International Journal of Scientific Research in Engineering and Management (IJSREM)
Volume: 06 Issue: 05 | May - 2022 Impact Factor: 7.185 ISSN: 2582-3930

Brain Tumour Segmentation from 3D MRI using U-net

Prof. D.D Pukale[1], Akanksha Kadam[2], Vrushali Gajare[3], Prachi Desai[4], Sakshi Patel[5]

[1]Head and Associate Professor, Department of Computer Engineering, Bharati Vidyapeeth's College of Engineering for Women, Pune

[2,3,4,5]Student, Department of Computer Engineering, Bharati Vidyapeeth's College of Engineering for Women, Pune

ABSTRACT

Brain cancers, despite their rarity, are extremely lethal. Among them, the most frequently seen dominant brain tumours are histological gliomas. In addition to diagnostic variables and heterogeneous histological sub-regions that include four tumour regions (peritumoural edema, necrotic core, enhancing and non-enhancing tumour cores), gliomas are highly invasive because they grow quickly and can infect the central nervous system. Magnetic Resonance Imaging (MRI) can be used for monitoring, analyzing, and treatment planning of tumours. To visualize the brain, the MRI uses four different modalities: T1-weighted, T2-weighted, T1ce-weighted, and flair. Though these modalities give complementary information about tumour core regions, they can be used together for monitoring and analyzing sub-regions of tumour cores. Segmentation is a technique that provides information about tumour - affected boundaries. Several tumours have irregular shapes, sizes, and ambiguous boundaries, making it difficult for physicians to manually segment the tumour. That is why the need for an automated segmentation system occurs. Taking into account the need, we present a system, tested and evaluated on BRATS 2020 (training + validation) dataset to automatically segment brain tumour, thereby eliminating human errors. The U-NET model, which is a fully convolutional neural network, is used to perform the segmentation task. Following a successful execution, our system generates segmented regions of necrotic, edema, and enhancing tumour core.

Key Words: Image Segmentation, U-net, 3D Magnetic Resonance Imaging, Brain Tumour, Multimodal

INTRODUCTION

The segmentation of tumour regions from magnetic resonance imaging (MRI) is considered a complex but essential procedure in biomedical image processing. The diagnosis of a brain tumours needs to be as early as possible to avoid negative consequences and increase the patient's chance of survival. Despite significant advances in medical image processing and the existence of many automated segmentation systems, brain tumour segmentation is still done manually by professional radiologists. Manual segmentation is not only time-consuming but also a lengthy procedure, with the outcome relying on human judgments. As a result, automated segmentation methods are becoming increasingly popular and in high demand. MRI images are preferred for brain tumour segmentation because they provide precise delineation, which is essential in surgical planning, and their use produces more accurate results and aids in diagnosis. In this paper, we present a system that aims to segment 3D MRI images using UNET, an image segmentation technique designed primarily for medical image analysis. Despite some inherent difficulties, multimodal image processing is advantageous because the information available in various modalities complements one another. Furthermore, we used a dice-based loss function to quantify the performance of medical image segmentation and evaluated our model using four different initializers and optimizers: adadelta he_normal, adadelta he_uniform, adam he_normal, and adam he_uniform. Based on the comparison of dice coefficients and accuracy after applying each initializer and optimizers, we choose adam he_normal for further analysis. Our system was trained and validated using the BraTS2020 training and validation dataset.

We obtained dice scores of 0.627, 0.727, 0.685, and 0.613 for whole tumour, necrotic tumour core, enhancing tumour core, and peritumoural edema tumour core respectively. In this paper, we present a genuine method for automatically segmenting brain tumours using multimodal MRIs that is faster than manual methods. As a result, it can save physicians time while also providing accurate, reproducible solutions for further tumours analysis and monitoring.

