An Efficient U-Net Based Deep Convolution Network for Brain Tumour Detection from MRI Image

Krishna Patel[1], Riddhi Bhavsar[2], Sweta Popat[3*], Priyanka Puvar[4], Bhagirath Prajapati[5]

[1,2,3]*B.E. Student, Dept. of Computer Engineering, A. D. Patel Institute of Technology Constituent, Anand, India*
[4]*Assistant Professor, Dept. of Computer Engineering, A. D. Patel Inst. of Technology Constituent, Anand, India*
[5]*Professor, Dept. of Computer Engineering, A. D. Patel Institute of Technology Constituent, Anand, India*
*Corresponding author: swetapopat12@gmail.com

***Abstract*: The brain tumour is one of the most aggressive and common disease, which leads to a very short life expectancy in its highest grade. Therefore, treatment planning is important to improve the quality of life of patients. Generally, various techniques such as Computed Tomography (CT), Magnetic Resonance Imaging (MRI) [1] and ultrasound images are used to diagnose the tumour in brain manually. But it has some limitations i.e. it can only provide accurate results for limited number of images. Therefore, trusted and automatic detection of brain tumour is essential to decrease death rate of human. This paper proposes fully automatic segmentation of brain tumour using U-net based deep convolution network. We have used BRATS dataset for training and validation purpose.**

***Keywords*: MRI images, CNN, Brain tumour, BRATS dataset, Tumour detection, Computed tomography (CT).**

1. Introduction

Brain tumour is an irregular mass of tissue in which cells grow and multiply feverishly, by the mechanisms that control normal cells. Generally, tumour is classified into primary and secondary tumour. Primary tumour begins within the brain and secondary tumour will expand to the other parts of the body.

The most frequent primary tumours in adults are primary central nervous system lymphomas and gliomas, where gliomas account for 80% of malignant cases. Lower-grade gliomas (LGG) are a varied group of primary brain tumours that generally arise in young, and if proper care is not taken then low grade gliomas will continue to grow and then develop into a higher grade tumour such as the grade 3 or grade 4 tumours [2]. In this article we have proposed method to diagnosis the lower grade glioma.

There are many medical imaging methods available like X-ray, CT (Computed Tomography) and MRI (Magnetic Resonance Imaging). The research article uses MRI brain images because of its high resolution and good quality of an image. After capturing MRI brain image, it is necessary to separate the tumour region from the MRI brain image. Accurate segmentation of medical images helps the radiologist for radiotherapy planning.

In our work we have used U-net which is built upon the Fully Convolutional Network and modified in a way that yields better segmentation in medical imaging.

Convolution Neural Network (CNN) is one of the classes of the deep learning. CNN is most commonly applied to analyse visual imagery [3]. There are mainly three types of layers in CNN such as input layer, output layer and multiple hidden layers. Hidden layers include multiple-convolution layer, pooling layers, normalization layer and fully connected layer.

The U-net model which we have used has 3 separate parts.

The contracting/down sampling path, bottleneck and expanding/up sampling path.

The U-Net combines the location information from the downsampling path with the contextual information in the upsampling path to finally obtain a general information combining localisation and context which is necessary to predict a good segmentation map [4].

We have used BRATS dataset for training and validation purpose. We have trained MRI images using U-net model.

2. Implementation

We have used U-net model for MRI brain tumour segmentation using TensorFlow. Normally, the segmentation is performed using various tools like MATLAB, LABVIEW etc. We have used TensorFlow based MRI brain tumour segmentation in order to improve segmentation accuracy, speed and sensitivity. Segmentation is performed on BRATS MRI brain images and results are compared in terms of dice co-efficient. Many researchers use MATLAB to implement the segmentation process. Our work utilizes the python programming to implement the segmentation of MRI brain tumour. The features to choose python programming for implementing the research workare listed below

1. Python code is more compact and readable than MATLAB
2. The python data structure is superior to MATLAB
3. It is an open source and also provides more graphic

International Journal of Research in Engineering, Science and Management
Volume-3, Issue-6, June-2020
www.ijresm.com | ISSN (Online): 2581-5792

498

packages and dataset [5].

Hence, the proposed work utilizes python programming instead of MATLAB. There are some additional python packages used during the implementation process of our research work through python.

A. Dataset Description

We have used BRATS'19 dataset to train and validate the model. BRATS' data set contains 259 volumes of HGG and 76 volumes of LGG and one volume contains 155 slices. These slices are MRI images. This system is proposed to detect LGG tumours so we have used LGG data set of BRATS'. The volumes are arranged into T1, T2, Flair and T1Ce sequences [6]. In the Flair sequence whole tumour is visible. For better result we have used flair images of LGG for training and validation.

