A Thesis/Project/Dissertation Report

on

Glioblastoma brain tumor segmentation and survival prediction using 3D U Net

Submitted in partial fulfillment of the
requirement for the award of the degree of

Bachelor of Technology(Computer Science)

UnderTheSupervision of
Dr. Dileep Kumar Yadav
Professor

Submitted By

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SCHOOL OF COMPUTING SCIENCE AND ENGINEERING
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GALGOTIAS UNIVERSITY, GREATER NOIDA
INDIA
05, 2023

SCHOOL OF COMPUTING SCIENCE AND ENGINEERING
GALGOTIAS UNIVERSITY, GREATER NOIDA

CANDIDATE'S DECLARATION

We (Prabhav Srivastava & Vanshika Misra) hereby certify that the work which is being presented in the thesis/project/dissertation, entitled **"Glioblastoma brain tumor segmentation and survival prediction using 3d u net "** in partial fulfillment of the requirements for the award of the B.Tech submitted in the School of Computing Science and Engineeringof Galgotias University, Greater Noida, is an original work carried out during the period of month, Year to Month and Year, under the supervision of **Dr. Dileep Kumar Yadav** Designation, Prof. Department of Computer Science and Engineering/Computer Application and Information and Science, of School of Computing Science and Engineering , Galgotias University, Greater Noida

The matter presented in the thesis/project/dissertation has not been submitted by us for the award of any other degree of this or any other places.

Prabhav   Srivastava ,19SCSE1010097

Vanshika Misra, 19SCSE101493

This is to certify that the above statement made by the candidates is correct to the best of my knowledge.

Supervisor Name

Dr. Dileep Kumar Yadav

Designation :(Professor)

CERTIFICATE

The Final Thesis/Project/ Dissertation Viva-Voce examination of Prabhav Srivastava (19SCSE1010097), Vanshika Misra (19SCSE1010493) been held on 15/05/2023 and his/her work isrecommended for the award of B.Tech .

Signature of Examiner(s)   **Signature of Supervisor(s)**

Signature of Project Coordinator   **Signature of Dean**

Date: 15/05/2023

Place: Greater Noida

Acknowledgment

[From Crimi, Alessandro; Bakas, Spyridon; Kuijf, Hugo; Keyvan, Farahani; Reyes, Mauricio; van Walsum, Theo (2019). *[Lecture Notes in Computer Science] Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries Volume 11384 (4th International Workshop, BrainLes 2018, Held in Conjunction with MICCAI 2018, Granada, Spain, September 16, 2018, Revised Selected Papers, Part II) || 3D U-Net for Brain Tumour Segmentation. , 10.1007/978-3-030-11726-9(Chapter 23), 254–266.* doi:10.1007/978-3-030-11726-9_23 **]**

Abstract

Convolutional networks are the most widely used method for egmenting three-dimensional (3D) medical images. Deep learning algorithms have recently attained human-level performance in a number of significant application tasks, including lung cancer volumetry and delineation ,preparing for radiation therapy However, cutting-edge topologies like UNet and Deep Medic are computationally intensive and necessitate workstations with graphics processing units for quick inference.

However, there has been little study into making fast central processing unit computations possible in such networks. This is where our paper comes in. To segment a 3D study, we present a new segmentation method that uses a human-like technique. We begin by analysing the image at a small scale to find areas of interest, then process only the feature-map patches that are relevant. Magnetic resonance (MR) imaging tumour segmentation is a vital step in giving objective assessments of glioma aggressiveness and response to therapy. It's useful for diagnosing, monitoring, and planning treatment for brain tumours. The goal of this study was to create a fully automated deep learning approach for segmenting brain tumours and predicting survival.. To segment the entire tumour (WT), tumour core (TC), and augmenting tumour, a three-group structure was built, with each group consisting of three 3D-Dense-UNets (ET). This method was used to break down a complex multi-class segmentation problem into separate binary segmentation problems for each sub-component. Different techniques and loss functions were used to train each group.

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1. Table for Student Data:

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2. Table for Faculty Data :

S.No	Supervisor Teacher Name	Course
01	Dr. Dileep Kumar Yadav	School of Computing Science and Engineering

CHAPTER-1

1.1 Introduction

Automatic brain tumor segmentation is one such task that will help doctors and radiologists detect and delineate tumor subtypes more accurately. Automated brain tumor segmentation is very wanted since it will aid clinicians in learning about prognostic factors, monitoring tumor progression, and therapy planning.On the Brats 2020 Challenge, we offer an approach based on a modified 3D UNet architecture that delivered state-of-the-art segmentation results.

In both paediatric and adult populations, gliomas are the most prevalent malignant primary brain tumours. Gliomas are cancerous tumours that grow from glial cells and are classified as low grade or high grade, with significant disparities in patient survival.

