

Brain Tumour Sub-Region Segmentation (BraTS21 Dataset)



End Semester Project Report

CS517: Digital Image Processing

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1 | Introduction

This project is based on **The Brain Tumor Segmentation (BraTS)** Continuous Challenge seeks to identify the current, state-of-the-art segmentation algorithms for brain diffuse glioma patients and their sub-regions.

This continuous challenge will culminate in an annual, state-of-the-field evaluation where we will ask participants to submit containerized versions of their best models which will be run against a held out testing data set, and the results presented at the annual MICCAI conference

2 | Objectives

The following are the objectives of the End Semester project challenge:

- Develop a method and produce segmentation labels of the different Gliomas.
- Identify various subregions of deadly Brain Tumour called Glioma.
- Test the developed methodology on provided BraTS21 dataset.

3 | Tools Used

For the implementation of this project, we used and explored various tools and technologies. Most of the work is done using the Python programming language in Google Colab.

Although, the project began with a simple segmentation model, various deep learning based models were utilized and explored in the implementation of this project. The models are enlisted below:

- **UNet Model:** based on Convolutional Neural Network architecture.
- **SwinUNETR Model:** Transformer-based Encoder-Decoder model
- **DeepLab Model:** based on Fully CNN architecture

4 | Methodology

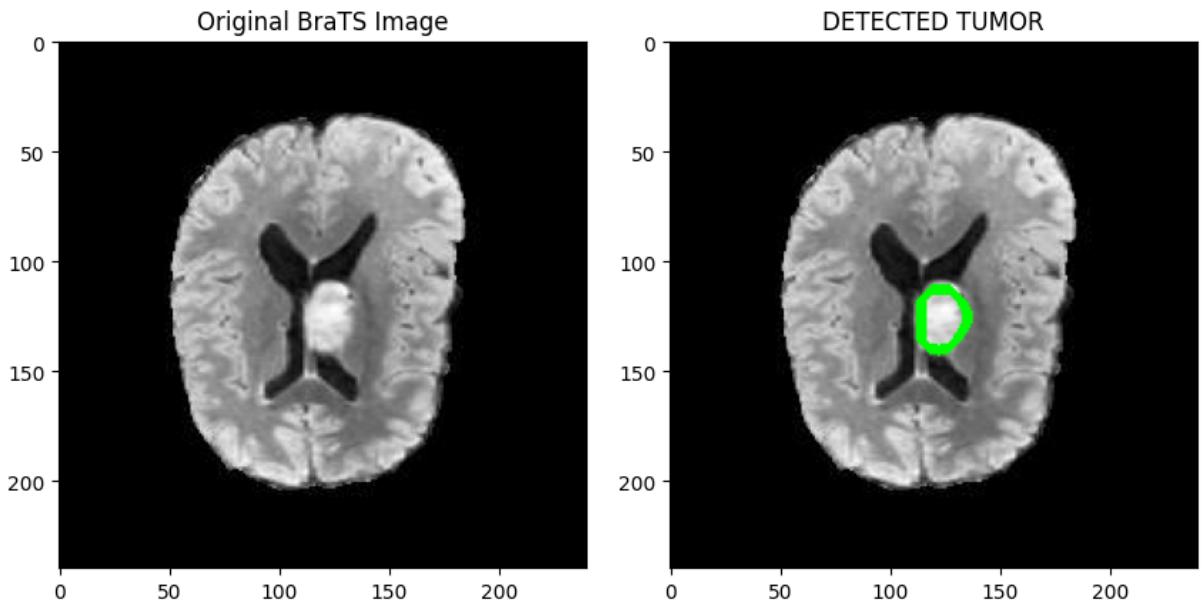
Here is the step-by-step description of our work done on this project

- We began with a simple model for segmentation. This model is based on the simple methodologies that we understood throughout the class and lab assignments.
After reading the image, we notice by plotting its histogram that it needs to be enhanced. Hence, we apply some standard techniques for its enhancement.
Gaussian blurring filter is applied on entire input image to obtain blurred version of it.
For enhanced homogeneity in the input image, the blurred image is added to the original grayscale image.
Further, owing to the edge-preserving and denoising properties of the median filter, we apply it on the image.
Then a kernel is generated as a morphological gradient. This improves the edge contrast across the entire image.
Then thresholding is applied.
Then we apply various morphological operations to develop a better region of interest after thresholding. Finally, we obtain the segmented model.

