

# Automated Segmentation of 2D Brain Tumor Using Back Propagation Model

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## ABSTRACT

Central to early detection and diagnosis of brain tumors- benign or malignant is accurate segmentation. Hitherto, manual segmentation techniques on Magnetic Resonance Imaging (MRI) modality have been employed extensively but with its inherent high labour intensity, time consumption and susceptibility to intra- and inter-operator variability errors. Semi-automated and automated segmentation approaches have addressed some of these identified drawbacks. However, fully automated techniques still suffers some challenges of accuracy. This paper presents a classifier, for automated segmentation, based on a back-propagation Neural Network, consisting of feature extraction, dimensionality reduction, and classification stages. BraTS 2021 datasets containing 3D MRI scans in four modalities- T1-Weighted, T2-Weighted, FLAIR and contrasted enhancing T1-Weighted (T1ce) was employed to train, evaluate and optimize the neural network for higher accuracy. Our results, as compared with Convolutional Neural Network (CNN) model and an automated segmentation method based on U-Net, depict that the back-propagation Neural Network classifier gives fast and more accurate classification than the other neural networks and can be effectively used for classifying brain tumors with a high level of accuracy. The model achieved a 99.4% accuracy.

**Keywords:** 2D, MRI, Brain tumor, Segmentation, Back-propagation, U-Net, CNN

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## 1. INTRODUCTION

The brain, as one of the most important organs in the human body, is made up of billions of cells and is in charge of control and decision-making. Because it is the controlling center of the nervous system, it is critical to keep it safe from harm and illness. Brain tumors are caused by the formation of abnormal cells within the brain. A brain tumor is defined as a tissue that grows in an area of our brain where it should not grow or uncontrolled growth of any tissue in an area where it should not grow. Tumors are classified as malignant or benign. Non-cancerous and less aggressive tumors that develop slowly and do not spread to other regions of the body are known as benign tumors. (Kalaiselvi et al., 2020).

Malignant tumors, on the other hand, are cancerous and rapidly grow, with a predisposition to spread to other regions of the body. One of the most serious diseases that can take a person's life is brain tumors. The correct understanding of brain tumor stages is critical for disease prevention and treatment. A popular medical imaging technology is magnetic resonance imaging (MRI). Radiologists frequently employ magnetic resonance imaging (MRI) to examine brain malignancies. This is because MRI uses a powerful magnetic field, radio-frequency pulses, and a computer to produce high-resolution, high-contrast images of organs, soft tissues, bone, and almost all other interior body components (Singh et al., 2015). The images can then be viewed on a computer monitor, electronically transmitted, printed, or copied to a drive. MRI does not use ionizing radiation (unlike x-rays).

Physicians can analyze various regions of the body and detect disorders using detailed MR images (Glassman N., 2010). Surgical planning, postsurgical assessment, anomaly detection, and a number of other medical applications all require medical image segmentation. Despite the availability of a variety of automatic and semi-automatic image segmentation approaches, they fail in the majority of cases due to unknown and irregular noise, in-homogeneity, poor contrast, and weak boundaries found in medical images. In image analysis and interpretation, image segmentation is crucial. Brain imaging applications include tissue classification, tumor identification, tumor volume estimation, blood cell delineation, surgical planning, and matching, to name a few (Tiwari et al., 2020).

Using a Convolutional Neural Network, brain tumor segmentation is applied to three-dimensional MR images in this study (CNN). Convolutional Neural Networks (CNNs) are a type of deep learning and artificial neural network that can take an input image and give importance (learnable weights and biases) to distinct objects or elements of the image, allowing them to be distinguished from one another.

An input layer, output layer, and n hidden layers make up the CNN layers. Hidden layers include multi-convolutional layers, pooling layers, completely linked layers, and normalization layers. The output of neurons connected to the input regions is computed by convolutional layers. Each neuron computes the sum of its weights. The pooling layers will perform a downsampling operation on the spatial dimensions (i.e., width, height) of the feature maps (Frniak et al., 2019).

