

# MRI Brain Tumors Detection by Proposed U-Net Model

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## **Abstract**

Brain tumor segmentation aims to distinguish between healthy and tumorous tissue. Early and accurate diagnosis of brain tumors increases the chances of people with this complication surviving. Manual tumor segmentation in three-dimensional Magnetic Resonance images (volume MRI) is a time-consuming and tedious task. Its accuracy depends heavily on the operator's experience doing it. The need for an accurate and fully automatic method for segmenting brain tumors and measuring tumor size is strongly felt. Attention to the construction and improvement of CAD systems to diagnose this complication can help experts in this field. In this project, using the ability of deep networks to learn and solve problems, we examined the methods of tumor segmentation in MRI images of the brain. The architecture used in this project is U-Net architecture, which consists of an Encoder and Decoder. An attempt has been made to comprehensively examine how different parameters in education affect the degree of accuracy of Network in two-dimensional version. Six different experiments with different parameters were performed on the Network, and their results were compared.

**Keywords:** BraTs 2018, U-Net network, Magnetic Resonance Images, brain tumor segmentation

## 1. Introduction

Cancer is defined as the uncontrolled and abnormal growth of a body of cells [1]. A brain tumor appears as an abnormal mass in the brain, its growth, and abnormal cell division in the brain tissue. While brain tumors are not very common, they are one of the deadliest cancers. Gliomas are a type of brain tumor made up of glial cells[2]. They are the most common type of brain tumor that brain tumor segmentation research is currently focusing on. Early detection of brain tumors plays an important role in increasing the likelihood of treatment and survival of patients. MRI images provide valuable information about brain tumors' shape, size, location, and metabolism and help diagnose them. MRI is an in vitro imaging technique that uses radio signals to stimulate target tissues to produce internal images under a strong magnetic field. Images of different MRI sequences are created by changing the stimulation and repetition times during the imaging process. These different MRI imaging techniques produce different types of tissue contrast images. They thus provide valuable information for tumor diagnosis and segmentation [3].

Before any treatment, tumor isolation is necessary to maintain the health of other tissues. Brain tumor segmentation involves identifying and isolating tumor tissues from other tissues. In standard clinical practice, this process is done manually. Because manual segmentation is a very time-consuming method, developing automated segmentation methods to provide efficient segmentation has become a research topic in recent years. The good performance of deep learning techniques in image segmentation has made them an excellent way to achieve this goal [4]. The BraTS Challenge has been held annually since 1996 and has always focused on evaluating new and advanced methods for locating brain tumors in MRI scanning images. This study selected data from the BraTS 2015 and BraTs 2018 brain tumor classification challenge to evaluate the system. In the collection of data for 2015, the training set includes 220 cases of high-grade tumors (HGG) and 54 cases of low-grade tumors (LGG). In the data set of 2018, the training set includes 210 cases of high-grade tumors (HGG) and 75 cases of low-grade (LGG). These images are presented in the dimensions of  $155 * 240 * 240$ . The zoned image related to the tumor area is also provided in proportion to each image with the same dimensions. In recent years, the use of deep networks in image processing work has led to significant improvements in results. The u-net [5] network is an architecture for fast and accurate segmentation of images, especially in the medical field. These networks are based on fully convolutional networks, and their design was created. Improvements in the structure of fully connected networks are necessary to reduce the number of images for the training process. There are several versions of u-net depending on the network input structure. Among these versions, we can mention U-Net 2D and U-Net 3D, the input image of these networks, are two-dimensional and three-dimensional, respectively. In [6], a two-dimensional version of the U-Net-based network is used. In this research, BraTS 2015 challenge data has been used. Data enhancement techniques and the Dice criterion for loss were also used, and an accuracy of 86% was reported to detect the entire tumor area. In [7], U-Net 3D with input dimensions  $128*128*128$  has been used. In addition, Dropout = 0.2 has been used. LeakyRelu is also used for activation and convolution in each layer is L2 regularization with a learning rate of 5–10. In [8], a three-dimensional version of U-Net with Batch Normalization and LeakyRelue is considered 2–10 activation. Also, the combination Loss function is the simple sum of Dice and Entropy Cross. Then post-processing is performed on the network output. Finally, %91 accuracies were reported to detect the entire area of the tumor. In [9], the three-dimensional version of the U-Net network has been used again. The difference between this research and previous research is that the input of this network has a larger dimension than the previous networks ( $160*192*128$ ). The output of this network is divided into two branches, one of which includes all three areas of the tumor. The second branch is used as a regularizer during the training process. Also, the combination of Entropy Cross Dice and KL-Divergence by weight has been used to calculate the loss. The proposed network uses L2 software for regularization. The reported accuracy for this network is 90%.

