

BRAIN TUMOR SEGMENTATION USING UNET-FEW SHOT SCHEMATIC SEGMENTATION

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Abstract—Early finding and determination of a proper therapy technique will build the endurance of cancer patients. Precise and dependable brain tumor segmentation is a significant part in its determination and therapy procedure. Glioma is one of the hardest brain tumors to find on account of its irregular shape and obscured borders. Programmed division of glioma mind growths is a moving issue because of critical varieties in their design. In this paper, improved UNet-based architectures are presented for automatic segmentation of brain tumors from MRI images. Training semantic division models requires an enormous measure of finely clarified information, making it hard to rapidly adjust to novel classes not fulfilling this condition. The original Few Shot Segmentation tackles this problem with many drawbacks. Hence in this paper we propose generalized Few-Shot Schematic Segmentation to break down the speculation capacity of at the same time sectioning the original classifications with not very many models also, the base classes with adequate models. We are also using Context-Aware Prototype Learning (CAPL) which would significantly increase the performance by 1) utilizing the co-occurrence of earlier information from help tests and 2) progressively enhancing logical data to the classifier, molded on the substance of each question picture.

Keywords- UNet, Few Shot Segmentation, CAPL.

I INTRODUCTION

The evolution of Deep Learning has contributed to essential performance gain in semantic segmentation methods. Current semantic segmentation methods have contributed to a wide range of applications for robotics, automatic driving, medical imaging, etc. Notwithstanding, when these systems are prepared, without adequate completely named information, they can't manage concealed classes in new applications. Regardless of whether the expected information of novel classes are prepared, tweaking costs extra time and assets. Hence in order to quickly learn and test novel classes with only limited labeled data, Few Shot Segmentation models are trained on a small dataset and are

tested on new data with an aim of obtaining as precise results as possible. Then again, supervised learning based strategies require preparing information and mark matches to gain proficiency with a grouping model, in view of which new examples can be characterized and afterward fragmented. A review was proposed in which very randomized woods were utilized for arranging both appearance and setting based highlights and 83% Dice score was accomplished. After training, both support and query samples are sent to FS-Seg models to yield query predictions on previously unseen classes based on the support information. Magnetic resonance imaging (MRI) technology is the most widely recognized imaging test to analyze a cerebrum cancer as it has innocuous, painless, and high-goal highlights. Additionally, MRI can get multimodal pictures of the cerebrum's interior tissues. The most widely recognized MRI modalities are T1-weighted (T1), contrast-improved weighted (T1ce), T2-weighted (T2), and Flair examines. In every mode, an explicit piece of the cerebrum tissue is better addressed. For instance, T1 pictures are great at secluding sound tissues in the cerebrum, while T1ce assists with isolating growth limits that seem more brilliant because of the differentiation specialist. Regardless of the many advantages of MRI, dividing a cerebrum cancer physically is drawn-out, tedious, and blunder prone. Accordingly, completely programmed and precise strategies are required. Up to this point, many mechanized frameworks have been planned, yet exact glioma mind cancer division is as yet a test. This is for certain reasons:

- 1) Gliomas can show up anyplace on the mind with various shapes, sizes, and appearances.
- 2) Diagnosing gliomas is troublesome due to the fuzzy limits with healthy brain tissue.
- 3) Absence of a proper meaning of grayscale values in a similar MRI mode

Four types of sequences for two patients are shown in Figure 1. As seen in Figure 1, the structures of tumors are different. Also in Flair mode, healthy cells are seen darker in the patient's image B. Depending on the specifications of the MRI machine (1.5, 3, or 7 T) and the acquisition protocol, the grayscale values of the brain tissue vary from one patient to another patient.

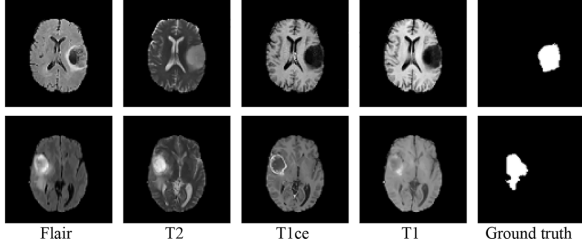


Fig 1. Examples of brain tumor in two patients A (top row) and B (bottom row) with 4 MRI modalities (Flair, T2, T1ce, T1) and physician's delineation of tumor region.

