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U-Net for Medical Imaging: A Novel Approach for Brain Tumor Segmentation

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In medical imaging, brain tumor segmentation is critical. The segmentation of a brain tumor might be done manually or automatically. Finding anomalies in magnetic resonance imaging (MRI) images manually is time-consuming and complex. Automatic segmentation, on the other hand, is incredibly accurate and time-saving. Any technique that can detect a brain tumor early would improve the diagnosis method. As a result, the number of cases of death will decrease. MRI (Magnetic Resonance Imaging) scans have proven to be quite helpful in the detection and segmentation of brain tumors in recent years. MRI images can aid in the detection of a brain tumor. MRI scans can detect abnormal tissue growth and blood blockages in the neurological system. The U-Net model is being used to segment the brain tumor region. The U-Net model is simply a more advanced version of CNN's algorithm. The U-Net model was created to segment biological pictures. We create a 3D U-Net design to segment the brain tumor infection zone in this paper. We combine clinical data with novel radiometric parameters based on the geometry, position, and shape of the segmented tumor to estimate each patient's survival length. The loss graph and accuracy graph are given together with the scores. Finally, we run the tests on various original photographs using the masks that correspond to them.

Keywords: Automatic, MRI images, U-Net, Brain Tumor, Machine Learning, Segmentation

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Introduction

A brain tumor, also known as an intracranial neoplasm, is caused by abnormal cells that form within the brain. The area of automatic segmentation of brain tumors is undergoing extensive development. Brain tumors are extremely dangerous to one's health and can result in death. Early detection of brain tumors is critical for lowering the death rate. Because of the shorter diagnostic time, automatic segmentation allows for the early detection of cancers in MRI images. Recent research has focused on developing effective and precise automated segmentation approaches, with deep learning techniques playing a key role in brain tumor segmentation [1].

The total tumor (WT) is made up of all of these subregions, whereas the core tumor (CT) is made up of non-enhancing and enhancing regions, and the active tumor (AT) is made up of enhancing regions. This is owing to its capacity to provide a good contrast for soft tissues. Furthermore, there are no known health risks associated with brief exposure to the MR environment. As a result, MRI is a useful tool for detecting brain tumors in humans. Brain tumor segmentation manually is time-consuming and perplexing [2,3]. The most common of these modalities is T1 weighted imaging, which is generally used for structural analysis and detecting healthy and diseased tissues. Because of their prominent appearance, gliomas pose the greatest risk of morbidity.

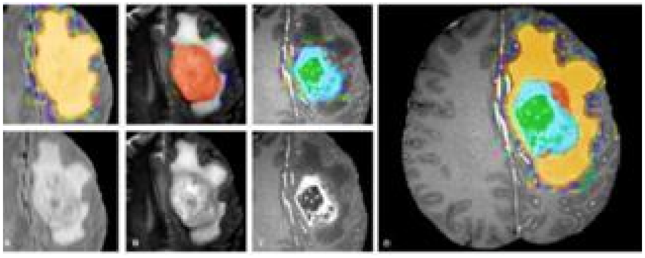


Figure 1: Samples of Different MRI Images

Handcrafted characteristics were retrieved manually in previous segmentation algorithms, resulting in a higher level of complexity. Because features are extracted directly from the inputs with a developing hierarchy in deep learning segmentation algorithms, the complexity of manually obtaining features has been reduced. As a result, rather than taking the usual way of manually extracting features, we should aim to create more effective deep architectures that learn the features On their own [4]. One of the main motivations for adopting deep learning to solve challenges like extracting tumor traits from brain pictures is this.

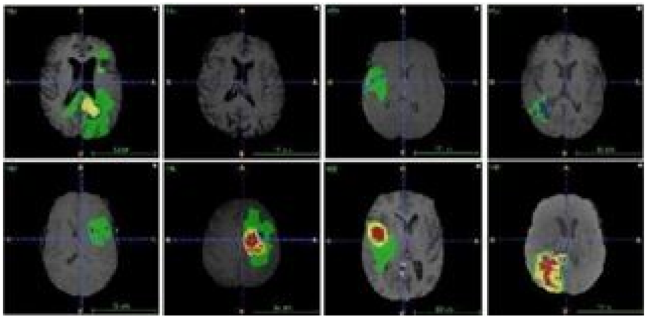


Figure 2: Different Patients Brain Tumor with same brain slice

The remaining articles are describing the mentioned section, for instance, section 2 will be literature work, section 3 will be methodology, section 4 will be results and discussion and finally, section will conclusion and future scopes parts.