## 2. Proposed method

Due to hardware and time constraints, the proposed model for this project is based on the U-Net 2D model [10]. The input of the network is  $128*128$  images from the MRI slices, and the output is the  $128*128$  black and white images, which identifies the tumor area in the input image. Figure 1

shows the first architecture used. As can be seen in the figure, this architecture consists of two paths, Encoder, and Decoder. In the Encoder path, each step consists of two Conv layers. Then the output of these two layers will be scaled to smaller dimensions and given to the next step. In the return path and the Decoder, each step consists of two layers of Conv. The difference is in scale. In the return path, the input images of each step will first go to a larger scale and then be given to the Conv layer. Each round trip consists of 4 stages. In the proposed architecture in this section, Batch Normalization and Dropout are used after each layer of Conv. The activation of this network is Relu, and the Coefficient Dice is used to calculate the network loss.

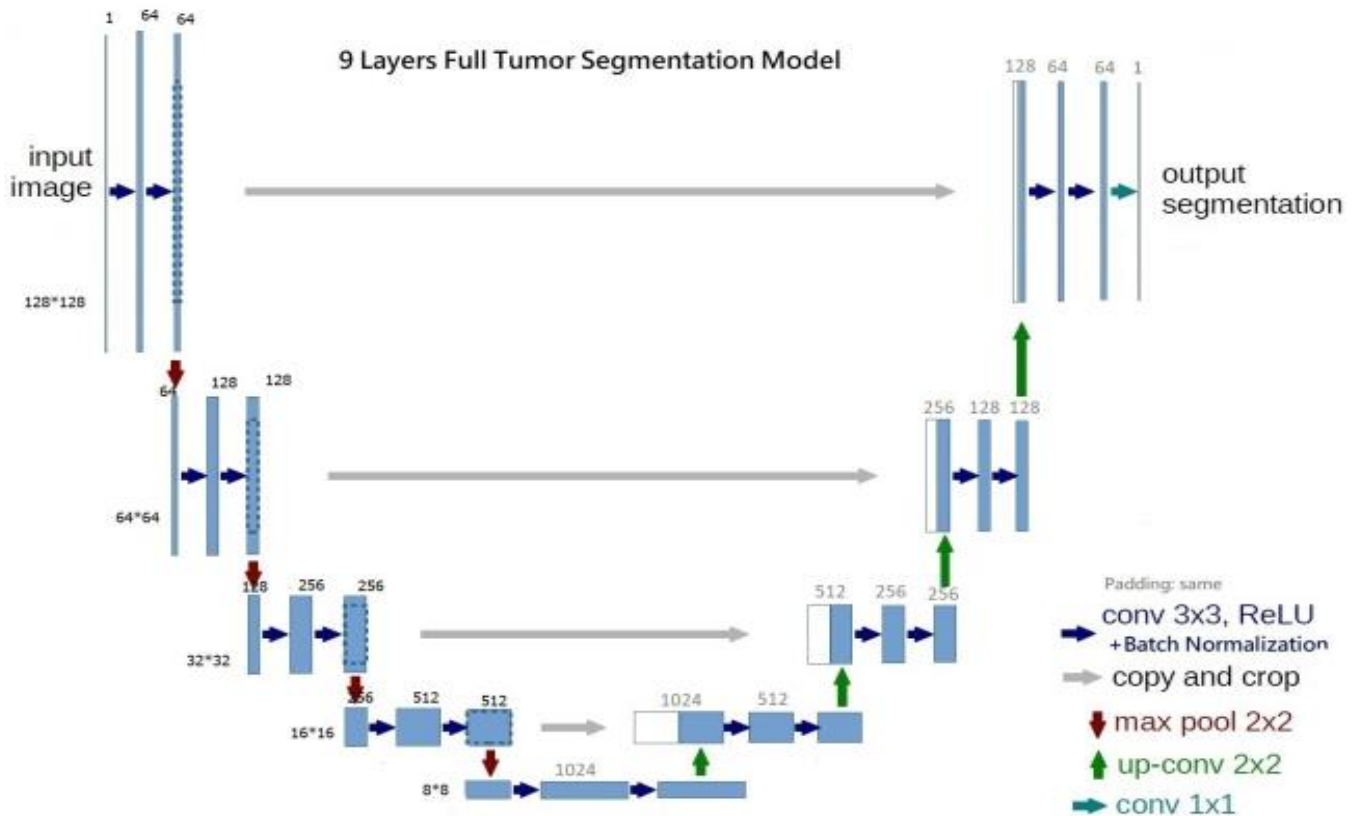


figure 1- Proposed network - the architecture

