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A Novel Activation Function for Brain Tumor Segmentation using V-NET Approach

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Abstract. This work emphasizes on automatic brain tumor segmentation from three dimensional magnetic resonance imaging (3D-MRI) scan images. We have used fully convolutional neural networks (FCNN) for extracting whole tumor. The proposed architecture is based on V-Net architecture. We have developed a new activation function for training the network. ReLU is used and in experiment 2, proposed activation function is used. We have conducted two experiments for brain tumor segmentation by varying the activation functions. In experiment 1, we have also used dice loss as loss function. The proposed method is trained and tested using BraTs 2021 training dataset which contains 2000 volumes of 3D-MRI scans. The proposed method's performance is closer to the manually segmented images by experienced neurologists available with BraTs 2021 datasets. We have obtained a mean dice score of whole tumor as 99% while using proposed activation function which is higher when compared to the existing methods. We conclude that our novel activation function proposed activation function produced enhanced accuracy and dice score when compared with ReLU activation function.

Keywords: Brain Tumor Segmentation, V-Net, Magnetic Resonance Imaging (MRI), Fully Convolutional Neural Networks (FCNN), Complete Tumor, Activation Function.

1 INTRODUCTION

Brain Tumor is the assembly of atypical cells in the brain. Brain tumors can either be harmless (benign) or malicious (malignant) in nature. Benign tumors are categorized into primary brain tumor since it is located inside the brain and it is not spread to any other parts of the body, whereas secondary brain tumor will spread to other parts of the body which is life-threatening [1]. Benign tumors can be surgically extracted easily than malignant tumors. Generally, malignant brain tumors are difficult to be entirely extracted from the surrounding normal cells.

Magnetic Resonance Imaging (MRI) is one of the popular imaging modality that is used for producing medical images with highest spatial resolution and contrast between soft tissues [2]. MRI provides very detailed information about the accurate shape, size and location of brain tumors which in turn enables proper diagnosis and appropriate treatment. MRI technique produces different types of images such as T1-weighted, T2-weighted, T1c-weighted, fluid attenuated inversion recovery (FLAIR). In the proposed work, all the modalities are fused together and the brain tumor segmentation is carried out.

MRI produces very large volumes of images for a single patient and it is very crucial for the medical professionals to annotate them manually and segment these images in a short time. So, the automatic segmentation process had gained its importance [3]. The process of segmenting abnormal cells such as complete, core and enhancing tumor from normal brain tissues such as grey matter (GM), white matter (WM) and cerebrospinal fluid (CSF) is called as brain tumor segmentation. The combination of enhancing, non-enhancing and edema are referred as complete tumor. The current brain tumor segmentation methods have not reached accurate results yet. In the proposed method, we have used V-Net for brain tumor segmentation. V in V-Net model refers to size of the input (volumetric input). For our research problem, we need volumetric input to tune the architecture for our dataset. So we chose V-Net architecture. We have used the existing V-Net architecture for our proposed work and the novelty of the article exists in developing a new activation function for model training.

There are many activation functions that are available for training neural networks. One of the popular activation functions for computer vision that is developed to train images to a neural network is ReLU. ReLU zeroes out all the negative values. It is acceptable for general images classification or segmentation. In case of medical image processing, minute details should be learnt by the neural networks. The proposed activation function learns the very negative values which preserves the minute details of the medical images. So we developed this proposed activation function for medical images. The proposed activation function eliminates vanishing gradient problem that is suffered by existing activation functions and it performs well in case of deeper neural networks when compared to the existing ones.

The rest of the article is organized as follows. In section 2, we have provided a detailed overview on the current segmentation methods using deep learning techniques for brain tumor segmentation. The materials and metrics used for the proposed work are explained in Section 3. The methodology of

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the proposed work is briefed in section 4. The results and discussion of the proposed work is given in section 5. Finally conclusion and future scope for brain tumor segmentation methods are described in section 6.