II RELATED WORK

In the early works, region-growing, thresholding, and mathematical morphology are frequently used as the foundation for segmentation algorithms. Threshold-based segmentation was utilized by Ilhan et al. to identify brain cancer. This technique is said to be 96% accurate. For two sets of photos, Gupta et al. suggested a new segmentation technique. Adaptive thresholding was used to segment the first set of photos, which included T1 and T1c images, while Canny edge detection filter was used to locate the tumor area in the second set of images, which included Flair and T2 images. Threshold-based techniques failed to reach high accuracy due to the intricacy of the brain's structure and the muddled tumor boundaries. Rahima et al. introduced the pairing of region growing methods and morphology for low-grade glioma segmentation using semi-automation. 19 pictures of gliomas were segmented using a mathematical morphology operator by Devkota et al. Increasing the quantity of samples may cause the high velocity and accuracy of morphological operation to produce less accurate findings. Using a combination of spatial fuzzy c-mean (SFCM) and region growth, Li et al. discovered the tumor. The procedures needed to initialize the seed locations in the region. When the initializations were inappropriate, their segmentations were typically not accurate enough. Their ability to successfully analyze more data sets is constrained

by these subpar initial conditions. Consequently, more advanced techniques are required.

Different convolutional neural networks (CNNs) have been developed for the segmentation of brain tumors. These networks are designed to immediately learn the intricate hierarchical features from domain data. Two-pathway architecture was introduced by Havaei et al. for efficient learning of tumor features and contextual information. Nexus structures were presented by Hussain et al. for the segmentation of gliomas. The output of a basic CNN is treated as an additional input for a succeeding CNN in the Nexus model. These CNNs are all built using a single-label prediction method. The core voxel of an image patch, or a tiny portion of the picture, is classified into a tumor or non-tumor class using a single-label prediction architecture. The core voxel of an image patch, or a tiny portion of the picture, is classified into a tumor or non-tumor class using a single-label prediction architecture. By estimating the core voxel class of the input picture patches, the segmented image is created. As a result, the conclusion step of single-label prediction networks is very slow. Dense prediction networks were introduced as a result of further developments in CNNs.

Medical picture segmentation problems have lately seen a significant increase in popularity for UNet and its variants. UNet gradually incorporates feature maps by concatenating its down-sampling layers to its up-sampling layers of the same resolution in order to achieve more precise segmentation. In the 2018 Brain Tumor Segmentation Challenge, Caver et al. employed UNet and obtained a dice similarity coefficient of 87.8%. (DSC). Abd-Ellah et al. proposed the use of two parallel UNet with asymmetric residual blocks. Performance of segmentation is enhanced by extracting local and global features along parallel routes. The WRN-PPNet network was proposed by Wang et al. [20] by fusing the local feature with the global priors under various pyramid scales. The network's strength is indicated by an increase in DSC to 91%.

In this paper, we propose an automated technique for brain tumor segmentation using MRI data with the skull removed. Our paper's main contributions are as follows: 1) We segment brain tumor images using a modified version of the basic UNet; 2) We then present a combination of a two-pathway architecture with the residual block as two-pathway-residual (TPR) architecture; and 3)

Finally, We propose Three Novel TPR-based UNet Models to Improve Segmentation Performance, Which Include TPR Blocks. While our models' computing costs were lower than those of the competition, they produced positive outcomes in the segmentation of glioma brain tumors. The suggested algorithm also doesn't need any post-processing operators, in contrast to prior approaches. Cabezas et al. introduced a 3D patch-based UNet that fully utilizes the 3D data on MRI images. On the basis of the BRATS 2018 data set, Hu et al. suggested the 3D-dilated-UNet and reported 86% for DSC. Chen et al. introduced a separable 3D UNet for efficient learning of the intra-slice and inter-slice representations in deep networks. MRI data in 3D can be processed directly by 3D networks.

