

3D U-Net for Brain Tumor Detection and Segmentation

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ABSTRACT

We describe a fully automated brain tumor segmentation approach based on Convolutional Neural Network in this paper. The suggested network takes the 3D Flair Magnetic Resonance Image (MRI) of glioblastomas as input. These tumors can appear anywhere in the brain and have practically any shape or size by their very nature. These factors compel us to investigate an artificial intelligence system that takes advantage of a flexible, high-capacity neural network while remaining incredibly efficient. We describe the U-Net model that we've found to be important for achieving effective performance in segmenting the tumor in brain and the stage of the patient.

Keywords : Convolutional Neural Network, U-Net architecture, 3D volumes, Brain Tumor (Gliomas), Segmentation.

Article Info

Volume 9, Issue 3

Page Number : 232-237

Publication Issue

May-June-2022

Article History

Accepted : 01 June 2022

Published : 05 June 2022

I. INTRODUCTION

A brain tumour is a collection of abnormal cells in your brain that forms a mass. Your brain is protected by a highly tough skull. Any expansion in such a small location can generate complications. Brain tumours can be malignant (cancerous) or benign (noncancerous) (benign). The pressure inside your skull might rise when benign or malignant tumours get larger. This can result in brain damage, which can be fatal.

There are two types of brain tumours: primary and secondary. The origin of a primary brain tumour is in the brain. The majority of initial brain tumours are harmless. A secondary brain tumour, also known as a metastatic brain tumour, develops when cancer cells from another organ, such as your lung or breast, migrate to your brain.

Glioblastoma is a type of brain cancer. It's the most common type of malignant brain tumor among adults. And it is usually very aggressive, which means it can grow fast and spread quickly.

Depending on its location and rate of growth, a glioma can damage brain function and be life-threatening. One of the most prevalent types of primary brain tumours is gliomas. The type of glioma you have influences your treatment options and prognosis. Surgery, radiation therapy, chemotherapy, targeted therapy, and experimental clinical trials are among methods for treating glioma.

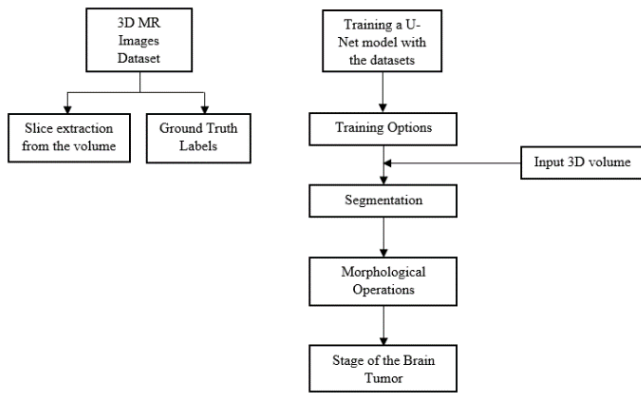


Figure 1: Block Diagram of Proposed System

II. Related Work

[1] Kalaiselvi, T., and Nagaraja, P: - Using fuzzy c-means (FCM) clustering and seeded region growing approaches, this research aims to build a semi-automatic method for detecting a brain tumour from T2-weighted MRI brain scans. FCM clustering is utilised to divide an image into four regions: background, grey matter, white matter, and cerebrospinal fluid at first (CSF). The tumour seems good in the CSF component and forms a mask of brain tissue from the CSF portion. The tumour region is then detected from the segmented portion using the applicable seeded region developing approach. The tumour component of the T2-weighted glioma MRI brain images was segmented in this study. The tumour area appeared to be in good shape in the CSF region, and it was also the most linked. The mask matching to significant sections of the brain is generated in the CSF section by removing the majority of non-brain elements such as background, bone, fat, and muscles. This mask is used to remove the substructure of the brain for future investigation. The SRG approach is then utilised to differentiate brain tumours from the substructures that were extracted. The seed points can be manually selected in the SRG section.