2 RELATED WORKS

Some of the brain tumor segmentation methods done on BraTs dataset using deep learning techniques are discussed below. Nema et.al [4] had developed a RescueNet based on generative adversarial networks. The advantage of their method is unpaired approach for reducing the time complexity. The value of dice score is low when compared to the existing methods. Mlynarski et.al [5] had developed a U-Net architecture with mixed supervision. They have trained the model both for brain tumor classification and segmentation which is different from traditional supervised learning. They have not used larger dataset for their experiments.

Wang et.al [6] had developed a multimodal brain tumor segmentation using PP-NET. Wide residual networks perform better in extracting features. Chen et.al [7] had developed dual force convolutional neural networks for enhancing the quality of hierarchical features and the time complexity is high. Sajid et.al [8] had developed a patch-based hybrid convolutional neural network. They had used a two path CNN and dropout to avoid overfitting. The major disadvantage of two path CNN is it requires more time for training process. Zhao et.al [9] had integrated the CNN and conditional random fields to ensure the spatal properties of segmentation results. Their method works for T2, T1c and FLAIR modalities. It didn't produce better results for T1 imaging modality.

Hussain et.al [10] had developed a patch based deep convolutional neural networks to overcome the problem of overfitting using dropout regularizer. The disadvantage of their method is only two co-centric patches are extracted from each slice. Pereira et.al [11] had developed a convolutional neural network with small 3 x 3 filters. They have used small kernels for deep architecture. Data preprocessing such as normalization of intensities and augmentation is used. It produced low dice score for enhancing tumor.

Havaei et.al [12] had developed a simultaneous local and global processing using cascaded two pathway CNN. Cascaded architecture is used for accurately modeling the local label dependencies. They have used GPU to enhance the speed of training time. Dvorak and Menze [13] had combined the convolutional neural networks and k-means algorithm for segmenting brain tumor. This work is based on correlating the pixels of different imaging modalities in 3D.

Davy et.al [14] had developed a double pathway CNN for extracting both the local and global features simultaneously. Urban et.al [15] had developed a 3D CNN for segmenting brain tumor. Zikie et.al [16] had developed patch based CNN architecture for brain tumor segmentation. They had used multichannel intensity information for patches extraction. The main disadvantage of their method is that their method is employed only for high grade gliomas.

3 MATERIALS AND METRICS

The experiment is carried out in 64-bit i5 processor with 8 giga bytes of RAM. We have used BraTS2021 dataset which consists of 2000 volumes of training images. A single volume is comprised of T1, T2, T1c, and FLAIR modalities. The MRI volumes were manually segmented and experienced neurologists approved the interpretations of segmented tumor regions. We took only 100 volumes from BraTs 2021 dataset for our experiments. Among them, 75 volumes were used for training and 25 volumes were used for prediction. We have implemented our experiment using python. We have used keras and TensorFlow libraries that are available in python for carrying out our experiments. The following are the metrics used in our experiments.

$$\text{Accuracy} = \frac{True\ Positives + True\ Negatives}{True\ Positives + True\ Negatives + False\ Positives + False\ Negatives} \quad (1)$$

$$\text{Dice Coefficient} = \frac{2 * Precision * Recall}{Precision + Recall} \quad (2)$$

True Positives denotes the number of tumor images identified precisely. True Negatives denotes the number of normal images detected precisely. False Positives denotes the number of tumor images erroneously identified. False Negatives denotes the number of normal images erroneously identified.

4 METHODOLOGY

Workflow of Proposed Segmentation Method

The algorithm for the proposed work is given below.

Algorithm for proposed work

Input : Volumes of MRI Brain Scans

Output : Segmented brain tumor region

Step 1: Load the Training volumes.

Step 2: Slicing the images by taking 90 central slices (30-120) and rest of the slices are eliminated.

Step 3: Images are cropped to eliminate the background.

Step 4: Creation of V-Net model with proposed activation function and Dice Coefficient loss function.

Step 5: Model training.

Step 6: Plot the accuracy and loss graph for training and validation data.

Step 7: Save model to the disk.

Step 8: Load the model from disk.

