Brain tumor segmentation using an extension of an encoder-decoder fully convolutional network

ISRAKA JAHIR and SADIA SULTANA, North South University, Bangladesh

1 ABSTRACT

Brain tumor is considered as one of the most serious causes of death in the world. There are various distinct steps that may be used to identify brain tumors using magnetic resonance imaging (MRI). In the field of medical imaging, segmentation is the key stage. Segmentation is carried out after classification and image analysis. The appropriate segmentation is crucial since a brain tumor's incorrect detection might have a number of negative effects. To automate and standardize segmentation procedure, we trained U-net convolutional network, backbone of U-net convolutional network and Link net model, on the BRATS 2020 dataset. The openly accessible dataset has 40GB data containing 371 NiFTI-format folders. To remove the brain tumor from the MRI images, we employed ensemble deep learning with VGG, Resnet, and Inception. Link-net was included purely for comparison's purposes. The main focus of our study is the ensemble model, which has a higher IOU score and accuracy of 97.21 %. The method outperformed currently used traditional methods for detecting brain tumors, achieving an IOU score of U-net 58 % Ensemble (VGG, Resnet, Inception) 61 % and Link-net 56 % in the testing dataset. The document also offers suggestions for future research in this sector.

ACM Reference Format:
Israka Jahir and Sadia Sultana. 2024. Brain tumor segmentation using an extension of an encoder-decoder fully convolutional network. 1, 1 (February 2024), 8 pages. https://doi.org/10.1145/nnnnnnn.nnnnnnn

2 INTRODUCTION

The brain is a complex organ which contains blood vessels and nerves, including neurons and glial cells. It is an organ which is considered the kernel part of the body [1]. Brain tumors are abnormal cells growing in human brains, regarded as a type of common neurological disease, which is harmful to human health extremely [2]. Primary brain tumors begin when normal cells develop changes (mutations) in their DNA. A cell's DNA contains the instructions that tell a cell what to do. The mutations tell the cells to grow and divide rapidly and to continue living when healthy cells would die. The result is a mass of abnormal cells, which forms a tumor. Brain tumors are threatening because they can put pressure on healthy parts of the brain or spread into those areas. Many different types of brain tumors exist, some brain tumors are noncancerous (benign), and some brain tumors are cancerous (malignant). A primary brain tumor is an abnormal growth that starts in the brain and usually does not spread to other body parts. Primary brain tumors may be benign or malignant. A benign brain tumor grows slowly, has distinct boundaries, and rarely spreads. Although its cells are not malignant, benign tumors can be life-threatening if located in a vital area. A malignant brain tumor overgrows, has irregular boundaries, and spreads to nearby brain areas. Although they are often called brain cancer, malignant brain tumors do not fit the definition of cancer because they do not spread to organs outside the brain and spine. [3]

They can cause problems if they block the flow of fluid around the brain, which can lead to an increase in pressure inside the skull. Meningiomas (benign tumor) are the most common brain tumor in adults, accounting for one out of three primary brain and spinal cord tumors. The risk of developing a meningioma increases with age, and they occur about twice as often in women. Gliomas (malignant) are the most prevalent type of adult brain tumor, accounting for 78 percent of malignant brain tumors. The growth rate of a brain tumor as well as the location of a brain tumor determines how it will affect the function of your nervous system. An estimated 700,000 Americans are living with a primary brain tumor. Among them approximately 71% of all brain tumors are benign, 29% of all brain tumors are malignant and 58 of all brain tumors occur in females where 42% of all brain tumors occur in males [4]. According to the International Agency for Research on Cancer (IARC), the mortality rate due to brain tumors is 76%. It is required to detect the brain tumors as early as possible and to provide the patient with the required treatment to avoid any fatal situation [5].

The process of diagnosing brain tumors is very complicated for many reasons, including the brain's synaptic structure, size, and shape. Tumor segmentation represents the correct identification of the spatial location of a tumor. Manual segmentation performed by a radiologist is considered the gold standard. In fact, an essential step is to exclude normal tissues by segmentation and extract more relevant characteristics of lesions for a better diagnosis. Machine learning techniques are employed to help doctors to detect brain tumor and support their decisions. Artificial intelligence, or AI, is currently highly popular in the research world, particularly in the field of medical research. Numerous AI applications are useful for early disease detection. Deep learning (DL), a component of AI, uses a variety of methods to diagnose diseases accurately. AI approaches are applied to the automated 2 segmentation of MR images to detect brain tumors. The segmentation of the brain tumors had been conducted on many studies. The outcomes of this study work have been enhanced by newly developed approaches as well as by current methods. For the detection of the brain tumors, the radiologists must use the computer-aided systems. Under typical circumstances, radiologists in the medical area may need more than half an hour or so to find tumors and complete the segmentation procedure. However, compared to older methods, new ones enable professionals to identify tumors with more accuracy and speed. MRI

Authors' address: Israka Jahir, israka.jahir@northsouth.edu; Sadia Sultana, sadia.sultana06@northsouth.edu, North South University, Bashundhara R/A, Block-B, Dhaka, Bangladesh.

