International Journal of Scientific Engineering and Science
Volume 5, Issue 9, pp. 45-50, 2021. ISSN (Online): 2456-7361

Brain Tumour Segmentation Using JeisloNet - a Unet Architecture

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Abstract**—** *Manual medical images segmentation is very tedious task. Accurate segmentation of brain magnetic resonance images (MRI) is a critical phase in measuring the irregularities in brain structure. In recent years, deep learning has gained popularity for its efficiency in brain image segmentation. In particular, Unet architecture is being deployed in several biomedical fields for segmentation. It has contributed immensely to solving clinical problems, which includes accurate segmentation of desired feature, efficient processing, and analysis of biomedical images, therefore enhancing an improved accuracy in biomedical images diagnosis and prognosis. In this research, JesloNet, a Unet architecture was developed for the automatic segmentation of abnormal tissues, brain tumours in MR scan images. MR scanned brain images were obtained from The Cancer Image Archives, the images were preprocessed and split in train and test set in the ratio 80:20. The experiment results showed that the Unet model, JeislоNet achieved good performance with the following results in Dice Coefficient Index (DSC) 0.9931, Mean IOU 0.9321, Global Accuracy 0.9928, and Error rate 0.0072. The result was also compared with other methods in the literature an JeislоNet performed better, hence, it can be adopted for other medical image segmentation*.

Keywords**—** *Brain tumour, unet, segmentation, magnetic resonance image, biomedical image*.

I. INTRODUCTION

Brain and nervous system cancer happen to be prominent cause and reason of death today, having a world ranking of number 10 [1] [2]. Over the years, there has been a rapid growth in brain cancer cases [2], this therefore calls for the need of an automated diagnosis systems which help to detect early-stage tumour and reduce the intervention of clinicians. In the past, accurate diagnosis of brain cancer was a laborious and tedious task for neurologists leading to the invention of modalities such as X-ray, Magnetic Resonance Imaging (MRI) and the computed tomography (CT) which provides visualization of the brain structure, thereby simplifying the task of brain cancer diagnosis. However, MR images are more preferable as they provide detailed information about the tumour position, type, size, and better contrast images with higher spatial resolution, thus making it an essential tool in treatment, diagnosis, and monitoring of disease [3]. MR imaging is widely used for medical images segmentation such as liver segmentation, brain tumour segmentation, and breast tumour segmentation among others, an important procedure for automated diagnosis system. Automated segmentation method is therefore necessary since manual segmentation which involves labelling of pixel/voxel can be difficult a task as well as large time consumption. The conventional brain tumour MR images protocol includes T1-weighted imaging, T2-weighted imaging (including Fluid Attenuated Inversion Recovery i.e., FLAIR) and gadolinium-enhanced T1-weighted imaging sequences. These structural MR images provide a quality prognosis and diagnosis in most cases [4]. Initially, traditional method such as boundary extraction, regionbased segmentation, threshold-based segmentation and clustering-based segmentation was used for brain tumour segmentation, but over time these traditional methods became difficult to learn manual features when large data are used, therefore being unable to assist neurologist in accurate diagnosis or analysis and treatment of disease [5].

In recent times, Deep Learning (DL) methods are becoming popular in the area of medical images segmentation due to the aptitude to efficiently process enormous quantity of data and extraction of useful image features, it allows direct learning of complex features from the original data making it a requisite for medical image analysis [5]. DL technology is a subclass of Machine Learning (ML) technology that acquires data representations by improving abstraction levels [6]. Among different DL models that exist, Convolutional Neural Networks (CNNs) has shown outstanding success in almost all sophisticated task of computer vision such as image segmentation, object detections and image classification, through the advent and success of AlexNet developed by Krizhevsky et al [7] which revolved the field of computer vision from customary ML algorithms towards CNNs. According to researchers, the perception of CNNs was an innovation. It began from the discovery of Hubel and Wiesel elucidating that in the primary visual cortex there are simple and complex neurons, these simple structures such as oriented edges are the basic step of visual processing. Hubel and Wiesel work greatly motivated Kunihiko Fukushima and he developed a multi-layered neural network named Neocognitron [8] with the use of simple and complex neurons which could identify outlines in images and spatial invariance [9]. Using the Neocognitron idea the LeNet [10] was developed by Yann LeCun which was used for identifying handwritten digits, LeNet however became the first CNN built [11]. The breakthrough by Krizhevsky et al. [7] was a result of a supervised and overseen training exercise of a huge network having eight layers and parameters in millions on the

