AI Driven Brain Tumor Segmentation using U-Net: A Deep Learning Approach

Okunade Temilola
Dept. of Comp. Sci.
Lagos State University
of Sci. and Tech
Lagos, Nigeria

Amusu Mary I.
Dept. of Comp. Sci.
Lagos State University
of Sci. and Tech.
Lagos, Nigeria

Aremu Idris A.
Dept. of Comp. Sci.
Lagos State University
of Sci. and Tech
Lagos, Nigeria

Tiamiyu Olalekan S.
Dept. of Comp. Sci.
Lagos State University
of Sci. and Tech
Lagos, Nigeria

Ganiu Serifat
Dept. of Cur. Tech & Le
Memorial University
Newfound Land
Canada

Davies Muyis
Dept. of Comp. Sci
Western Govr University
Utah USA

ABSTRACT
Brain tumors are brought on by the growth of aberrant cells in an unfavorable region of the brain. There are two types: malignant tumors, which are more aggressive and carcinogenic and can spread to other parts of the body, and benign tumors, which are less aggressive and non-cancerous. One of the deadliest types of cancer, a brain tumor is a life-threatening condition. Early identification and precise segmentation constitute the first step in the treatment of brain tumors. The most used medical imaging technique for assessing brain tumors is MRI (Magnetic Resonance Imaging). Manual segmentation requires a lot of time and effort and is subject to human error and judgment. An automatic segmentation technique based on U-Net, a Convolutional Neural Network (CNN), was proposed in this study, developed for biomedical imaging. The BraTS 2021 dataset, which includes three-dimensional MRI images in four different modalities (T1, T1ce, T2, and T2 Flair, each with four labels), was used to train and test the network. The final model has a 99.4 percent accuracy rate.

Keywords
Image segmentation, MRI, Brain tumor, CNN, non-cancerous

1. INTRODUCTION
According to Kalaiselvi etal (2020), one of the most important organs in the human body is the brain. It consists of billions of cells and is responsible for decision-making and control. It is vital to protect it from harm and illness because it is the controlling center of the neurological system. A brain tumor is a tissue that grows in an area of the brain where it shouldn't. It can also be characterized as unregulated tissue expansion. The growth of aberrant cells within the brain causes brain tumors and it can be cancerous or non-cancerous. Benign tumors are non-cancerous, less aggressive tumors that grow slowly and do not spread to other parts of the body. Malignant tumors, on the other hand, are tumors that develop quickly and have a proclivity for spreading to other parts of the body. One of the most dangerous diseases that can lead to death is a brain tumor, therefore it is critical to understand the stages of a brain tumor's growth in order to avoid and treat them. Magnetic Resonance Imaging (MRI) is a technique used by radiologists to examine brain tumors. This is because MRI produces high-resolution, high-contrast images of organs, soft tissues, bone, and practically all other inner body components using a powerful

magnetic field, radio-frequency pulses, and a computer Singh et al (2015). The images can then be seen on a computer monitor, transferred electronically, printed, or copied to a hard disk. Ionizing radiation is not used in MRI (unlike x-rays). Using comprehensive MR pictures, doctors may examine various parts of the body and discover problems (Glassman N., 2010). Medical image segmentation is required for surgical planning, postsurgical assessment, anomaly identification, and a variety of other medical applications. Human mistake and subjective judgments can occur during manual segmentation, which is a time-consuming and labor-intensive job. This raises the chances that various witnesses may come to different conclusions about the presence or absence of tumors, or that the same observer will come to different judgments at different times. As a result, automatic segmentation is necessary to assist doctors in precisely segmenting tumor areas and making decisions in the diagnosis of brain tumors, as opposed to manual segmentation and decision-making.

Despite the fact that a range of automatic and semi-automatic image segmentation algorithms are available, they fail in the majority of cases due to unknown and irregular noise, inhomogeneity, poor contrast, and weak borders present in medical images. Picture segmentation is critical in image analysis and interpretation. Tissue classification, tumor detection, tumor volume calculation, blood cell delineation, surgical planning, and matching are just a few of the brain imaging uses (Tiwari et al., 2020). The Convolutional Neural Network (CNN) is used in this study to segment three dimensional (3D) MR images of brain tumors.

