

# Brain tumor segmentation using UNet-few shot schematic segmentation

*Pavithra L K<sup>2</sup>, Nirmala Paramanandham<sup>1\*</sup>, Tanya Sharan<sup>1</sup>, Ronit Kumar Sarkar<sup>1</sup>, Samraj Gupta<sup>1</sup>*

<sup>2</sup>School of Computer Science and Engineering, Vellore Institute of Technology, Chennai, India

<sup>1</sup>School of Electronics Engineering, Vellore Institute of Technology, Chennai, India

**Abstract.** Early finding and determination of a proper therapy technique will build the endurance of people with cancer. A key step in the diagnosis and treatment of brain tumors is accurate and reliable segmentation. Given its uneven shape and opaque borders, gliomas are among the most difficult brain cancers to detect. Because of significant differences in their design, programmed division of glioma brain growths is a fluid topic. Improved UNet-based designs for the automatic segmentation of brain tumors from MRI images are reported in this article. Training semantic division models requires an enormous measure of finely clarified information, making it challenging to quickly acclimatize to unfamiliar classes that don't meet this requirement. The original Few Shot Segmentation attempts to address this issue but has other flaws. Hence in this paper a generalized Few-Shot Schematic Segmentation is discussed to break down the speculation capacity of at the same time sectioning the original classifications with the base classes and adequate models. A Context-Aware Prototype Learning (CAPL) which is used for improving the performance by utilizing the co-occurrence of earlier information from help tests and progressively enhancing logical data to the classifier, molded on the substance of each question picture. Results reveal the outperformance of the developed model.

## 1 Introduction

The development of deep learning has significantly improved the performance of semantic segmentation techniques. Many different applications, including those for robots, automated driving, medical imaging, etc., have benefited from the use of modern semantic segmentation techniques. However, even when these systems are ready, they cannot handle hidden classes in new applications without sufficient completely identified metadata. Whether or whether the anticipated information for unique classes is ready, modifying requires additional time and resources. Consequently, using only a small amount of labelled data, in order to quickly learn and test novel classifications, Few Shot Segmentation models are trained on a small dataset and are tested on new data with an

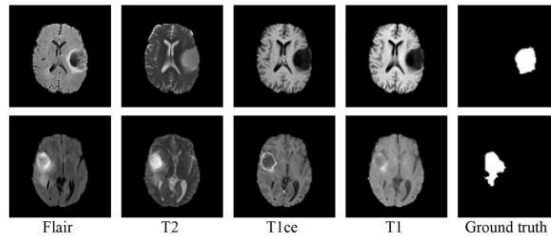
---

\* Corresponding author: [nirmalvp.ece@gmail.com](mailto:nirmalvp.ece@gmail.com)

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 put forth that achieved an 83% Dice score that used very random forests to arrange both appearance- and setting-based highlights. After training, FS-Seg models are used to provide query predictions on classes that had not yet been observed based on the support data. Magnetic resonance imaging (MRI) is one of the familiar domains to detect the brain tumor, which has a low risk of harm and a high success rate. Additionally, multimodal images of the tissues inside the cerebrum can be obtained using MRI. The T1-weighted (T1), contrast-improved (T1ce), T2-weighted (T2), and Flair examines are the most popular MRI modalities. Every mode better addresses a certain area. For instance, T1 images are excellent at separating unhealthy parts in the brain, whereas T1ce isolates growth restrictions that seem more brilliant due to the differentiation expert. 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 and discussed in the following:

- 1) Gliomas can show up anyplace on the mind with various shapes, sizes, and appearances.
- 2) It is troublesome to diagnose gliomas due to the fuzzy limits with normal brain tissue.
- 3) The meaning of in a similar MRI mode is difficult to comprehend.

Figure 1 displays four different sorts of sequences for two patients. The structures of tumors vary, as shown in Figure 1. In Flair mode, healthy parts were seen darker in the image B. Usually brain tissue's grayscale values vary from patient to patient depending on the MRI machine's parameters (1.5, 3, or 7 T) and the acquisition methodology.



**Fig. 1.** Examples of brain tumors of 2 patients with four different MRI techniques (Flair, T2, T1ce, T1) and a doctor's delineation of the tumor location are shown in rows A and B, respectively.

## 2 Literature Survey

In the previous works, region-growing, thresholding, and mathematical morphology are frequently used as the foundation for segmentation algorithms. Threshold-based segmentation was utilized by [6] D.N.H. Louis et al. to identify brain cancer. This technique is said to be 96% accurate. For two sets of photos, [5] H. Ohgaki 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 in the second batch of photos, which contained Flair and T2 images, the tumor region was found using one of the types of edge detectors (i.e.) Canny. Threshold-based techniques failed to obtain pinpoint efficiency due to the intricacy of the brain's anatomy and the fuzzy tumor

boundaries. [13] Jafari 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 [7] Vijay 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, [10] Wu 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.