RELATED WORK

Using U Net-based deep convolutional network in this research paper, a fully automatic method has been proposed by the authors [1] for brain tumour segmentation. It uses BRATS 2015 datasets that contain 220 high-grade glioma and 54 low-grade glioma patient scans. A comprehensive data augmentation technique and soft dice-based loss function were used to boost the segmentation accuracy for better results. This method worked on both LGG and HGG patients. Dice scores of 0.90, 0.86 and 0.73 were obtained for complete, core and enhancing tumours respectively

Olaf Ronneberger, Philipp Fischer, and Thomas Brox presented a [2] training and network technique that uses extensive data augmentation to ensure that available automated samples are used in the best way possible. It employs a U-Net architecture with contracting and expanded paths to record context and enable exact localization. This aided in attaining excellent results in a variety of segmentation applications. U-Net produces a wrapping error of 0.000353 with an average IoU of 92% for data set “PhC-U373” and 77.5% for data set “DIC-HeLa” which is significantly better than the other algorithms used.

The authors [3] examined the existing U-Net model to later propose a hybrid model of VGG16 and U-Net with transfer learning to simplify the architecture of U-Net. The accuracy provided by this method is high (96.1%) in the learning dataset. For validation purposes, the calculation of the Correct Classification Ratio is done by comparing the segmentation result with the ground truth (CCR Value - 95.69%). Given the minimal value of loss and the great value of accuracy, the model outperforms the U-Net model.

[4] Peter X. Liu, Jing Huang and Minhua Zheng present a method based on UNet Architecture for multimodal 3D MRIs, for the same BRATS 2017 dataset was used. It contains two parts, a 3D segmentation network (for more detailed sub-region segmentation) and ROI extraction (region of interest - obtains areas of whole tumours and provides the input for the 3D network). The average Dice scores for the entire tumour, tumour core, and enhancing tumour were 0.9089, 0.7165, and 0.8398, respectively. This aided in the automated segmentation of brain tumours.

[5] A technique for detecting brain tumours and categorizing tumourous MRIs into malignant and benign, as well as malignant brain MRI into glioma and meningioma, is proposed in this study by Sunita M. Kulkarni and Dr. G. Sundari. Preprocessing techniques are used to detect brain tumours, which are then followed by skull stripping and brain tumour segmentation. This method appears to be successful in separating the brain tumour from the MRI. Using CNN-based AlexNet transfer learning techniques, the tumourous pictures are further

identified as malignant or benign. The proposed method achieved a precision of 0.9375, recall of 1, and f-measure of 0.9677.

METHOD

1. Data Acquisition

The dataset used here is BraTS2020 Dataset (training + validation)) [6]. It contains MRI Images from 355 patients, with each patient dataset containing 5 images in NIfTI files (. nii.gz) format that is commonly used in medical imaging format to store brain imaging data obtained using MRI and describe different MRI settings. All BraTS multimodal scans are available as NIfTI files (. nii.gz) and describe a) native (T1) and b) post-contrast T1-weighted (T1ce), c) T2-weighted (T2), and d) T2 Fluid Attenuated Inversion Recovery (T2-FLAIR) volumes, and were acquired with different clinical protocols and various scanners from 19 institutions, are the data contributors. Along with this mask is present in the dataset its annotations are label 0 (Unlabelled), label 1 (Necrotic and non-enhancing tumour core), label 2 (Peritumoural edema), label 3 (missing that is no pixel have label 3) and label 4 (GD - enhancing tumour). All the imaging datasets have been segmented manually and were approved by experienced neuro-radiologists. Along with this, the manual annotations in the dataset were approved as well.