XXXX-XXXX/2024/2-ART $15.00
https://doi.org/10.1145/nnnnnnn.nnnnnnn

scans are used for the quick and simple detection of tumors. Imaging technique that is most frequently employed is magnetic resonance imaging, or MRI. MRI employs a number of modalities, such as T1CE, T2, and FLAIR (Fluid- attenuated inversion recovery). These modalities depict each mode of the brain in a distinctive manner [1].

In order to predict and segment brain tumor, many approaches have been proposed. The efficient classification and segmentation of tumors from surrounding brain tissues is a crucial task. Therefore, they suffer from different problems such as the necessity of the intervention of a specialist, the long-required run-time and the choice of the appropriate feature extractor [6]. To address these issues, we proposed brain tumor segmentation using an extension of an encoder-decoder fully convolutional network. Our segmentation models for MR images included Ensemble Deep Learning using VGG, Resnet, Inception. Link-net was included for comparison purpose. There is no ensemble model based on U-net backbone (VGG, Resnet, Inception). Our project is focused on ensemble model with better accuracy and IOU score.

The main contributions of this paper can be summarized as follows:

1. The BRATS 2020 dataset uses a model which is based on encoders and decoders. They used 371 folders of NiFTI files in this dataset, and each folder comprises 5 different types of images, which is based on MRI modalities in Figure 1 as well as segmentation images also.

2. We suggest an extension of encoder-decoder architecture and employ U-net architecture for image segmentation and mask prediction.

3. We contrasted the findings of various segmentation models, including the proposed model, standard U-Net, Backbone of U-net (VGG, Resnet, Inception), and Link net.

3 LITERATURE REVIEW

3.1 AResU-Net: Attention Residual U-Net for Brain Tumor Segmentation

In this paper, they proposed an end-to-end 2D brain tumor segmentation network, attention residual U-Net (AResU-Net), which simultaneously embeds attention mechanisms and residual units into U-Net for the further performance improvement of brain tumor segmentation. AResU-Net incorporates a series of attention units into the corresponding down- and up-sampling processes, and it adaptively rescales features to effectively improve. They extensively evaluate AResU-Net on two MRI brain tumor segmentation benchmarks, the BraTS 2017 and BraTS 2018 datasets. In their study, experiment results show that the proposed AResU-Net outperforms its predecessors. To attain a better result, achieve performance equivalent to traditional brain tumor segmentation methods. Compared to the U-Net baseline, AResU-Net improves performance by 1.60%, 2.00 %, and 0.60% on the total tumor, core tumor, and enhanced tumor segmentation, respectively. In compared to several previous approaches, AResU-Net also gets the greatest performance on tumor segmentation enhancement. [7]

3.2 UNet-VGG16 with transfer learning for MRI-based brain tumor segmentation

In this work, the MRI brain tumor is segmented to provide a clearer view of the 1.5 Tesla machine's MRI image and attempt a comparison between the suggested model and the previous state-of-the-art model. We use 100 epochs for the training procedure, which is run on a machine with an Intel Core i7 processor, 32 GB of RAM, a 128 GB SSD, and no GPU or VRAM. The convolutional network used in this study, UNet-VGG16, has a new architecture. This model or architecture combines Transfer Learning with U-Net and VGG16. It has a high accuracy in the learning dataset of roughly 96.1%. The visualization of segmentation results demonstrated that the sample sequence's segmentation results could identify the tumor area as ROI in a range of tumor sizes and locations, both on the left and right sides of the brain.The suggested model outperforms the U-Net model (in four scenarios) because it has the lowest loss and highest accuracy values.The segmentation outcomes for each brain tumor MRI image under the suggested methodology typically come quite close to the ROI target. The results of segmentation from testing data were obtained with a CCR value of 95.69%.[10]

3.3 A Modified U-Net Based Architecture for Brain Tumor Segmentation on BRATS 2020

In this paper, they present an encoder-decoder U-shaped 3D model based on deep learning for automatic segmentation of brain tumors from MRI data.In the suggested system, the U-Net model is applied to improve the performance of the conventional model.For the research work,they have used the BRATS 2020 dataset which is publicly available.It may be useful for radiologists and medical researchers in the early detection of tumors.The proposed model is compared to the traditional 3D U-Net model, FPN, and Linknet models.By doing this, they demonstrate how the model reacts to different changes, such as the addition of layers. Include dropout changes in the model's layers as well. The performance of the state-of-art models' is not as impressive as the one that is proposed. The accuracy of the proposed model is 0.9819, while the IOU score is 0.6588. It might be used to segment tumors accurately in real-time systems.[1]