III PROPOSED WORK

The proposed methodology shows how well deep neural networks function when segmenting brain tumors. After a two-step pre-processing stage that improves the input images, the brain tumor images are segmented using UNet-based designs. The resolution of the tumor tissue in the T1 picture is lower than that of the other MRI sequences. Because of this, only three sequence types—Flair, T2, and T1ce—have been utilized to identify the tumor's location. 3D MRI examines the composition of 2D slices from the pivotal, coronal, and sagittal sees. In our proposed technique, just 2D cuts from the pivotal view are utilized as information pictures as the 2D pivotal cuts have discriminative data to separate growth tissues. A few cuts toward the start also, the finish of the MRI pictures are totally dark (no cerebrum image), which isn't useful. so dark cuts are disposed of in the initial step of the pre-handling. Then, at that point, since the intensity values across MRI cuts are extremely huge, image normalization is performed. At the time of training the model, Soft Dice metric was used in the form of cost function of the network instead of cross entropy based or the quadratic expense capability. Soft Dice is basically taken as a differentiable form of the first Dice Similarity Coefficient (DSC). Stochastic gradient-based optimization is required to limit the cost function for training Deep Neural Networks. We embraced

the versatile second assessor (Adam) to appraise the boundaries. The second and third moments of gradients are used by Adam for revising and refreshing the moving average of the ongoing gradients. For our model the parameters of the Adam optimizer were set as:

- 1) Learning rate = 0.0001
- 2) Maximum number of Epochs = 100
- 3) Batch Size = 32

U-Net is an advancement of the conventional CNN (Convolution Neural Network), which was first designed in 2015 to help process biomedical images. This adjusted rendition of the U-Net has three slices used in the improved U-Net configuration with the same order in three MRI modalities separately as data inputs. These information sources are handled by a down-sampling/encoder way with down-sampling tasks and an up-sampling/decoder way with up-testing activities. To improve the precision of segmentation, the feature map of both paths are linked through a skip connection. There are similar linear blocks on both U-Net paths hence U-net is a symmetric path. Overall U-Net performs well in segmenting brain tumors, however it also has two downsides:

- 1) Normally the size of brain tumors is smaller than the entire image. AS the quantity of linear blocks in the U-Net builds, a few small tumors in the upcoming blocks might vanish on the grounds that after each block (with an exception of the final remaining one) a max-pooling layer is utilized to lessen the size of the feature maps. Consequently, some data is lost and ensuing blocks have less ability of identifying tumors.
- 2) The size of all channels in the linear block are small, so linear blocks start learning more about the local features as compared to the global ones.

These issues limit U-Net's capacity to recognize various tumors. The proposed strong block based on the blend of two pathways and residual block has great ability to recognize various growths of various different shapes and sizes.

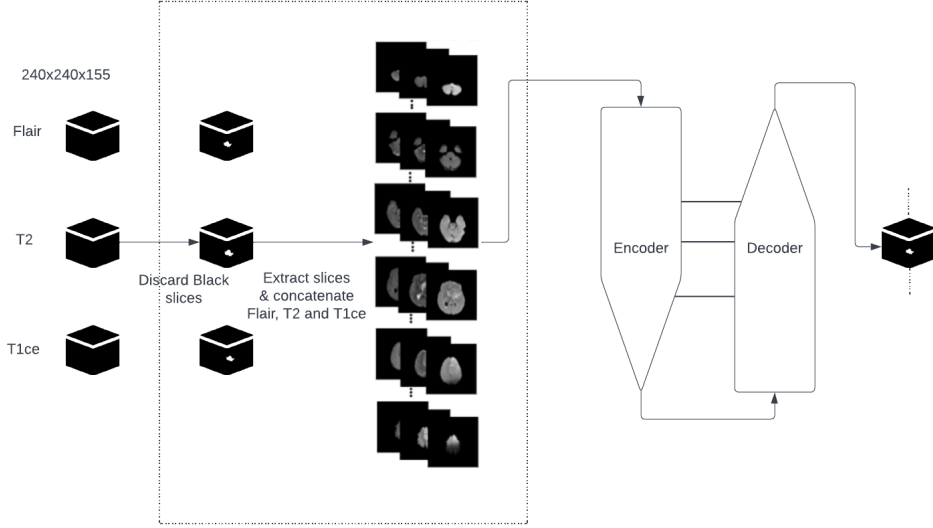


Fig. 2. Graphical abstract of the proposed methodology

IV RESULTS

Since the dataset contained different varieties of tumor images, at times images containing only black slices, so the first task was to remove these black slices from all three Flair, T2 and T1ce images. Figure 3 shows the statistics for images with tumor and no tumor from the dataset used.