The BRATS'19 dataset is in NIFTI format, so SimpleITK library is used to read images of this format.
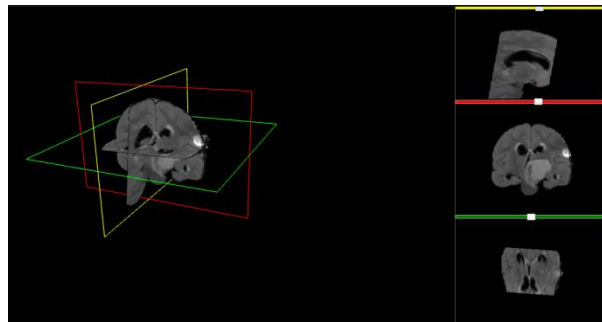

Fig. 1. Original image

Figure 1 shows the 2D representation of a NIFTI image. Three axis are seen, x, y and z which shows the brain from different angle.

B. Data Preprocessing

The images we have used are in NIFTI format. Biomedical images generally have NIFTI format which is high resolution format. Therefore, we've used SimpleITK library to read these images. We used the SimpleITK library for performing Data pre-processing and Data Augmentation.

ITK or Insight Segmentation and Registration Toolkit is an open-source and cross-platform system that provides developers with an extensive suite of software tools for image analysis. Among them, SimpleITK is a simplified layer built on top of ITK, intended to facilitate its use in rapid prototyping, education and interpreted languages. SimpleITK is an image analysis toolkit with a large number of components supporting general filtering operations, image segmentation and registration [7]. SimpleITK itself is written in C++ but is available for a large number of programming languages including Python.

The ground truth is available in dataset. And the images are stored in numpy array, so that it becomes easy to train and validate.
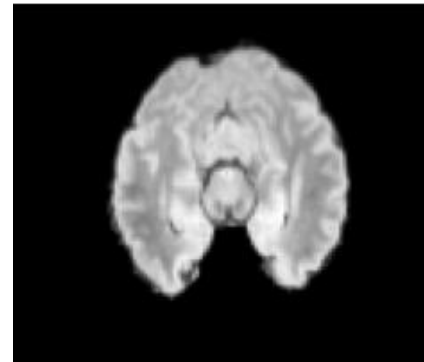

Fig. 2. Pre-processed image

We have 76 volumes and from each volume we have fetched 80 images, so we did data augmentation in order to increase the number of images. After data pre-processing and augmentation we have 12160 images in numpy array. Out of which 9120 images are used for training and 3040 are used for validation purpose.

Figure 2 shows the pre-processed image which is obtained after performing the pre-processing on NIFTI image. The image is of 124x120 pixels.

C. U-Net Based Deep Convolutional Network Architecture

Biomedical images usually contain detailed patterns of the imaged object (e.g., brain tumour) and the edge of the object is variable. To cope with the segmentation for the objects with detailed patterns, Long et al. proposed to use the skip architecture that combined the high-level representation from deep decoding layers with the appearance representation from shallow encoding layers to produce detailed segmentation [8]. Olaf Ronneberger et al. introduced the U-Net for Bio Medical Image Segmentation, which employed the skip-architecture to solve the cell tracking problem. We use only one U-net model to do three different segmentation tasks Full Tumour, Tumour Core, Enhancing Tumour.

The architecture contains three paths:

1. Contraction path (also called as the encoder):

It is used to capture the context in the image. The encoder is just a traditional stack of convolutional and max pooling layers. As shown in Figure 3(left side path), it consists of the repeated application of two 3x3 convolutions (unpadded convolutions), each followed by a rectified linear unit (ReLU) and a 2x2 max pooling operation with stride 2 for down-sampling [9]. At each downsampling step we double the number of feature channels.

2. Bottleneck:

This part of the network is between the contracting and expanding paths. As shown in Figure 3(Bottom most block), the bottleneck is built from simply 2 Convolutional layers (with batch normalization), with dropout.

3. Symmetric Expanding path (also called as the decoder or Expansive Path):

It is used to enable precise localization using transposed convolutions. As shown in Figure 3(Right side path) Every step in the expansive path consists of an upsampling of the feature

International Journal of Research in Engineering, Science and Management
Volume-3, Issue-6, June-2020
www.ijresm.com | ISSN (Online): 2581-5792

499

map followed by a 2x2 convolution ("up-convolution") that halves the number of feature channels, a concatenation with the correspondingly cropped feature map from the contracting path, and two 3x3 convolutions, each followed by a ReLU. The cropping is necessary due to the loss of border pixels in every convolution.