3.4 3D MRI brain tumor segmentation using autoencoder regularization

In this paper, they present the BraTS 2018 winning semantic segmentation method for volumetric 3D brain tumor segmentation from multimodal 3D MRIs. They use an asymmetrically big encoder to extract deep image features, and a decoder that reconstructs dense segmentation masks. This is similar to the encoder-decoder structure of CNN. In order to regularize the shared encoder, they additionally add the variational autoencoder (VAE) branch to the network, which reconstructs the input pictures alongside segmentation. Only the primary segmentation encoder-decoder component is used during inference. They also tested more advanced data augmentation approaches, such as random histogram matching, affine picture transforms, and random image filtering, but found no additional benefits. Without using any additional internal data, they built their network in Tensorflow and trained it on an NVIDIA Tesla

V100 32GB GPU with the training dataset (285 instances).They provide the outcomes of their approach to validation sets (66 cases) and testing sets (191 cases). The average dice for the testing dataset are 0.7664, 0.8839, and 0.8154 for enhanced tumor core, entire tumor, and tumor core, respectively. Finally, the additional VAE branch assisted in regularizing the shared encoder, which not only increased efficiency but also helped to achieve good training accuracy for any random initialization. [8]

3.5 Brain tumor segmentation with self-ensembled, deeply supervised 3D U-net neural networks: a BraTS 2020 challenge solution

In [9], the author looks towards automating and standardizing brain tumor segmentation. On the Multimodal Brain Tumor Segmentation Challenge (BraTS) 2020 training dataset, they trained many U-net-like neural networks with on-the-fly data augmentations using dice loss and deep supervision. Two ensembles of models were trained using two different training techniques, and each produced a segmentation map for a brain tumor. The Multimodal Brain Tumor Segmentation Challenge 2020 consisted of three distinct tasks. The major evaluation measures were an overlap metric and a distance metric. In addition to the Dice metric, the Hausdorff distance quantifies the maximum separation between the margins of the two outlines. They performed as follows on the online validation dataset with test time augmentation: Dice values of 0.81, 0.91, and 0.85, respectively, and Hausdorff (95%) values of 20.6, 4.3, and 5.7 mm for the enhancing tumor, whole tumor, and tumor core. Similarly, their solution received Dice values of 0.79, 0.89, and 0.84 on the final test dataset, as well as Hausdorff (95%) values of 20.4, 6.7, and 19.5 mm, putting them in the top ten teams. They used a 3D U-Net-like neural network architecture and a rigorously planned pre-processing, training, and inference technique to complete the task with excellent accuracy.

3.6 Brain Tumor Analysis Using Deep Learning and VGG-16 Ensembling Learning Approaches

This study set out to develop a convolutional neural network (CNN) model framework, critically evaluate the suggested literature solutions, apply the Visual Geometry Group (VGG 16) for finding brain tumors, and establish parameters to train the model for this issue. Because of its effectiveness, VGG is one of the best CNN models employed.In addition, the study created a useful method for MRI-based brain tumor detection to help with making prompt, effective, and accurate decisions. Convolutional feature maps were created by Faster CNN using the VGG 16 architecture as its primary network. A dataset for the diagnosis of brain tumors using MR images, consisting of 253 MRI brain pictures, of which 155 showed tumors, was used to test their proposed methodology. In MR images, our method could spot brain cancers. For a remarkable accuracy rate, the suggested model combined deep learning and transfer learning techniques. In this study, the optimization of training models was increased in order to decrease the requirement for high computational power as compared to comparable methodologies from earlier literature. The system beat existing traditional methods for identifying brain tumors in the testing data (Precision = 96%, 98.15%, 98.41% and F1-score = 91.78%, 92.6% and 91.29% correspondingly) and achieved an excellent accuracy of CNN 96%, VGG 16 98.5%, and Ensemble Model 98.14%. The paper also makes future research recommendations based on the proposed research. [14]

3.7 DeepMedic for Brain Tumor Segmentation

When trained on either the large BRATS 2015 database or the rather small BRATS 2013 database, CNNs have demonstrated a promising level of accuracy. However, the qualitative differences between the two databases prevent estimating the impact of database size. A network's required capacity for the task hasn't been studied, despite the fact that several architectures have previously been proposed. The network's performance on the tumor segmentation task in light of the two aforementioned variables. 40 datasets were picked at random from the remaining 198 datasets to serve as a validation fold. All experiments in this section used the same validation fold. Then, using a smaller set of training data and the remaining 158 datasets, trained DeepMedic's original version. In addition, versions of the network with all layers' filters reduced to 50% and 33% were trained on all 158 datasets in the training fold. Even when trained with little data or when its capacity is drastically reduced, the network still maintains the majority of its performance for the three merged classes of the challenge even when accuracy is negatively impacted. A closer examination of the accuracy results for the task's four non-merged classes reveals that the challenging necrotic (NC) and non-enhancing (NE) classes have experienced the biggest declines, though this has less of an impact on the segmentation of the overall core. The observed trends indicate that both a large training database and a large number of network filters are necessary, even though the precise quantitative results can be affected by training randomness.