Step 9: Model Prediction and Evaluation.

The workflow of proposed segmentation method is represented in Figure 1.

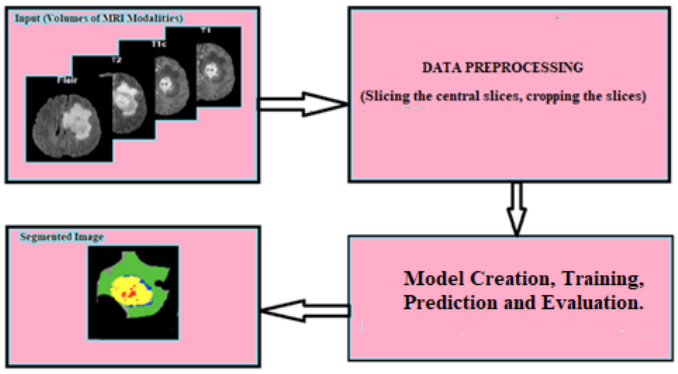

Figure 1. Workflow of Proposed Segmentation Method

Data Preprocessing

We have performed two data preprocessing techniques in the training data. Each volume in BraTs 2021 dataset is comprised of 155 slices. The dimension of each slice is 256 x 256. Initial and final slices will be generally blank and it won't contain any valuable information. The central slices contain more important details. The training images are sliced by taking the central slices (30 to 120) and rest of the slices are eliminated. After slicing the images, they are cropped to eliminate the background.

Model Creation

The proposed brain tumor segmentation is based on V-Net architecture. The architecture of the proposed model is shown in Figure 2. The leftmost part of the V-Net model is classified into different stages which operate in various resolutions. At each stage, the network learns a residual function. In each stage, the input is processed with non-linearity function in the convolutional layers and are added to the last convolutional layer's output and makes it to learn the residual function. V-Net architecture guarantees convergence when compared with U-Net architecture, which is a non residual learning. The convolutions in every level use volumetric kernels with the size of 5x5x5 voxels. In the contracting path, there is reduced resolution by convolution with 2x2x2 voxels wide kernels with stride 2. The feature map's size is halved as done by pooling layers and there is doubling of feature channels at each stage of V-Net's contracting path. Here, the pooling operations are replaced by convolutional operations since it consists of smaller memory consumption during training process. Down sampling increases the receptive field. ReLU and proposed activation function are used as the non linearity activation function. In the right side of the V-Net architecture, the features are extracted by the network. The spatial support of the feature maps with lower resolution is expanded to interpret the important information to produce a volumetric segmentation output. A deconvolution operation is performed in each stage to expand the input size which is followed by three convolutional layers by involving 5x5x5 kernels that were employed in previous layer. As in the left part of the V-Net architecture, the residual function is learnt in the right part also. The last convolutional layer computes two feature maps with 1x1x1 kernels. The outputs are provided as the same size of the input. These probabilistic segmentations are done by applying softmax function. The location information gets lost in the left contraction path. The features that are extracted from early stages of the left part are forwarded to the right part through horizontal connections. These connections improve the model's time of convergence. The architecture of V-Net is shown in Figure 2.

For experiment 1, ReLU activation function is used in V-Net and the model is trained. For experiment 2, proposed activation function is used in the same architecture and their results are compared.