### 2.1. Preprocessing

As mentioned, the given images are provided in three-dimensional images format. Because we will be using a 2D version of the network, we must first convert the data to fit the network input structure. For this purpose, we consider each 3D image with 155 slices as 155 separate 2D images. Since not all 155 sections contain meaningful image information, only sections 60 to 130 are used. Totally, we have 285 x 70 images with two-dimensional operations. These images are 240 x 240, which we resize to 128 x 128. Figure 2 shows a slice of these images.

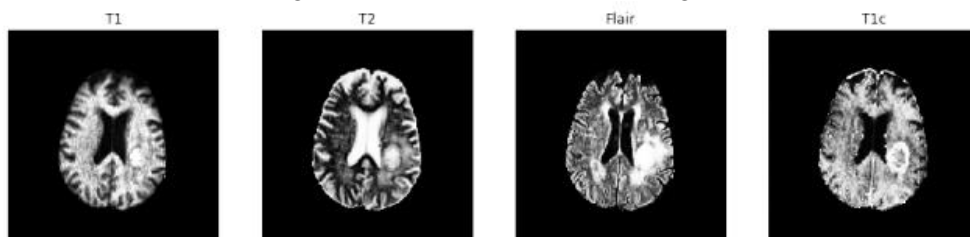


Figure 2- Image of a slice after histogram balancing

### 3. Experiments and results

### 3.1. The first experiment

In this experiment, the configuration of Figure 1 is used. Dropout is not considered here. Normalization was used on the whole image in preprocessing, and histogram balancing was not applied. In addition, only the usual methods were used to increase the training data, and no elastic deformation was used.

The Dice index is also used for loss. The DSC method shows the degree of overlap between the brain tumor area obtained by the automatic and manual methods. This is how the Dice criterion is calculated:

$$DSC = \frac{2TP}{FP + 2TP + FN}, \quad (1)$$

In the above formula FP = False Positive, FN = False Negative and TP = True Positive. Figure 4 shows the training process. BraTS 2015 data set has been used to train this network.