3.8 Brain Tumor Segmentation with Deep Neural Networks

CNN model is a M M 2D patch with a number of modalities.The convolutional layer is the primary component used to create a CNN architecture. An arrangement of layers that form a hierarchy of features is possible. The output of a single convolutional layer, which accepts a stack of input planes as input, is a number of output planes or feature maps. Each feature map can be thought of as a topologically organized map of the responses of a specific, sliding-window, spatially local non-linear feature extractor (whose parameters are learned). This feature extractor is applied uniformly to each spatial neighborhood of the input planes. Individual input planes in the case of a first convolutional layer correspond to various MRI modalities (individual input planes in typical computer vision applications correspond to the red, green, and blue color channels).The weights of the connections between neurons in one layer and neurons in another are also represented by a kernel's value. With each kernel tuned to a different spatial frequency, scale, and orientation as appropriate for the statistics of the training data, it is frequently observed in practice that the learned kernels resemble edge detectors. Brain tumor segmentation is a highly data-imbalanced problem where 98% of the total voxels are healthy (i.e., label 0). Necrosis makes up 0.18% of the remaining 2% pathological voxels (label).Label 1 corresponds to tumor, Label 2 to edema, Label 3 to non-enhanced,

and Label 4 to enhanced tumor (label 4). When training out CNN models, choosing patches from the true distribution would result in the model being overrun by healthy patches.

3.9 Automatic Brain Tumor Detection and Segmentation Using U-Net Based Fully Convolutional Networks

The BRATS 2015 datasets, which include 220 high-grade glioma (HGG) and 54 low-grade glioma (LGG) patient scans, were used to test and evaluate the proposed method. Each patient has access to multimodal MRI data in the BRATS 2015 datasets and four MRI scanning sequences using T1-weighted (T1), T1-weighted imaging with gadolinium enhancing contrast (T1c), T2-weighted (T2), and FLAIR were carried out for each patient. The T1, T2, and FLAIR images were co-registered into the T1c data, which had the highest spatial resolution, for each patient. The T1c data was then resampled and interpolated into 1 11 mm3, resulting in an image size of 240 240 155. By dividing by its standard deviation and subtracting its mean, we applied data normalization for each sequence of the multimodal MRI. Flipping, rotating, shifting, and zooming are examples of straightforward transformations that can result in displacement fields to images but do not produce training samples with drastically different shapes. To minimize the cost function with respect to its parameters, stochastic gradient-based optimization is needed when training deep neural networks. For cases of brain tumors scanned using T1- and T2-weighted sequences, region-growing achieved a segmentation accuracy of 73%. Even with the best performance described in this study, accuracy was still only 77%. Extremely random forest was used in a study that was proposed to classify both appearance-based and context-based features, and 83% Dice score was attained.

3.10 S3D-UNet: Separable 3D U-Net for Brain Tumor Segmentation

They employ separable 3D convolutions to fully utilize 3D volume information while minimizing the amount of calculation. They create a novel separable 3D convolution architecture by breaking each 3D convolution into three parallel branches, each with a distinct orthogonal perspective, namely axial, sagittal, and coronal. This is done in order to address the peculiarities of the isotropic resolution of brain tumor MR images. They also suggest a separable 3D block that makes use of modern residual inception technology. Finally, utilizing the widely used U-Net structure and separable 3D convolutions, they propose the S3D-UNet architecture. The network under consideration received average Dice scores of 0.68946, 0.83893, and 0.7733 for the segmentation of the enhancing tumor, total tumor, and tumor core, respectively, on the BraTS 2018 Challenge testing dataset. The scores of the testing set are lower than those of the training and validation sets' performances. The testing set's challenging instances may be to blame for this, since the median values are high.[15]

4 METHODOLOGY

4.1 Implementation procedure:

The methodology, as outlined in Figure-2, was followed while evaluating brain tumor segmentation. First, we took the raw dataset and pre-processed the dataset. In the pre-processing phase we have cropped the images, resized it and split it. After that, we select the model for the research work and select the hyperparameter for the model. Then we trained the model and validated the data. The models were trained from the train set and applied on the test set. Accuracy, dice loss, focal loss, IOU-score of each model is also measured separately based on the hyper parameters.