The fully connected layer, as the name implies, will have complete connections to all activations in the previous layer. CNN systems can perform a variety of activation functions, including Identity Binary step Logistics (Soft step), TanH, ArcTan, Rectified Linear Unit (ReLU), Parametric Rectified Linear Unit (PReLU), Exponential Linear Unit (ELU), and SoftPlus (Kalaiselvi et al., 2020). In this study, ReLU and Softmax are used.

## **2. RELATED LITERATURE**

Researchers have put in a lot of effort in the research to partially or fully automate the task of brain tumor segmentation. Some key works are discussed below:

Mohsen H et al. (2018) proposed a methodology for classifying brain tumors into three types of malignant brain tumors using a combination of discrete wavelength transform (DWT) and Deep Neural Network (DNN). They stated that DNN classifiers outperform traditional classifiers in terms of accuracy.

Kamnistas et al., 2017 proposed an 11-layered deep 3D CNN for brain lesion segmentation. They created this architecture to investigate the shortcomings of current networks proposed at the time for brain lesion segmentation applications. In order to reduce the processing time of 3D scans, a dense training scheme was introduced.

Kleesiek et al. (2016) proposed a method for dealing with various modalities, such as contrast-enhanced scans. This method works with MRI data that has four channels: T1, T1c, T2, and FLAIR contrast. They tested their method on a clinical dataset with 53 tumor sets and obtained a dice accuracy of around 95.19. The method's sensitivity is increased by adjusting the cut-off threshold used to generate binary masks from CNN results.

Pereira et al. (2016) proposed an automatic segmentation method based on CNN with 3 x 3 kernels. They concluded that using small kernels aids in the design of a deeper architecture and provides confidence against overfitting issues when the number of weights is low. Intensity normalization is included in their pre-processing step, which is uncommon in CNN-based segmentation methods.

Afshar et al. (2018) presented a method for classifying brain tumor images that they developed. They used 1 convolutional layer with 64 feature maps and 16 primary capsules in the method they recommended. They had an 86.56 percent accuracy rate. They obtained an accuracy value of 72.13 when they compared the model they developed with CNN in the same study.

In their study, Saxena et al. (2019) classified brain tumor data using the Vgg16, InceptionV3, and Resnet50 models. They obtained the highest accuracy rate in the Resnet50 model with 95 percent in this study using transfer learning methods.

Shahzadi et al. (2018) classified brain tumor cells using the Cnn - Lstm hybrid construct. They claimed to have classified the network with 71 percent accuracy using Alexnet-Lstm, 84 percent accuracy using VggNet-Lstm, and 71 percent accuracy using Resnet-Lstm. They achieved the highest accuracy rate of 84 percent in the VggNet-Lstm architecture.

Charfi et al. (2014) presented a method for classifying MR images of brain tumors. In his proposed machine learning method, he stated that he used the histogram equalization method for image segmentation. He then used PCA to reduce the size of the resulting data. Finally, for the classification process, a feed-forward back propagation neural network was used. He achieved 90% accuracy in classifying images as normal or abnormal. He stated that this accuracy rate is extremely high.

