

# Gliomas Autonomous Segmentation Using Advanced Deep Learning Techniques

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**Abstract.** Segmentation of brain Gliomas from MRI autonomously is one of the important tasks for accurate diagnosis and efficient treatment procedures. Lot of recent researches involves many deep learning models for predicting the results in a proficient manner. Some researches include Convolutional Neural Networks, both 2D and 3D approach. But results gained through CNN are not promising and it is time and memory consuming. In our proposed work, a computer vision based package FastAI based Dynamic\_UNet model is utilized. The model is fine tuned by comparing the results with Classical\_UNet. The model results are visualized and the optimized parameters are chosen for segmentation process using Neptune AI logger tool. The accuracy obtained is nearly close to the ground truth results. The loss obtained is less than 0.005% with an accuracy of more than 87%. The model results helps to overcome the uncertainty information obtained due to false-segmentations and helps to perk up the prediction accuracy.

**Keywords:** Convolutional Neural Networks, Dynamic\_UNet, Classical\_UNet, Neptune AI, FastAI.

## 1. INTRODUCTION

For the past few decades, taking the snap of the brain and the technology behind it has grown enormously and that leads to many studies of the brain and its segmentation techniques. Previously, the brain imaging technique was less efficient compared to today's technology and retrieving information from such imaging techniques was also a tedious process. But with recent brain MR imaging technologies, it is possible to extract more information about the brain through segmentation process. Brain segmentation is a computerized process of analyzing the MRI images of the brain, which will be accurate in analyzing the data and consumes very less time when compared to manual process of analysis. Segmentation is a momentous step in processing MRI images. Majorly, it helps in visualizing, measuring and analyzing the parts of the brain's interior structure and arrangement. MRI plays a vital role in

diagnosing any abnormalities in the brain structure and in the detection of tumor cells in the brain. Again, the process of segmentation is the first step in achieving the above mentioned tasks in MRI images.

The most common cause of brain tumors in adults are the Gliomas. The Gliomas used to initiate the glial cells of the brain. Depending upon the origin and the size, the Gliomas are categorized as different stages like High-Graded Gliomas (HGG) and Low-Graded Gliomas (LGG). HGG is the most malignant form of the tumor and is big in size with rapid growth whereas the LGG are slow-developing tumors with an initial prediction stage [1]. The most common method of diagnosis of such brain Gliomas is through MRI (Magnetic Resonance Imaging). Diagnosis and further planning of treatments are made through the proper examination of MRI images by oncologists. In MRI, different categories of the examination are possible such as T1-weighted imaging, T2-weighted imaging, increasing the contrast on MRI (T1ce), and FLAIR (Fluid Attenuation Inversion Recovery) imaging. Among the all, T2-weighted and FLAIR sequence draw attention to the complete region of the tumor with infiltrative edema inclusion whereas t1-weighted and T1ce sequence focuses on the core region of the tumor by enhancing the contrast on imaging without including infiltrative edema [2]. All these sets of imaging are considered and compared for better analysis of the brain Gliomas.

The proposed model uses Dynamic and classical U-Net architecture for the segmentation task of the Gliomas. Neptune AI has been used for comparing the various metrics and to do model performance variations during hyper parameter tuning. The structural overview of the paper involves: Section 2 overviews about the models projected by various authors related to segmenting brain Gliomas. Section 3 details about the dataset used and the methodology description with analysis and results discussion are detailed in Section 4. Section 5 concludes the results obtained from the proposed model.

## 2. RELATED ART

As noted by Ivana et al. 2015 [3], the basic concepts behind the brain image segmentation on 2D and 3D images are image definition, intensity distributions and features related to the diagnosis. The process that has to be done before actual segmentation may include removal of non-brain cells, correcting bias fields and registration. The proper implementation of these steps affects the effectiveness of the segmentation process. Since many models of segmentation are available, it is necessary to decide upon the proper technique for a required application. Most of the time, a combination of segmentation techniques provides the better segmentation results.