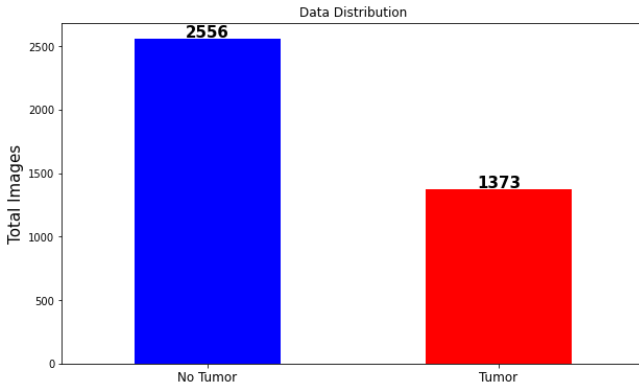


Fig 3. Data distribution of the total dataset between images containing and not containing tumors.

The above data concluded 2556 images containing no tumor while 1373 image contained tumor, the latter being the required data to take ahead for further processing of tumor shape detection.

After performing data generation, data augmentation and adjusting the data, the U-Net model is trained on the final dataset at a learning rate of 0.0001 and 100 epochs. The model performance is visualized on 3 main factors: Loss function, Intersection over Union (IoU) and Dice Coefficient.

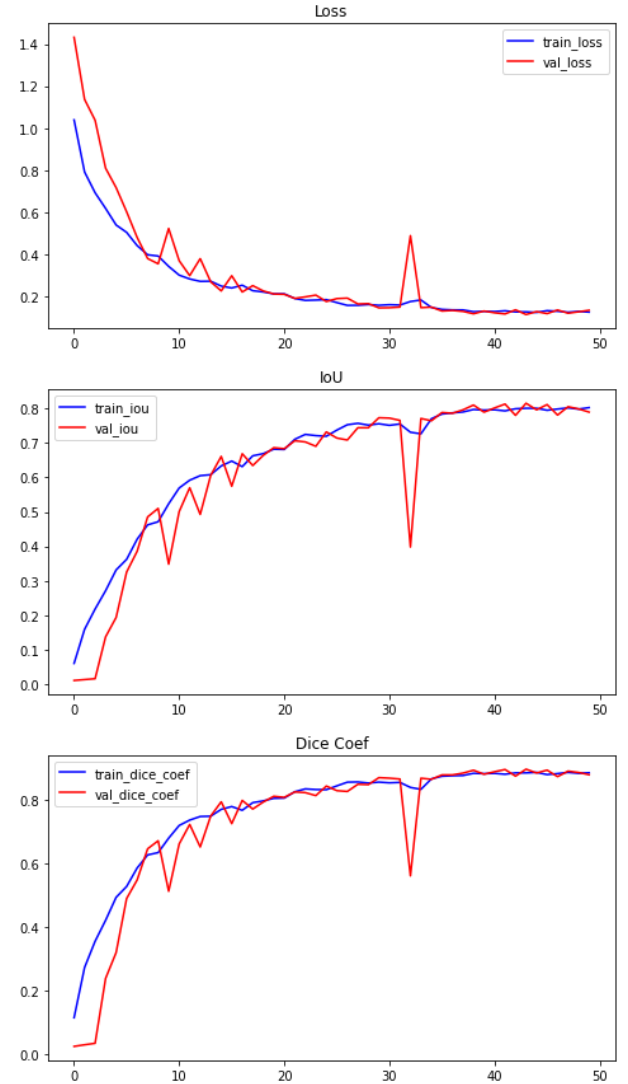


Fig 4. Visualization of the model based on loss function, IoU and Dice Coefficient.

While testing the model, the U-Net performance based on the same Loss, Intersection over Union and Dice coefficient were obtained at part with the visualized data based on 590 image filenames.

Table 1

Loss	IoU	Dice Coeff
0.1264	0.7920	0.8830

Finally the original tumor images are passed through the model and the results are compared with the original mask to the predicted ones. Figure 5 shows the obtained results.