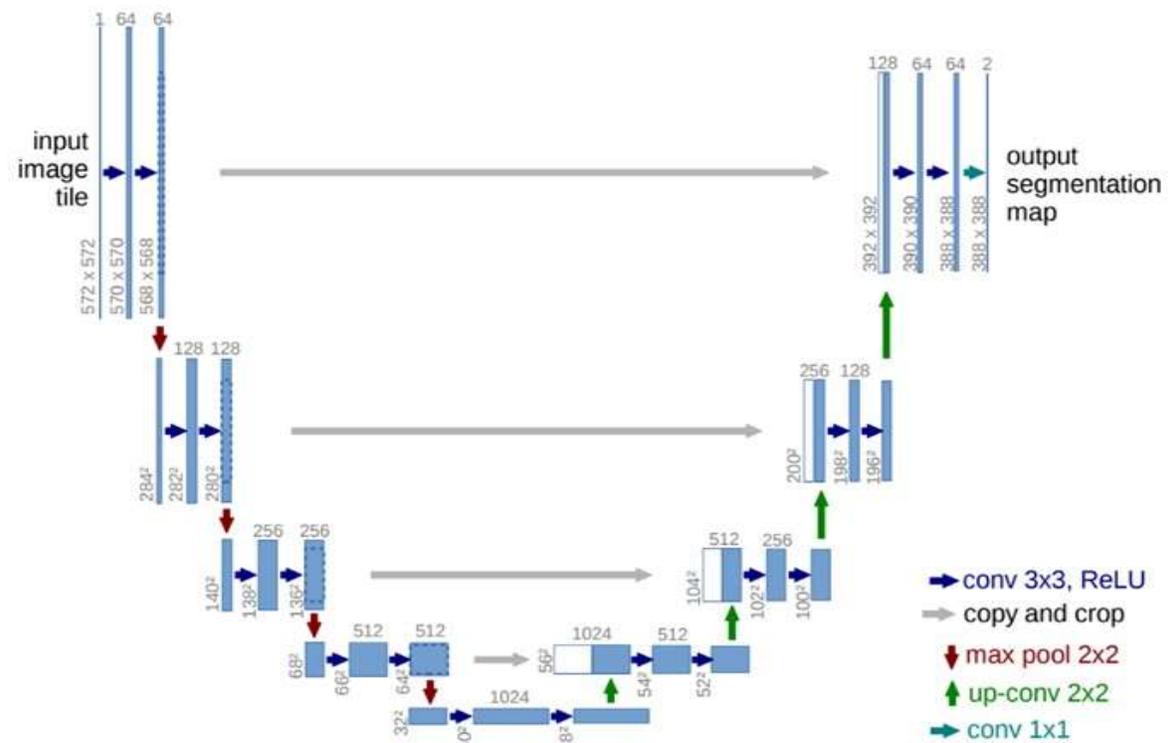
Citak et al. (2018) stated that in their brain tumor study, they used three different machine learning algorithms. These algorithms are SVM, multi-layer perceptrons, and logistic regression, according to them. As a result, they were able to achieve 93 percent accuracy.

## **2.1 Research Gaps**

Manual segmentation is a time-consuming and labor-intensive task that is subject to human error and subjective judgments, increasing the possibility that different observers will reach different conclusions about the presence or absence of tumors, or that the same observer will reach different conclusions on different occasions. As a result, automatic segmentation is required to aid doctors in accurately segmenting tumor areas compared to manual segmentation and making decisions in the diagnosis of brain tumors.

### 3. METHODOLOGY

The model is built on U-Net, a convolutional neural network developed in 2015 by Olaf Ronneberger, Philip Fischer, and Thomas Brox at the University of Freiburg's Department of Computer Science for biomedical imaging. The network has a u-shaped design with a contracting path (encoder) and an expanding path (decoder). Convolution layers are followed by a rectified linear unit (ReLU) and max-pooling layers in the encoder, which downsample the image by lowering spatial information and enhancing feature information. The image resolution is halved and the feature map is doubled with each downsampling step. Through a series of up-convolutions and concatenations with high-resolution features from the contracting path, the decoder combines feature and spatial information. Low-resolution images with high-resolution features from the encoder are concatenated with high-resolution images with low-resolution features from the decoder across the network.



**Fig 1: U-Net**

Source: <https://arxiv.org/pdf/1505.04597.pdf>

#### 3.1 Datasets

The dataset utilized in this paper is the BraTS 2021 dataset obtained from Kaggle. The MRI scans in the dataset are divided into four volumes: native (T1), post-contrast T1-weighted (T1ce), T2-weighted (T2), and T2 Fluid Attenuated Inversion Recovery (T2-FLAIR). They have all been manually annotated and approved by an expert neuroradiologist. Enhancing tumor, necrosis or non-enhancing tumor, edema, and healthy tissue are the four main classes in the dataset.