The life expectancy of patients with aggressive high-grade gliomas is fewer than two years. Glioblastoma (GBM) is a type of severe brain cancer defined as stage IV by the World Health Organization (WHO).

The overall survival rate for GBM patients is low, ranging from 12 to 15 months. Surgical removal of the tumour is usually followed by radiotherapy and chemotherapy. Gliomas are frequently licenced under the Creative Commons Attribution-NonCommercial-NoDerivatives-NoDerivatives-NoDerivatives-NoDerivatives-NoDe The author/funder (who has granted bioRxiv a perpetual permission to display the preprint) is certified by peer review.

This preprint's copyright holder (which did not include active tumour tissue, necrotic tissue, or surrounding edoema) Because of its superior soft tissue contrast, magnetic resonance imaging (MRI) is the most often utilised modality to assess brain malignancies.

It's commonly utilised in patients' clinical work-ups for brain tumour diagnosis, progression tracking, and therapy planning.

Accurate segmentation and quantitative analysis of brain tumor are critical for diagnosis and treatment planning. Generally, manual segmentation of brain tumor is known to be time-consuming, tedious and error-prone.Therefore, there is a strong need for a fully automatic method for brain tumor segmentation.

However, brain tumor segmentation is a challenging task because MR images are typically acquired using various protocols and magnet strengths, which results in the non-standard range of MR images. In addition, brain tumors can appear anywhere in the brain, and their shape and size vary greatly. Furthermore, the intensity.

Brain tumor causes abnormal functioning of brain cells which affects the nervous system in a disastrous manner. It has various stages of serious issues with Brain that may lead to decrease the general life span of a normal human being whose brain is tumorized. Brain Tumor [1] is also of 2 types, i.e., Cancerous and Non-Cancerous. The motion inside the skull can affect the stage of Brain Tumor. If it is not detected at an early stage, it may lead to brain damage and can have life threatening affects for a human being. According to research, around 308,102 people all over the world were diagnosed with Brain Tumor out of which 251,329 people died because of primary cancerous brain and central nervous system tumor that is the reason we have decided to focus on prediction of early-stage brain tumor. MRI (Magnetic Resonance Imaging) [1] scans are used to detect such disease and according to the results, doctor advices the most suitable treatment for the same. These treatments are done based on size, shape, stage, and part of brain where tumor is detected. In this project, we are focusing on detection of brain tumor using various Deep Learning techniques. There are various deep learning techniques which could help in building this project such as Artificial Neural Network (ANN), Convolutional Neural Network (CNN),

Classic Neural Network, Recurrent Neural Network (RNN) etc. but we are focusing to work using the CNN model to get the most efficient result with high accuracy and less time consuming. The basic purpose of using the CNN model is to get the excellent performance to classify the tumors.

Keywords— deep learning ; medical image segmentation

Formulation of Problem

- Make prediction of Age and Survival Days for each unique identifier in the data.

  - **Segmentation** ----- algorithm used in segmentation is 3D Unet **.**

  - **Prediction** ----------- algorithm used in prediction is 3D autoencoder.

Tools and Technology used

- Anaconda [Jupyter Notebook]
- Language [Python]
- Library : pandas
    matplotlib,
    sklearn ,
    PyTorch
    Nilearn

What is Brain Tumor

A brain tumor 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 tumors can be malignant (cancerous) or benign (noncancerous) (benign). The pressure inside your skull might rise when benign or malignant tumors get larger. This can result in brain damage, which can be fatal.

A cancerous or non-cancerous mass or growth of abnormal cells in the brain. Tumours can start in the brain, or cancer elsewhere in the body can spread to the brain.

Symptoms include new or increasingly strong headaches, blurred vision, loss of balance, confusion and seizures. In some cases, there may be no symptoms. Treatments include surgery, radiation and chemotherapy.

Type of Brain Tumor

It can be any of the following, depending on the types of cells in a tumor:

Mainly three types are described her

- **Benign:**
  There are no cancerous cells in the tumour.
  A benign tumour is a collection of cells that lacks the potential to penetrate or spread to other tissues (spread throughout the body). When benign tumours are excised, they usually do not return, whereas malignant tumours do sometimes.

- **Premalignant or precancerous :** is a term used to describe a condition that is not yet cancerous. It contains aberrant cells that have the potentialto become malignant.
  The cells in these tumours aren't currently cancerous, but they have the potential to become so. Malignant tumours are malignant tumours. The cells have the ability to multiply and spread to other places of the body.