Related Work: The literature on brain tumor detection using MRI scan pictures has grown dramatically, necessitating a review and summary of the methodology utilized, associated datasets, and results obtained. The research in this field employs machine learning approaches to detect brain tumors. To learn the tumor detection system, machine learning models require feature data [13-15]. Deep learning approaches based on CNNs necessitate a large amount of data, making it a difficult and costly endeavor. To successfully train tumor identification and segmentation, large features are required [5]. On the other hand, the CNN U-net model has proven to be quite useful in medical picture segmentation prognostication. Methods for segmenting brain tumors (particularly those devoted to MRI) can be loosely separated into two categories: generative models and discriminative models [12]. WHO (World Health Organization) categorization of central nervous system tumors is a conceptual and practical summary of the predecessor. The WHO classification for CNS tumors is based on molecular markers for diagnosis. More recently, the CNS WHO has identified additional diffuse gliomas and other tumors, as well as novel features such as histology and chemistry. In 2007, the World Health Organization (WHO) released the third version of their diagnosis of central nervous tumors. Glioma, papillary, and glioneuronal tumors are among the new titles and data lists.

Various edge distribution, position, symptoms, and therapeutic characteristics are all possible with histological variances [6]. The MICCAI-BRATS Challenge results from 2012, 2013, and 2014 imply that random forest-based approaches are among the most accurate [7,8]. Fuzzy clustering is a biomedical image detection technology that is commonly employed. In aberrant MR brain picture segmentation, the effective fuzzy clustering approach is applied. We can reliably determine the cancer region by employing clustering in brain tumor segmentation. Magnetic resonance pictures are used to improve the identification of brain tumors. Because brain tumors are now one of the most dangerous diseases, early identification is essential. It is possible to achieve this using automated tumors detection techniques on medical imaging, one of which is MRI images, which specify the tumor growing region and edges detection. In comparison to previous procedures, this provides more accurate as well as clear results, and the benefits of automated tumors identification techniques are used for tumors removal if necessary [9]. Neural networks are a novel technology that has recently been found. The neural network is a "hot" study area in fields such as cardiology, radiology, and cancer. It allows for the solution of exceedingly complicated problems by combining neurons into layers. In medical applications, neural networks are similar to artificial neural networks (ANNs) that are used to map given output into an expected outcome [10]. The very uneven borders of tumors tissues are visible in an MRI picture. The deformable modes and region basis approaches are employed in the segmentation of medical images. In MRI pictures, the most common issues are imprecise tumors localization, undetected boundaries or data loss at boundaries, and a silent edge that has not been stretched. The quiet edge is expanded and the boundary of the site or area of the tumor is discovered using this approach, and the boundary or location of the tumor is seen. The tumors can then be surgically removed [11].

Methodology

The basic block diagram of brain tumor identification and segmentation is shown in Figure 3. For processing, MRI pictures of the brain are acquired.

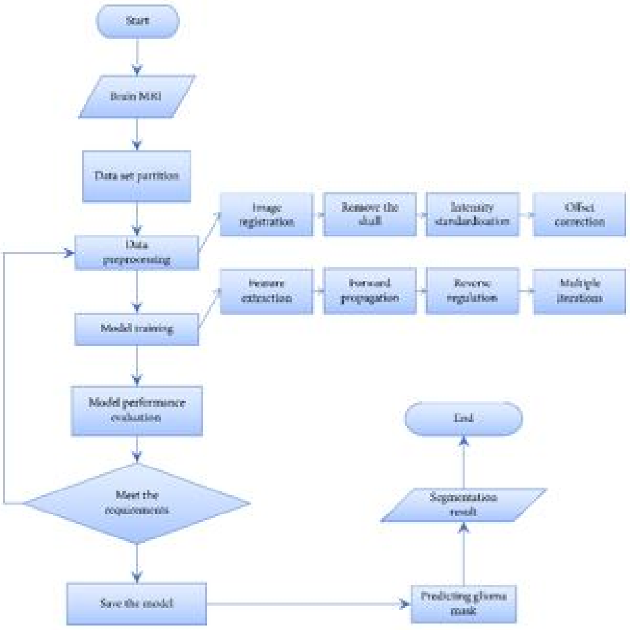


Figure 3: Flow Chart of Brain Tumor Segmentation.