El-Amir et al (2020) in their research, found out that CNNs are a sort of deep learning and artificial neural network that can take an input image and assign levels of relevance (learnable weights and biases) to different objects or aspects of the image, allowing them to be distinguished from one another. The quantity of pre-processing required by a CNN is much smaller than that required by other classification algorithms. An input layer, an output layer, and n hidden layers make up a CNN. Multi-convolutional layers, pooling layers, totally linked layers, and normalization layers are all examples of hidden layers. Convolutional layers compute the output of neurons connected to the input layer. Each neuron calculates the total of its many weights. The pooling layers perform a down sampling operation on the feature maps' width and height (spatial dimensions) (Frniak et al., 2019). All activations in the

previous layer are fully connected in the fully connected layer. A multitude of activation functions are carried out by the CNN system. TanH, ArcTan, Rectified Linear Unit (ReLU), Parametric Rectified Linear Unit (PReLU), Exponential Linear Unit (ELU), and SoftPlus are among them (Kalaiselvi et al., 2020). ReLU and Softmax are employed in this research. The goal of this research is to create a deep Convolutional Neural Network model for detecting and segmenting brain tumors using MRIs. MRIs will be used to train and test the developed model.

2. REVIEW OF RELATED LITERATURES

Researchers have worked hard to partially or completely automate the task of brain tumor segmentation and identification, with some of the results highlighted below:

Using a combination of Fuzzy C-means for segmentation, Discrete Wavelength Transform (DWT) for feature extraction, and Deep Neural Network (DNN) for classification, Mohsen H et al. (2018) suggested a methodology for classifying brain tumors into three categories of malignant brain tumors. In terms of accuracy, they claim that DNN classifiers surpass classical classifiers. Extending the application of DWT to CNN has been identified as a research topic for the future.

For brain lesion segmentation, according to Kamnistas et al (2017), suggested an 11-layered deep 3D CNN. Their design was created to look at the flaws in the available networks for brain lesion segmentation applications at the time. To speed up the processing of 3D scans, a dense training system was implemented in their research. The researchers realized that the inference method needed to be made more understandable.

Pereira et al. (2016) proposed a CNN with 3 x 3 kernels-based automatic segmentation method. When the number of weights is low, they found that using small kernels aids in the design of a deeper architecture and provides confidence against over fitting issues. Their pre-processing step includes intensity normalization, which is uncommon in CNN-based segmentation methods.

A strategy for categorizing brain tumor images was presented by Afshar et al. (2018). One convolutional layer with sixty-four (64) feature maps and sixteen (16) main capsules was used in the approach. The investigation yielded an accuracy rating of 86.56 percent. Investigations are currently ongoing into how adding more capsule layers would affect classification accuracy.

Saxena et al. (2019) in their study, used the VGG16, InceptionV3, and ResNet50 models to classify brain tumor data in their study. In this study, they used transfer learning methods to get the best accuracy rate in the ResNet50 model, with 95% accuracy. Hyper-parameter tuning and better preprocessing methods were identified as ways to improve the model's performance after examining the effect of newer architectures.

In Shahzadi et al (2018) study, brain tumor categorised cells using the CNN - LSTM hybrid design. They claimed to have classified the network with 71 percent accuracy using AlexNet-LSTM, 84 percent accuracy using VGGNet-LSTM, while that of ResNet-LSTM is 71 percent.

Charfi et al. (2014) in their research reported a method for categorizing MR images of brain malignancies. The proposed machine learning method used in their study applied the histogram equalization method for picture segmentation and Principal Component Analysis (PCA) to reduce the size of the resultant data. Finally, for the classification procedure, a feed-forward back propagation neural network was deployed. 90 percent accuracy was attained in identifying pictures (as normal or pathological). The challenge of providing generalized CAD systems that work for all database size and quality and the need for collaboration to build larger datasets were identified as worthy of future research efforts.

According to Citak-Er et al. (2018) in their study of brain tumor image segmentation, used three different Machine Learning algorithms. These algorithms are Support Vector Machines (SVM), Multi-layer Perceptions, and Logistic Regression. The research achieved 93 percent accuracy. However, there is need to investigate the use of machine-learning algorithms for brain tumor classification in a larger collection of patients.

In Ronneberger et al. (2015), a U-Net architecture was developed, a network and training strategy that strongly uses data augmentation so that the available annotated samples can be used more efficiently. The structure consists of a contracting path to capture context and a symmetric expanding path that enables precise localization. The network can be trained end-to-end from very few images.