In contrast, general technique for brain segmentation is not yet provided. Ali Ahmadvand et al. 2014 [4] discussed the efficiency of unsupervised segmentation with supervised segmentation and derived the conclusion. It states that no prior information is handled by unsupervised methods and hence such techniques follow unsupervised methods will not generate high accurate results and hence cannot be used in real time datasets where accuracy is highly expected. On the other hand, in supervised learning, it requires prior information for training and hence it needs more training data from clinical experts. Though it generates comparatively accurate results, it is tagged as most expensive methods. On the concluding note, the brain image segmentation has to be treated more sensitively than other image segmentation processes [4].

Deep Neural Networks (DNN) based segmentation of brain images provides a better

solution for both high quality and low quality images of the brain. Mohammad Havaei et al. 2017 [5], proposed a new Convolutional Neural Networks (CNN) architecture where it is completely remodeled from its traditional structure and made suitable for analyzing brain image data. This implements a 2-phase functioning procedure that mainly focuses on normalizing the variants in tumor features. It also includes a final cascading architecture that fetches the outcome of CNN model which is used as extra information for processing.

Alexander de Brebisson et al. 2015 [6], proposed the first segmentation process for segmenting the entire brain using deep neural networks. The method automatically processes and segments the brain MR image into its expected interior regions. As mentioned, deep neural networks are behind the automatic segmentation process, where each voxel of the brain image is segmented and categorized based on its anatomical region. Each layer of the network captures the input at different dimensions as required for the application and an important note is that it does not require image registration which is considered as one of the most important preprocessing steps for brain image segmentation.

Brain image segmentation itself is a vital process as discussed; segmenting 3D images is again a complex task. Also, 3D brain image segmentation has greater importance with which detection and diagnosis will be highly accurate when comparing to normal images. Hao Chena et al. 2018 [7], proposed a new segmentation method known as novel voxelwise residual network (VoxResNet) that uses 25 layers to provide high accuracy in detecting features. Preprocessing methods like wavelet denoising are required to clearly categorize the various interior parts of the brain before actual segmentation occurs. Automatic segmentation of brain images is possible through Convolutional Neural Network and along with this introducing parallel computing capabilities will enhance the effectiveness of the segmentation proposed by Zhenglun Kong et al. 2019 [8][27][28]. Compared to semi automatic or other types of segmentation, automatic segmentation will provide better accuracy and efficiency and consume more training samples in no time.

On the other hand, using deep neural networks, there are problems like loss of information during the conversion process since there is more number of parameters under consideration. Wentao Wu et al. 2020 [9] proposed a hybrid model that consists of a deep convolutional neural network with Support Vector Machine (SVM). This algorithm trains the deep convolutional neural network as the initial step and the extracted parameters are fed into SVM and finally the deep convolutional neural network and SVM classifier are connected and a deep classifier is built to achieve accurate segmentation. SVM based segmentation of breast cancer cells is proposed by Sountharajan et al in [10][29].

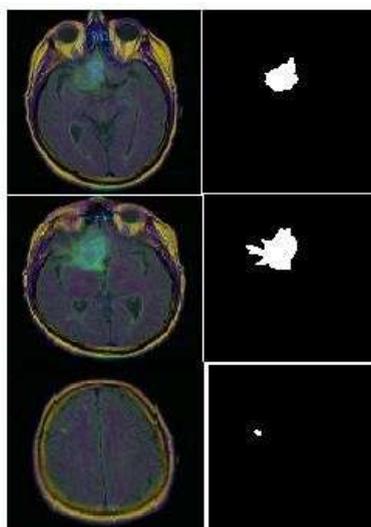
From the MRI images, the tumor regions and its related sub-regions have to be segmented automatically for the absolute diagnosis and better treatment approach and evaluation [2], [11]. But the automatic segmentation of the tumor regions is a tough job with multi-modal MRI images due to its unpredictable boundaries between normal and affected regions. The boundaries of the other parts of the body like liver [12] and heart [13] remain the same in all the people whereas the boundaries, size and location of the brain tumor varies from patients to patients and this makes automatic segmentation one of the toughest job. Hybrid-SVM based classification of Glioblastoma multiforme is proposed by Sountharajan et al in [14]. The proposed work uses hybrid swarm based optimization techniques to select the appropriate features for classification. Through recent advancements in technologies like Deep learning methods such as Convolutional Neural Networks (CNNs) facilitate the automatic segmentation of brain tumors [11]. CNN is capable of learning the most optimised features undoubtedly without the need of any manual design and features selection in contrast to the traditional machine learning algorithms like Decision trees [15] and Support Vector