A. Data Collection: The information is collected from the Kaggle repository. The dataset includes MRI Images as well as FLAIR abnormalities segmented masks created by hand.

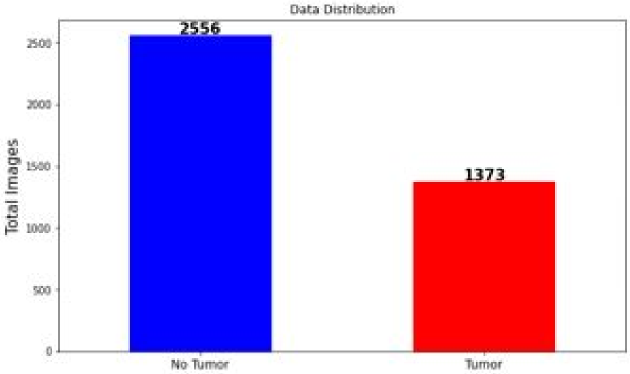


Figure 4: Data Distribution (Tumor and No tumor)

"LGG Segmentation Dataset" is the name of this dataset. The dataset includes 110 patients Brian Images with lower glioma. The dataset contains total MRI images are 3,929. The number of Negative images is 2556 and Positive images are 1373.

The dataset also contains the Mask images of all the MRI images because of that we do not need to extract the Mask images. Otherwise, we have to extract the mask images.

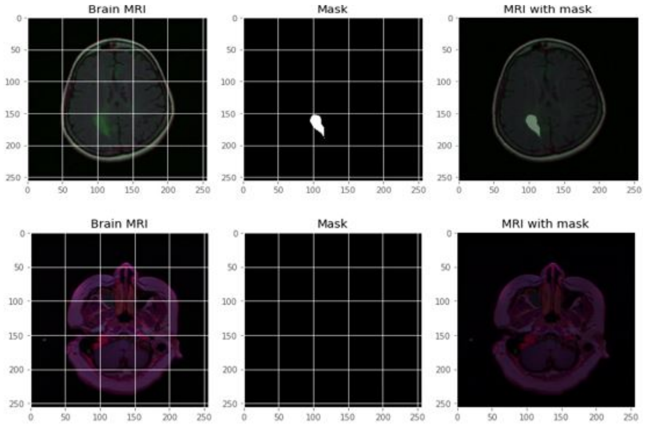


Figure 5: Sample of Positive and Negative image with Mask

B. Data Pre-processing

All four modalities were layered during the first step of data pre-processing, giving each instance the size (4, 240, 240, 155) the input tensor is in the (X, Y W, Z) layout, with (channels, height, width, and depth). Noise removal is part of the pre-processing stage, and it can be done with a variety of spatial filters, both linear and nonlinear (Median filter). Some morphological techniques remove other artifacts, such as text. Additionally, in this phase, RGB images convert to Grey and change the shape size. MRI images might be carrying noise because of the thermal effect. So, removing the noise, there is a median filter [16].

Image processing is the is nothing but a transforming technique where a physical image is transforming into a digital image. After converting, many different extraction operations are used to extract the useful information. At the very first time of using specified image processing algorithms, it’s basically treated as a 2D images. [17]

c. Train-Test Split: Trian Data: A sample collection is nothing but more than a training dataset that is utilized to suit the learner throughout the learning process. The training data is quite large (2838, 3) [8].

Validation Data: This piece of data is used to provide an independent assessment of a process that happens on the training sample while optimizing hyperparameters. Other parts of development and establishment, such as selecting features and thresholds cut-off selections, are influenced as well. The size of the validation data is (501, 3) [8].