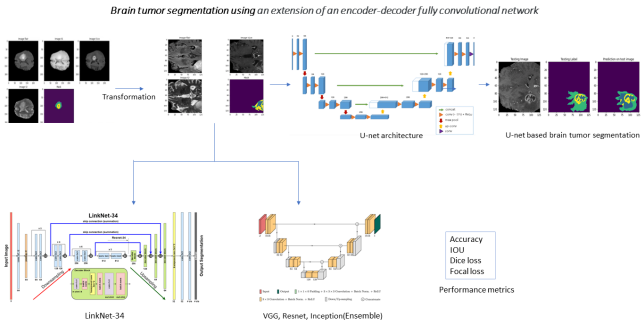

Fig. 1. Visualization of proposed system

4.2 Dataset and preprocessing:

For our evaluation of the Proposed system, we used the Brats 2020 dataset. In this dataset there are 371 such folders and each folder have 5 different images that are flair.nii, seg.nii, t1.nii, t1ce.nii and t2.nii.Additionally, this includes multimodal scans that were previously accessible as NiFTI files (nii.gz). There are four information channels, which translates to four distinct volumes of the same region: T2-Fluid Attenuated Inversion Recovery (FLAIR), Native(T1) and post-contrast T1-weighted(T1CE) volumes. Each image dataset in this was manually segmented and were approved by the experienced neuro-radiologists. Here are some annotations (labels):

Label 0 : Unlabeled volume.

Label 1: It is identified as having an, or Necrotic (NCR) and Non-enhancing tumorcore (NCR/NET).

Label 2: This volume is Peritumoral edema (ED)

Label 3: It is Missing volume

Label 4 : This volume is GD- enhancing tumor (ET)

Data is separated into training data, and validation data. We used the nibabel library to read the files from the dataset. Every volume was scaled using Min-Max Scaler. T2, T1CE, and Flair are three non-native volumes that should be combined into a single multi-channel volume. The volumes are then cropped to 128x128x128 and saved to the local disc as numpy arrays. Since we are scaling them anyhow, we can now reassign the pixels (.npy). Finally, we separate the train and validation datasets from the images and the mask volumes. The training sets are 360 images, and the validation sets are 125 images. We divided the training data into train and test set into 80:20. It is therefore necessary to create the custom data generator such that it may only be used with.jpg,.png, and .tif images. Since the custom generator won't accept npy files, it must be declared in order to load the data. The 3D U-Net model is then defined.

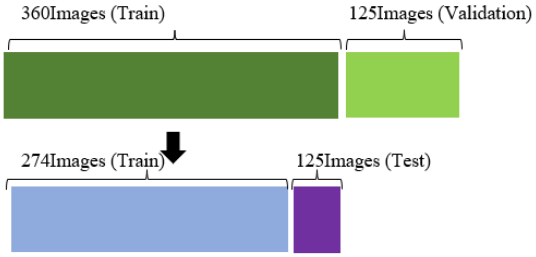

Fig. 2. Division of data

4.3 Proposed model Architecture

In the proposed model for the semantic segmentation of the MRI images of the brain tumor. A U-shaped fully convolutional deep network has 6 layers of encoder and a base layer with 6 layers of decoder. A Relu activation function is placed after each layer's two blocks of the 3x3x3 convolutional blocks. The 2x2x2 max-pooling method was then used to minimize the feature maps' spatial dimensions. For the decoder to produce richer semantic features and serve as a shortcut connection for the indirect flow of gradients to earlier layers without degrading, each layer includes skip connections that give it more information. The decoder block starts with a 2x2x2 up convolution. The number of neurons decreases by half after each set of two 3x3x3 convolutions and a Relu activation function for each convolution. Convolutional 1x1x1 with sigmoid activation is the output of the final decoder. Up to the seventh layer, which has 1024 neurons, there are 32 neurons in the second layer, and in the first layer there are 16 neurons and so on. The neurons in the decoder layers are reduced in the same 10 way at each stage, with dropout starting at 10% for the first two layers, 20% for the next two levels, and 40% for the base layer. Dropout then starts to decline for the decoder in a similar way in Figure 3.