[2] Wafa M, Zagrouba E: - Two automated techniques for brain tumour segmentation have been developed in this research, with the goal of determining which one would produce accurate segmentation that is

similar to manual results. Each axial slice through the head was segmented using three weighted MR feature images (improved T1, proton density (PD), and T2). The first method uses a multi-feature Fuzzy-c-means (FCM) algorithm, which is then followed by a post-processing step that uses prior knowledge of the tumour region. The three-pass method is the second approach. To begin, the FCM algorithm classifies each individual modality MRI independently. Second, the final brain tissue labelling is obtained by fusing classified images using the Dempster-Shafer evidence theory. Finally, prior knowledge is applied to fine-tune the tumor's location. A total of 200 multimodal MRIs were utilised to validate ten tumour instances of various sizes, shapes, and locations in the brain. The ground truth is a comparison of the brain tumour segmentation findings to a manual segmentation performed by two independent medical professionals. In comparison to the first strategy, our experiments show that the second approach yields results that are comparable to hand tracing.

[3] Fletcher-Heath LM, Hall LO, Goldgof DB, Murtagh FR: - On two 1.5 Tesla GE Signa MR Scanners (General Electric Company, Milwaukee, WI) from two institutions, six data sets from four patients with brain tumours were obtained. Patient volume 6 was obtained from the University of Texas Medical Branch in Galveston. The remaining five volumes were obtained through the Department of Radiology at the University of South Florida. With a 256x192 acquisition matrix, a field of view of either 240 mm (volumes 1 and 2) or 220 mm (volumes 3 - 6) and one full excitation (NEX=1), axial, 2D, 5 mm thick slice images at the level of and superior to the lateral ventricles were acquired at the level of and superior to the lateral ventricles. Volumes 1 through 5 are contiguous slice data, however volume 6 was recorded with a 2 mm slice gap. A normal spin-echo (SE) sequence was used to capture T1-weighted pictures, while a fast spin-echo (FSE) sequence was used to take PD and T2-weighted images. Although none of the six

patients had hyper-intense tumour regions in T1 post-contrast imaging, all T1-weighted pictures used for categorization were those taken before the contrast agent gadolinium was injected.

[4] A. Mustaqeem A. Javed and T. Fatima: - Images are obtained via an MRI scan and shown in a two-dimensional matrices with pixels as its elements in this paper. The size of the matrix and the field of view affect these matrices. The images are saved in MATLAB and shown as a 256*256 grayscale picture. A grey scale image's entries range from 0 to 255, with 0 representing complete black and 255 representing complete white. From black to white, the entries in this range vary in intensity. Thirty female and thirty male patients, ranging in age from 20 to 60 years, were examined for the objective of the investigation. Their MRI scans were archived in a JPEG image database.

[5] S. Sivanand: - In this work, an unique method for picture segmentation is proposed. An adaptive local threshold algorithm is suggested to solve the difficulty of conventional threshold segmentation methods. With photos that have non-uniform illumination, this approach works effectively. Using a kernel-based clustering strategy, the problem of the Fuzzy C-Means clustering method can be avoided. For photos with unequally sized clusters, the Kernel Fuzzy C-Means clustering algorithm might be utilised. Experiments on medical images show that the proposed technique performs better at clustering.

[6] R. B. Dubey, M. Hanmandlu, and S. K. Gupta: - The goal of this study is to see how different merging criteria effect segmentation quality and processing time in this paper. The merge criteria are determined by four key features of segmentation output: region merge ability, boundary correctness, merge rejections, and the number of iterations necessary. Based on local feature analysis, the system either automatically or manually sets segmentation thresholds. The method is reliable and generates high-quality segmentation on a variety of textured and grayscale pictures. Seeds can be chosen automatically or manually for growing in a

certain region. The brightest pixel in an image can serve as a seed pixel, and their automatic selection can be based on detecting pixels of interest. They can also be figured out by looking at the peaks in a picture histogram. Seeds, on the other hand, can be individually selected for each object in the image. Using a set of seeds, the method is used to segment an image into various sections. A set S represents each seeded region, which is a connected component with one or more points. It is estimated the collection of immediate neighbours that surround the pixel.