2. Implementation Details

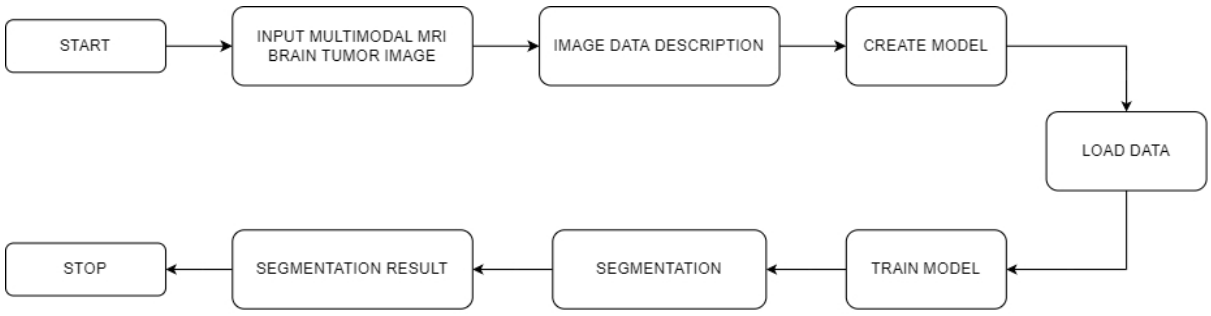


Fig. 1. System Architecture

We have used Unet convolutional neural network architecture , for its implementation we can import the model from keras unet 0.1.2, this is a package with multiple U-Net implementations in Keras , in place of importing pre-existing model we have created it from scratch using keras that is useful utility tool helpful in the field of image segmentation along with this Tensorflow which is a foundation library used for building Deep Learning models. Here U-Net algorithm is used for fast and precise segmentation of images. The hyperparameters used for our model are as follows:

Sr.No	Optimizer	Initializer
1	adadelta	he_normal
2	adadelta	he_uniform
3	adam	he_normal

4	adam	he_uniform

Table 1. Hyper-Parameter Details

The best from this is chosen in terms of accuracy and dice coefficient. Few other hyperparameters are the number of iterations (epochs) in training is 32. Batch size for our model is 1, with the drop-out ratio being 0.2. The initial learning rate is 0.001. The ratio of Train, Valid and Test data is as follows: Train data - 68%, Valid data - 20%, Test Data - 12%

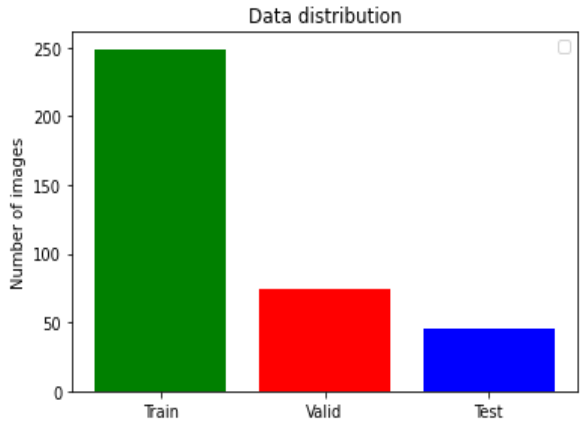


Fig. 2. Dataset Distribution

3. U-Net Algorithm

U-Net was created by [7] Olaf Ronneberger, Philipp Fischer, Thomas Brox in 2015 in the paper "U-Net: Convolutional Networks for Biomedical Image Segmentation". The network has a u-shaped architecture because it has a contracting path and an expansive path. The architecture consists of two parts - encoder and decoder. [8] The encoder is made up of two 3x3 convolutions that are applied repeatedly. After each conv, there is a ReLU and batch normalization. The spatial dimensions are then reduced using a 2x2 max pooling operation. We double the number of feature channels while halving the spatial dimensions at each downsampling step. For the decoder, every step in the expansive path starts with an upsampling of the feature map and then a 2x2 transpose convolution, which reduces the number of feature channels in half. We also have a concatenation with the contracting path's matching feature map, as well as a 3x3 convolutional neural network (each followed by a ReLU). A 1x1 convolution is used to map the channels to the desired number of classes in the final layer. [9] The skip connections used in the architecture are an important notion for preserving the loss from prior layers so that it may be seen more clearly in the total values. They've also been scientifically demonstrated to deliver superior results and accelerate model convergence.The original architecture of the model follows image size of 572x572. We have customized the architecture as per our needs to 128x128.The U-Net does not require numerous runs to do image segmentation and can learn from a small number of annotated images, making it ideal for image segmentation in biology and medicine. While running faster and using less labeled input, U-Net got lower errors than the other traditional convolutional neural networks.