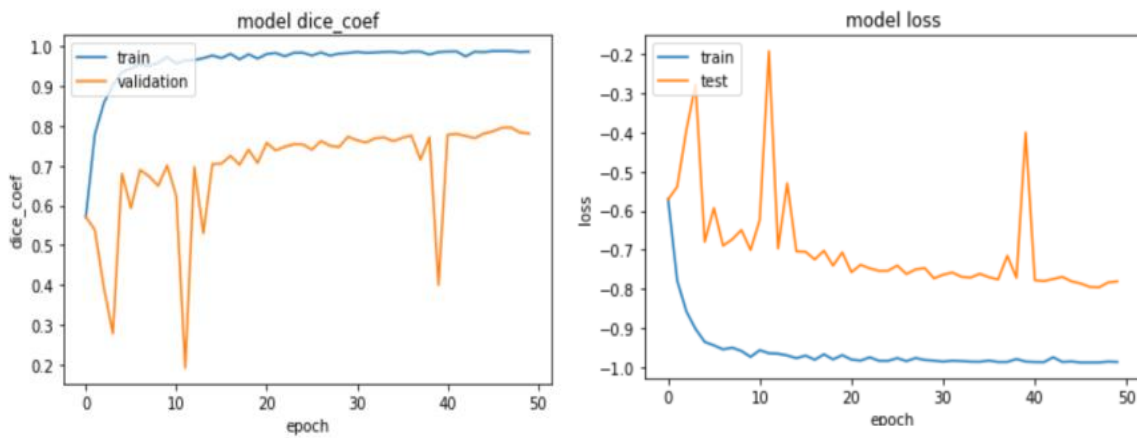


Figure3- The first training process

### 3.2. The second experiment

The difference between this test and the first test is that the Dropout = 0.1 is used here. Figure 4 shows the training process. BraTS 2018 datasets have been used to train this network.

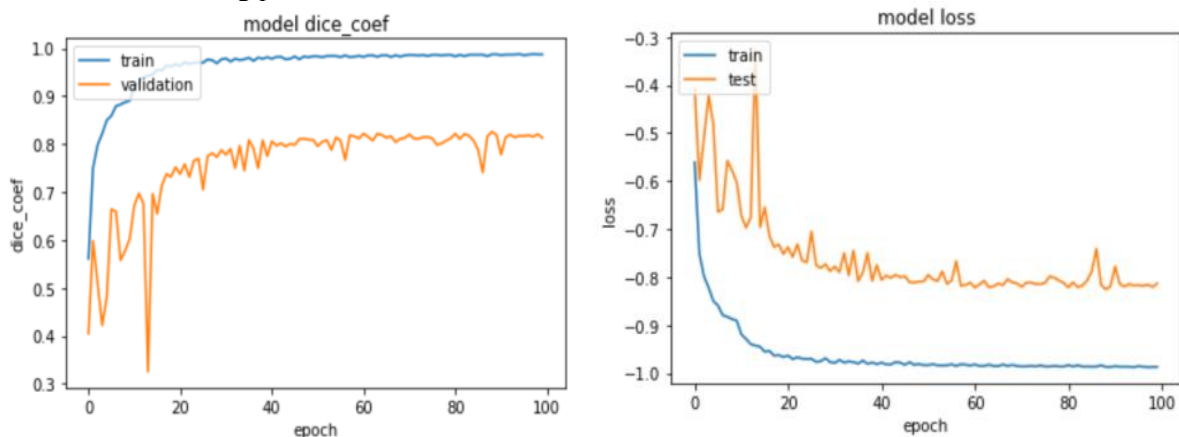


Figure4- The second training process

### 3.3. The third experiment

The changes of this experiment compared to the previous two experiments are the use of Dropout = 0.2 and the normalization of images only on the part containing the brain image. The results of this experiment are given in figure 5.