In Feng et al. (2020) a model based was developed on the U-Net structure, with adaptations in the training and testing strategies, network structure and model parameters for brain tumor segmentation. Instead of picking the best model, it uses an ensemble (6) of multiple models trained with different hyper-parameters to reduce random errors from each model and improve performance. However, there were no objective measures to achieve optimal combination of models, the number of models and the corresponding hyper-parameters that were empirically determined.

3. METHODOLOGY

3.1 The U-NET Architecture

The research model is built on U-Net, a Convolutional Neural Network developed in 2015 by Olaf Ranneberger, 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 precedes a rectified linear unit (ReLU) and max-pooling layers in the encoder. The image is down sampled by lowering spatial information and enhancing feature information. The image resolution is halved and the feature map is doubled with each down sampling step. The decoder combines feature and spatial information through a series of up-convolutions and concatenations with high-resolution features from the contracting path. 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.
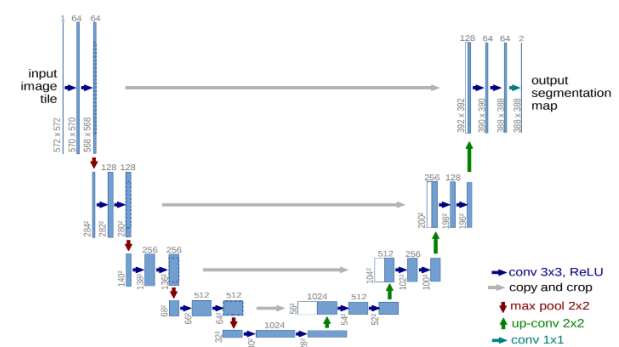

Figure 3.1: U-Net Diagram

3.2 Network and Training

The size of the input image in the network is 128 x 128, 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.

The softmax function is represented as equation
$$\sigma(\vec{z}) = \frac{e^{z_i}}{\sum_{j=1}^{K} e^{z_j}} \qquad (3.1)$$

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.

The softmax function is the activation function in the final convolution.

Categorical cross entropy function was used as the loss function. It is given as:
$$Loss = -\sum_{i=1}^{output\ size} y_i\ log\ log\hat{y}_i \qquad (3.2)$$

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.

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:

$$DSC = \frac{2|X \cap Y|}{|X|+|Y|} \qquad (3.3)$$

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:

$$Precision = \frac{True\ Positive}{True\ Positive + False\ Positive} \qquad (3.4)$$

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

$$Sensitivity = \frac{True\ Positive}{True\ Positive + False\ Negative} \qquad (3.5)$$

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

$$Specificity = \frac{True\ negatives}{True\ negatives + False\ positives} \qquad (3.6)$$

4. EXPERIMENTAL SETUP

4.1 Dataset

The dataset utilized in this research 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 Neuro-radiologist. Enhancing tumor, necrosis or non-enhancing tumor, edema, and healthy tissue are the four main classes in the dataset (Baid et al., 2021, Bakas et al., 2017 & Menze et al., 2015). The total dataset used was 1666, partitioned into 1219 for training and 447 for testing.
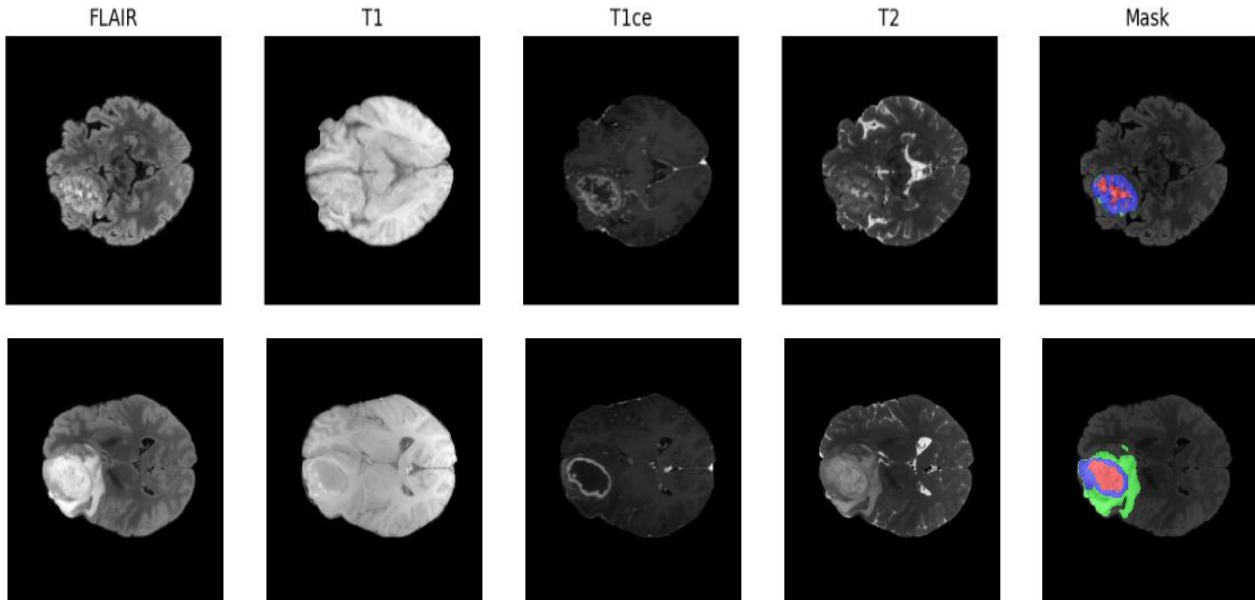