- **Malignant:** Cancerous cells are present in the tumour.
Malignant tumours have uncontrollable cell growth that spreads locally and/or to distant locations. Tumors that are malignant are cancerous (ie, they invade other sites). They spread through the bloodstream or lymphatic system to distant locations. Metastasis is the medical term for this type of spread.

Summary: Tumors are non-cancerous growths on the body's surface. They might be harmless or cancerous. Tumors that aren't cancerous are referred to as benign tumours. They're cancerous. Tumors that are benign can only grow in one location. They can't spread to other sections of your body or infiltrate them. Even so, if they press against essential organs like your brain, they can be harmful.

Grades of Tumor :

If a grading system for a tumor type is not specified, the following system is generally used (1)

- **GX:** Grade cannot be assessed (undetermined grade)
- **G1:** Well differentiated (low grade)
- **G2:** Moderately differentiated (intermediate grade)
- **G3:** Poorly differentiated (high grade)
- **G4:** Undifferentiated (high grade)

Grading is a method of classifying tumour cells into groups depending on their appearance. An professional clinician known as a pathologist examines a sample of brain tumour cells under a microscope to determine the grade.

The lower the grade, the more normal the cells appear. The higher the grade, the more aberrant the cells appear.

Purpose of the Project:

The main purpose of this project was to build a CNN model that would classify if subject has a tumor or not base on MRI scan. In this project, we are going to discuss the early prediction of Brain Tumor using Deep Learning We'll be creating a CNN model (Convolutional Neural Network) for the same. Based on some images, we are going to classify the brain tumor in order to cure or prevent the seriousness of increasing of dangerous stage. Through this project, you will get familiar with the exploratory data analysis and feature engineering techniques that need to be applied to process data. Machine learning and Data Science are one of the fastest-growing technological fields. This field results in amazing changes in the medical field, production, robotics etc. The main reason for the advancement in this field is the increase in the computational power and availability of large amounts of data. In Data Science, this data is analyzed and made suitable for creating machine learning models and products. And Deep Learning is a subpart of Machine Learning. 1

Target beneficiary:

The motivation for using deep learning in the Brain tumor classification is to improve the accuracy and performance and create better strategies in order to prevent from increasing to a dangerous state.We used Convolutional Neural Network. With the help of this DL Network we predicted the probability of a person having brain tumour which are in the form of Boolean results i.e. Yes (1) or No (0).

Project Scope:

Our aim is to detect the brain tumor is or not from the CNN model we have build based on the input images. the early detection of brain tumor will prevent the patient from its dangerous stage, later on we will apply the model two or three different datasets. • Input: A collection of images of brain tumor. These images are of different sizes with varied lighting conditions. • Output: The primary goal is to extract

meaningful and accurate information from these images with the least error possible . The first step is pre-processing which is used for reduction of impulsive noises and image resizing. The next step is feature extraction, mser features and etc. The last step is model building ,A Convolutional Neural Network (ConvNet/CNN) is a Deep Learning algorithm which can take this input image to differentiate one from the other. the evaluation of result is done on the basia of different parameters like accuracy, precision , recall values etc.

Project Description:

Reference algorithm: CNN Convolutional neural network (CNN) is one of the most popular and used of DL networks Because of CNN, DL is very popular nowadays. The main advantage of CNN compared to its predecessors is that it automatically detects the significant features without any human supervision which made it the most used.

Data:

First of all we want the data which we are going to pre-process and using that we will train our model. So we collected the data Brain Tumor Detection CNN v1.0||vgg16 given by Ruslan Klymentiev from the website named Kaggle. They include information like images. There were two folders named as Yes and No. In the Yes folder, it consists of 259 images of Tumor whereas in the No folder,100 images where no tumor exists. No quality data means no quality results. This is the basic line behind the success of any algorithm. Because before using any algorithm we have to process the data in advance if we expect the best results from it. There are many potential problems with data such as incorrect values, inconsistencies, imperfections etc. Firstly we have collected the data then we have imported the data after that we have extracted the data then splitted it into training and testing and validation after that we have preprocessed the data then we have build the model, after that we have predicted the result that the images has tumor or not. The most crucial libraries for data analysis are Numpy and Matplotlib and other libraries used are

tqdm, Imutils, Plotly, Tensorflow. We have used numpy for array size of data and matplolib for plotting the graph and confusion matrix.

SWOT Analysis:

• Strength: As an image is one of the strongest way to analyze the functioning and defects, that is why it is able to be constructed from any object that we pull from an image. A Convolutional Neural Network (ConvNet/CNN) is a Deep Learning algorithm which can take in an input image, assign importance to various aspects/objects in the image and be able to differentiate one from the other. The network learns to extract features while training, we just feed the image to the network, it helps the model to generate more accurate data. We are collecting datasets from Kaggle, that's a website which allows the user to access multiple datasets that are required. we use the pre-trained model that has been already trained on large datasets and extract the ,mser features and etc, from the images and use them for our tasks.