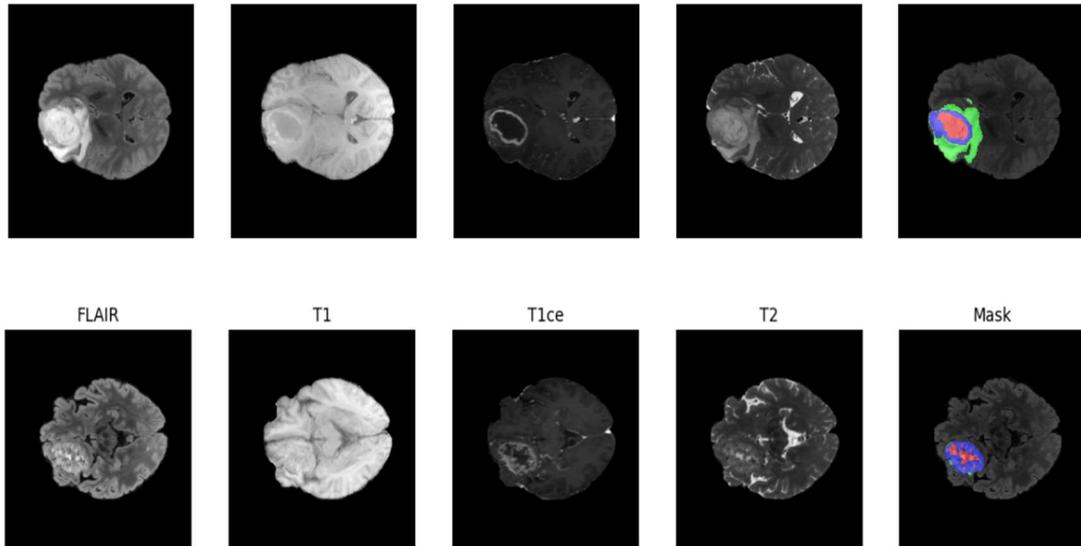


Fig 2: Sample cases from the Datasets

### 3.2 Network And Training

The size of the input image in the network is 128x128, the padding was set to same to ensure that the size of the output image is the same as the size of the input image After the last block in the contracting pathway, a dropout layer with a ratio of 0.2 was added. The softmax function was used to generate values for each class based on probabilistic calculations performed on the network. This function uses the following equation to compute the probabilities for each class (Szegedy C. et al, 2015).

$$\sigma(\vec{z}) = \frac{e^{z_i}}{\sum_{j=1}^K e^{z_j}} \quad \text{.....1}$$

Where  $\vec{z}$  is the input vector,  $e^{z_i}$  is the standard exponential function for the input vector, K is the number of classes in the multi-class and  $e^{z_j}$  is the standard exponential function for the output vector was used as the activation function in the final convolution. Categorical cross entropy function given as:

$$Loss = -\sum_{i=1}^{output\ size} y_i \log \hat{y}_i \quad \text{.....2}$$

Where  $\hat{y}_i$  is the i-th scalar value in the model output,  $y_i$  is the corresponding target value and the output size is the number of scalar values in the model output. was used as a loss function. The model was trained over twenty-five epochs on an Intel graphics processor with 1.5GB of graphics memory. The Adam optimizer with an initial learning rate of 0.001 which was set to reduce when a metric has stopped improving with minimum learning rate of 0.000001 was used.

### 3.3 Evaluation Metrics

Dice coefficient (DSC), precision, sensitivity, and specificity were used to evaluate the performance of the model. The Dice coefficient score is used to measure the degree of overlap between the ground truth and the predicted output using the formula:

$$DSC = \frac{2|X \cap Y|}{|X| + |Y|} \dots\dots\dots 3$$

where |X| and |Y| are the number of elements in the two sets. Precision measures the accuracy in classifying a sample as true positive. It is calculated as:

$$Precision = \frac{True\ Positive}{True\ Positive + False\ Positive} \dots\dots 4$$

Sensitivity is the measure of the precision of true positive. It is calculated as:

$$Sensitivity = \frac{True\ Positive}{True\ Positive + False\ Negative} \dots\dots\dots 5$$