III. Methodology

3D-UNet is made up of a contractive and expanding path that uses a combination of convolution and pooling techniques to create a bottleneck in its centre. The image is then reconstructed using a combination of convolutions and up sampling after this bottleneck. UNET is a U-shaped encoder-decoder network architecture made up of four encoder blocks and four decoder blocks linked by a bridge. At each encoder block, the encoder network (contracting path) has half the spatial dimensions and double the number of filters (feature channels).

3D Volume dataset: The 3D volume of the Flair MRI dataset is acquired from the Kaggle Public dataset under Brain Tumor Segmentation (BraTS20).

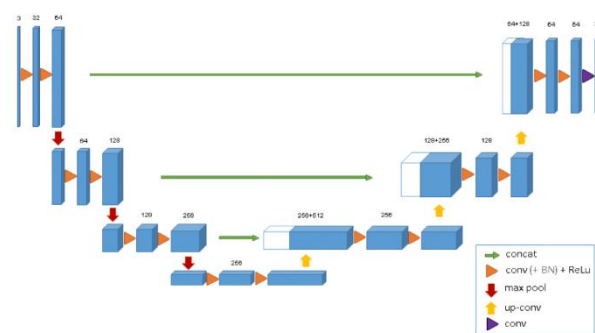


Figure 2: Layers of U-net

U-net can be separated into two types of paths: encoder-decoder and contracting-expansive. The encoder (left side) 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 down sample step. Decoder path (right side): Every step in the expanded route starts with an up sample of the feature map, which is followed by 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.

Sliding convolutional filters are applied to the input by a 2-D convolutional layer. Convolution2dLayer creates a 2-D convolutional layer. The convolutional layer is made up of several parts. Filters and Stride are convolutional layers that are made up of neurons that link to subregions of the input images or the previous layer's outputs. While scanning through an image, the layer learns the features localised by these regions. The filter Size input argument can be used to specify the size of these sections when constructing a layer with the convolution2dLayer function.

Dilated Convolution: A dilated convolution is one in which the filters are enlarged by inserting spaces between the filter elements. The 'Dilation Factor' parameter is used to specify the dilation factor. Increase the layer's receptive field (the area of the input that the layer can see) without increasing the number of parameters or computation by using dilated convolutions. By putting zeros between each filter element, the layer widens the filters. The dilation factor controls the sample step size for the input, or the filter's up-sampling factor. It equates to a filter size of (Filter Size - 1) in terms of effective filter size. * Add 1 to the dilation factor.

Feature Maps: A feature map is formed when a filter advances along the input using the same set of weights and bias for the convolution. Each feature map is created by convolution with a separate

combination of weights and bias. As a result, the number of feature maps and filters is identical. $((h*w*c + 1)*\text{Number of Filters})$ is the total number of parameters in a convolutional layer, where 1 is the bias.

The 'Padding' name-value pair option can also be used to apply zero padding to input picture borders vertically and horizontally. Padding is the addition of zeros to the picture input's borders in rows or columns. By adjusting the padding, you can control the output size of the layer. This image shows a 3-by-3 filter scanning through the input with padding of size 1. The lower map represents the input and the upper map represents the output.

Rectified Linear Unit (ReLU): As a non-linear activation function, a Rectified Linear Unit is used. If the value is less than zero, a ReLU says to round it up to zero. Using reluLayer, create a ReLU layer. Each element of the input is subjected to a threshold operation by a ReLU layer, with any value less than zero being set to zero. A nonlinear activation function, such as a rectified linear unit (ReLU), is commonly specified by a ReLU layer after the convolutional and batch normalization layers. Batch normalization improves the predictability of a network's output, reduces overfitting through regularization, and speeds up training by an order of magnitude.

Batch normalization is the process of doing normalization inside the current batch's scope activation layer by subtracting the mean of the batch's activations and dividing by the batch's standard deviation. Using batch-Normalization-Layer, create a batch normalization layer. Each input channel is normalized over a mini-batch via a batch normalization layer.