Machines[16].

A disadvantage of CNN is that it has to be modeled with suitable networks architecture and specified training criteria. A two-dimensional CNN offers a requirement of low-memory [17] whereas three-dimensional CNN affects the performance of the model. A three-dimensional CNN offers better exploitation of the features but it needs high memory so the batch size of the inputs, depth and number of features explored are affected [18]. As a variation of the two CNNs, 2.5 dimensional CNN have been introduced to model using inter-sliced features as like 2D CNN and with low memory requirement in contrast to 3D model. For medical diagnosis, unambiguous segmentation results are most important for clear decisions as these could enable proper understanding of the affected regions [19] with identification of the challenges associated with it during expert's diagnosis and review [20]. Voxels occurs in brain tumor images around the boundary due to low contrast between the neighboring tissues and segmented parts with low confidence. These ambiguous voxels leads to misclassified tumor segments and these in turn could be resolved by manual interactions [21]. Added to it, the datasets available for CNN-based clinical image segmentation are petite and this leads to incorrect segmentation prediction results thereby resulting structure-wise ambiguity in measuring the tumor region volume. In [22], Fish swarm based optimization techniques are utilized to select the optimized features and this also slightly helped in improving the results. From the surveyed researches, deep learning based techniques helps to improve the segmentation accuracy. So, computer vision based techniques are used in the proposed model.

### 3. PROPOSED WORK

For segmenting the brain Gliomas, classical and dynamic U-Net architecture is utilized. The U-Net was proposed by Olaf Ronneberger in 2015 [23][24]. It is an advancement of fully convolutional networks [24]. The dataset used for the model is gathered from Kaggle [26]. This dataset comprises of MRI images of the brain with FLAIR masks of segmentation. These images are gathered from Cancer Imaging Archive (TCIA). The below Fig. 1. shows the sample images chosen for the proposed model.



**Fig. 1.** Original image with FLAIR masked segmented images

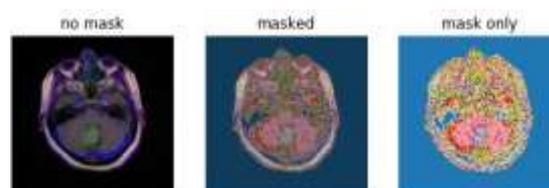
For medical image classification, the results should not reveal the identification of disease but also should aim in correctly posturing the position of the affected regions. Convolutional Neural Networks results in correctly labeling the image with ailments whereas UNet methodology is capable of absolutely determining the affected region and distinguish them from other body cells by importing classification on each and every pixel. The name for UNet is obtained due to its ‘U’ shape structure. In ‘U’, left side is known as contraction area and the right side is expansion area. Left constitutes general process of convolution and right constitutes as an up-sampling process. The process of contraction uses layer1\_convolution followed by layer2\_convolution followed by max\_pooling layer then finally dropout. Dropout may be optional. There are two convolutional layers in each step and as the image depth increases the channels also changes from one to sixty four. The image size is halved during the max\_pooling layer. This process is 3 times repeated. In the bottom layer, only two convolutional layers are built and there is no max\_pooling. The size of the image is 28\*28\*1024 at that moment.

