International Journal of Advance Research in Science and Engineering
Volume No.08, Issue No.06, June 2019
www.ijarse.com
IJARSE
ISSN: 2319-8354

# DEEP NEURAL NETWORK SEGMENTATION OF BRAIN TUMOR IMAGES

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**Abstract**

The process of segmenting and classifying brain tumours is critical for evaluating malignancies and making treatment decisions. Because of its improved picture quality and lack of ionising radiation, magnetic resonance imaging (MRI) is extensively utilised for cancer diagnosis. Deep learning is a branch of machine learning that has lately demonstrated impressive results, particularly in segmentation and sub-segmentation challenges. The BRATS dataset 2017 is used to propose a Deep Learning model based on a convolutional neural network for segmentation of brain tumours in this study.

**Key words:CNN, KNN, Convolution Layer, RcLU Layer, Types of brain tumor**

## INTRODUCTION

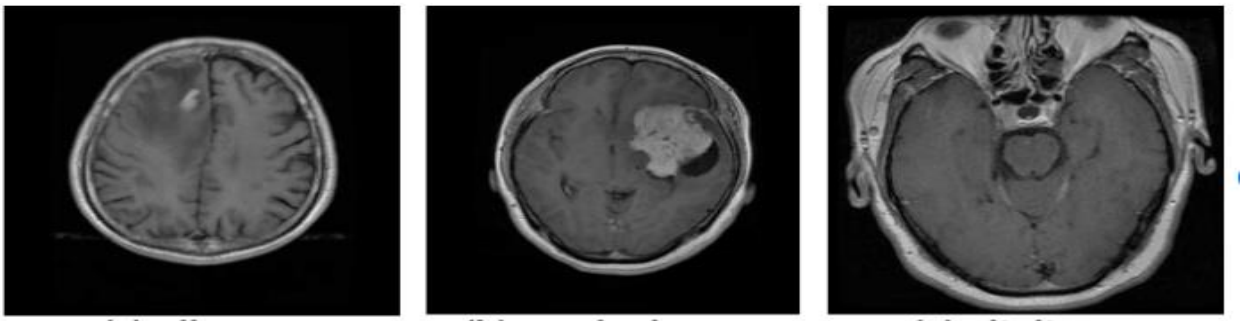
The brain is one of the most complicated organs in the human body, with billions of cells working together. When cells divide uncontrollably, they create an abnormal clump of cells surrounding or inside the brain, which is known as a brain tumour. These cells have the ability to disrupt the regular functioning of brain activity as well as kill healthy cells. According to a research issued by the World Health Organization (WHO), brain cancer accounts for fewer than 2% of all cancers in humans, yet it causes significant morbidity and consequences. According to the United Kingdom's Agency for Cancer Research Corporation, brain, other Central Nervous System (CNS), and intracranial cancers cause over 5,000 fatalities each year[3].

Brain cancers are classified in a variety of ways, including primary and secondary tumours, as well as metastatic brain tumours. The former accounts for around 70% of all brain tumours, whereas secondary tumours account for the remaining 30%. ( percent ).

This classification is based on the tumor's origin, much as primary tumours are those that begin in the brain. Secondary tumours, on the other hand, start in another region of the body and then spread to the brain, and the majority of them are malignant[1].

Brain tumour classification is based on the tumor's origin, and primary tumours are those that start in the brain. Tumors that start in another region of the body and then spread to the brain are known as secondary tumours, and the majority of them are cancerous. Tumors can be cancerous (also known as malignant) or non-cancerous (also known as benign)[2].

(or in a good way). Cancerous Malignant brain tumours develop quickly and spread to other parts of the brain and spine, making them more life-threatening than benign tumours. It might be either main or secondary. Tumors are divided into four categories in a more precise classification. 1st Figure Adults with gliomas have the most prevalent kind of primary brain tumour. Gliomas are classified according to the World Health Organization's severity grading system, which ranges from I to IV. Grade 1 tumors have benign cells that appear normal. Cells in grade two tumors appear to be slightly aberrant. Grade 3 tumors have malignant and aberrant cells. Fourth-degree brain tumors are the most dangerous because they involve rapidly spreading and abnormal cells. Meningioma tumors arise from the meninges, a layer of tissue that surrounds the brain and spinal cord. The Material The meninges protect the brain and spinal cord by covering them. Because meningioma tumors develop slowly and are less likely to spread, they are usually classified as benign tumors. Pituitary tumors arise in the pituitary gland and account for 14% of all primary intracerebral tumors, with most occurring spontaneously[3].