Test Data: A defined as information that can be used to provide a neutral assessment of a final version that has been matched to the training examples. The size of the Test data set is (590, 3) [8].

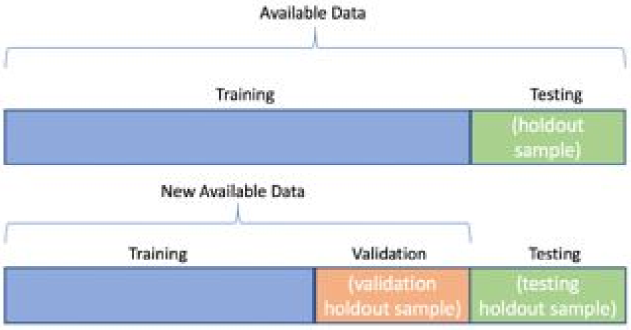


Figure 6: Training, Validation, and Testing structure

D. Model

U-Net Architecture: Due to the need for localization in biomedical signal processing, specialized deep learning algorithms are required to get the desired result. For biomedical image segmentation, the Localization technique is used because Localization can pixel label classification. On the other hand, Standardized CNN is not effective for segmentation because of is designed for classification tasks for instance it can assign a class level to every image instead of identifying the segmented region.

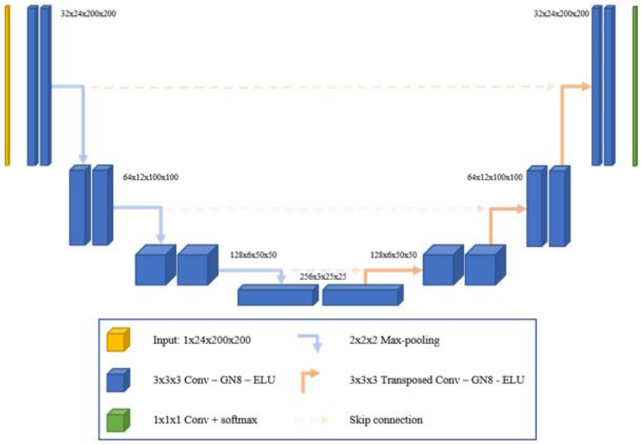


Figure 7: U-Net Architecture

U-Net is a fully convolutional encoder-decoder with few changes in the CNN architecture [18]. U-Net has invented only biomedical images where the target is not only a classifier whether where the target is not only classified but also to identify the area of infection. This model predicts the mask of an object present in the image. Following are the specifications of the U-net.

- This model has two parts called contraction or encoder or expansion or decoder.
- Every encoder has two consecutive convolutional layers and one carpooling layer.
- Before using Carpooling layer, we use a skip connection to store the feature values that will use in the decoder part.
- For encoder input/2 and filters*2
- For decoder input*2 and filters/2
- In the decoder phase, first, increase image dimension using up-sampling (trans convolution) and concatenation with a feature from the skip connection.
- We are using the same padding in convolution to ensure our image size does not decrease.
- For loss function, we are using Binary cross-entropy
- Activation function Relu and Sigmoid

Down sampling

The left side of the architecture is called down sampling which is made by two of 3x3 convolutional layers and it is continue till up sampling start.

After each convolutional operation, we have ReLU activation function and batch normalization. Additionally, a 2x2 max pooling layer is used for reducing the dimensions.

Decoder (right-side)

The abstract representation is utilized to produce a semantic segmentation mask using the decoder network. A 2x2 transpose convolution is used to begin the decoder block. It is then concatenated with the encoder block's associated skip connection feature map.

According to the channel's complexity, these skip connections give features from prior layers that are sometimes lost. Afterwards when, two 3x3 convolutions are utilized, followed by a ReLU activation function for each convolution.

The outputs of the final decoder is convolutional 1x1 with sigmoid activation.

The segmentation mask representing pixel-wise categorization is obtained using the sigmoid activation function.