• Weakness: The images if not uploaded correctly may give the incorrect results. The dataset used to predict the result should be preprocessed properly.

• Opportunities: Predicting the Tumor will help us to know the result faster.

• Threats: An incorrectly predicted Tumor may result in putting the human life in danger.

Project Features:

a. Collecting Dataset: First of all we want the data which we are going to pre-process and using that we will train our model. So we collected the brain tumor dataset from Kaggle. There are Two fifty files and two folders in this dataset :- a) Yes b) No

b. Data import and pre-processing:

No quality data mean there will be no quality results. This is the basic line behind the success of any algorithm. Because before using any algorithm we have to process the data in advance if we expect the best results from it. There are many potential problems with data such as incorrect values, inconsistencies, imperfections etc. that's why we need to filter the correct data without getting any kind of errors in it.

There are many pre-processing steps to deal with these issues such as data cleaning, data consolidation, data modification, data reduction, data segmentation etc. The most crucial libraries for data analysis are Numpy and Matplotlib and other libraries used are tqdm, Imutils, Plotly, Tensorflow. We have used numpy for array size of data and matplolib for plotting the graph and confusion matrix .

Data Pre-processing: It improves the standard of the brain tumor MR images. Pre-processing techniques used are as follows:-
 • cv2.erode() method is used to perform erosion on the image.
 • Conversion of RGB color to gray-scale.
• The dilation operation is performed by using the cv2. dilate() method.
 • Gaussian Blur() method of cv2 library to blur an image.
 • Interpolation is the way the extra pixels in the new image is calculated.
 • cv.draw: Contours function is used. It can also be used to draw any shape provided you have its boundary points.

Data Augmentation: Techniques used to increase the amount of data by adding slightly modified copies of already existing data or newly created synthetic data from existing data. a) Zoom in, zoom out. b) Left shift, right shift. c. Training and Testing Splitting the data set:
 • Testing data: The Convolutional Neural Network (CNN or ConvNet), Its built-in convolutional layer reduces the high dimensionality of images without losing its information algorithm is trained using this data. The data scientist gives the algorithm with

input data that matches to an expected output. The model evaluates the data repeatedly in order to gain a better understanding of its behaviour and then modifies itself to accomplish the goal.

• Training data: A huge dataset used to train a Convolutional Neural Network is referred to as training data. Prediction models that apply deep learning algorithms are taught how to extract features that are important to certain goals using training data.

Chapter 2: Literature Survey

We demonstrated how a simple CNN network like 3D U-net can be successfully applied for the task of tumour segmentation. U-net process the input multi-modal MR images at multiple scales, which allows it to learn U-Net for Tumour Segmentation 265 local and global context necessary for tumour segmentation. The network was trained using a curriculum on class weights to address class imbalance, showing competitive results for brain tumour segmentation on BraTS 2018 testing dataset. Our method performed well and we got following Dice scores for enhancing tumour, whole tumour, and tumour core on BraTS 2018 validation and testing datasets: 0.788, 0.909, and 0.825 (validation dataset), and 0.706, 0.871, and 0.771 (testing dataset). But our method showed degradation in performance on the testing dataset in the categories of Enhancing Tumours (ET) and Tumour Core (TC)

For training datasets, the network achieves equivalent DSC to existing leader board approaches, while the validation dataset produces somewhat worse results.

Pre-processing techniques, as well as Z-score normalisation and augmentation, improved decoding module design, and post- processing, will be implemented in the future. The network output will be compared to that of a deeper network as well as other state-of-the-art networks. The age, statistical, and necrosis shape aspects of the ground truth are used to train RFR for OS prediction using five-fold cross-validation. Then, for cases with GTR, network segmentation is used to evaluate RFR for OS prediction. To partition brain tumour into three substructures of brain tumour and backdrop, we present a cascaded V-Nets architecture. For the total tumour, tumour core, and enhancing tumour, the experimental results on the BraTS 2018 online validation set reach average Dice scores of 0.9048, 0.8364, and 0.7768, respectively.

For the BraTS 2018 online testing set, the equivalent values are 0.8761, 0.7953, and 0.7364, respectively. For the clinical testing set, the equivalent values are 0.8635, 0.8036, and 0.7217, respectively. Pictures acquired using 2D MRI sequences achieve higher average Dice scores than images acquired using 3D MRI sequences in the clinical data set, demonstrating that the proposed method is useful and practicable in clinical practise. The results show that V-Net is a promising network for medical imaging segmentation tasks, and that the cascaded architecture and ensemble method are effectivein improving segmentation performance.