Use batch normalization layers between convolutional layers and nonlinearities, such as ReLU layers, to speed up convolutional neural network training and reduce sensitivity to network

initialization. Down-sampling is accomplished with a max pooling layer, which divides the input into rectangular pooling sections and computes the maximum of each zone. The `maxPooling2dLayer` is used to create a maximum pooling layer. By dividing the input into rectangular pooling regions and determining the average values of each zone, an average pooling layer performs down-sampling. Using `averagePooling2dLayer`, make a pooling layer with an average

For downsampling, pooling layers come after the convolutional layers, lowering the number of connections to the subsequent layers. They don't learn anything themselves, but they do lower the amount of parameters that need to be learned in the layers that follow. They also aid in the reduction of oversizing. The desire to use a transformation that goes in the opposite direction of a normal convolution, i.e., from something that has the shape of a convolution's output to something that has the shape of its input while maintaining a connectivity pattern that is compatible with said convolution, leads to the need for transposed convolutions.

A concatenation layer accepts many inputs and concatenates them along a single axis. In all dimensions except the concatenation dimension, the inputs must be the same size. When creating the layer, specify the number of inputs. 'in1','in2','inN' are the names of the inputs, where N is the number of inputs. The input is softmaxed via a softmax layer. Softmax layer can be used to create a softmax layer. For multi-class classification problems with mutually exclusive classes, the cross-entropy loss is computed by a classification layer. Using `classification Layer`, create a layer for classification. The final fully linked layer must be followed by a softmax layer and finally a classification layer for classification tasks.

The Layers of Pixel Classification: For each picture pixel or voxel, a pixel classification layer assigns a

categorical label. For semantic picture segmentation networks, `PixelClassificationLayer` generates a pixel classification output layer. For each visual pixel or voxel processed by a CNN, this layer outputs a categorical label. During training, the layer excludes pixels with ambiguous labels.

Semantic segmentation: The technique of providing a label to each pixel in an image is referred to as semantic segmentation. In comparison, categorization assigns a single label to the entire image. Multiple objects of the same class are treated as a single entity when semantic segmentation is used.