ImageNet dataset, using a million set of images for training, resulting in the training of larger and deeper networks [12].

The drawback of deep learning techniques is the need for a huge quantity of data for training. However, in analysis of images involving medical it is challenging to come by such a huge quantity of labeled data for training and large computing power. It then becomes essential to mitigate these limitations by improving DL networks that can effectively perform, with however small the quantity of training data maybe.

In the 2015 ISBI cell tracking challenge, Olaf Ronneberger et al., [13] presented a model to outperform the existing best method for segmentation medical image by Ciresan et al. [14] This model was called Unet. The Unet model is a salient semantic segmentation framework in CNN [15]. It shows a good segmentation performance even with few training images as a result of its U-shape architecture nature which allows end-to-end training of medical image and analysis. The model mainly constitutes a down-sampling (contracting) and an up-sampling (expansion) respectively. Convolution alongside pooling is done in the encoding or down-sampling path while up-convolution is done in the decoding or up-sampling path to yield a segmented tumour. Unet was initial proposed for segmentation of structures of the neurals in electron microscopic stacks [13]. It is an extension of the architecture known as fully convolutional network (FCN) which is used for segmentation [16]. The FCN architecture solitary comprises of the encoder path involving sequential convolution and max pooling processes. The input image is down-sampled, and the last down-sampled feature map is inputted into an activation map for evaluations (perdictions) on each of the pixels. Compared to the sliding window-based architecture, the architecture called U-net has shown an improved and much faster execution for segmentation [17], it is a breakthrough of DL in medical image study and also a foundation set for clinicians to acquire accurate pathologic diagnosis [5].

In this study, we used the based Unet architecture for MR brain image tumour segmentation. However, in the process of the data training augmentation scheme [13] was not needed because the training process was carried out using only the available training data. This automatic method used a dataset of LGG patients for validation. Dice similarity coefficient (DSC) [18] and Mean IoU which is also known as Jaccard Index [19] methods for segmentation evaluation which showed promising results when equated with the manual delineated ground truth. The other part of this paper is in this order: In section 2, reviewed related works, in section 3 the adopted method is elaborated, discussion of experimental result in section 4 and the paper is concluded in section 5.