At the final layer a 1x1 convolution is used to map each 64-component feature vector to the desired number of classes. In total the network has 23 convolutional layers.

Thus it is an end-to-end fully convolutional network (FCN), i.e. it only contains Convolutional layers and does not contain any dense layer because of which it can accept image of any size.

In machine learning, ground truth is a term used in statistics and machine learning that means checking the results of machine learning for accuracy against the real world. In other words, the term "ground truth" refers to the accuracy of the training set's classification for supervised learning techniques. This is used in statistical models to prove or disprove research hypotheses. The term "ground truthing" refers to the process of gathering the proper objective (provable) data for this test.
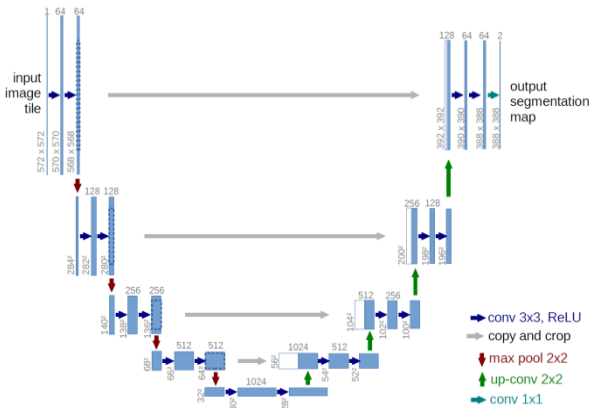

Fig. 3. U-Net model architecture

Our Modifications in U-Net Model

In the proposed system we have modified the u-net architecture according to our input image. Figure 4 shows the U-Net model used in this system.

In total this network has 18 convolution layers with batch normalization. And there are total 7 blocks. 3 blocks of Contraction path, 1 block of bottleneck and 3 blocks of Expansive path.

1. Contraction path:

Initially the size of input image is 120x120 pixels in first layer and number of channel is 1. And then the number of channel changes from $1 \rightarrow 64$ as convolution process will increase the depth of the image. The red arrow pointing down is the max pooling process which halves down size of image.

In 2nd block the number of channels is doubled from $64 \rightarrow 128$ and the size of image is halved from 120 pixels $\rightarrow$ 60 pixels as we have applied the max pooling layer with stride of 2. Then again after applying max pooling layer with stride 2 the image

size is halved.

In 3rd block the number of channels is 256 and the image size is 30x30 pixels. After this, max pooling layer with stride of 2 is applied.

2. Bottleneck:

In this block, 2 convolution layers are built and there is no max pooling. At this point the size of image is 15x15 pixels and channels are 512.

3. Expansive path:

In expansive path image is upsized to its original size. The 1st layer of this block is Transpose Convolution. It is an upsampling technique that expands the size of images. After the transposed convolution with stride 2, the image is upsized from 15x15x512 to 30x30x256, and then, this image is concatenated with the corresponding image from the contracting path and together makes an image of size 30x30x512. The reason is to combine the information from the previous layers in order to get a more precise prediction.
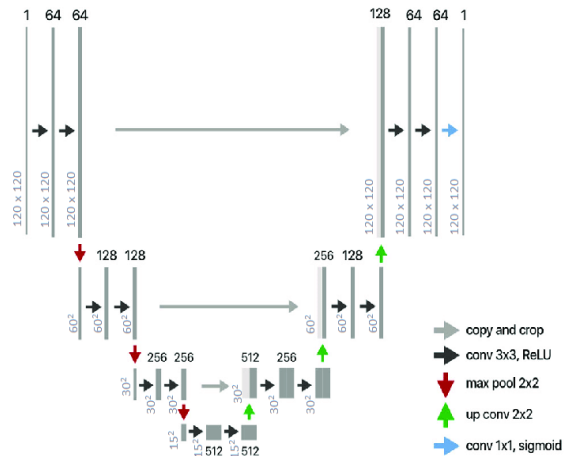

Fig. 4. U-Net Model used in this system

In the 2nd block of this path after the transposed convolution with stride 2, the image is upsized from 30x30x256 to 60x60x128 and is again concatenated with the corresponding image from the contracting path and together makes an image of size 60x60x256.

In the 3rd block of this path after the transposed convolution with stride 2, the image is upsized from 60x60x128 to 120x120x64 and is again concatenated with the corresponding image from the contracting path and together makes an image of size 120x120x128. The last layer is a convolution layer with 1 filter of size 1x1 which gives out the desired output [10].