Due to the challenge of brain tumor segmentation and the broad medical prospect, many researcher shave proposed various methods to solve the problem of brain tumor segmentation.Brain tumor segmentation methods can be divided into different categories according to different principles . Broadly, these methods can be divided into two major categories: generative methods and discriminative methods. Generative methods typically rely on the prior information about the appearance of both healthy tissues and tumors. The proposed models often regard the task of segmentation as a problem of aposteriori distribution estimation. On the contrary, discriminative methods use very little prior information and typically rely on a large number of low-level image featuresto learn the distribution from the annotated training images.More recently, due to the success of convolutional neural networks (CNNs), great progress has been made in the field of computer vision. At the same time, many deep learning based brain tumor segmentation methods have been proposed and achieved great success. Hava ei et al.proposed a two-pathway architecture with a local pathway and a global pathway, which can simultaneously exploit both local feature sand more global contextual features.

Kamnitsas et al. [4] proposed an efficient fully connected multi-scale CNN architecture named deep medic that uses 3D convolution kernels and reassembles a high resolution and a low resolution pathway to obtain the segmentation results. Furthermore, they used a 3D fully connected conditional random field to effectively remove false positives. Isensee et al. [5] proposed 3D U-Net, which carefully

modified the popular U-Net architecture and used a dice loss function to cope with class imbalance. They achieved competitive results on the BraTS 2017 testingdata. Kamnitsas et al. introduced EMMA, an ensemble of multiple models and architectures including deepmedic, FCNs and U-Net. Due to the heterogeneous collection of networks, the model is insensitive to independent failures of each component and has good generalization performance. They won first place in the final testing stage of the BraTS 2017 challenge among more than 50 teams.Although so many achievements have been made, the progress of medical image analysis is slower than that of static images, and a key reason is the 3D properties of medical images. This problem also occurs in the tasks of video understanding. To solve this problem, Xie et al. [7] proposed S3D model by replacing 3D convolutions with spatiotemporal-separable 3D convolutions. This model significantly improved on the previous state-of-the-art 3D CNN model in terms of efficiency.Inspired by S3D architecture for video classification and the state-of-the-art U- Net architecture for medical image segmentation, we propose a novel framework namedS3D-UNet for brain tumor segmentation. To make full use of 3D volumes, we design anew separable 3D convolution by dividing each 3D convolution into three branches in a parallel fashion, each with a different orthogonal view, namely axial, sagittal and coronal. We also propose a separable 3D block that takes advantage of the state-of-the-art residual inception architecture.

During the testing stage we achieved competitive results with Dice

scores of 0.68946, 0.83893, and 0.78347 for enhancing tumor, whole tumor, and tumor core, respectively

Chapter 3 Methodology

Methodology Uses
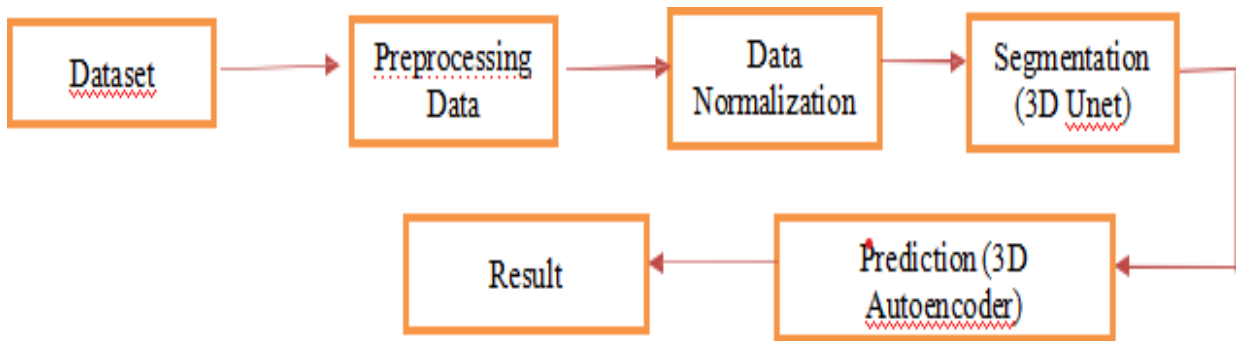
- **Step 1:** Dataset is used from BraTS2020 .

- **Step 2:** Data preprocessing describes any type of processing performed on raw data to prepare it for another processing procedure

- **Step 3:** Data normalization is the organization of data to appear similar across all records and fields.

- **Step 4:** Brain tumor segmentation is the process of separating the tumor from normal brain tissues. In segmentation we use 3D Unet algorithm.

- **Step 5:** In Prediction we use 3D Autoencoder algorithm.