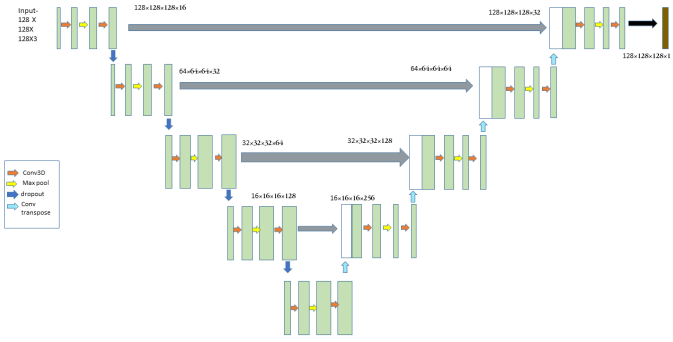

Fig. 3. U-net Architecture for brain segmentation

VGG was born out of the need to reduce the number of parameters in the CONV layers and improve on training time. Hence, VGG16 model concentrates on having 3x3 filters and max pooling layer of 2x2 filters with a stride of 2. The outcome part of the model consists of 2 Fully connected layers and a SoftMax output layer. In this work, VGG16 network has more than 3.5 million trainable parameters. The problem of training very deep networks has been relieved with the introduction of these Residual blocks and the ResNet model is made up of these blocks. A residual block is a stacking of layers in which the output of a single layer is taken and added to a layer further down in the block. ResNet's central concept is to introduce "identity shortcut connections" that avoid one or even more tiers in the convolution layer. The exact dimensions must be enforced directly in order to implement the "identity shortcut connections". [16]

Inception-v3 is a convolutional neural network architecture from the Inception family that makes several improvements including using Label Smoothing, Factorized 7 x 7 convolutions, and the use of an auxiliary classifer to propagate label information lower down the network (along with the use of batch normalization for layers in the sidehead). [17]

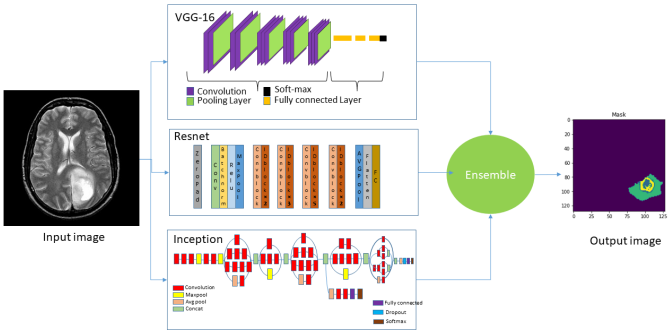

Fig. 4. Ensemble (VGG, Resnet, Inception) Architecture for brain segmentation

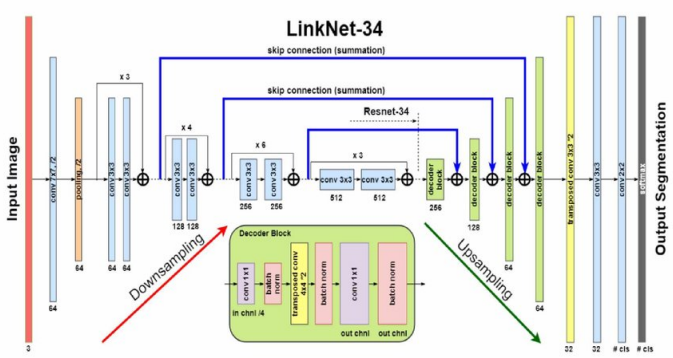

Fig. 5. Link-net Architecture for brain segmentation

4.4 Evaluation Metrics:

The effectiveness of our models is quantified using evaluation metrics. When a model is trained on a dataset, it is used to produce

predictions on a dataset that was not used during training. The performance of the model is then assessed by contrasting these predictions with the values that the standard models would have predicted. Some terminologies are utilized in the performance metrics, which are: TP means for True Positive, TN represents True Negative, FN represents False Negative, and FP represents for False Positive, to evaluate the performance of the suggested approach.

• Dice:

Dice loss is defined as 1 subtracted from the dice coefficient. The dice coefficient, which is frequently used as a loss function as well as a measure for pixel segmentation, was developed for this purpose. And the dice coefficient is determined by the following formula: Dice loss = 1-Dice Dice= (2*TP)/(2*TP+FN+FP)

• Focal Loss:

Focal loss is represented as FL. this commonly used loss function for segmentation which is pixel-wise cross-entropy loss. Total Loss Total loss is equal to the dice loss is getting added into the 1 multiply into the focal loss which represents the total loss. Total Loss=Dice Loss + (1*FL)

• Accuracy: In terms of predictions, accuracy is the proportion of accurate predictions to total predictions. ACC = (TP+TN)/(FP+FN+TP+TN)

IOU Score: It also goes by the name of the Jaccard Index, which is a different way to evaluate the model's performance. The IOU, which is another name for this metric, is intersection over union. The IOU's formulas are as follows: IOU Score = TP/(TP+FP+FN)

5 EXPERIMENT SETUP

We developed an extension of encoder and decoder model based on deep learning that could segment the MRI images into five different modalities. We tested different state-of-art segmentation models (U-Net, Ensemble using U-net backbone, Link-Net) and compared the outcomes.

5.1 Ensemble model

The best image segmentation on the MRI images is achieved by the ensemble model we have suggested in this research. The proposed model's IOU rating is 0.6079. The training and validation accuracy is 0.9676.