(a) glioma (b) meningioma (c) pituitary

Supervised learning uses an algorithm to find a mapping function between input variables and associated output labels to anticipate new subject labels. Using methods such as Artificial Neural Networks (ANN), Support Vector Machines (SVM) and K-Nearest Neighbors, the main aim is to uncover basic patterns within the training data (ANN) and to extract features from the training photos, which are often grayscale , texture, and statistical features to determine learning, which in most situations may require segmentation of the tumor prior to the feature extraction step.

These traits are called handmade traits and require an expert with extensive expertise and therefore the ability to grapple with the most important aspects[4].

Furthermore, because this task requires a lot of time and involves a lot of information, it is prone to errors.

Deep learning is a man-made intelligence function that mimics the human brain's data processing and pattern-making processes to be employed in higher cognitive processes. Deep learning technology is a subset of machine learning in artificial intelligence (AI) that uses networks to learn unsupervised from unstructured or unlabeled data. Also known as deep neural network or deep neural learning. Convolution Neural Network (CNN) is a type of deep learning that is often used in image analysis and is meant to need little preparation. It is based on biological processes in the human brain and is used to manage data from many arrays. The key advantages of Convolution Neural Networks over typical machine learning neural networks are feature learning and limitless accuracy, which can be obtained by increasing training samples and consequently resulting in a more robust and accurate model. Feature extraction is accomplished by convolving tiny lters with the input patterns and then selecting the most important differentiating features to begin coaching the classification network. The key advantages of Convolution Neural Networks over typical machine learning neural networks are feature learning and limitless accuracy, which can be obtained by increasing training samples and consequently resulting in a more robust and accurate model. Feature extraction begins with the convolution of tiny lters with the input patterns, followed by the selective extraction of the most important differentiating features[1].