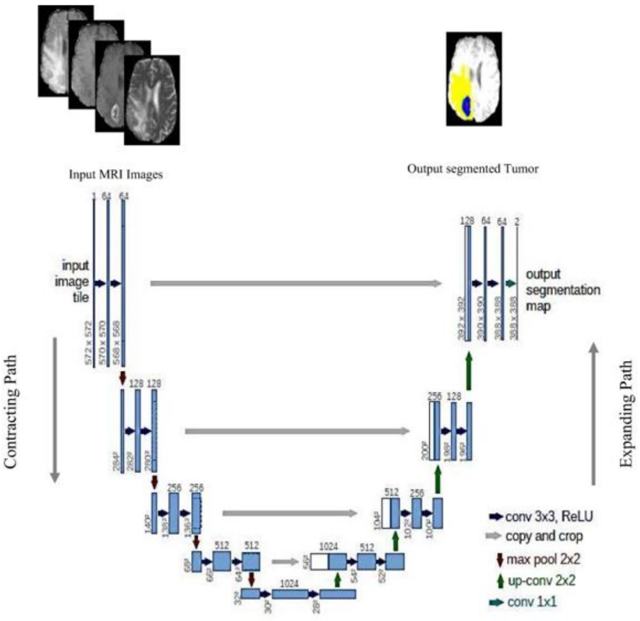


Figure 8: Proposed Model

Implementation U-Net for Brain Tumor Segmentation:

- Import requires Library: We'll use the TensorFlow deep learning framework to develop the U-Net architecture, as we've already covered. As a result, we'll use the TensorFlow library as well as the Keras framework, which is now a standard feature of TensorFlow model structures. Then we'll apply some extra layers, such as the Conv2DTranspose layer, which will up sample our desired decoder blocks. The Batch Normalization layers will be used to stabilize the training process, and the Concatenate layers will be used to combine the necessary skip connections.
- Building the Convolutional Block: We can now continue to develop the U-Net structure after exporting the essential libraries. As illustrated in the architecture diagram, we'll use three iterative blocks: the convolution block, the down sampling, and the up sampling. We can easily construct the U-Net architecture using these three elements. Let's go over each of these function code blocks one by one and see how they work.

The principle of operation of the convolutional operator blocks is to execute a double layer of convolution operations using the provided input parameters.

- **Construct Encoder – Decoder:** The left side of the architecture is called down sampling which is made by two of

- 3x3 convolutional layers and it is continue till up sampling start. After each convolutional operation, we have ReLU activation function and batch normalization. Additionally, a 2x2 max pooling layer is used for reducing the dimensions.

The abstract representation is utilized to produce a semantic segmentation mask using the decoder network. A 2x2 transpose convolution is used to begin the decoder block. It is then concatenated with the encoder block's associated skip connection feature map. According to the channel's complexity, these skip connections give features from prior layers that are sometimes lost. Afterwards when, two 3x3 convolutions are utilized, followed by a ReLU activation function for each convolution. The outputs of the final decoder is convolutional 1x1 with sigmoid activation. The segmentation mask representing pixel-wise categorization is obtained using the sigmoid activation function.

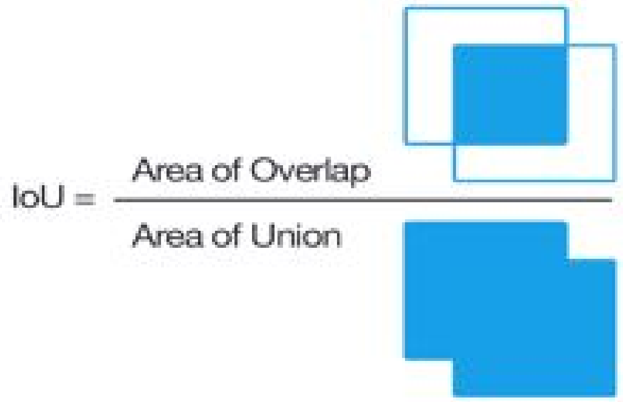
The incoming input, the skip connection inputs, and the filter size in the given building block will all be parameters in the decoding module. The Conv2DTranspose layers in our model will be used to upsample the entered data. To get the final value of the skip connections, we'll concatenate both the receiving input and the freshly upsampled layers. We'll then utilize this combined function to get to another layer and conduct our convolution blocks operations, returning this output value.