For the segmentation of brain tumors, a lot of convolutional neural networks (CNNs) based models have been used. These networks are intended to quickly pick up on the complex hierarchical structures seen in domain data. [1] Collins et al. presented the dual-pathway design. Network designs for the delineation of gliomas were offered by [2] Hussain et al. These CNNs are all built using a single-label prediction method. Using a mono prediction architecture, the core pixel of an input image, or a small piece of the image, is grouped into a tumor or non-tumor class. Using a single-label prediction architecture, the core voxel of an image patch, or a small piece of the image, is categorized into various class. By estimating the core voxel category of the input picture patches, the segmented image is created. As a result, the conclusion stage in single-label prediction networks proceeds slowly. 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. To acquire more precise segmentation, UNet appends its up-sampling layers with the same granularity including its down-sampling layers in order to incrementally add feature maps. Using UNet, Caver et al. achieved an 87.8% dice similarity coefficient in the 2018 Brain Tumor Segmentation Challenge (DSC). Asymmetric residual blocks with two parallel UNets were suggested by [12] Soltaninejad et al. Extraction of local and global information along parallel paths improves segmentation performance. By combining the local feature with the global priors at different pyramid sizes, [4] Batchelor et al. presented the WRN-PPNet network.

Using MRI data with the skull removed, we suggest an automated method for segmenting brain tumors in this work. 1) By including another layer of the CNN based model, brain tumors are segmented. 2) Following this, the final layer of the model is changed such that it would associate the segmented part instead of trying to classify it. 3) Thus, a novel TPR-based UNet models is developed for improve segmentation performance.

Although our models required less computer power than those of the competitors [1, 3, 8 & 9], they successfully segmented 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 of the input images.

### 3 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 T1 image has a worse resolution of the tumour tissue than the other MRI sequences. Because of this, the tumor's location has only ever been determined using the three sequence types Flair, T2, and T1ce. 3D MRI analyses the structure of 2D segments from the coronal,

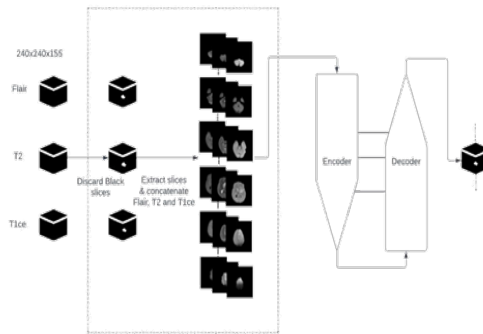
sagittal, and pivotal angles. Only 2D pivotal cuts from the pivotal view are used as information images in our suggested method since they provide discriminatory information to distinguish growing tissues. A few cuts toward the start also, the finish of the MRI pictures are totally dark (no cerebrum image), which isn't useful. So, the first pre-handling process is getting rid of the dark cuts. Image normalisation is then carried out since the intensity values across MRI cuts are so enormous at that moment. Instead of using cross entropy-based or quadratic expense capabilities, the Soft Dice metric was employed to train the model as the network's cost function. The first Dice Similarity Coefficient is essentially treated as a differentiable form in soft dice (DSC). Optimisation technique based on Stochastic Gradient becomes necessary to limit the cost function for training the DNN. 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 rolling mean of the ongoing gradients. For our model the following parameters were assigned:

- 1) Learning rate = 0.0001
- 2) No. of Epochs = 100
- 3) Batch Size = 32

The traditional CNN (Convolution Neural Network), which was initially developed in 2015 to assist in the processing of biological pictures, has been improved by U-Net. Three slices are utilized in the upgraded U-Net configuration with identical order in three different MRI modalities for this modified version of the U-Net. Both a down-sampling/encoder approach with down-sampling duties and an up-sampling/decoder way with up-testing activities are used to manage these information sources. By using a skip connection, the feature maps of the two pathways are connected to increase segmentation accuracy. Since both U-Net pathways have comparable linear building components, U-Net is a symmetric path. U-Net segments brain tumors effectively overall, however it also has two drawbacks:

- 1) Brain tumors are often smaller than the overall picture. A few minor tumors in the next blocks may go away when the U-number Net's of linear blocks increases because, except from the final block, every other block uses a max-pooling layer to create a smaller feature maps. As a result, few data is lost, and remaining parts poorly perform on detecting tumours.
- 2) Since each channel in a linear block is quite small, it starts to learn more about local features than global ones.