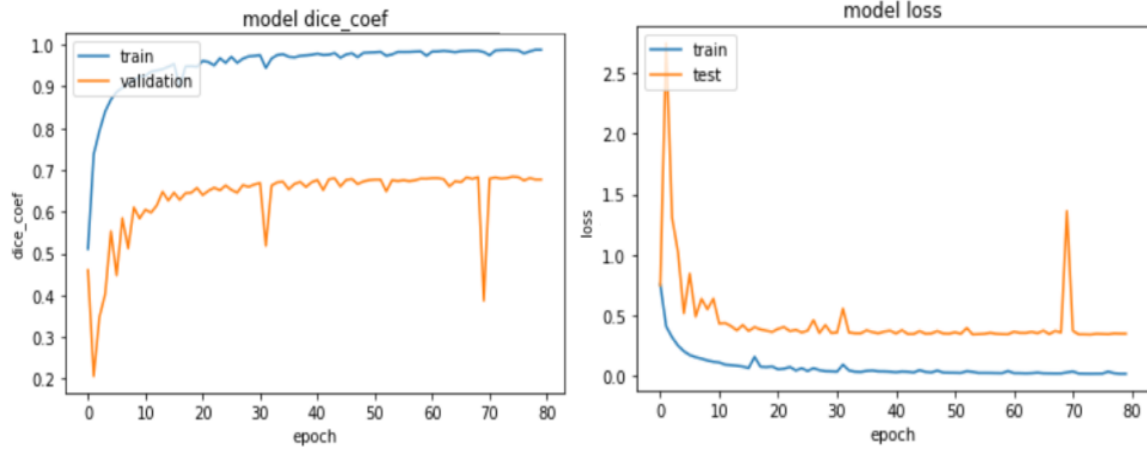


Figure 5- The third training process

### 3.4. The fourth test

In this experiment, Dropout = 0.1 was used. For data preprocessing, in addition to the cases mentioned in the previous methods, histogram balancing has also been used. In addition to previous experiments, Elastic deformation has also been used to increase training data. The results are given in figure 6.

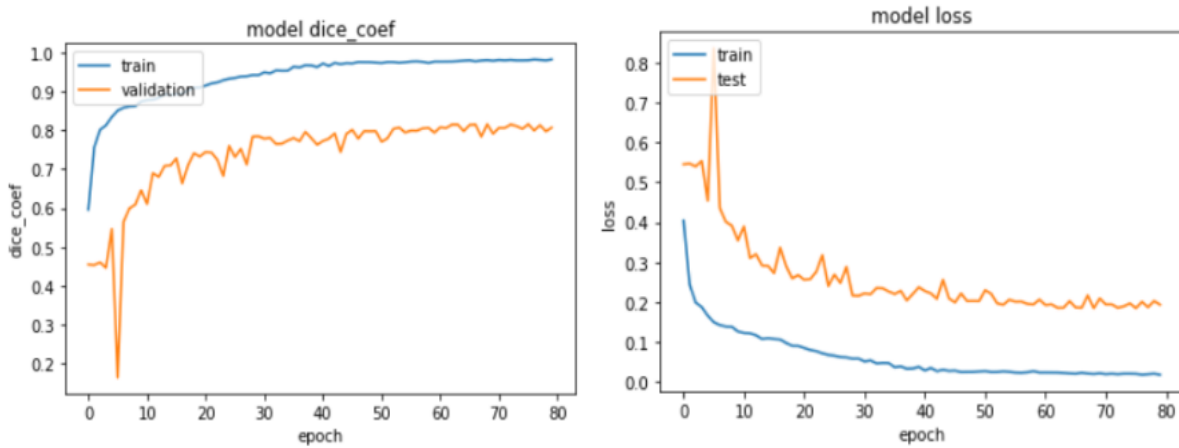


Figure 6- The fourth training process

### 3.5. The fifth experiment

In this experiment, a combined loss was used. To calculate the Loss addition, Dice uses the Entropy Cross criteria KL-Divergence is used. The sum of these three criteria is considered as Loss. The results of this change were very poor and unreproducible. (2) and (3) show the Formulas for calculating Cross-Entropy and KL-Divergence.

$$(y \log(p) + (1 - y) \log(1p)) \quad (2)$$

$$L_{KL} = \frac{1}{N} \sum \mu^2 + \sigma^2 + -\log \sigma^2 + 1 \quad (3)$$

### 3.6. The sixth experiment

Histogram balancing was not used for preprocessing. The Dice and Cross-Entropy were used to calculate the Loss. The results are given in figure 7.