- **Step 6:** Make prediction of age and survival days for each unique identifier in the data .

Formula used

- **Jaccard Index :**

$$J(A,B) = \frac{|A \cap B|}{|A \cup B|} = \frac{|A \cap B|}{|A| + |B| - |A \cap B|},$$

- **Dice Cofficient :**

When applied to Boolean data, using the definition of true positive (TP), false positive (FP), and false negative (FN), it can be written as

$$DSC = \frac{2TP}{2TP + FP + FN}$$

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Chapter 4: Results Analysis and Discussion

Results:

For GBM segmentation, the VGG-Seg acquired a mean Dice coefficient of 0.86 across 163 individuals with GBM. The C-index for the handcrafted signature was 0.64 (95 percent confidence interval: 0.55-0.73), whereas the C-index for the DL-based signature was 0.67. (95 percent confidence interval, 0.57-0.77). The DL-based signature successfully separated tested patients into two prognostically distinct groups, unlike the handcrafted signature.

Segmentation Result :

1. Quantitative Results :

For the validation set, we use the statistical metrics Dice Coefficient, Sensitivity, Specificity, and Hausdorff Distance to calculate the results of the suggested approaches for Enhancing tumor, Whole tumor, and Tumor core. Leaderboard - Zillella Brats 2020 Challenge

Parameters	Dice_ET	Dice_WT	Dice_TC	Sensitivity_ET	Sensitivity_WT	Sensitivity_TC	Specificity_ET	Specificity_WT	Specificity_TC	Hausdorff95_ET	Hausdorff95_WT	Hausdorff95_TC
Mean	0.80661	0.89414	0.85721	0.81519	0.9251	0.84795	0.99971	0.99884	0.99953	23.19044	5.56554	5.44695
StdDev	0.23953	0.08177	0.12749	0.25155	0.07596	0.16678	0.00043	0.00116	0.0007	85.62448	10.87704	9.90171
Median	0.87871	0.91993	0.91058	0.89553	0.94956	0.90561	0.99985	0.99918	0.9998	1.73205	3.16228	3
25quantile	0.80214	0.87042	0.82128	0.82766	0.90596	0.81328	0.99957	0.99858	0.9995	1	2.23607	1.73205
75quantile	0.92648	0.94299	0.93417	0.94811	0.97373	0.95586	0.99996	0.99958	0.9999	3	5.47723	5.47723

2. Visualization Results

❑ **Axial View**
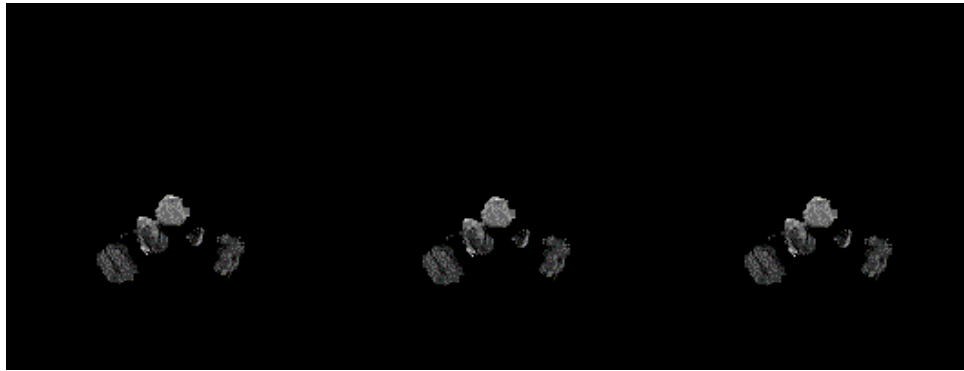
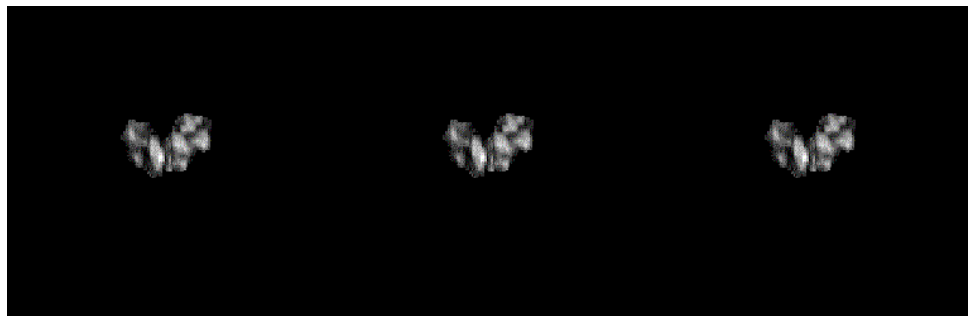**Brain MRI**   **Ground Truth**   **Predicted Tumor**

