppressing the lower frequency content in the image [19], [20]. The high-pass filtering operation used for edge sharpening is mathematically expressed in (1).

$$H(s) = \frac{s}{s+\omega_c} \quad (1)$$

2.3. Contrast-limited adaptive histogram equalization

This is an image processing method aimed at enhancing the contrast of images [21], especially images with non-uniform illumination [22]–[24]. CLAHE achieves this by mapping the histogram of the image to another histogram in which the intensities are spread throughout the range. The method achieves this by placing limits on the amount of contrast enhancement in each area. This ensures that no over-amplification of noise occurs without enhancing the contrast [25]. The CLAHE procedure is described by the transformations in (2) to (4), which define the histogram-based contrast enhancement process.

$$x = [x_{max} - x_{min}] * p(f) + x_{min} \quad (2)$$

$$x = x_{min} - \frac{1}{a} * \ln[1 - p(f)] \quad (3)$$

$$cdf = p\left(f\left(\frac{x}{b}\right)\right) = \int_0^x \frac{x}{b^2} e^{\frac{-x^2}{2b^2}} \quad (4)$$

2.2. DeepLab V3+

DeepLab v3+ is an innovative encoder-decoder architecture that uses DeepLab v3 as the encoder part [26]–[28]. Arous spatial pyramid pooling (ASPP), which is capable of extracting features at different levels and with varying resolutions, is adopted by the DeepLabV3+ network to solve the issue of information loss caused by the pooling operations [29], [30]. This proposed segmentation framework is based on the DeepLabv3+ architecture, using a residual network (ResNet)-50 backbone as the encoder. The DeepLabv3+ formulation and its associated feature-processing operations are summarized in (5) and (6).

$$y[i] = \sum_{k=1}^{K} x[i + r \cdot k] w[k] \quad (5)$$

$$\mathrm{L} = \alpha \cdot \mathrm{L_{CE}} + \beta \cdot \mathrm{L_{Dice}} \quad (6)$$

The weighting parameters α and β were empirically set to 0.5 to balance region-based and boundary-based learning. Table 1 outlines the training hyperparameters used in the experiment. The proposed method for tumor segmentation follows a structured algorithm, detailed as Algorithm 1.

Algorithm 1. Algorithm of proposed method

Input: Images (Ik)
Mask (Mk)
Output: Segmented tumor
For k=0 to N
Read images I_k, M_k,
I_R = resize (I_k)
I_E = hispass filter (I_R)
$I_C = CLAHE(I_E)$
$Deeplabv3+ = Initialize(Training\ parameter)$
$Deeplabv3+ = Train(Deeplabv3, I_E, M_R)$
EndFor
For k=0 to N
Read Testing Images IT_k, T_k
$S_k = Test(Deeplabv3+, IT_k)$
Read testing images I
Segmented image = Test($Deeplabv3+$, I)

Table 1. Training hyperparameters

Hyperparameters	Value
Number of epochs	50
Learning rate	0.0010
Momentum	0.9
Batch size	16
Optimizer	Stochastic gradient descent with momentum
Weight decay	0.0005

3. RESULTS AND DISCUSSIONS

These experiments were conducted using a computer that is running Windows OS, which consists of an Intel(R) Xeon(R) Silver 4214 processor, 2.20 GHz and 256 GB RAM, as well as an NVIDIA Tesla T4 GPU. The development of the proposed architecture has been carried out in the Python programming language. Training and testing have been done using Google Colab.

3.1. Dataset

In this regard, the BraTS 2020 test dataset has 166 samples, whereas the training dataset contains 369 samples. The only difference between these datasets is the number of samples present in each one of them. The distribution of MRI tumor classes can be seen in Table 2. The number of samples present with

Meningioma tumors is 306, whereas 300 samples have Pituitary tumors, 300 have Gliomas, and 405 have no tumors. In order to provide reliable tuning of hyperparameters and unbiased evaluation of the model's performance, the dataset was split into three parts: 70%, 10%, and 20%.

Table 2. Description of dataset

Characteristics	BraTS 2020
Labels	3
No of testing images	166
No of training images	369
Volume	240 × 240 × 155

3.2. Performance metrics

The proposed method shows great performance on all used datasets. Quantitative results demonstrate high overlap accuracy [31]–[33], which is expressed by the high Dice similarity coefficient (DSC) [34] and intersection over union (IoU) [35], [36] values. The results of low boundary-based metrics indicate accurate target region localization without over-segmentation. The evaluation metrics used to quantify segmentation performance are defined in (7) to (12), including the measures used to assess classification accuracy and overlap between predicted and reference tumor regions.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{7}$$