In the expansion process, the image is resized to its original. The process involves 2Dtranspose\_convolution followed by concatenation then layer1\_convolution and finally layer2\_convolution. In convolution transpose, images are expanded by padding original image then a convolution operation. After this step, the image size is now 56\*56\*512. The corresponding image from the contraction process is then concatenated with the image 56\*56\*512. After concatenation, the final image size is 56\*56\*1024. This concatenation is performed to obtain the correct information from the previous layers and in turn leading to absolute prediction results. The final step involves image reshaping with 1\*1 sized filters in last convolutional layer.

As contrast to Classical\_UNet, an encoding-decoding based structure is employed in Dynamic\_UNet. In the proposed model, the top of the encoder is occupied by UNet serving as a pre-trained model with n\_classes output. The intermediate size of the features is determined by utilizing Hooks during initialization by providing dummy values of inputs and automatically creating an upward path in the model. The expansion path is also created automatically in the model.

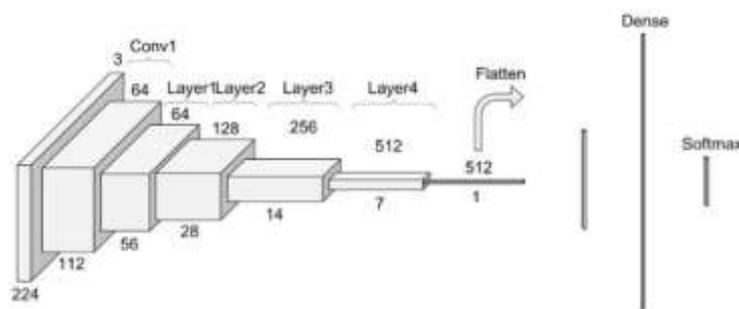
#### 4. RESULTS AND ANALYSIS

The architecture of Dynamic\_UNet from the fastai.vision package is utilized in the proposed model. The dataset is gathered from Kaggle [25]. The sample datasets are downloaded and visualized first to know in depth about the quality of the normal and masked images. The visualized images are represented in below Fig. 2.



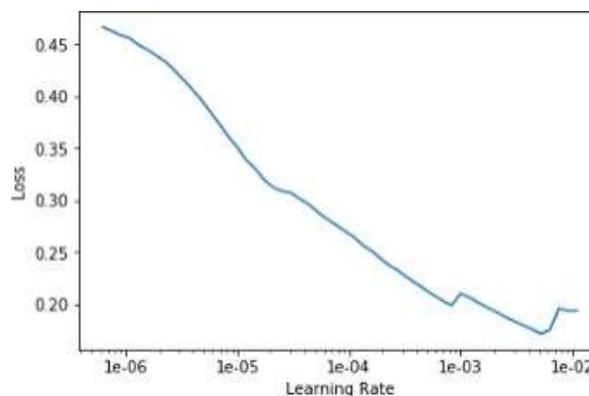
**Fig.2.** Sample MRI images

The encoder utilized in our model is ResNet34. The Deep Residual learning model is basically utilized for image classification. It acts as a pre-trained model. Its configuration helps in saving the time and memory with deeper operation in each block ensuring the quality of the work with limited number of layers. The overall view of ResNet34 architecture is illustrated in the below Fig. 3. For model evaluation metric, DICE is utilized. DICE: coefficient of DICE is 2 multiplied by overlap area divided by total pixels in the image chosen. The weight\_decay parameter utilized is L2regularisation. This diminishes overfitting, by adding the total sum of squares of all weights of model to loss function.



**Fig.3.** ResNet34 architecture

To determine the learning\_rate in an optimum fashion, learn.lr\_find(), a built-in FastAIs' method is utilized and this offers a Learning\_Rate range\_based test. The output result obtained from the Learning\_Rate test is represented in the below Fig. 4. The variation of loss with respect to learning\_rate could be visualized in the below Fig. 4. The graph depicts that as the learning\_rate increases the weight of the model get updated periodically thereby resulting in decrease of loss of the model.