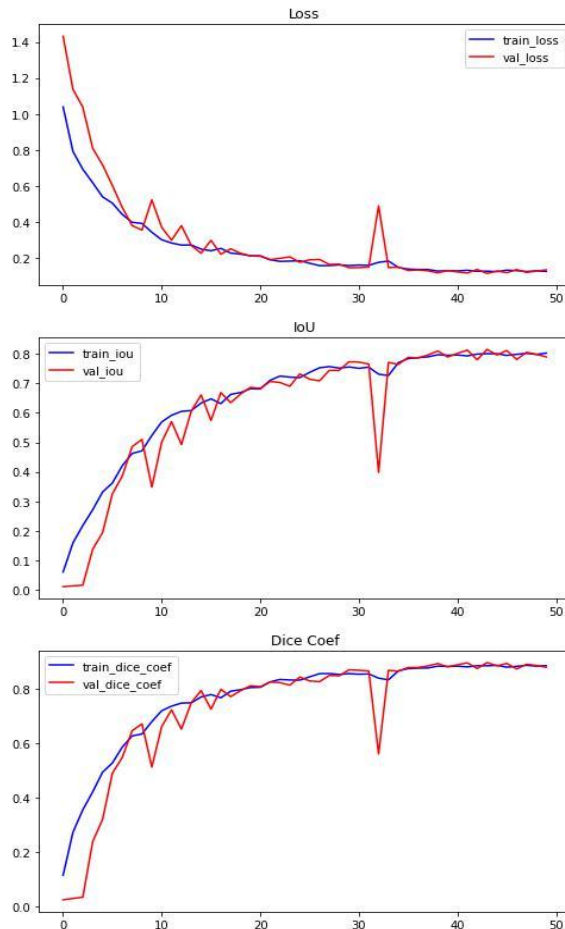
These limitations restrict U-ability Net's to distinguish between different cancers. The suggested strong block, which combines two paths and residual block, has excellent recognition capabilities for a wide range of growths in a wide range of varied forms and sizes.



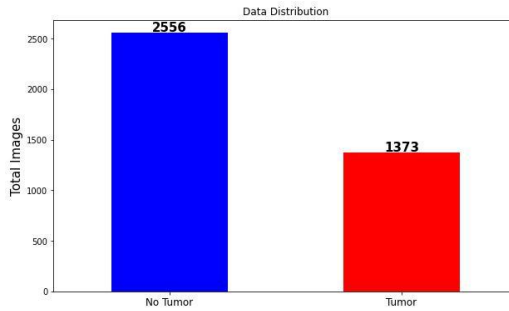
**Fig. 2.** An illustrated summary of the suggested method

### 4 Results

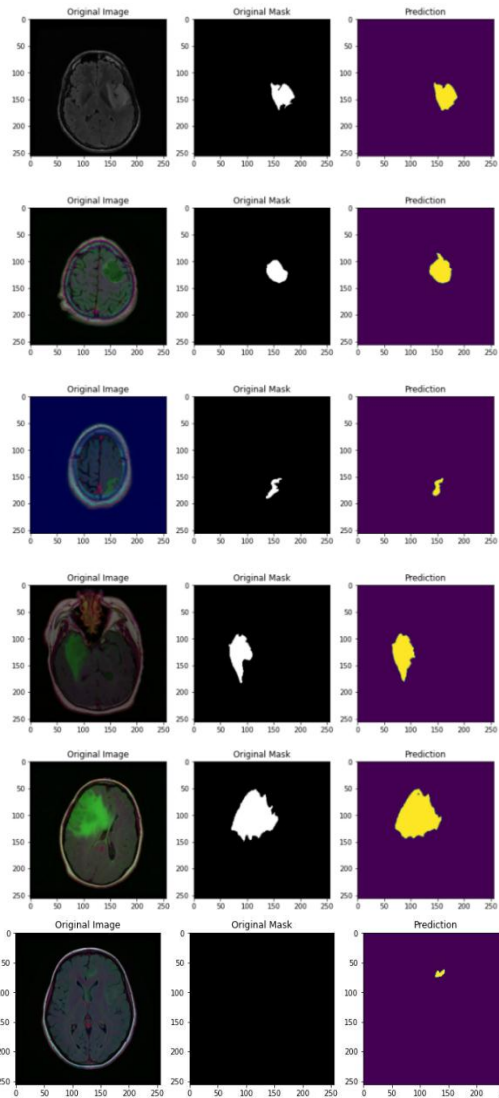
Since the dataset contained different varieties of tumor images, at times images containing only black slices, so the first task was to remove these blacks slices from all three Flair, T2 and T1ce images. Figure 4 shows the statistics for images with tumor and no tumor from the dataset used.