II. Related Works

This section reviewed methods that have been successfully used for brain tumour segmentation. Wu et al. [20] presented a method of detecting and segmenting tumour in the brain with a Conditional Random Fields (CRF) structure using which uses super pixel features, however, they were great variations in results amidst diverse patient cases, nonetheless its performance in images of LGG was small. Pinto et al. [21] proposed a study in which brain tumour segmented was built on extremely randomized forest (RF) for categorizing both context-based features as well as appearance, the Dice score gotten was 83%. Soltaninejad *et al*. [22] this method used super pixel based extremely randomized trees (ERT) classification for automatic segmentation of MR image scan of a solo FLAIR and got an total DSC of 88% for both the HGG and LGG cases, but the change of super pixel size and density can affect the final delineation since it can be complicated. Kermi *et al*. [23] in this study a new automated technique for brain tumour segmentation was introduced. The segmentation was performed as a three-stage process. Pre-processing of was carried out at the first process to remove the noise. During the second process, the tumour de-formable model was located by performing symmetry analysis. In the last process, the final tumour is obtained by using geodesic level set and region growing methods. This work was evaluated using BraTs 2017 dataset with two hundred and eight five subjects of 3D MRIs using diverse sorts and forms of tumours in the brain. T2 and FLAIR achieved a sensitivity score of 81.59% and 89.01% correspondingly. A deep voxel-wise residual network proposed by Hao *et al.* [24] a using a set of patterns for training. The two-dimensional(2D) residual learning is protracted into a three-dimensional(3D) variant which is used to solve the segmentation tasks through a deeper network. 25 layers were allotted for the training of the deep networks coupled with inadequate training data for the segmentation of the brain. Outcomes were evaluated with Brains 2013 dataset and attained dice similarity of 89.46%. Wu et al. [25] used sparse representation to perform feature extraction and selection, it differentiated the two clinical problems with based radionics framework. Discovery and diagnosis of the regions where the tumour is located is done by dictionary learning with depiction sparse based feature extraction. An accuracy of 98.51% was attained with the use of a secluded dataset of hundred and two patient. Chen *et al.* [26] developed a lightweight dilated multifibre network to achieve real-time tumour segmentation. A set of convolutions is done to discover multi-fiber units; the multi-scale feature representation is built using 3D opened convolutions. BraTS 2018 challenge dataset was used to estimate the work and it obtained a dice similarity of 90.62%. Another approach more recently used for brain tumour segmentation is SegNet network which semantic-wise CNN architecture [27]. Nevertheless, SegNet has a likeliness of neighboring details being lost during the up-sampling from a feature map having low resolution and it also tends to focus more on training and testing the central slices with no results for non-central slices. So therefore, when compared with other existing method does not show a promising result in segmentation [27].

Brain Tumor Image Segmentation (BRATS) is a yearly workshop and challenge used to evaluate various developed brain tumour segmentation algorithm [28]. There are some limitations CNN has in the applications of segmentation, this is as result the reconstruction which ought to be done form the vector in the process of the segmentation, where conversion of feature map is meant not only into vector but likewise a brain image reconstruction from the vector. Although, a lot of

International Journal of Scientific Engineering and Science
Volume 5, Issue 9, pp. 45-50, 2021. ISSN (Online): 2456-7361

attention has been towards the Unet due to its reconstruction which is an advantage over the CNN proficiency. According to [13], the U-net can achieve better results in segmentation areas such the biomedical owing to its ability to lower distortion which preserve the structural integrity of the image. Images in biomedical fields typically encompasses comprehensive outlines of the imaged object such as brain tumor. However, the imaged object edge is inconstant and in other for the segmentation of the object image to be meticulously patterns, skip architecture proposed by Long et al. [29] which united the high-level depiction to yield a comprehensive segmentation by starting from the decoding layers which are deep with appearances depiction from low encoding layers. The Unet solved the cell tracking problem by the use of the skip architecture which showed an auspicious outcome on natural images, making it application to medical images possible [30]. In this study, a fully convoluted segmention system of two dimension(2D) was used based on the Unet architecture.

III. The Developed Method

A The Jeislonet

The model architecture which is based on the Unet, comprises a contracting or down-sampling or encoding path and the up-sampling or decodingor expansion path as presented in Figure 1. Input slices of 256x256. The contracting path consists of four processes, each constituting two convolutional layers trailed by a ReLU and down-sampling operation. A two-dimension (2D) 3x3 up-padding convolution with 1 stride is done, after the convolution the number of channels changes from 3 to 192. The 192 channels are gotten as a result of 64 filters (kernels) used in each convolution layer. The ReLU which occurs after each convolutional layer is an activation function that increases the nonlinearity in the images. During the down-sampling operation, a 2x2 max pooling task using stride was carried out. At each process of the down-sampling, the feature channel number is doubled, while the image size is halved. The contracting stage secures context via a compact feature. Before the expansion stage at the bottommost area of the flow diagram in Figure 1, which is the bridge between the contracting stage and expansion stage, another process of 2 convolutional layers each trailed by ReLU but with no down-sampling occurs. In the decoding or expansion path, the image is to be increased to its original size, it also contains three processes. Each process constitutes a transposed (C^T) convolution and two layers of convolution each trailed by a ReLU. The C^T is an up-sampling technique that expands the size of images. It does some padding on the image inputted into the expansion stage, trailed by a 2x2 up convolution that splits the number of feature channels equally. This image is then concatenated or joined with the matching image from the contracting stage. The concatenation is essential owing to border pixels loss in each convolution. After the up-sampling, two convolutional layers each trailed by a ReLU are carried out similar to the contracting stage processes. At the final process step, the last of the two convolutional layers, which is a convolution of 1x1 carried out to map each of the 64 components feature of the vector to the preferred segmentation map.