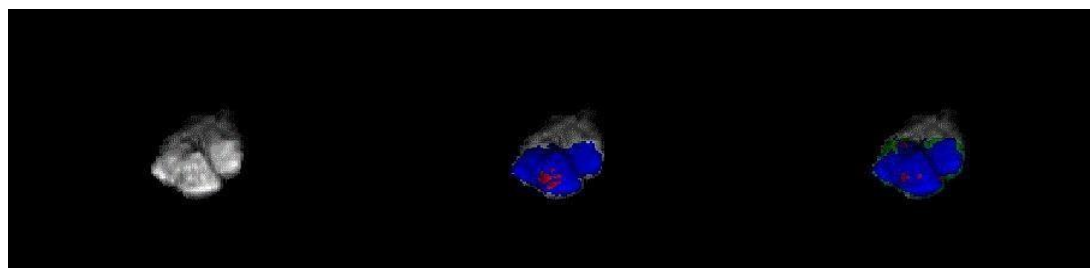❖ **Coronal View**

Brain MRI   Ground Truth   Predicted Tumor

❑ Sagittal View

Brain MRI   Ground Truth   Predicted Tumor

■ Region in red indicates the tumor core
■ Region in green indicates the whole tumor
■ Region in blue indicates the enhancing tumor region

Discussion

For automatic brain tumour segmentation, we suggest an S3D-UNet architecture. We use separable 3D convolutions to make full use of 3D volume information while decreasing the amount of computation. We create a new separable 3D convolution architecture for the isotropic resolution of brain tumour MR images by separating each 3D convolution into three branches in a parallel fashion, each with a different orthogonal perspective, namely axial, sagittal, and coronal. We also offer a separate 3D block that utilises the most up-to-date residual inception architecture. Finally, we propose the S3D-UNetarchitecture, which is based on separable 3D convolutions and uses the widely used U-Net structure.

On the BraTS 2018 Challenge testing dataset, this network received average Dice scores of 0. 68946, 0. 83893, and 0. 78347 for enhanced tumour, entire tumour, and tumour core segmentation, respectively. The testing set's scores are lower when compared to the training and validation sets' results.

This could be owing to the testing set's difficult instances, as the median values are high. We will try to improve the network's robustness in the future. 3D contextual

information is a crucial aspect in volumetric medical picture segmentation to achieve high-performance findings.

Using 3D convolutions is a simple technique to capture such 3D context. The adoption of a large number of 3Dconvolutions, on the other hand, will significantly increase the number of parameters, making the training process more difficult. The separable 3D convolutions with greater computing efficiency were used in the video interpretation challenges.

We show that the U-Net with separable 3D convolutions can produce promising results in the field of medical image segmentation in this research.

The proposal uses three-layer deep U-net based encoder-decoder architecture for semantic segmentation. Each layer of the encoding side incorporates dense mod-ules and decoding side convolution modules. The network achieves comparable DSC for training datasets with other methods of the leader board but generates little poor results for the validation dataset. In the future, pre- processing techniques, in addition to Z-score normalization and augmentation, better design of the decoding module, as well as post-processing, will be incorporated. The network output compared with the more deeper network as well as other state-of-art networks will be incorporated. Age, statistical, and necrosis shape features of the ground truth are provided to train RFR with five-fold cross-validation for OS prediction. Later, network segmentation for cases with GTR tests RFR for OS prediction

The handcrafted signature achieved a C-index of 0.64, while the DL-based signature achieved a C-index of 0.67. The DL-based signature achieved numerically higher AUCs,evaluated at the OS of 300 days and 450 days, than the handcrafted signature.

Additionally, the DLbased signature, unlike the handcrafted signature, resulted in prognostically distinct groups using eitherXtile generated or median threshold.

Should et al12 did not report the C-index but did report an accuracy of 0.52 in

classifying patients with GBM into 3 survival outcome groups. However, DL-based radiomic featureswere not investigated in this study.

It is also difficult to know whether significant patient stratification was achieved for testing patients with GBM in thisstudy because log-rank tests were not conducted

To segment brain tumours, we offer a cascaded V-Nets system. The cascaded framework divides a challenging segmentation task into two simpler subtasks: separating the whole tumour from the background and separating the tumour substructures from the complete tumour. Unlike other approaches, ours considers the impact of preprocessing on segmentation outcomes and employs a tailored preprocessing approach to analyse the data and train several models. Only given data, dataaugmentation, and a focal loss formulation are used to train the cascaded V-Nets. On the BraTS 2018 validation set, we achieve state-of-the-art results. For the total tumour, tumour core, and enhancing tumour, the experimental results on the BraTS 2018 online validation set reach average Dice scores of 0.9048, 0.8364, and 0.7768, respectively. The corresponding values for BraTS 2018 online testing set are 0.8761, 0.7953, and 0.7364, respectively.