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

$$Specificity = \frac{TN}{TN + FP} \tag{9}$$

$$Precision = \frac{TP}{TP+ FP} \tag{10}$$

$$DSC = 2\frac{|A \cap B|}{|A|+|B|} \tag{11}$$

$$IoU = \frac{|A \cap B|}{|A \cup B|} \tag{12}$$

Figure 2 shows the sample segmented image. Table 3 presents the performance metrics based on various training and testing ratios. When using a 40/60 training/testing split, the metrics achieved were 55.13% accuracy, 56.79% sensitivity, 53.02% specificity, 56.97% precision, a DSC of 0.35, and an IoU of 0.46. Further improvements were observed with a 70/30 split, achieving 85.16% accuracy, 81.02% sensitivity, 86.39% specificity, 88.94% precision, a DSC of 0.72, and an IoU of 0.82. The highest performance was recorded with an 80/20 split, showing 99.79% accuracy, 99.19% sensitivity, 99.78% specificity, 99.02% precision, a DSC of 0.96, and an IoU of 0.97. Figure 3 illustrates the gradient-weighted class activation mapping (Grad-CAM) visualizations of the proposed model for representative brain MRI samples.

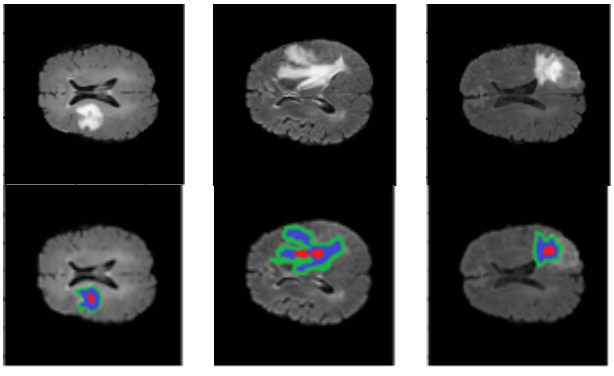

Figure 2. Sample segmented image

Table 3. Performance based on the training and testing ratio

Training / testing	Accuracy	Specificity	Precision	Sensitivity	DSC	IoU
40/60	55.13	53.02	56.97	56.79	0.35	0.46
50/50	62.31	61.60	63.41	63.46	0.51	0.53
60/40	75.69	76.19	78.96	79.64	0.64	0.68
70/30	85.16	86.39	88.94	81.02	0.72	0.82
80/20	99.79	99.78	99.02	99.19	0.96	0.97

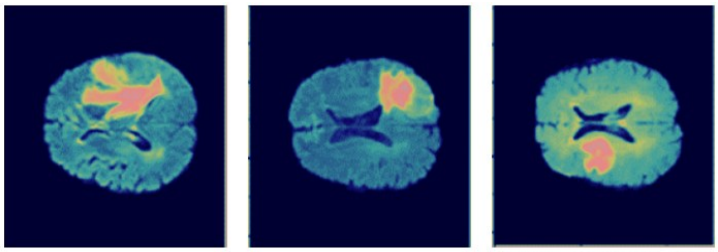

Figure 3. Grad-CAM visualization of the proposed model on representative brain MRI images

Table 4 shows the comparison of the performance of the proposed method with some other methods. As shown from the above results, it is clear that the model has achieved the highest accuracy rate of 99.79% with a sensitivity of 99.19% and a specificity of 99.78%. All these rates are higher compared to UNet, packet bytes-based convolutional neural network (PBCNN), adaptive layer cascaded residual network (ALCResNet), and DeeplabV3+. Figure 4 shows the accuracy and validation accuracy of the proposed method in 50 epochs.

Table 4. Comparative performance with existing methods

Methods	Accuracy	Sensitivity	Specificity
UNet [17]	98.70	98.70	99.50
PBCNN [16]	98.63	85.19	99.01
ALCResNet [18]	99.64	99.07	99.49
DeeplabV3+ [26]	94.36	92.25	93.26
This work	99.79	99.19	99.78

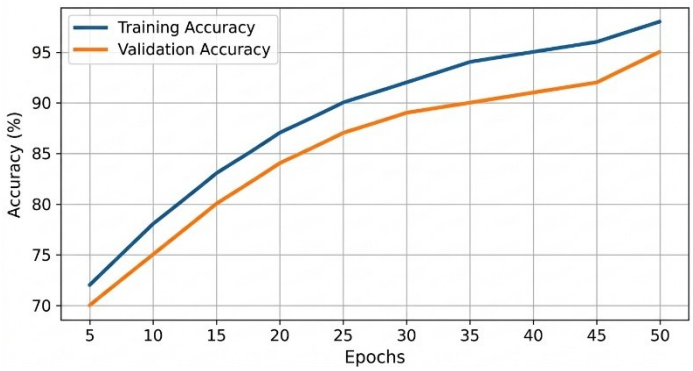

Figure 4. Training accuracy DeeplabV3+

Table 5 shows the per-fold performance results. The proposed model demonstrates consistent performance across five folds, achieving an average accuracy of 99.79%, sensitivity of 99.19%, and specificity of 99.78%, with low standard deviation indicating strong robustness. A p-value < 0.05 was considered statistically significant, indicating that the performance gains of the proposed DeepLabv3+ method are unlikely to be due to random chance.