IV. Experimental Results

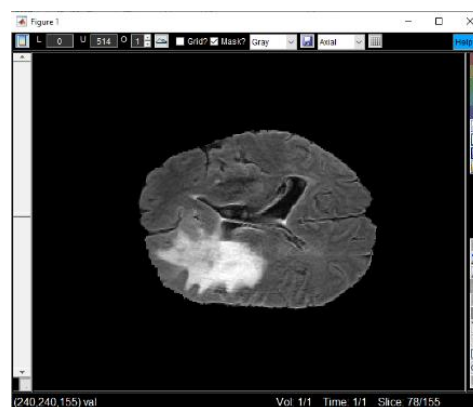


Figure 3: Viewing the 3D Volume as slices

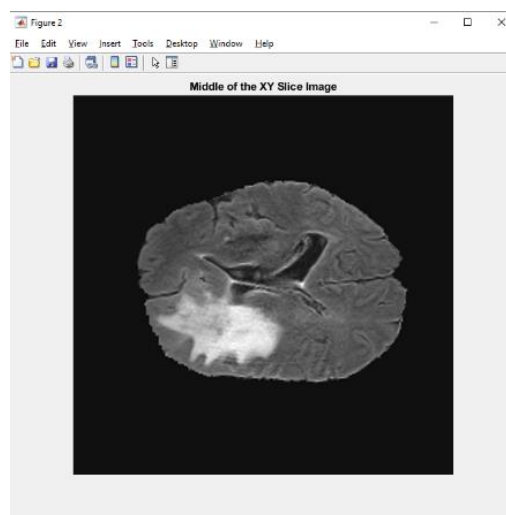


Figure 4: Input

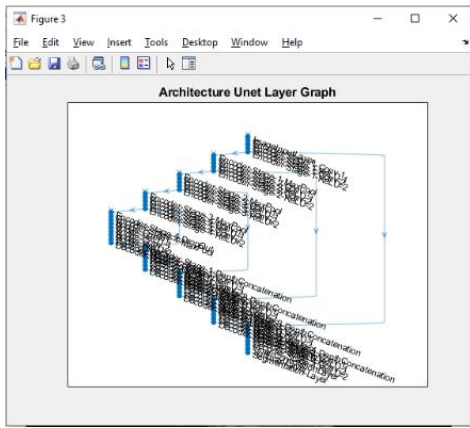


Figure 5: U-Net Layers and Architecture

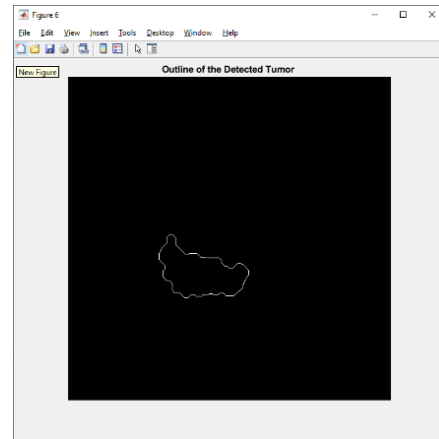


Figure 9: Outline of the tumor

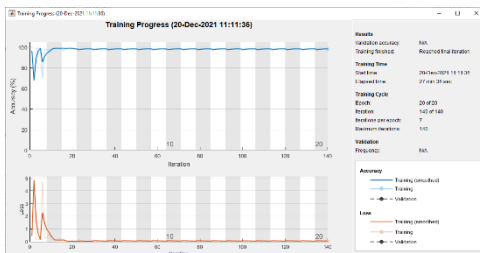


Figure 6: Training Progress

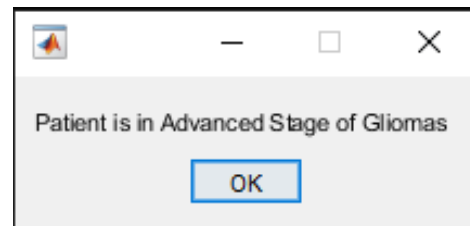


Figure 10: Output

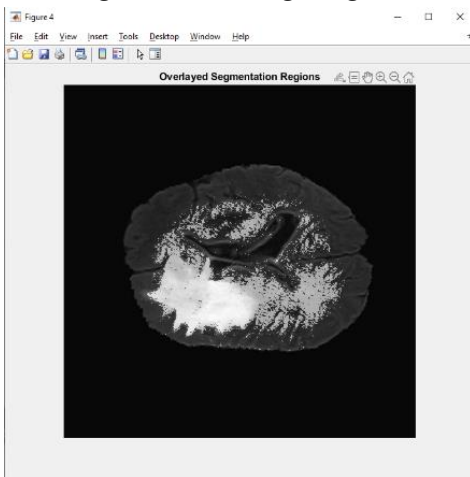


Figure 7: Overlaid Segmentation after training

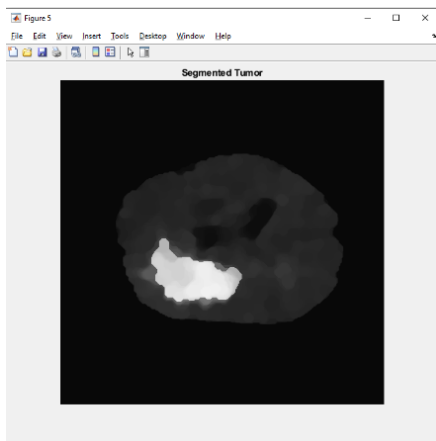


Figure 8: Segmented Tumor

V. Conclusion

The proposed method involves the Gliomas, the most common Brain Tumor is being detected with using U-Net modal network. This model trains on the sliced images and ground truth labels and works excellent for the brain tumor medical images. Brain Tumor is being segmented successfully and the tumor size is used to determine the stage of tumor.

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Cite this article as :

P Swathi, M Narayana Ramakrishna, K Vilasini, M Sai Hemanth, J Nirmal Sumanth, "3D U-Net for Brain Tumor Detection and Segmentation", International Journal of Scientific Research in Science and Technology (IJSRST), Online ISSN : 2395-602X, Print ISSN : 2395-6011, Volume 9 Issue 3, pp. 415-421, May-June 2022.
Journal URL : <https://ijsrst.com/IJSRST229377>