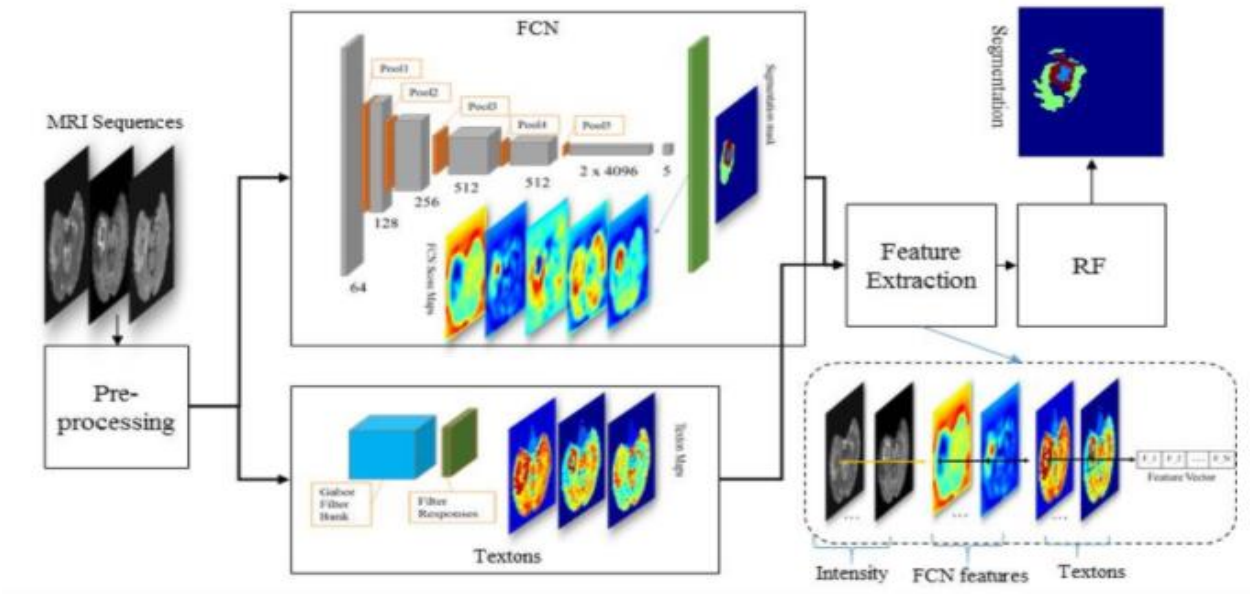



FIGURE 2: SYSTEM MODEL

Figure 2 shows the proposed method for tumor segmentation in brain MRI using a deep neural network model. The system starts loading in the first step. Start preprocessing by extracting images and captions from dataset files. After that, the dataset was divided into three sets: training, validation, and testing. The setting of hyperparameters, the regularization approach, and the optimization procedure will all be discussed once the proposed system is presented. The last stage proposes network training and performance calculation. Convolution neural networks are used in the proposed system in two phases. Phase I is used to segment the MRI image into a full tumor segmentation while Phase II is used to segment the tumor region into a full tumor region that enhances the tumor region and the tumor core region[2].

**IMPLEMENTATION**

a. DATASET

This project makes use of the BRATS 2017 dataset. MICCAI - Medical Image Computing and Computer-Aided Interventions Conference has issued a challenge. There are 210 folders of high-grade Glioma (HGG) training data, 66 folders of validation data, and 75 folders of low-grade Glioma (LGG) Cases in this collection. T1 (native), T1 contrast enhanced (T1ce), T2 weighted, FLAIR (T2 Fluid Attenuated Inversion Recovery), and ground-truth are the four information sequences found in each region. T1-weighting is the most often utilised structural analysis sequence, and it also allows for straightforward healthy tissue annotation. The tumour margins look brighter in T1 contrast-enhanced pictures because the contrast agent accumulates there due to breakdown of the blood-brain barrier within the proliferative tumour area[3].

The necrotic and active tumor regions can be clearly separated in this sequence. The zone of edema surrounding the tumor appears bright on T2 MRI. Since the free water signal is reduced, T2FLAIR could be a specific sequence that helps distinguish the edema area from the body fluid (CSF). Manual segmentation of ground truth labeled as follows: 1 for necrotic (NCR) and non-enhancing (NET) tumors, 2 for edema (ED), 4 for enhancing tumors (ET), and 0 for everything else, including normal tissue and background ( black upholstery). The tumor segmentation score is determined by combining the predicted markers into three regions: the entire tumor (1 + 2 + 4), the tumor core (1 + 4), and the tumor border (1 + 4)[5].

Promotion of tumor growth (4). These data sets were pre-processed, which includes co-registration to the same anatomical template, interpolation to the same resolution (1 mm3), and skull stripping. Each MRI sequence is 240 x 240 x 155 pixels.

b. PREPROCESSINGI

Isotropic, skull-stripped, and co-registered MR volumes are included in the BraTS2017 dataset. The following four data file sequences are preprocessed: T1, T1ce, T2, and T2 Flair. The data are

normalized by subtracting the mean and dividing by the standard deviation to reduce the intensity of the volumes. SimpleITK is used to read data in NIFTI format and convert it to numpy array format. Each subject's data is 240 x 240 x 155 pixels, but we only use the 60-120. axial slices as training data since the rest of the brain is not used.

c. CNN ARCHITECTURE

There are two parts to this brain tumour segmentation model experiment. To begin, we utilise a 9-layer U-net design (Figure 3.4) to segment the whole tumour. Second, the tumour core and augmenting tumour are segmented using the segmentation results as input for two seven-layer U-net designs. The proposed architecture can be thought of as an auto-encoder, with a contraction network attempting to find image features and an expanding network attempting to reconstruct an occasional dimensional data representation of the image, similar to the bottom truth of information, using these features[3].