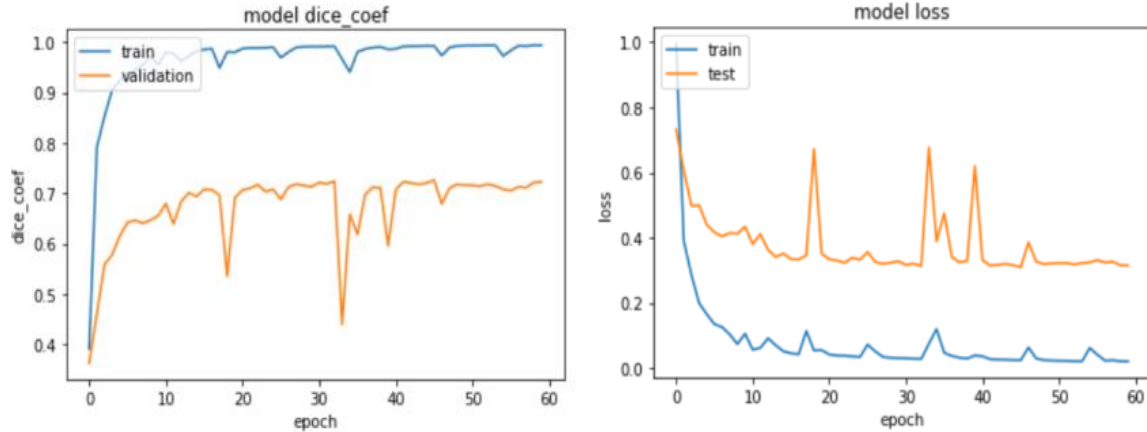


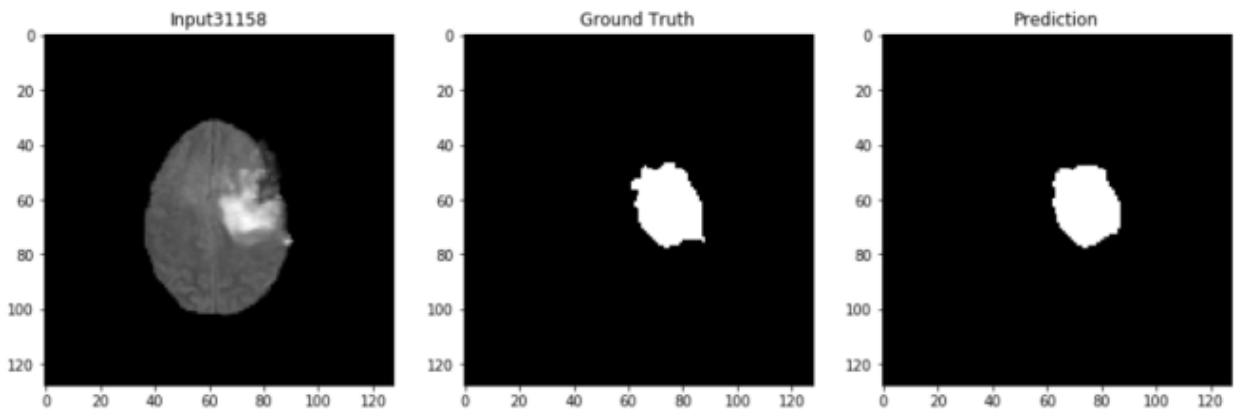
Figure 6- The sixth training process

## 4. Conclusion

Table 1 compares the accuracy obtained in the different methods. Table 1 compares the accuracy obtained in the different methods. Figure 7 shows an example of brain segmentation. The trained network does not seem to learn boundaries or sudden changes and small details. In addition, there are cases in which the jump in the training process is accurate, which should also be considered. But the network has produced acceptable results (% 0.82) with a slight change from the original U-Net architecture, i.e., adding dropout, normalization, and using Batch Normalization. The training data for the network is still low and more data should be used because we do not have a significant increase in the accuracy of the method from one place to another in the experiments.

Table1- Compare methods

method	Dice accuracy
<b>The first experiment</b>	<b>77%</b>
<b>The second experiment</b>	<b>82%</b>
<b>The third experiment</b>	<b>81%</b>
<b>The fourth experiment</b>	<b>69%</b>
<b>The fifth experiment</b>	<b>45%</b>
<b>The sixth experiment</b>	<b>70%</b>



**Figure7- an example of image segmentation using the proposed model**

## 5. References

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