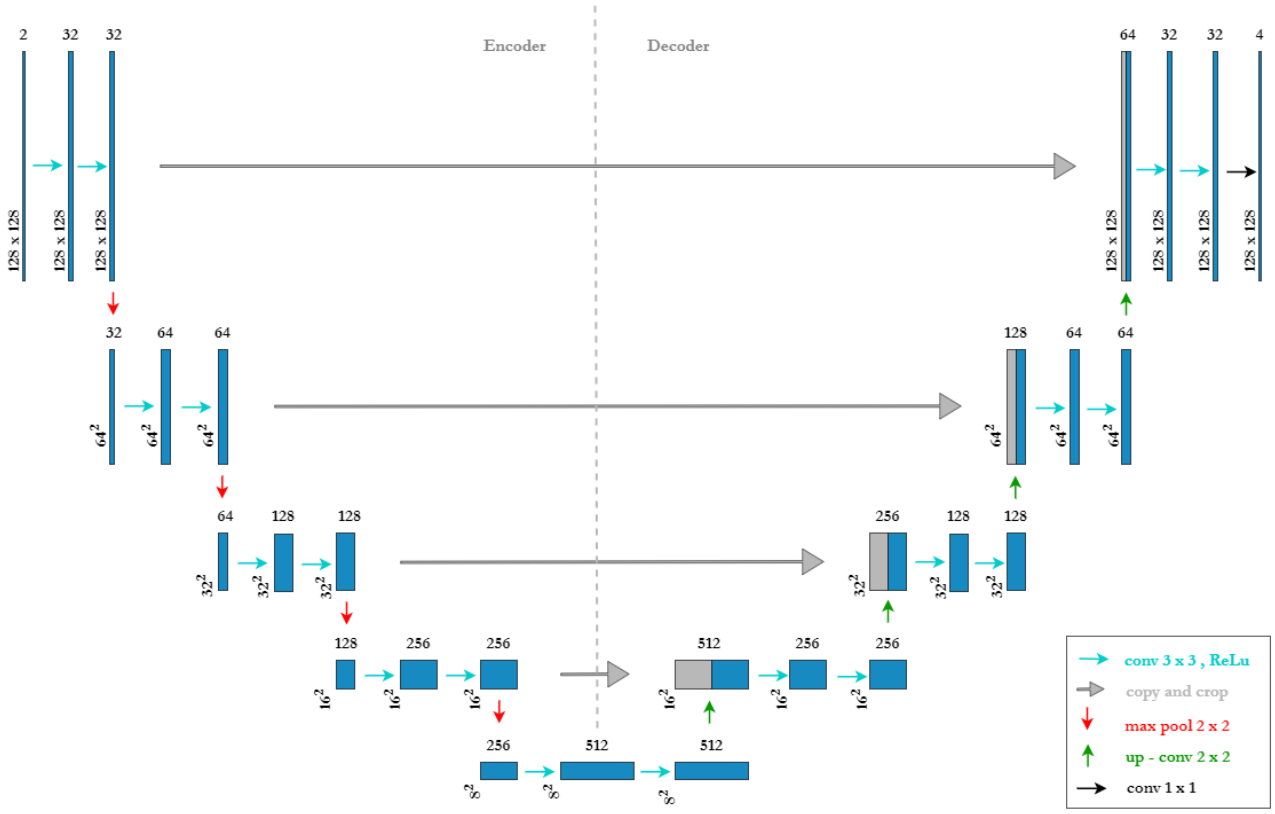


Fig. 3. U-Net Architecture

4. Performance Evaluation

Image segmentation is a crucial step in using MRI data in brain tumour research. We have used 4 segmentation classes for the model. The labels for the same are as follows:

1. Label 0 - Unlabeled volume
2. Label 1 - Necrotic and non-enhancing tumour core (NCR/NET)
3. Label 2 - Peritumoural edema (ED)
4. Label 3 - GD - enhancing tumour

The results of the U-Net algorithm with 3D MRI brain scan of modality flair and t1ce as the input of the network, to obtain the segmentation results of necrotic, edema and non-enhancing tumours. The segmentation results are evaluated from the following factors: Dice coefficient measures similarity between the sets of data provided. The calculation of the same is done using the following formulas:

Term/Factor	**Basic Formula**
Dice coefficient (calculated for all classes)	2TP / (2TP+ FP + FN)
Precision	TP / TP + FP

Sensitivity	TP / TP + FN
Specificity	TN / TN + FP
Mean IoU	TP / TP + FP + FN

Table 2. Formulas Used

Where TP, TN, FN and FP represent true positive, true negative, false positive and false negative, respectively. For our model, we derived formulas for calculations of the factors needed to measure the model's performance. For a perfect segmentation, the value of the dice coefficient is one, and in the case of no overlap between segmentation and reference, the lowest possible value is zero. In our model , dice coefficient for each segmentation class is calculated and displayed.

RESULT

The process of training any model involves choosing optimal hyperparameters. For our model we choose adam and adadelta optimizer and he_normal and he_uniform initializer combination.

	Hyper-Parameter : adadelta		Hyper-Parameter : adam	
	he_normal	he_uniform	he_normal	he_uniform
Accuracy	0.984	0.984	0.994	0.993
Loss	0.079	0.073	0.019	0.019
Dice Coefficient	0.287	0.288	0.627	0.604
Dice Coefficient: Necrotic Core	0.208	0.194	0.747	0.727
Dice Coefficient: Enhancing	0.152	0.099	0.686	0.670
Dice Coefficient: Edema	0.054	0.094	0.613	0.565

Table 3 Hyper-Parameters Comparison

Table 3 is the comparison, we got after applying this hyperparameter combination to our model. Here, adadelta he_normal and adadelta he_uniform give approximately the same and good accuracy but the dice coefficient for the whole region and individual tumour region is not precise. Both show poor performance on segmenting individual tumour regions. The segmentation performance ranges from 5% to 15% percentage which is very low.

In contrast, adam he_normal and adam he_uniform both are giving approximately the same result. The performance checking parameters for both the cases are nearly equal. Still after comparing dice coefficient of every single tumour core classe adam and he_normal combination gives slightly better performance than adam he_uniform .hence we choose adam optimizer and he_normal initializer combination as optimal hyperparameter for our model to correctly map i/p features (independent variable) to targets or label.

Performance Parameter	Hyper-Parameter : adam he_normal	
	Training	Testing
Accuracy	0.994	0.993
Loss	0.019	0.020
Mean IOU	0.769	0.767
Dice Coefficient	0.627	0.599
Dice Coefficient : Necrotic	0.747	0.726
Dice Coefficient : Enhancing	0.686	0.642
Dice Coefficient : Edema	0.613	0.542