The expanding network is made up of up-sampling/transposed convolution layers, whereas the contracting layer is made up of stacked convolution/pooling layers. High-resolution characteristics from the contracting route are concatenated with the up-sampled output of successive stages in order to localise. These are referred to as "skip connections." The advantages of skip connections are that they send feature information to lower layers, making it easier to categorise minute features[4]. When you execute maximum pooling, some spatial information is lost. Because the nal layer feature will contain more information, skipping connections can assist improve classification accuracy. They distinguish between long and short skips that cover more than one residual block. The difference between the original U-net and our U-net is that after each convolution layer, we connect a batch normalisation to keep the gradient levels controlled, speed up training, and reduce the effect of internal covariate shift, so the network parameters don't change rapidly during back propagation.We employ the same padding to keep the output size of convolution layers unchanged, which is also different from the original U-net. Two layers of convolution/batch normalisation are added to expand the receptive led at the lowest resolution. They quadruple the number of feature channels with each down-sampling step. Every step in the expansive path starts with an upsampling of the feature map, then a 2 x 2 transposed convolution (transposed convolution ") that halves the number of feature channels, a concatenation with the correspondingly cropped feature map from the down-sampling path, and two 3 x 3 convolutions. The ultimate procedure might be a 1 x 1 because every model is binary segmented[2].

d.Convolution Layer

Layers of convolution The primary building components used in convolutional neural networks are depicted in Figure 3.5. A convolution is the simple application of a lter to an input that results in activation application of the identical lter to input results in a map of activations known as a feature map, which indicates the positions and intensity of a recognised feature in an input, similar to a picture. CNN - convolutional neural networks - are unique in its capacity to automatically learn an enormous number of lters in parallel specific to a training dataset within the restrictions of a chosen predictive modelling task, such as image classification. The end result is a set of extremely specific characteristics that can be found anywhere on the input photos[1].

e. ReLU Layer

Each convolution layer is followed by a non-saturated activation function termed ReLU, which is primarily used to reduce training time. The following equation defines the ReLU model as a function of x, with the output equaling the input when x is positive and 0 otherwise. The ReLU function is depicted visually in gure 3.6 f (x) = max (0, x)

f. Max pooling

This allows us to reduce the number of factors, which both shortens training time and combats over tting. Stacking layers Figure 3.7: Independently down sample each feature map, lowering the peak and breadth while maintaining the depth. The most common type of pooling is max pooling, which simply takes the maximum value in the pooling window. There are no parameters in the pooling operation. It simply moves a window over its input and takes the maximum value within the window. The window size and stride are specified in the same way as for a convolution.

g. Batch normalization

Each batch, that is, makes a modification that keeps the mean activation close to 0 and hence the activation variance close to 1.

Tumor classification

There are two types of data training and validation. The training data are divided into two categories: HGG (Higher Grade Glioma) and LGG (Lower Grade Glioma) (Lower grade Glioma). Each category has four les: T1, T1CE, T2, T2 FLAIR, and Ground Truth. HGG has 210 les folders, whereas LGG has 66 les folders. Validation additionally contains 75 information folders. To identify the tumour location, we use labelling inside the ground truth as shown below.

The whole tumour zone was identified by examining non-zero values in the data. The image's necrosis region is identified in the array with the value 1 and cleared. every other value Value 4 identifies the tumour area and clears all other vales. Value 2 identifies the edoema area.

The tumour area prediction is completed by running the model numerous times. Initially, run the model to train the data for the entire tumour area, and it will output a weighted le. This type of system operation was used for Necrosis, Enhancing tumour, Non-enhancing tumour, and Tumor core. Second, the tumour location in an image is recognised by loading the model with the needed training weighted le and inputting a specific slice[1].

The planned model is perfected by comparing our system output to the relevant ground truth slice. The following approach is used to identify the tumour core and enhancing tumour during a full tumour area. When you run the model with weighted le for enhancing tumour and input projected whole tumour picture, the model will detect the region of enhancing tumour component inside the input image. The same procedure is used to identify tumour cores across the tumour area.

In this study, a deep neural network - U-net - is used for training to be told the features of segmented regions inside 3D MRI images such as total tumour (WT), enhancing tumour (ET), and tumour core (TC).

We are labelling areas such as the whole tumour, necrosis, edoema, tumour core, enhancing tumour, and non-enhancing tumour. All of the modalities listed above were utilised to segment WT, TC, and ET.

During the preprocessing step, 3D photos are transformed to 2D images with dimensions of 155 x 240 x 240, and then to numpy array format of type oat32. Then, as previously described, create a deep neural network in the form of a U-net architecture. During this architecture, a model is created by invoking a model function inside Keras and using slices of a 2D input picture as input and output from the final layer within the U nett as output. The model is then compiled using the following steps[2].