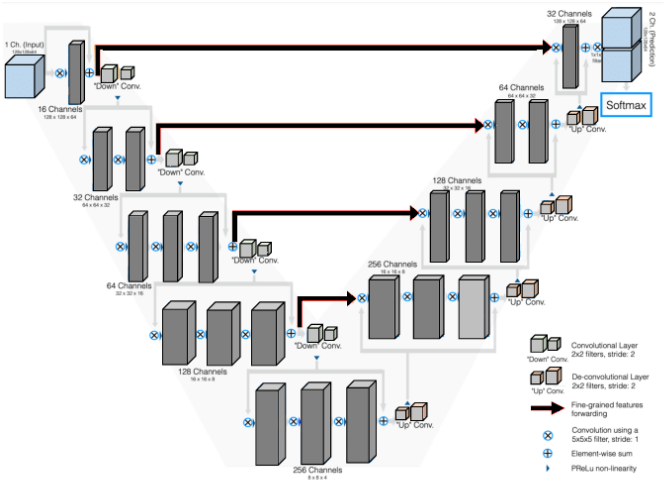

Figure 2. V-Net Architecture for `Proposed Segmentation Method

Model Training

The model is trained with 75 volumes of training images taken from BraTs 2021 dataset. The activation function used in our model is a novel activation function which was developed for deeper networks. The plot of proposed activation function and its derivative is shown in Figure 3 and Figure 4 respectively

$$\boldsymbol{F}(\boldsymbol{x}) = = \propto * \boldsymbol{x} * \boldsymbol{tanh^2}(\boldsymbol{x}) \quad (\mathbf{3})$$

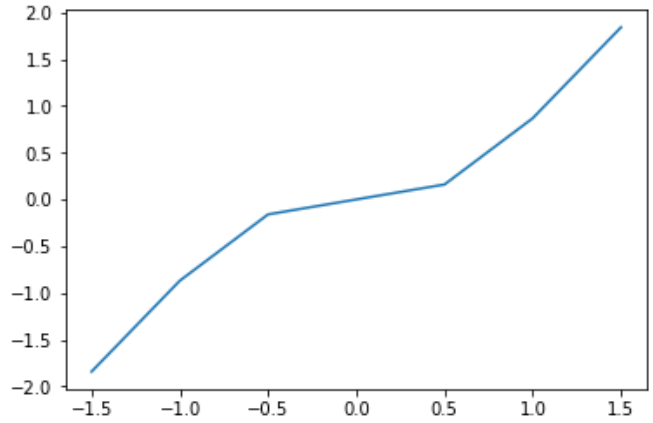

Figure 3. Plot of Proposed Activation Function

The derivative of this activation function is given below.

$$\boldsymbol{F^1}(\boldsymbol{x}) = \boldsymbol{tanh}(\boldsymbol{x})[2\boldsymbol{x} * \boldsymbol{Sec^2}(\boldsymbol{x}) + \boldsymbol{tanh}(\boldsymbol{x})] \quad (\mathbf{4})$$

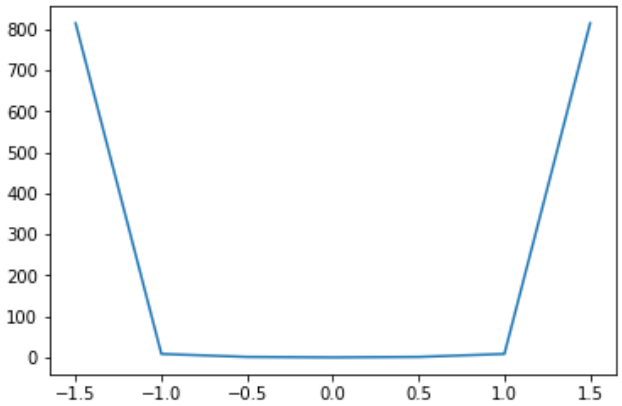

Figure 4. Plot of proposed Activation Function's Derivative

The model is trained for 30 epochs with a batch size of 8. We have used Adam as the optimizer during training process. The learning rate was set to 10^-5. The dice loss is used as the loss function in our model. The dice loss is defined as follows.

$$D = \frac{2\sum_i^N pi\ gi}{\sum_i^N pi^2 + \sum_i^N gi^2} \quad (5)$$

Where N is the voxels, pi is the predicted voxels and gi is the ground truth voxels. Finally, the trained model is saved to the disk.

Model Prediction and Evaluation

The saved model is loaded from the disk and predictions were made. We have tested 25 unseen volumes of BraTs 2021 dataset. We have evaluated our model using metrics such as accuracy, dice coefficient and dice loss.

5 RESULTS AND DISCUSSIONS

We have conducted two experiments using the same V-Net architecture. The results and discussion of two experiments is given below.