Table 4. Performance of Optimal Hyper-Parameter

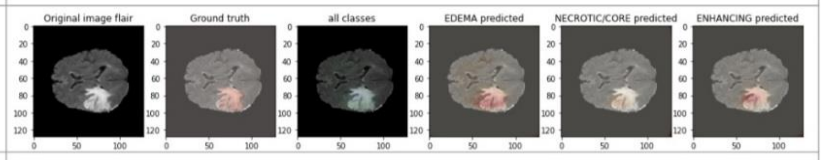
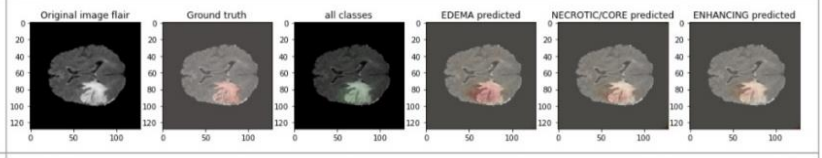
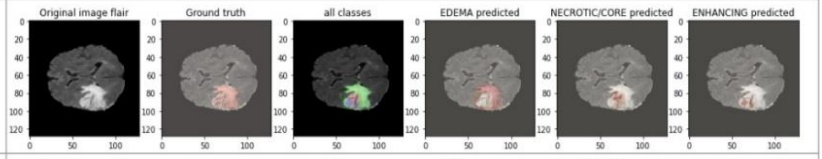
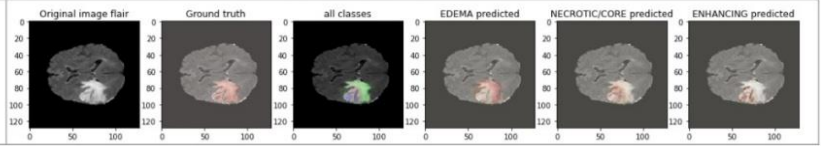
Optimizer	Initializer	Output Images
Adadelta	he_normal	
Adadelta	he_uniform	
Adam	he_normal	
Adam	he_uniform	

Fig. 4. Segmentation Output

Figure 4. shows, The Segmentation output of all the models in comparison. The final output for our model is a segmentation map which shows different segmented parts of brain tumour which includes original flair image, ground truth image, whole tumour region and individual sub regions of tumour. Here, for adadelta he_normal and adadelta he_uniform the sub regions are not predicted properly as the dice coefficient is also low. In case of adam he_uniform it shows proper whole region separation but the quality of separation is not clearly visible as compared with adam he_ normal. While in adam he_normal, the segmentation of input image, ground truth image and predicted segmentation are matching well.

CONCLUSION AND FUTURE WORK

Brain tumour segmentation is considered a difficult task due to the complexity of MRI brain images. In recent days, there has been a lot of work done on brain tumour MRI image segmentation using deep learning approaches. Still, MRI is a difficult field with a lot of room for improvement. In this paper, we present a system that uses U-Net architecture to segment and classify the brain tumour regions using multimodal MRI. This segmentation gives the physician a significant advantage in the form of a second opinion based on automated results and also saves a lot of time. Our model shows better performance than existing segmentation techniques.

The presented approach can be further improvised to explore 3D-based networks to improve the performance of segmentation. The system can also be integrated with MRI machines, which will directly give segmented regions as output.

REFERENCES

1. Automatic Brain Tumour Detection and Segmentation Using U-Net Based Fully Convolutional Networks - Hao Dong , Guang Yang , Fangde Liu, Yuanhan Mo , Yike Guo

2. U-Net: Convolutional Networks for Biomedical Image Segmentation - Olaf Ronneberger, Philipp Fischer, and Thomas Brox

3. UNet-VGG16 with transfer learning for MRI-based brain tumour segmentation - Anindya Apriliyanti Pravitasari, Nur Iriawan, Mawanda Almuhayar, Taufik Azmi ,Irhamah, Kartika Fithriasari, Santi Wulan Purnami, Widiana Ferriastuti

4. Automatic Brain Tumour Segmentation Using 3D Architecture Based on ROI Extraction - Peter X. Liu , Jing Huang and Minhua Zheng

5. A Framework for Brain Tumour Segmentation and Classification using Deep Learning Algorithm - Sunita M. Kulkarni, Dr. G. Sundari

6. WWW: https://www.kaggle.com/datasets/awsaf49/brats20-dataset-training-validation

7. U-Net: Convolutional Networks for Biomedical Image Segmentation Olaf Ronneberger, Philipp Fischer, Thomas Brox

8. Nikolas Adaloglou in an overview of U-Net architectures for semantic segmentation and biomedical image segmentation

9. U-Net Architecture For Image Segmentation by Bharath k