Adam optimizer-the Adam optimization technique is a stochastic gradient descent variant that has lately gained traction for deep learning applications in computer vision and linguistic communication processing. Examine the loss function using the dice coe cient function. Loss and metrics are assessed with the dice coe cient function.

To train the model, build an instance of the U-net model with the settings shown below. X as a numpy array of raw data input and Y as a numpy array of ground truth output, batch size determining the set of input picked, here set to four. Validation divided the entire set of data into

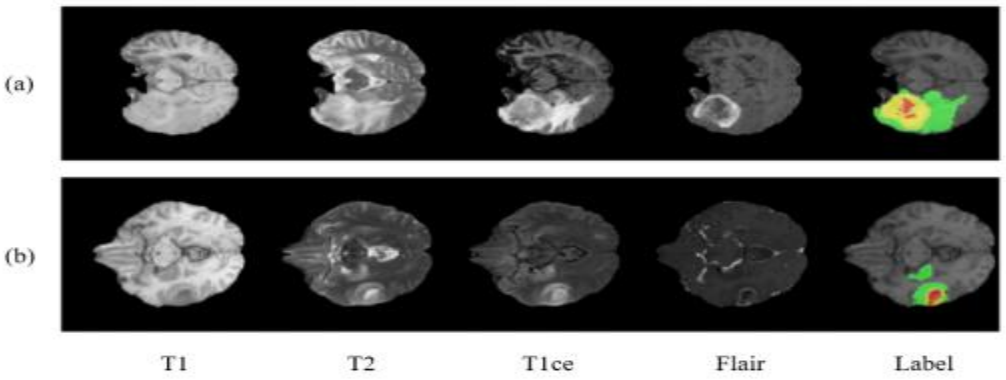
training and validation. Epochs determine how many times the iteration is repeated; as more epochs are considered, the perfection of coaching becomes obvious[3].

The model returns a weighted e called lename at the end of coaching. h5.

**RESULT**

Brain tumour segmentation divides the tumour into three regions: (a) the whole tumour (WT), (b) the tumour core (TC), and the Enhancing tumour (ET). First, DNN segments the whole tumour area. The qualitative outcome of this approach is seen in Figure 3.

Second stage 7 layers U-net segments tumour core and tumour promoting zones. The qualitative result of tumour core and Enhancing tumour is shown in Figure 4. Following the post-processing stage, the whole tumour region is labelled, including the tumour core and augmenting tumour region.




Three Evaluation metrics are used for tumor segmentation
*Dice Coe cient.*

The Dice-Coe cient is the primary measure used in biomedical picture segmentation. Table 1 shows the dice coe cient value of sample data with training, and Figure 5 depicts its curve. Figure 6 depicts the system's loss function with sample data. This metric reflects the degree of similarity between prediction and annotation[4].

3. Dice = (2 x TP + FN + FP)/(2 x TP + FN + FP)

Sensitivity and the city of Speci.

Sensitivity is the ratio of correctly predicted voxels to true positive voxels. Speci city represents the projected percentage of true negatives. These measures can assist us in determining if our strategy over-segments or under-segments tumour areas.

TP/(TP + FN) = Sensitivity

Speci city = (TN + FP)/(TN + FP)

Confusion matrices are used to assess the performance of a system. The number of positive anticipated instances that are actually positive is referred to as the True Positive (TP). True Negative (TN) is the number of anticipated negative situations that are also genuinely negative. False Negative (FN) is the number of anticipated negative cases that are really positive, also known as (type two) error[5].