Specificity measures the precision of true negatives. It is calculated using the formula:

$$Specificity = \frac{True\ negatives}{True\ negatives + False\ positives} \dots\dots\dots 6$$

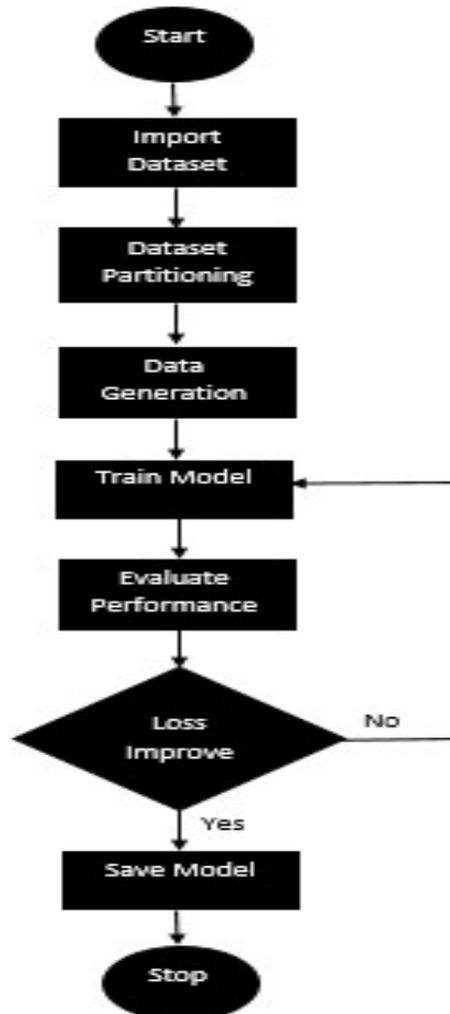


Fig 3: Program flowchart

### 3.4 Implementation Details

The algorithm was implemented with Python programming language using tensorflow, keras, numpy, nilearn, nibabel, and matplotlib libraries in Pycharm IDE. Keras is an open-source software that provides a Python interface for artificial neural networks. It acts as an interface for the tensorflow module Slicing and patch extraction from 3D MRI images were done with Numpy. Because the MRI pictures are in the nifti format, nilearn and nibabel were utilized to load them. For visualization, Matplotlib was used. After training, testing, and evaluating the model, I created an application (named "NeoTumor") using Qt Designer (a user interface design application) and the Python programming language to implement the model to segment brain tumors.