- **Finalize the Model:** Make sure your image forms can be divided by 16 or multiples of 16. We don't want to run into the divisibility of any odd number forms because we're employing four max-pooling layers throughout the down-sampling method. As a result, make sure your architecture's dimensions are identical to (48, 48), (80, 80), (160, 160), (256, 256), (512, 512), and other similar forms.

Result and Discussion

In this article, we introduce a new model for MRI image segmentation using the U-Net model. For evaluating the model performance of validating the approach to segment the brain tumor region, we are using Dice coefficient, Loss values, and accuracy. To implement the model, we are using several packages from python like sckit-learn, matplotlib, seaborn, etc. Additionally, we are using TensorFlow, Kear, Pip package, etc.

Dice Coefficients: Performance reviews were used to examine the training model's effectiveness on the training and testing for the deep learning prediction. The U-net learned in the classroom detection approach created the image representing the confined tumor. By matching the output to the original development truth image, the difference between both the genuine and forecasted MRI images was calculated. The dice coefficient was thought to be a more straightforward way to assess the picture



Segmentation problem's output effectiveness. It was used to calculate the % overlap between the ranges of the two photos, which ranged from 0 to 1. A value of 1 on the dice coefficient indicates perfect and full overlap. In most known medical imaging situations, the dice coefficient has been employed to evaluate the model. As a result, picture segmentation efficiency was evaluated using the dice score/coefficient. Dice score is a statistic for comparing the similarity of two items. The magnitude ofthe overlapping in between forecast area as well as its true equivalent is the score for a given class C.

$$Dice\ coefficient\ score = \frac{2 * |X \cap Y|}{|X| + |Y|}$$

It is calculated as the overlap of the two segmentations divided by the overall area of the two objects. The dice coefficient indicates the amount of spatial overlap between the ground truth (X) and expected segmentation (Y). The method for computing the dice point total is equation (1)

IOU (Intersection over Union): When computing means average precision, intersection over union (IoU) is employed (mAP). It's a value between 0 and 1 that indicates how much the expected and ground truth bounding boxes overlap.