Fig. 6. Performance of proposed model, a) Training and validation loss b) Training and validation accuracy of the ensemble model

In Figure 6(a) Losses for training and validation can be observed in the curves. The real image closely resembles the one that were expected. The proposed model successfully separated the images into the three classes. We could see the predicted s next to the original image in Figure-7. The predicted image resembles the original accuracy very well.

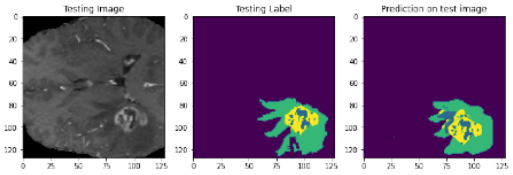

Fig. 7. Prediction of the proposed methodology

5.2 U-net model

U-net model managed to attain a 0.5829 IOU score while suffering a 0.8432 loss. With rising epochs, the training IOU consent declines, and Figure 8 (a). shows the validation accuracy fluctuates somewhat at 0.9721

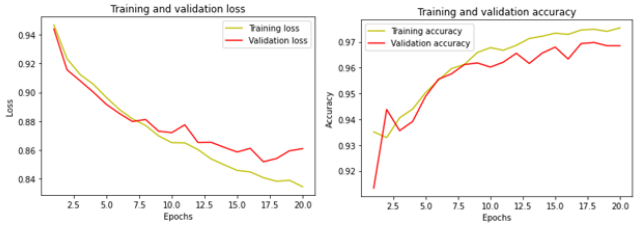

Fig. 8. Performance of proposed model, a) Training and validation loss of U-net model b) Training and validation accuracy of U-net model

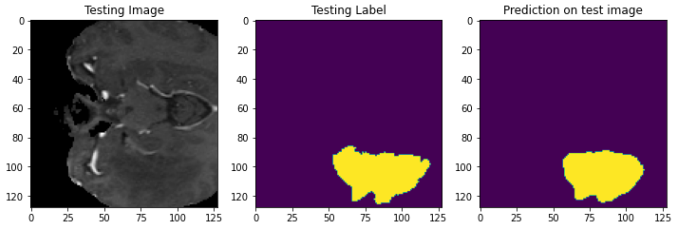

Fig. 9. Performance of proposed model, a) Training and validation loss of U-net model b) Training and validation accuracy of U-net model

5.3 Link net model

The Link-Net model, performance isn't all that impressive; the model earns an IOU score of 0.5636 and training and validation loss of 0.8885. In Figure 10(a) shows the accuracy of Link-net which is 0.9610

Fig. 10. Performance of proposed model, a) Training and validation loss of U-net model b) Training and validation accuracy of linknet model

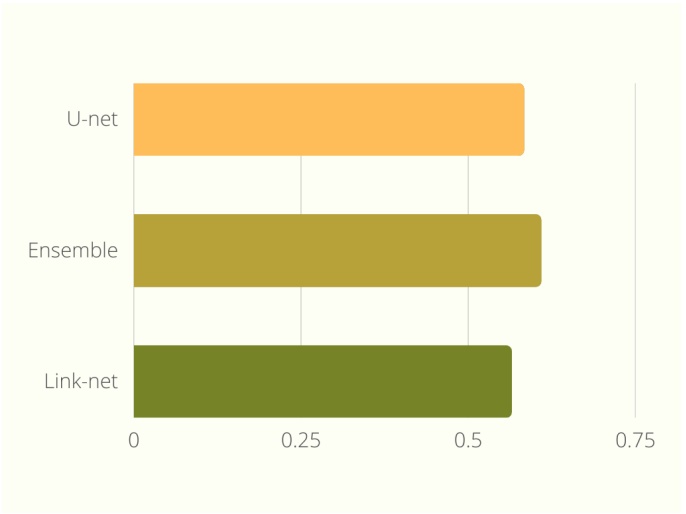

Fig. 13. Comparison of the IOU of the segmentation models

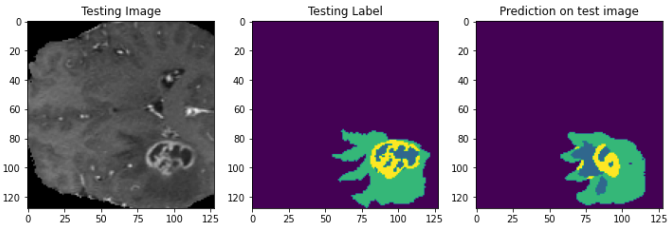

Fig. 11. Performance of proposed model, a) Training and validation loss of U-net model b) Training and validation accuracy of link model

5.4 Results and Analysis

Table-1: Compared experiment results on the BRATS 2022 dataset

Model	Validation Loss	Validation Accuracy	IOU Score
U-net	0.8694	0.9676	0.5829
Ensemble (VGG, Resnet, Inception)	0.8432	0.9721	0.6079
Link-net	0.8885	0.9610	0.5636