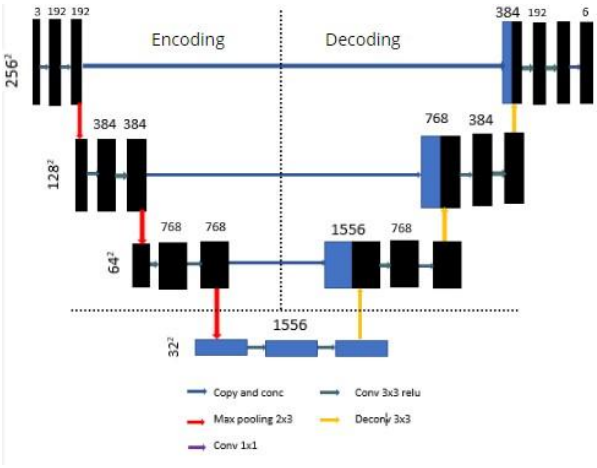

Figure 1. The developed JeisloNet architecture.

B Training and Optimization

The method entails of two stages, namely the training stage and the testing stage which were split in the ratio 80 to 20. At the training stage, the MRI slices with their corresponding manual delineated ground truth were processed with the following parameters; Stochastic Gradient Descent with Momentum (SGDM) having a default momentum value of 0.900 and Maximum number of Epochs and Initial Learning Rate of 20 and 0.001 respectively. The L2 Regularization Rate or Weight decay was set to 0.0001 (default). A MiniBatchSize of 128 was used, to update the learned weights, the categorical cross-entropy. Batch normalization method was used to initialize the weights [20]. Binary segmentation is done to predict the background and foreground of the MR images and their corresponding ground truth.

IV. Experimental Results

The developed model was implemented on MATLAB R2020a and evaluated on brain magnetic resonance images from The Cancer Images Archives (TCIA) [18]. The dataset obtained consists of Brain MRI composed with Ground Truth (manual FLAIR abnormality segmentation masks). It includes lower grade glioma (LGG) of the Cancer Genome Atlas (TCGA) assembly which corresponds to 110 patients with genomic cluster and at least a sequence data of fluid-attenuated inversion recovery (FLAIR). The dataset was organized into 110 folders. However, only 41 patient's folders were downloaded due to certain restrictions. From the 41 patient folders downloaded, 30 Brain MR images of various tumour shapes with corresponding segmentation masks were randomly selected. The model used a total of 24 MRIs training and 6 MRIs for testing. Every input slice of the TCIA dataset had a dimension of 256x256x3 (height x width x depth). All the results of segmentation shown in this study were gotten devoid of the use of data augmentation. Figure 2,3,4,5,6 and 7 show the GUI outputs of the six LGG patients' images used for testing. The first and second image in each of the figures illustrates the original image and the matching ground truth