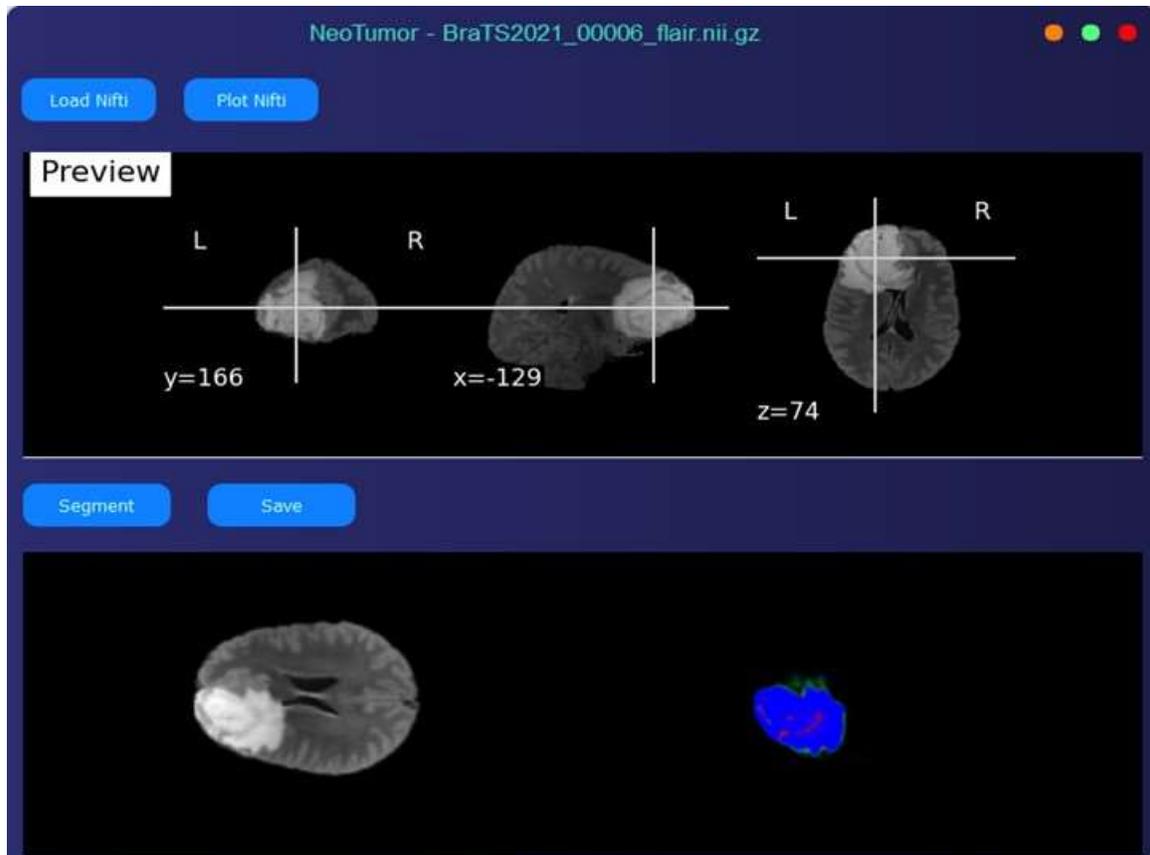


Fig 4: Segmenting the loaded MRI image

#### 4. RESULTS AND DISCUSSION

The model was trained using real patient data from the BraTS 2021 dataset. Due to the lack of resolution in the 3D images, 2D patches were extracted from the axial view to train the model. The model was trained on an Intel GPU with 1.5GB of memory. It took roughly 96 hours to train and 2500ms to test. The network was trained using the dataset's two modalities (T1ce and T2-FLAIR).