Fig. 12. Comparison of the IOU of the segmentation models

6 CONCLUSION

In this paper, we reviewed the state-of-the-art data segmentation methods applied in the context of segmenting brain tumors from BraTS 2020 dataset. We carefully investigated various papers and analyzed data segmentation techniques. We experimented with different models. First, we used U-net model and got accuracy of 0.9676 along with 0.5829 IOU score. After that, we trained our model with U-net backbone (VGG16, Resnet, Inception) and introduced our proposed ensemble model. Furthermore, we applied another model called Link-Net. We compared our models. Based on the results and analysis we can conclude that the proposed model namely U-net backbone ensemble is running well. The results of segmentation from testing data were obtained by accuracy value of 0.9721 and IOU score of 0.6079. For future research, the different architecture or convolutional block scenario could be obtained to get more alternative models. We aim to explore the optimum epoch with the goal to further reduce model complexity and training time increasing metrics scores.

7 REFERENCE

[1] Kajal, M., Mittal, A. (2022). A Modified U-Net Based Architecture for Brain Tumour Segmentation on BRATS 2020. https://doi.org/10.21203/rs.3.rs-2109641/v1

[2] Cui, S., Mao, L., Jiang, J., Liu, C., Xiong, S. (2018). Automatic semantic segmentation of brain gliomas from MRI images using a deep cascaded neural network. Journal of healthcare engineering, 2018.https://www.mdpi.com/2073-8994/12/5/721 [3]https://www.hopkinsmedicine.and-diseases/brain-tumor [4] https://braintumor.org/brain-tumors/about-brain-tumors/brain-tumor-facts/

[5](https://pubmed.ncbi.nlm.nih.gov/34561990/)

[6] (Aboussaleh, I., Riffi, J., Mahraz, A. M., Tairi, H. (2021). Brain tumor segmentation based on deep learning's feature representation. Journal of Imaging, 7(12), 269.https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8703)

[7] (Zhang, J., Lv, X., Zhang, H., Liu, B. (2020). AResU-Net: Attention residual U-Net for brain tumor segmentation. Symmetry, 12(5), 721. , https://www.mdpi.com/2073-8994/12/5/721)

[8] (Myronenko, A. (2019). 3D MRI brain tumor segmentation using autoencoder regularization. In International MICCAI brainlesion workshop (pp. 311-320). Springer, Cham. https://arxiv.org/abs/1810.11654)

[9] (Henry, T., Carré, A., Lerousseau, M., Estienne, T., Robert, C., Paragios, N., Deutsch, E. (2021). Brain tumor segmentation with self-ensembled, deeply-supervised 3D U-net neural networks: a BraTS 2020 challenge solution. In International MICCAI Brainlesion Workshop (pp. 327-339). Springer, Cham. , https://arxiv.org/abs/2011.01045)

[10] http://telkomnika.uad.ac.id/index.php/TELKOMNIKA/ article/view/14753)

[11]Havaei, M., Davy, A., Warde-Farley, D., Biard, A., Courville, A., Bengio, Y., ... Larochelle, H. (2017). Brain tumor segmentation with deep neural networks. Medical image analysis,35,1831. https://www.sciencedirect.com/science/article/abs/pii/S1361841516300330

[12] Dong, H., Yang, G., Liu, F., Mo, Y., Guo, Y. (2017, July). Automatic brain tumor detection and segmentation using U-Net based fully convolutional networks. In annual conference on medical image understanding and analysis (pp. 506-517).Springer,Cham.https://link.springer.co 3-319-60964-5$_4$4

[13] Kamnitsas, K., Ferrante, E., Parisot, S., Ledig, C., Nori, A. V., Criminisi, A., ... Glocker, B. (2016, October). DeepMedic for brain tumor segmentation. In International workshop on Brainlesion: Glioma, multiple sclerosis, stroke and traumatic brain injuries (pp. 138-149). Springer,cham. https://link.springer.com/chapter/10.1007/978-3-319-55524-9$_1$4

[14]Younis, A., Qiang, L., Nyatega, C. O., Adamu, M. J., Kawuwa, H. B. (2022). Brain Tumor Analysis Using Deep Learning and VGG-16 Ensembling Learning Approaches. Applied Sciences, 12(14), 7282.

[15] Chen, W., Liu, B., Peng, S., Sun, J., Qiao, X. (2019). S3D-UNet: separable 3D U-Net for brain tumor segmentation. In International MICCAI Brainlesion Workshop (pp. 358-368). Springer, Cham.

[16] Md. Shakib Khan1, Kazi Nabiul Alam1, Abdur Rab Dhruba1, Hasib Zunair2, Nabeel Mohammed1, Knowledge Distillation approach towards Melanoma Detection, https://ui.adsabs.harvard.edu/abs/2022arXiv2

[17] https://arxiv.org/abs/1512.00567v3