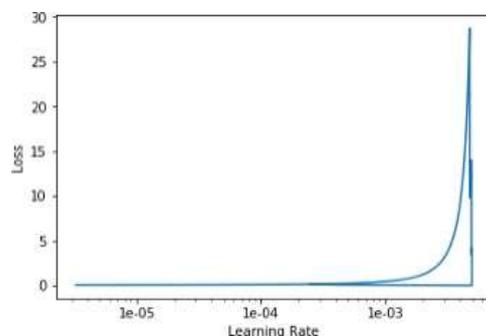
**Fig.4.** Learning\_Rate Vs Loss curve

For training the model, the policy named as Leslie Smith's 1cycle is utilized [10]. As per this

policy, cyclic based momentum is used wherein maximum value of momentum is initialized and gradually decreased in contrast to increasing value of learning rate. This kind of cyclic momentum helps to stabilize the model convergence with maximum learning\_rate values. Optimal value of learning\_rate is determined using this policy during model training. The optimal results are obtained with a learning\_rate values within a constant range of  $2e-03$  to  $6e-03$ . So in the training total of 5 epochs with learning\_rate value equal to  $5e-03$  is executed. The epochs used with training loss, validation loss and the DICE metric value is represented in the below Table 1. From the Table 1, it is understandable that as the number of epochs increases the training loss and validation loss diminishes in contrast to the increasing nature of DICE metric value. The resultant training loss Vs learning\_rate graph is visualized from the below Fig. 5.

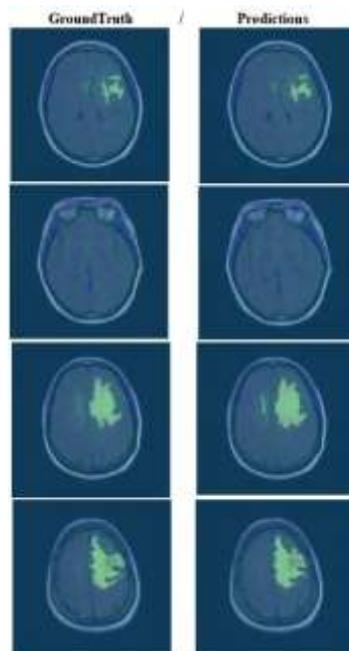
**Table 1.** Training of the model details.

Epochs	Training loss	Validation loss	DICE metric	Time taken
0	0.03	0.01	0.81	01:26
1	28.55	0.16	0.76	01:24
2	3.41	0.02	0.77	01:23
3	0.41	0.02	0.81	01:23
4	0.06	0.01	0.81	01:23



**Fig.5.** Training loss Vs Learning\_rate

In order to increase the model accuracy using FastAIs, number of epochs is increased and the total number of epochs utilized is 20. Finally at the end of 20th epoch, the accuracy of the model obtained is 87% with less than 0.005% training loss and validation loss. A powerful tool for visualizing the results, Neptune AI is used in the proposed work to enhance the understanding of the important parameters and the metrics to be involved to increase the accuracy. The segmented brain Gliomas using FastAIs is more or less similar to the original results and this proved that the model performs good in segmenting the brain Gliomas with an enhanced accuracy. The below figure 6 visualizes a sample of Gliomas segmentation by comparing the ground truth results and predicted results.



**Fig.6.** Comparison of GroundTruth Vs Predicted results of Gliomas segmented

## 5. CONCLUSION

Brain Gliomas, a leading type of brain tumor results in an increased rate of mortality in humans due to its faster growth and the inability to determine the stage of the Gliomas in advance. One method of diagnosing the tumor is through brain MRI. The results of the brain MRI is very difficult to diagnose and the proposed work aims in diagnosing the Gliomas efficiently paving an easy way to classify the stage of Gliomas. FastAI based computer vision package Dynamic\_UNet architecture is utilized in the work for segmentation. The model is compared with Classical\_UNet and the results are fine-tuned to enhance the accuracy. The parameters to be utilized are well selected using Neptune AI visualization tool. The model accuracy obtained is more than 87% with less than 0.005 % loss and error. Experimental results depicts that the model predicted near equal to the ground truth results and this shows that the proposed model is the best among the various computer vision models.

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