D. Training and Validation

During the training process, we used Dice metric as the cost function of the network. Training of convolution neural networks requires stochastic gradient-based optimization to minimize the cost function with respect to its parameters. We adopted the adaptive moment estimator (Adam Optimiser) to estimate the parameters. Adam optimiser is used to calculate the individual adaptive learning rate for each parameter from

International Journal of Research in Engineering, Science and Management
Volume-3, Issue-6, June-2020
www.ijresm.com | ISSN (Online): 2581-5792

500

estimates of first and second moments of the gradients [11].

3. Result and Analysis

To detect the tumour an image is provided and by using predict function it is detected whether tumour is present or not.
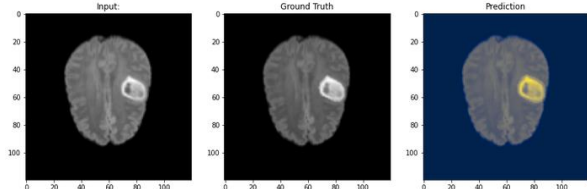

Fig. 5. Result 1

Figure 5 shows the prediction on image with tumour. As seen from ground truth there is tumour and also same is predicted in final image.
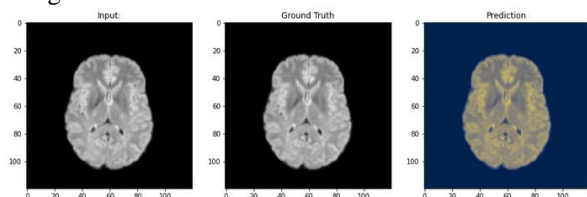

Fig. 6. Result 2

Figure 6 shows the prediction on image without tumour. As seen from ground truth there is no tumour and also same is predicted in final image.

4. Conclusion and Future Scope

Using this system tumour can be detected with upto 90% accuracy. In addition to that this method is quick and reliable to detect tumour in early stage with just MRI image. In future we can take large database and can also detect different types of tumour using this system. Along with this a desktop application can be created based on this system to detect tumour.

References

[1] NeethuOuseph C. "A Reliable Method for Brain Tumor Detection Using Cnn Technique," IOSR Journal of Electrical and Electronics Engineering.

[2] Elizabeth B. Claus, Kyle M. Walsh, John Wiencke, Annette M. Molinaro, Joseph L. Wiemels, Joellen M. Schildkraut, Melissa L. Bondy, Mitchel Berger, Robert Jenkins, and Margaret Wrensch "Survival and low grade glioma: the emergence of genetic information" Neurosurg Focus. 2015 Jan; 38(1).

[3] Rikiya Yamashita1, Mizuho Nishio, Richard KinhGian Do, Kaori Togashi, "Convolutional neural networks: an overview and application in radiology" Insights Imaging (2018) 9:611–629

[4] JiaxuLeng, Ying Liu, Tianlin Zhang, Pei Quan, Zhenyu Cui "Context-Aware U-Net for Biomedical Image Segmentation" Conference Paper. February 2019.

[5] M. Malathi, P. Sinthia "Brain Tumor Segmentation Using Convolutional Neural Network with Tensor Flow."

[6] Gaurav Shukla, Gregory S. Alexander, Spyridon Bakas, Rahul Nikam, KiranTalekar, Joshua D. Palmer, Wenyin Shi "Advanced magnetic resonance imaging in glioblastoma: A review," CCO Vol. 6, No. 4, August 2017.

[7] Ziv Yaniv, Bradley C. Lowekamp, Hans J. Johnson, Richard Beare "SimpleITK Image-Analysis Notebooks: A Collaborative Environment for Education and Reproducible Research" J Digit Imaging, 2018, 31:290–303.

[8] Hao Dong, Guang Yang, Fangde Liu, Yuanhan Mo, Yike Guo, "Automatic Brain Tumor Detection and Segmentation Using U-Net Based Fully Convolutional Networks," June 2017.

[9] Olaf Ronneberger, Philipp Fischer, and Thomas Brox "U-Net: Convolutional Networks for Biomedical Image Segmentation," May 2015.

[10] Ruirui Li, Wenjie Liu, Lei Yang, Shihao Sun, Wei Hu, Fan Zhang, Wei Li, "DeepUNet: A Deep Fully Convolutional Network for Pixel-level Sea-Land Segmentation," Sept. 2017

[11] Diederik P. Kingma, Jimmy Lei Ba "ADAM: A Method Forstochastic Optimization," Jan. 2017.