International Journal of Scientific Engineering and Science
Volume 5, Issue 9, pp. 45-50, 2021. ISSN (Online): 2456-7361

segmentation map respectively. While the third and fourth image in each of the figures shows the binary prediction map and the DSC respectively. DSC and JI or Mean IoU are usually used to estimate performances of segmentation algorithms, to empirically evaluate the performance of our work we employed DSC and JI. The scores of DSC and JI between the ground truth segmentation map and prediction map is defined as (1) and (2)

$$\text{DSC}(I,I') = \frac{2|I \cap I'|}{|I|+|I'|} \quad (1)$$

$$\text{DSC} = \frac{2TP}{2(TP+FP+FN)} \quad (2)$$

$$\text{Mean IoU}(I, I') = \frac{|I \cap I'|}{|I \cup I'|} \quad (3)$$

$$\text{Mean IoU} = \frac{TP}{TP+FP+FN} \quad (4)$$

Where TP is the True Position, TN is the True Negative, FP is the False Positive, FN is the False Negative, and |. | represents the cardinality of the set. True positive is the values of the that are model predicted correctly as actually positive, true negative is the values of the model that are correctly predicted as actually negative, false positive is the negative values of the model that are wrongly predicted as positive, and false negative is the positive values of the model wrongly predicted as negative.