**Fig 4.1: Sample Cases from the Dataset**

4.2 Setup

The model was trained using real patient's 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).

5. RESULTS AND DISCUSSION
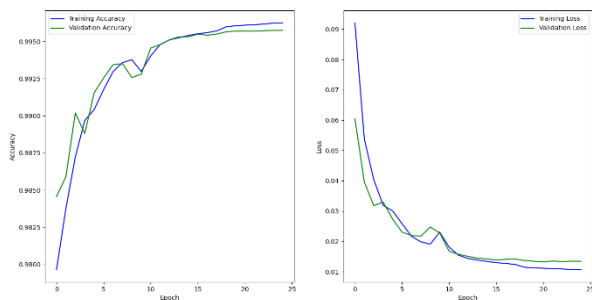
Fig. 5.1: Accuracy and loss of training and validation against the number of epochs
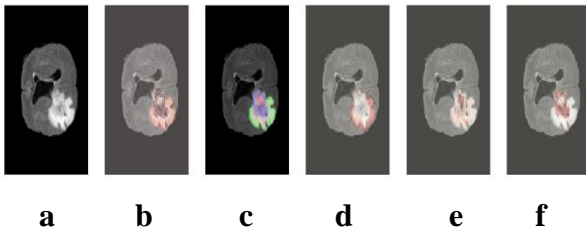
a   b   c   d   e   f
Fig 5.2: Ground Truth and Prediction

Figure 5.2 shows the original image (a), ground truth (b), prediction of all classes (c), prediction of tumor core (d), edema (e) and (f) and enhancing tumor regions respectively.

The results of the experiment are reported using five (5) metrics: Accuracy, Dice Score Coefficient, Precision, Sensitivity and Specificity as seen in figure 5.3. 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.
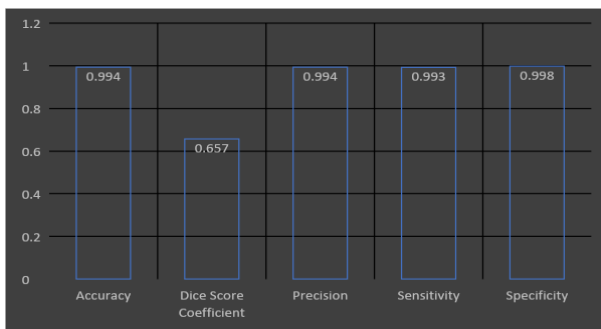
Fig 5.3: Performance Chart

5.1 CONCLUSION

This study introduced an effective technique for automatically segmenting brain tumors from MRI data by fine-tuning the parameters of the U-Net architecture. The proposed approach involved converting three-dimensional MRI images into two-dimensional slices for network training, optimizing both computational efficiency and performance.

The accurate and early detection of brain tumors is critical for effective treatment planning. Manual segmentation, being time-consuming and error-prone, highlights the need for automated solutions. This study addressed this challenge by developing a Convolutional Neural Network (CNN) based on the U-Net architecture. The network was trained on the BraTS 2021 dataset, which provided 2D slices extracted from 3D MRI scans, achieving an impressive accuracy of 99.4%.

The implementation leveraged Python and advanced machine learning libraries, demonstrating the potential of automated techniques to significantly enhance medical imaging workflows.

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