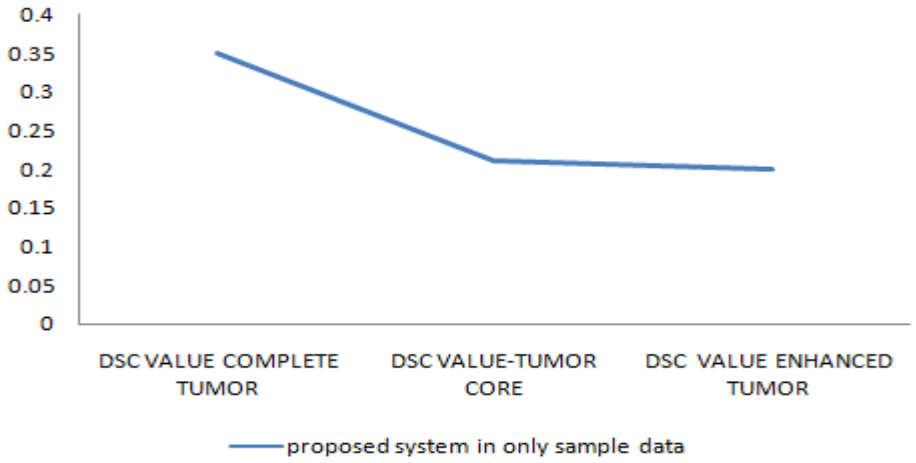



Figure 5: Dice Coe cient value of training data and validation data at different Epochs

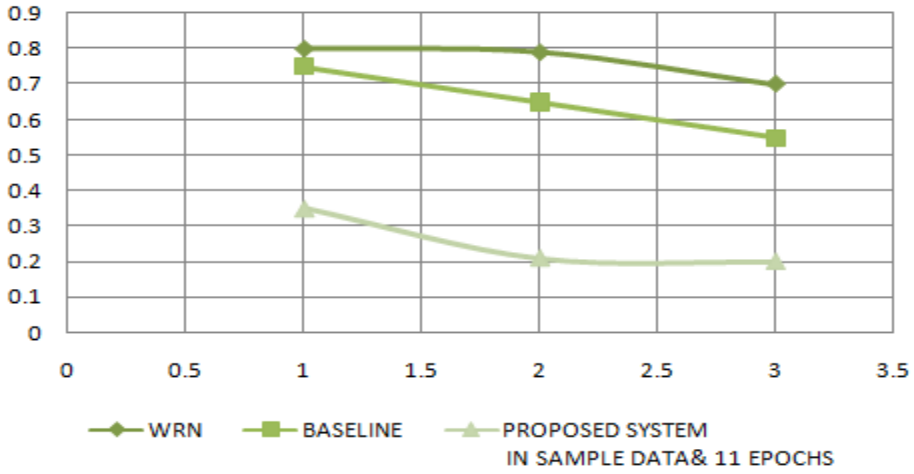



Figure 6:Loss function value of training data and validation data in different Epoch

## ACCURACY COMPARISON

| CNN model | DSC VALUE COMPLETE TUMOR | DSC VALUE-TUMOR CORE | DSC VALUE ENHANCED TUMOR |
|---|---|---|---|
| **proposed system in only sample data** | **0.35** | **0.21** | **0.2** |

Table 1: Dice Coe cient value in training dataset of BRaTs 2017

| CNN model | DSC VALUE COMPLETE TUMOR | DSC VALUE-TUMOR CORE | DSC VALUE ENHANCED TUMOR |
|---|---|---|---|
| **WRN** | 0.8 | 0.79 | 0.7 |
| BASELINE | 0.75 | 0.65 | 0.55 |
| PROPOSED SYSTEM IN SAMPLE DATA& 11 EPOCHS | 0.35 | 0.21 | 0.2 |

Table 2: Comparison with Di erent Networks

## CONCLUSION

In conclusion, a deep convolutional U-net network for brain tumour segmentation is proposed. We use a deep convolutional neural network with four MRI image sequences as input: T1, T1CE, T2, and T2 FLAIR. The three segmentation results are the output of our network. In contrast to existing DNN-based segmentation methods that focus on enhancing the quality of the collected features, our technique incorporates past information into brain tumour sub segmentation. The first stage of 9 layer U-net segments has finished the tumour area. In the second step, a 7-layer U-net loads the input from the first stage. This DNN divides the entire tumour into the tumour core and the increased tumour area. The 9 layer DNN technique learns how to extract more abundant features for identifying the tumour location by adding batch normalisation methods and a padding mechanism to various levels. According to the results, our approach is of moderate level in terms of multi-staged segmentation.

This initiative divides brain tumours into three categories: full tumour, tumour core, and enhancing tumour. The suggested network was tested using the BRATS 2017 dataset. Our suggested technique performed well on the BRaTs dataset, with average DSC values of 0.37, 0.25, and 0.19 for entire tumour, tumour core, and enhanced tumour, respectively. Overall, our technique performs moderately well in this area of DNN.

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