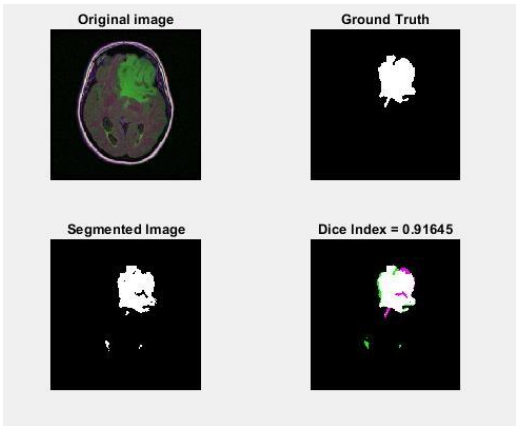

Figure 2. Segmented result for LGG MRI 2

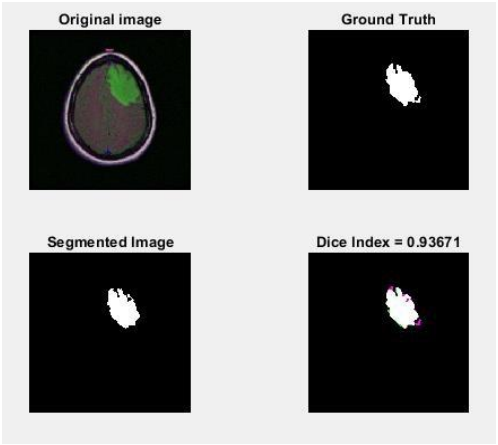

Figure 3. Segmented result for LGG MRI 3

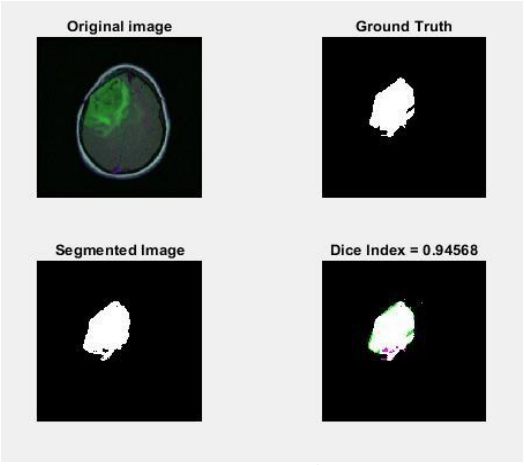

Figure 4. Segmented result for LGG MRI 4

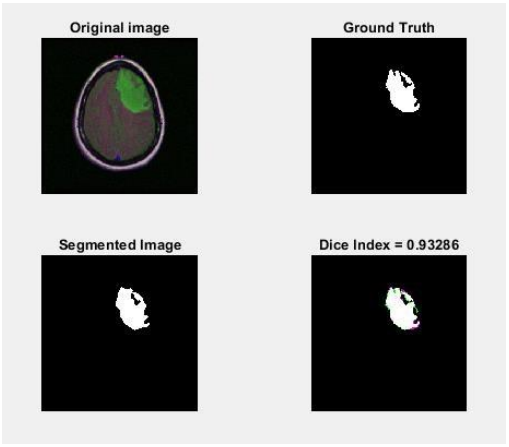

Figure 5. Segmented result for LGG MRI 5

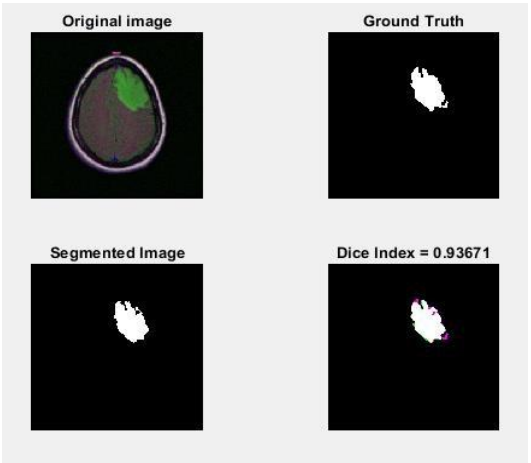

Figure 6. Segmented result for LGG MRI 6

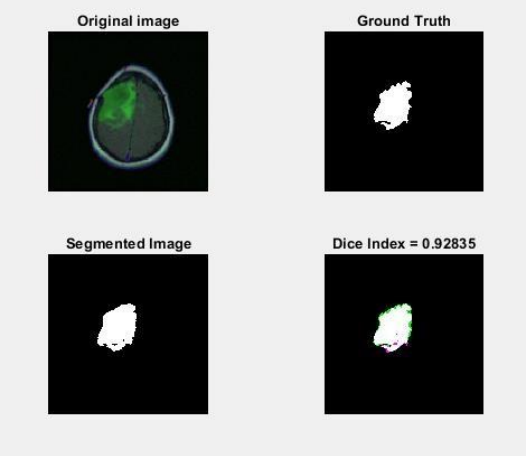

Figure 7. Segmented result for LGG MRI 7

The segmentation performances were further using Global accuracy and the Error Rate The global accuracy ratio of properly classified pixels to total pixels, irrespective of class as defined in (3), while error rate is differences between the model prediction and real mask (ground truth) as defined in (4).

$$\text{Global Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (5)$$

$$\text{Error Rate} = \frac{FP+FN}{TP+TN+FN+FP} \quad (6)$$

The performance of the segmentation in terms of the metrics discussed above is shown in table 1. Table 2 shows the DSC related to brain tumour segmentation.

TABLE 1: Performance metrics

Performance metric	Value
Dice similarity coefficient	0.9931
Mean IoU	0.9321
Global accuracy	0.9928
Error rate	0.0072

TABLE 2: DSC related to brain tumour segmentation

Author(s)	Method(s)	DSC
Pinto *et al* 2015	RF	0.83
Soltaninejad *et al* 2016	ERT	0.88
Hao *et al* 2018	VoxResNet	0.89
Chen *et al* 2019	DMF	0.90
JeisloNet	Unet	0.99

V. CONCLUSION

The analysis and processing of medical images have a great influence on clinical application such as setting a foundation for clinicians to obtain accurate pathologic diagnosis. JeisloNet has become a cutting-edge in semantic segmentation of biomedical images. The developed system used JeisloNet to segment the MR database attained from the Cancer Imaging Archive (TCIA) into tumour and background, this was achieved by predicting the image pixel by pixel. The developed Jeislonet has also shows significant performance in terms of metrics such as the Global Accuracy, Mean IoU, Dice Coefficient Index and Error Rate, achieving a good overall performance. Unet is a contemporary tool to address not only MR images segmentation but also different biomedical segmentation applications. However, this Unet is not proficient in some imaging systems. Therefore, its necessities to further upgraded in future studies for application in various imaging systems. The developed system has contributed immensely to solving clinical problems which include accurate segmentation of desired feature objective, efficient processing, and objective analysis of biomedical images. furthermore, it helps to increase accuracy in the diagnosis of biomedical images.

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