Experiment 1

We have trained the proposed segmentation model using ReLU activation function. The trained model is then evaluated with the test set (25 volumes from BraTS2021 dataset). We have evaluated the model using the dice score, accuracy and dice loss metrics for training, validation and testing datasets. The results of

experiment 1 are inferred in Table 1. The segmented brain tumor that is obtained by using ReLU activation is shown in Figure 5. The loss and accuracy of training and validation data are shown in Figure 6.

Table 1. Average segmentation results of experiment 1 obtained from proposed method.

S.NO	Dataset	Dice Loss	Dice Coefficient	Accuracy
1	Training	0.004	0.9826	0.9846
2	Validation	0.005	0.9813	0.9858
3	Testing	0.0052	0.9790	0.9812

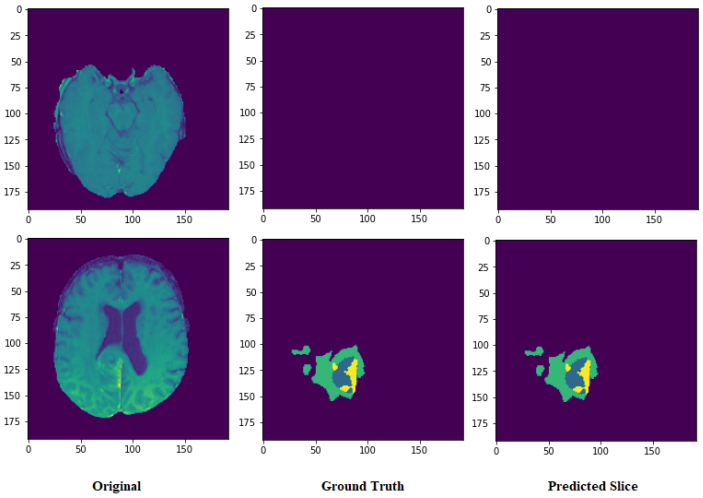

Figure 5: Segmentation Results of Experiment 1

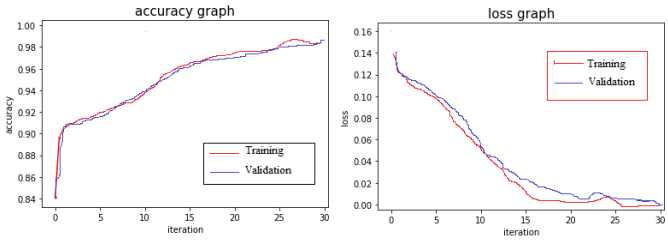

Figure 6: Accuracy and Loss Graph plotted from Experiment 1

Experiment 2

We have trained the proposed segmentation model using proposed activation function. The trained model is then evaluated with the test set (25 volumes from BraTS2021 dataset). We have evaluated the model using the dice score, accuracy and dice loss metrics for training, validation and testing datasets. The results of experiment 2 are inferred in Table 2. The segmented brain tumor that is obtained by using proposed activation is shown in Figure 7. The loss and accuracy of training and validation data are shown in Figure 8.

Table 2. Average segmentation results of experiment 2 obtained from proposed method.

S.NO	Dataset	Dice Loss	Dice Coefficient	Accuracy
1	Training	0.0035	0.9964	0.9959
2	Validation	0.0045	0.9954	0.9948
3	Testing	0.0046	0.9953	0.9947