**Fig. 3.** Train Loss, Dice Coefficient and IoU charts for the model.



**Fig. 4.** Data distribution of the total dataset between images containing and not containing tumors.



**Fig. 5.** Visual results of the U-Net based Architecture, the actual pictures are displayed in the first column while the unique mask is displayed in the second. The last column is the result predicted by the U-Net model.

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 training is performed 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.

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.

## 5 Conclusion and Future Work

In this article, an automated technique for segmenting brain tumors from MRI sequences is put on display. To get rid of the black slices of MRI, a two-step pre-processing was applied. The brain tumor was subsequently segmented using the indicated models. To aid in the creation of these models, two-pathway-residual (TPR) blocks were included in the UNet architecture. TPR blocks simultaneously benefit from additional local and international features. TPR blocks in the UNet structure have assisted in reducing the count of the parameters in the resultant model and also helped to increase the assessment criteria like DSC and sensitivity. In conclusion, the benefits of the models discussed here include lower computing costs, faster delineation, and an absence of post-processing. One limitation of the suggested strategy is the presumption that skull-stripped MRI scans will be used. The skull stripping pre-process can be used to distinguish brain tissues from non-brain areas in MRI images.

Studies on CNN based models, notably the UNet study, show how well these designs perform in segmentation tasks. Therefore, the goal of future deep neural network research will be to identify the optimal structure architecture for object-aware segmentation tasks.

## References

1. V. Collins, Brain tumors: Classification and genes. *Journal of Neurology, Neurosurgery & Psychiatry*. 2004;75(suppl 2):ii2-ii11.
2. S. Hussain, S.M. Anwar, M. Majid, Segmentation of glioma tumors in brain using deep convolutional neural network, *Neurocomputing* 282 (2018) 248–261.
3. Robert, Christian., *Machine learning, a probabilistic perspective*. 2014:62-63.
4. T. Batchelor, Patient information: high-grade glioma in adults (Beyond the Basics), *UpToDate* (2013) 1–6.

5. H. Ohgaki, P. Kleihues, Population-based studies on incidence, survival rates, and genetic alterations in astrocytic and oligodendroglial gliomas, *Journal of Neuropathology & Experimental Neurology* 64 (6) (2005) 479–489.
6. D.N.H. Louis, O. Ohgaki, D. Wiestler, W.K. Cavenee, WHO classification of tumors of the central nervous system, *World Health Organization classification of tumors*, World Health Organization. 2007.
7. Vijay Badrinarayanan, Alex Kendall, and Roberto Cipolla. Segnet: A deep convolutional encoder-decoder architecture for image segmentation. *TPAMI*, 2017.
8. Mazzara, G.P., Velthuizen, R.P., Pearlman, J.L., Greenberg, H.M., Wagner, H.: Brain tumor target volume determination for radiation treatment planning through automated MRI segmentation. *Int. J. Radiat. Oncol. Biol. Phys.* 59, 300–12 (2004).
9. Jones, T.L., Byrnes, T.J., Yang, G., Howe, F. a, Bell, B.A., Barrick, T.R.: Brain tumor classification using the diffusion tensor image segmentation (DSEG) technique. *Neuro. Oncol.* 17, 466–476 (2014).
10. Wu, W., Chen, A.Y.C., Zhao, L., Corso, J.J.: Brain tumor detection and segmentation in a CRF (conditional random fields) framework with pixelpairwise affinity and superpixel-level features. *Int. J. Comput. Assist. Radiol. Surg.* (2013).
11. Gotz, M., Weber, C., Blocher, J., Stieltjes, B., Meinzer, H., Maier-Hein, K.: Extremely randomized trees based brain tumor segmentation. In: *Proceeding of BRATS Challenge-MICCAI* (2014).
12. Soltaninejad, M., Yang, G., Lambrou, T., Allinson, N., Jones, T.L., Barrick, T.R., Howe, F.A., Ye, X.: Automated brain tumour detection and segmentation using superpixel-based extremely randomized trees in FLAIR MRI. *Int. J. Comput. Assist. Radiol. Surg.* (2016)
13. Jafari, M., Kasaei, S.: Automatic brain tissue detection in MRI images using seeded region growing segmentation and neural network classification. *Aust. J. Basic Appl. Sci.* 5, 1066–1079 (2011).