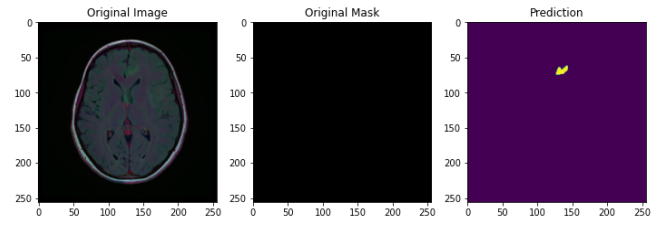
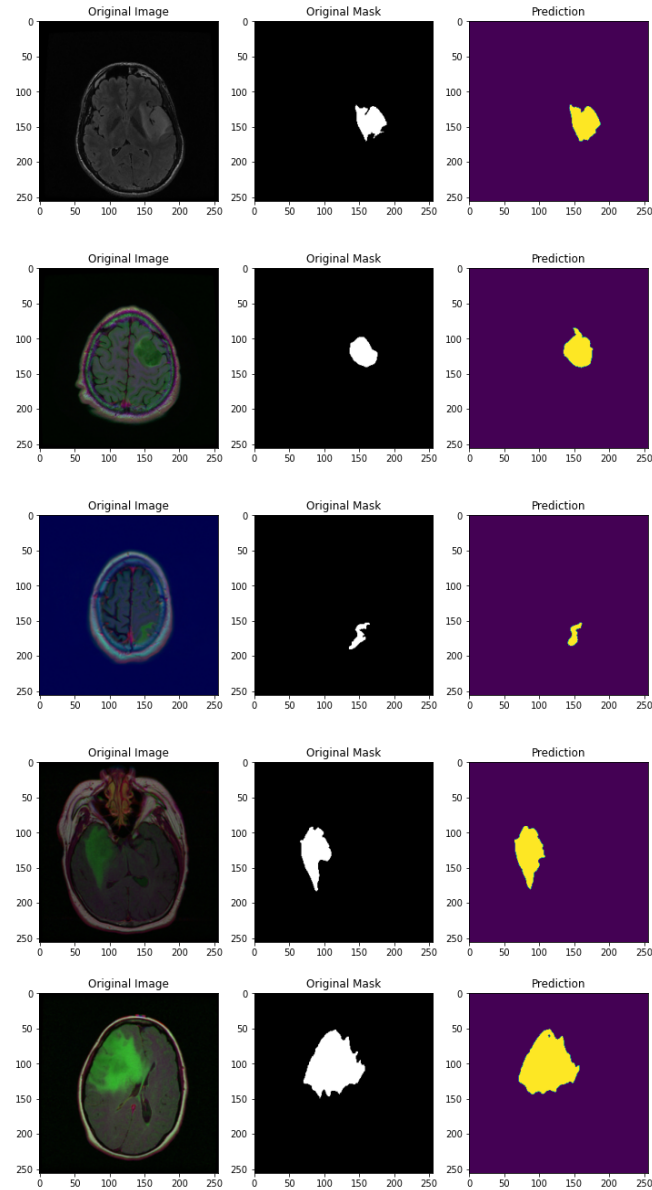


Fig 5. Visual results of the U-Net based Architecture, the first column shows the original images while second one shows the original mask. The last column is the result predicted by the U-Net model.

V CONCLUSION

In this paper, the segmentation of brain tumors from MRI sequences using an automated method is demonstrated. A two-step pre-processing was used to discard the b.

lack slices of the MRI image. The suggested models were then used to segment the image of the brain tumor. Two-pathway-residual (TPR) blocks were added to the UNet framework to help develop these models.

Two-pathway residual blocks concurrently take advantage of more regional and global features. In addition to improving evaluation criteria like DSC and sensitivity, TPR blocks in the UNet structure have also helped to minimize the number of parameters in the suggested models. In conclusion, the proposed models' benefits include lower computing costs, faster segmentation, and a lack of post-processing. One restriction of the suggested approach is the presumption that skull-stripped MRI images will be used. It is possible to separate brain tissues from non-brain regions in MRI images by using the skull stripping pre-process.

Deep neural network studies, particularly that of UNet, demonstrates the excellent capability of these architectures for segmentation tasks. Determining the best structural design for object-aware segmentation tasks will therefore be the focus of future research employing deep neural networks.

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