In general, when comparing the testing and validation sets, all three average Dice scores degenerate. The explanation for this could be that the testing set has a significantly greater sample size than the validation set, which includes more anatomical variants. In clinical testing sets, images acquired using 2D MRI sequences earn 2% better average Dice scores than images acquired using 3D MRI sequences. The explanation for this could be that the MICCAI BraTS 2018 organisers' public dataset contains more pictures taken using 2D MRI sequences than images acquired using 3D MRI sequences. As a result, the trained model prefers 2D testing data over 3D testing data. The resulting model, however, may be more practical and useful, considering that 2D MRI sequences are extensively used in clinical practise for

shorter acquisition times.

As a result, for sites with a lot of 3D photos, the training set might be expanded and a specific 3D model trained. Using a cascaded framework has various advantages. To begin, the cascaded structure divides a complex segmentation task into two subtasks. As a result, even a simple network V-Net can function well. In fact, V-Net performed better in our experiment when segmenting the tumour substructures one by one than when segmenting the backdrop and the three tumour substructures simultaneously. Second, the V-Net 1 segmentation results aid in reducing the receptive field from the entire brain to simply the entire tumour. As a result, certain false positives can be prevented.

Ensemble strategy, in addition to the cascaded architecture, contributes to segmentation performance. Models 1–3 are included in V-Net 1 of our cascaded V-Nets system, whereas models 4–5 are included in V-Net 2. Every model employs the V-Net network structure.

The training data, on the other hand, is preprocessed using the various pipelines indicated in section 2.1. According to our testing, the Dice scores will plummet as a result of the false positive results. While we tried a number of different approaches to improve the training data preparation techniques or the segmentation task model, the false positive findings persisted.

Surprisingly, false positive outcomes can be found in a variety of fields and models. As a result, the ensemble technique operates by averaging probability maps from several models. The ablation experiments also show that the proposed ensemble method is effective.

In addition, there are three noteworthy aspects of the experiment. For starters, a mix of data preparation processes is critical for multimodal MR imaging. To put it another way,

various MRI modalities should be processed separately. For example, bias field correction was only applied to T1 and T1Gdpictures in our first preprocessing pipeline.

The reason for this is that the histogram matching method may exclude high-intensity tumour structural information, which has a negative impact on the segmentation process. Second, we processed the training and validation data using three different preprocessing approaches and compared the segmentation outcomes.

As a result, in the three average Dice scores for total tumour, tumour core, and enhancing tumour, there is essentially no difference across preprocessing approaches. The three average Dice scores all increased by at least 2% following the ensemble of various models. This shows that data preparation methods are not the most critical component in segmentation performance, but that diverse data preprocessing approaches are complementary and can be used together to improve segmentation performance. Finally, the post-processing procedure is critical because it has a significant impact on the average Dices scores. If the threshold is set too high, some little clusters will be incorrectly eliminated.

If the threshold is set too low, some false positives will be kept. To improve performance, we evaluate a variety of criteria and select the two most appropriate thresholds as the upper and lower bounds. The average segmentation probabilities of the components between the upper and lower boundaries are calculated as a second criterion. Of course, these limits may notbe appropriate in all circumstances.

Conclusion and Future Scope

Conclusion

When compared to the winners of the Brats 2020 Challenge, state-of-the-art segmentation results for Enhancing tumor were obtained using the suggested modified 3D UNet architecture, with a dice coefficient improvement of approximately 1%. The model is computationally efficient, segmenting brain tumors from a complete brain MRI scan in less than 2 seconds.

For semantic segmentation, the proposal employs a three-layer deep U-net based encoder-decoder architecture. Dense modules and decoding side convolution modules are included in each layer of the encoding side.

Future Scope

1) More features can be embedded to enhance classification precision Shape feature is one of those features which can help raise an accuracy level of classification being done. Getextra information from patient like history, age to increase classification accuracy.

2) More efficient deep learning ModelMajor problem in automatic brain tumor segmentations the similarity between background and tumor pixels.Some background pixels are misclassified as brain tumor pixels. So, in future a more efficient deep learning model can be developed that can differentiate between tumor and background pixels with more accuracy.

3) To train Deep CNN a more efficient loss function can be chosen. A more effective loss function helps indifferentiating between background and tumor pixels with improved accuracy25

4) Colored images may also be considered. This study targets onlygrey-scale images. Besides, it could beintensifiedto augment colored images

Chapter 5: References

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