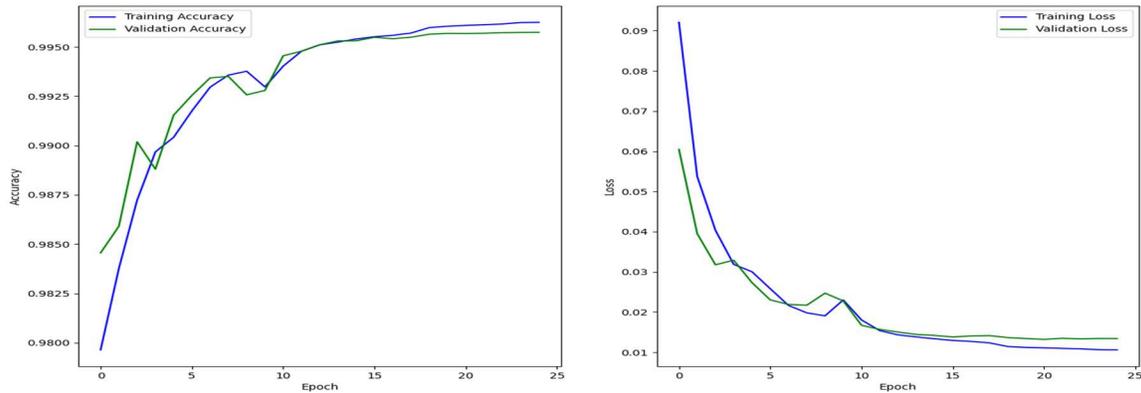


Fig 5: Accuracy and loss of training and validation against the number of epochs

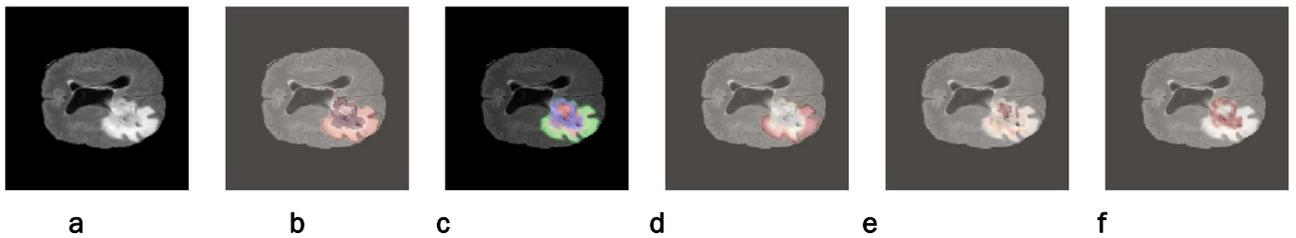


Fig 6: Ground Truth and Prediction

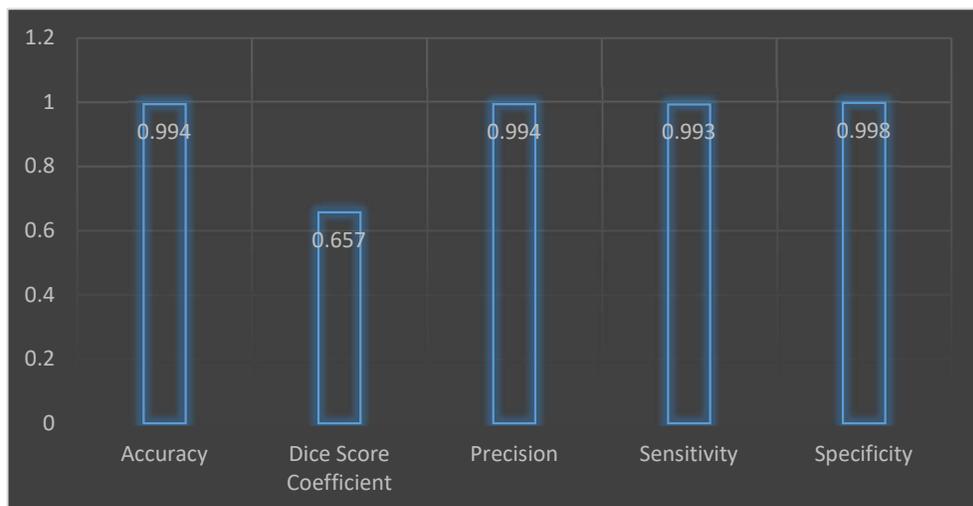


Fig 7: Performance Chart

Fig 6 shows the original image, ground truth, prediction of all classes, prediction of tumor core, edema and enhancing tumor regions respectively. The results of the experiment are reported using five metrics: accuracy, dice score coefficient, precision, sensitivity and specificity as seen in fig 7 above. Precision defines the ability of the model to make correct positive predictions. Sensitivity specifies the capability of the model to predict true positives. Specificity measures the model's ability to predict true negatives.

## 5. CONCLUSION

This research work presented a method for automatic brain tumor segmentation from MRI images. This method was achieved by modifying the parameters of the U-Net architecture. The MRI images used in this proposed method were three-dimensional from which two-dimensional images were extracted to train the network. In addition, for the purpose of brain tumor segmentation, an application that supports graphical user interaction to implements this model was developed.

For treatment planning, it is critical to have an early and precise diagnosis as well as segmentation of a brain tumor. Manual segmentation is time-consuming, exhausting, and prone to inaccuracy. As a result, employing a convolutional neural network based on the architecture of the U-Net, this paper offered a method for automatic segmentation of brain tumors. BraTS 2021 dataset was used to train the network, which contains 3D MRI scans from which 2D slices were removed for training. As seen in Fig 7, the network achieved a 99.4% accuracy. This was accomplished with the help of machine libraries and Python programming language.

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