Figure 5 presents the confusion matrix for the four segmentation classes: normal, enhancing tumor, peritumoral edema, and non-enhancing tumor core. The large diagonal counts (23,650–23,737) represent

correct class predictions, whereas the smaller off-diagonal counts (421–473) indicate misclassifications between classes. This pattern indicates that most evaluated pixels were assigned to their corresponding classes, although some confusion remains between tumor regions.

Table 5. Per-fold performance results

Fold	Accuracy (%)	Sensitivity (%)	Specificity (%)
1	99.75	99.10	99.74
2	99.82	99.18	99.80
3	99.78	99.15	99.76
4	99.81	99.22	99.82
5	99.79	99.30	99.78
Mean ± Std	99.79 ± 0.03	99.19 ± 0.07	99.78 0.03

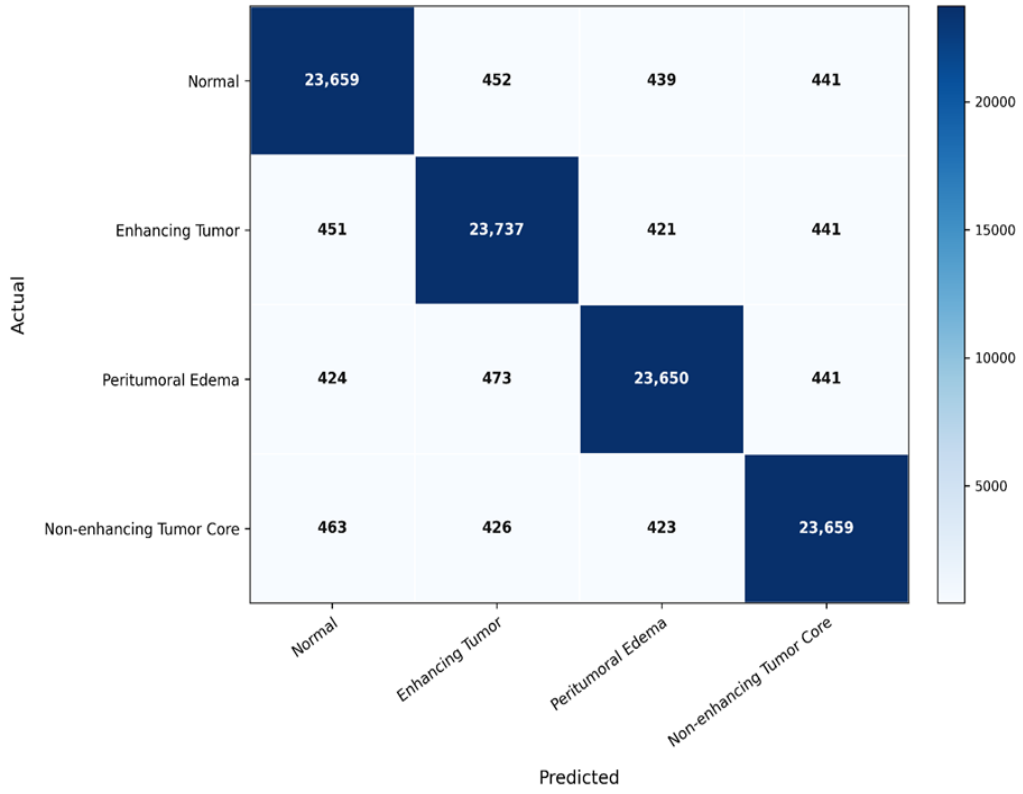

Figure 5. Confusion matrix for BraTS

4. CONCLUSION

This study demonstrates a highly efficient BraTS technique using state-of-the-art image preprocessing methods along with the DeepLab v3+ model. The DeepLab v3+ model has been shown to perform efficiently in this segmentation task due to its ability to capture multi-scale contextual information and improve the segmentation boundary. The combination of image preprocessing with DeepLab v3+ makes an efficient segmentation pipeline to effectively distinguish between brain tumors in MRI images. This method can prove to be very useful to enhance the accuracy of detection and segmentation of brain tumors, which will further assist in diagnostic and treatment purposes. This study has achieved 99.79% accuracy, 99.19% sensitivity, 99.78% specificity, and 99.02% precision. Further research may include optimizing the preprocessing parameters and experimenting with other models.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data supporting the findings of this study are available from the BraTS 2020 dataset, which was used for BraTS and evaluation.

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