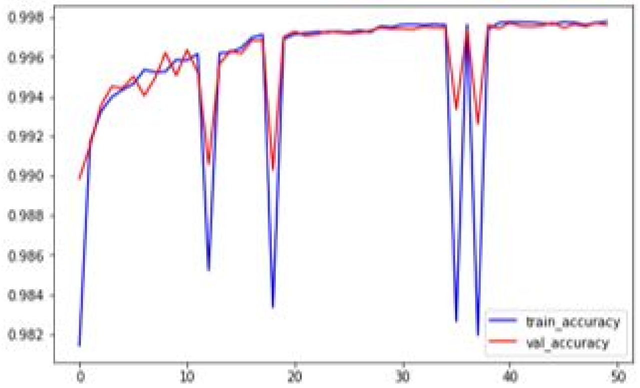


Figure 9: U-Net Train accuracy vs Validation accuracy performance

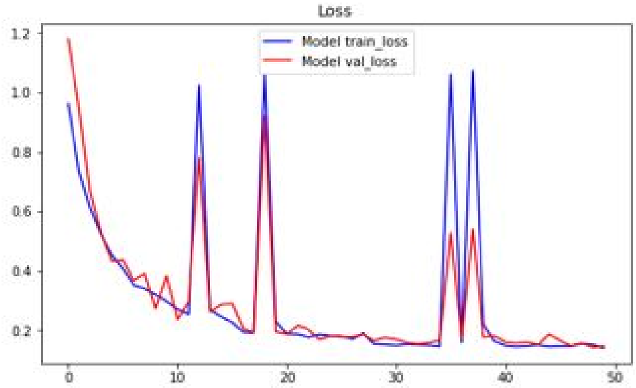


Figure 10: U-Net Train loss vs Validation loss performance

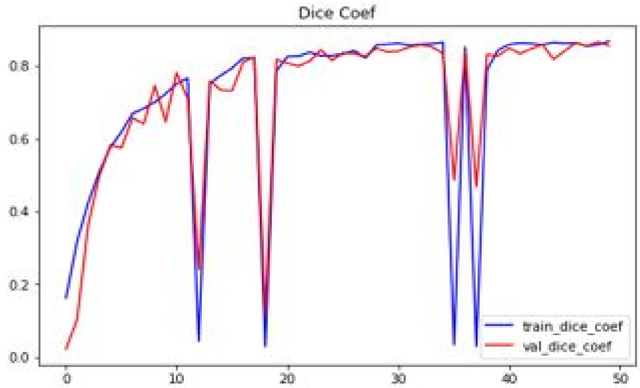


Figure 11: U-Net Train vs Validation Dice coefficient performance

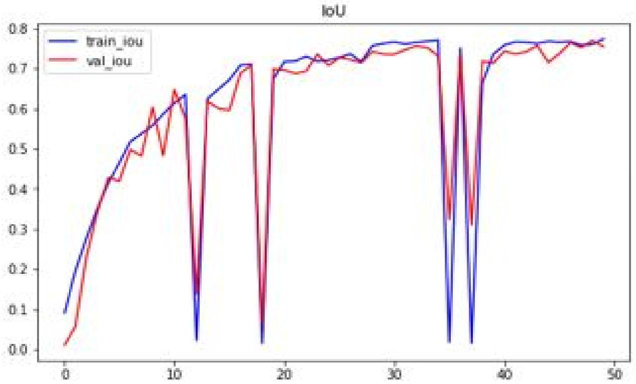
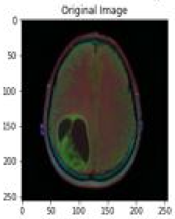
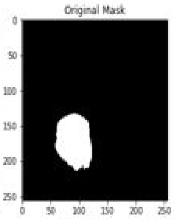
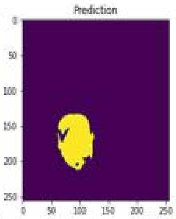
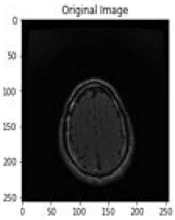
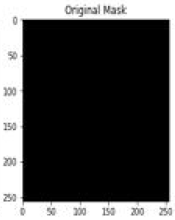
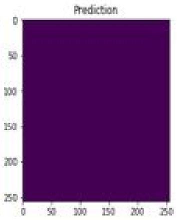
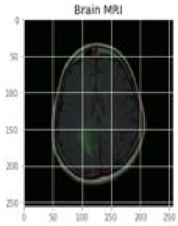
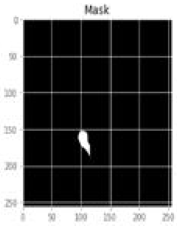
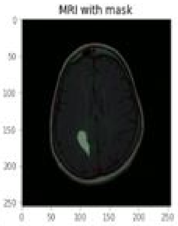


Figure 12: U-Net Train vs Validation IOU performance

From Figure 9, we can see that the training accuracy and validation accuracy are almost the same that is almost 100% and in Figure 10 the loss graph is a sketch showing very equal loss values. Furthermore, Figures 11 and 12 represent the Dice Coefficient and IOU perforce.

Table 1: Sample Test Case by U-Net Architecture

	Image	Ground Truth	Prediction
Test 1			
Test 2			
Test 3			

Conclusion and Future Scope

This project is mainly focused on MRI brain tumor segmentation by using U-net is an upper extenuate version of CNN. To evaluate the accuracy, we are adding the graph of Loss, accuracy, Iou, and Dice coefficients. The accuracy of the model is 99.75% and that is the best accuracy than other models. The contextual aspects of MRI scans are given special attention since they have proven to be useful in tumor segmentation. Although there are still areas for development and future investigation, the following are some of them:

- Creating a dependable system for the proposed model with an easy-to-use user interface. The interface would allow clinicians to upload an image and receive information on the tumor's location and classification.
- The model can be improved to predict the prognosis of patients with a brain tumor.

- Investigate a more robust solution for the massive database of clinical photos that may be noisy, influenced by external influences, and of worse quality.
- Apply the model to the detection and segmentation of cancers in various body parts.

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