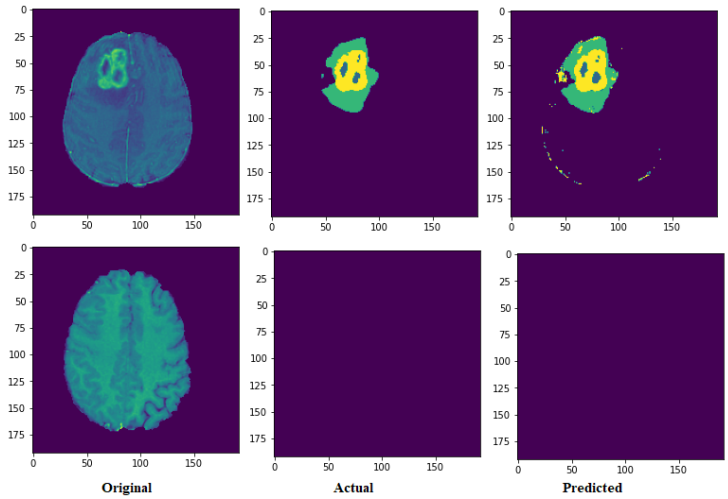

Figure 7: Segmentation Results of Experiment 2

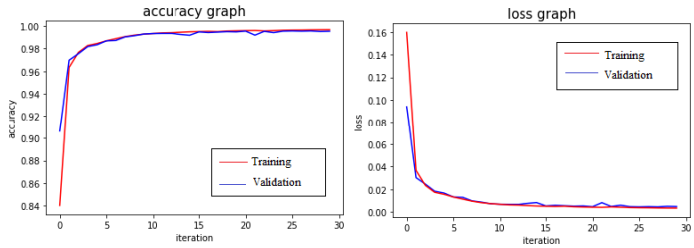

Figure 8: Accuracy and Loss Graph plotted from Experiment 2

The proposed segmentation methods are equated with the recent methods that were developed using deep learning techniques with BraTS dataset. In the proposed segmentation methods, we had obtained a highest dice score for whole tumor. The results of the comparison of dice score with other methods in literature are inferred in Table 3.

Table 2. Comparison of Existing Deep Learning Methods with Proposed Method for Brain Tumor Segmentation.

Author	Year	Method	Dataset	Dice of Whole Tumor
Nema et.al. [4]	2020	RescueNet based on generative adversarial networks	BRATS 2017	0.9463
Mlynarski et.al. [5]	2019	U-NET with mixed supervision	BRATS 2018	0.80
Wang et.al. [6]	2019	Multimodal brain tumor segmentation using PP-NET	BRATS 2018	0.94
Chen et.al.[7]	2019	Dual force convolutional neural networks	BRATS 2017	0.89
Sajid et.al. [8]	2019	Patch-based hybrid convolutional neural networks	BRATS 2013	0.86
Zhao et.al. [9]	2018	Integration of CNN and conditional random fields	BRATS 2015	0.81
Hussain et.al. [10]	2018	Patch based deep convolutional neural networks	BRATS 2015	0.86
Pereira et.al. [11]	2016	Convolutional neural networks with small 3x3 filters	BRATS 2013	0.88
Havaei et.al. [12]	2016	Simultaneous local and global processing using cascaded two pathway CNN	BRATS 2013	0.88
Dvorak and Menze [13]	2015	Combination of convolutional neural networks and k-means algorithm.	BRATS 2013	0.83
Davy et.al. [14]	2014	Double pathway convolutional neural network	BRATS 2013	0.85
Urban et.al. [15]	2014	Three dimensional convolutional neural network architecture	BRATS 2013	0.86
Zikie et.al. [16]	2014	Patch based convolutional neural network architecture	BRATS 2013	0.84
Proposed Method (Experiment 1)	2021	V-Net using ReLU activation	BRATS 2021	0.98
Proposed Method (Experiment 2)	2021	V-Net using proposed activation	BRATS 2021	**0.99**

6 CONCLUSIONS AND FUTURE ENHANCEMENTS

In the proposed method, an automatic method for brain tumor segmentation was developed based on V-Net architecture. We had performed two experiments using V-Net architecture by changing the activation functions. In experiment 1, we have used ReLU activation function in V-Net and in experiment 2, we have used proposed activation. Proposed activation gave better accuracy when compared to ReLU activation. ReLU converts all the negative values to zero whereas proposed activation function learns some negative values near to zero. The proposed method produced a significant performance in segmenting the whole tumor when compared to all the existing segmentation methods. In future, the model architecture of brain tumor segmentation will be fine tuned to produce better results in segmenting brain tumor substructures.

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