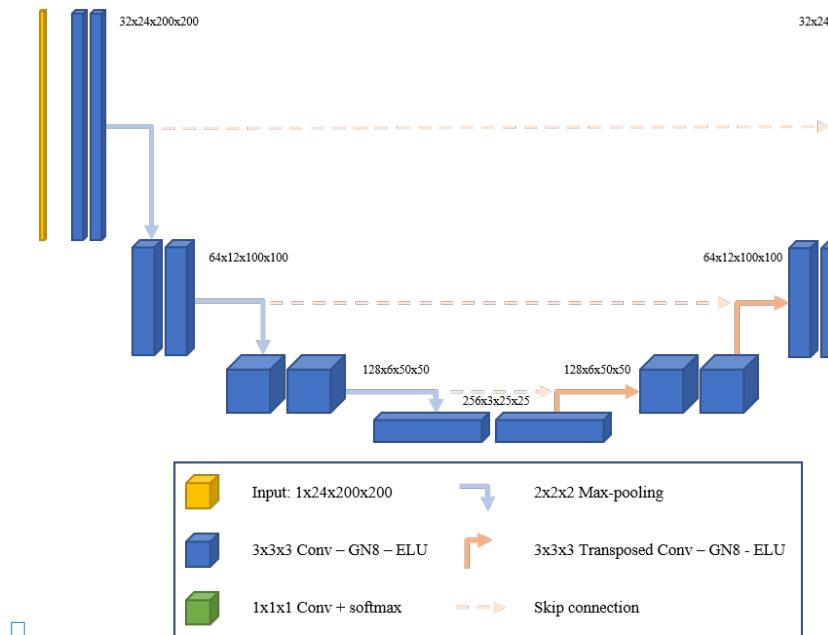
Limitations: This method is case specific as for different data, it needs different thresholding values and morphological operations. This can lead to unreliable results in real life problems.



Hence we moved towards more deep learning based models.



- As the simple segmentation using thresholding and Morphological Operations had various shortcomings, we moved to the deep learning based model called UNet Model.
 - UNet Model gets its name after its architecture. It is a U-shaped model that comprises of convolutional layers and two networks. It consists of an encoder followed by decoder. With the UNet model it is possible to solve two problems:
 - What part of image is the tumor?
 - Where is the tumor in the image?



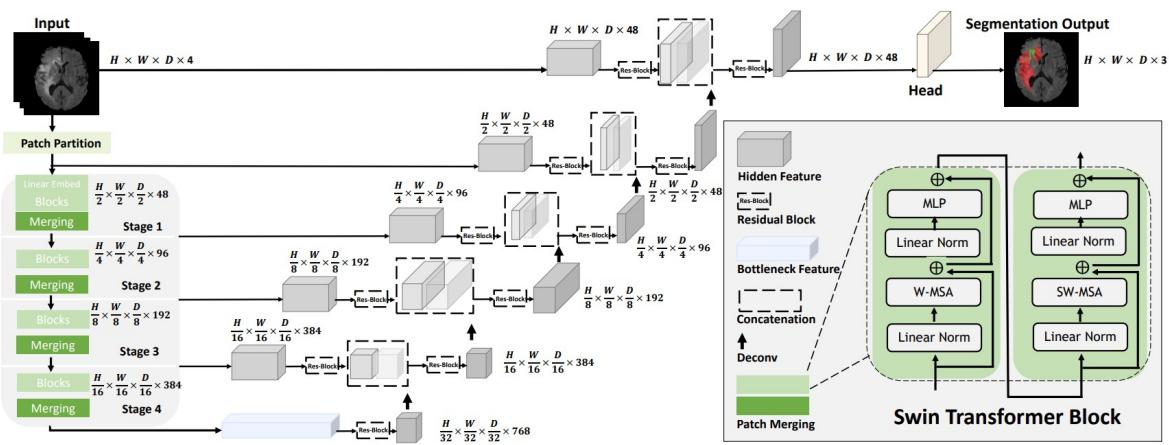
UNet Model Architecture

- The popular "U-shaped" network architecture has achieved state-of-the-art performance benchmarks on different 2D and 3D semantic segmentation tasks and across various imaging modalities. However, due to the limited kernel size of convolution layers in FCNNs, their performance of modeling long-range information is sub-optimal, and this can lead to deficiencies in the segmentation of tumors



with variable sizes. On the other hand, transformer models have demonstrated excellent capabilities in capturing such long-range information in multiple domains, including natural language processing and computer vision.

We came across a novel segmentation model termed Swin UNETR (Swin UNETR). In this model, the task of 3D brain tumor semantic segmentation is reformulated as a sequence to sequence prediction problem wherein multi-modal input data is projected into a 1D sequence of embedding and used as an input to a hierarchical Swin transformer as the encoder. The Swin transformer encoder extracts features at five different resolutions by utilizing shifted windows for computing self-attention and is connected to an FCNN-based decoder at each resolution via skip connections.



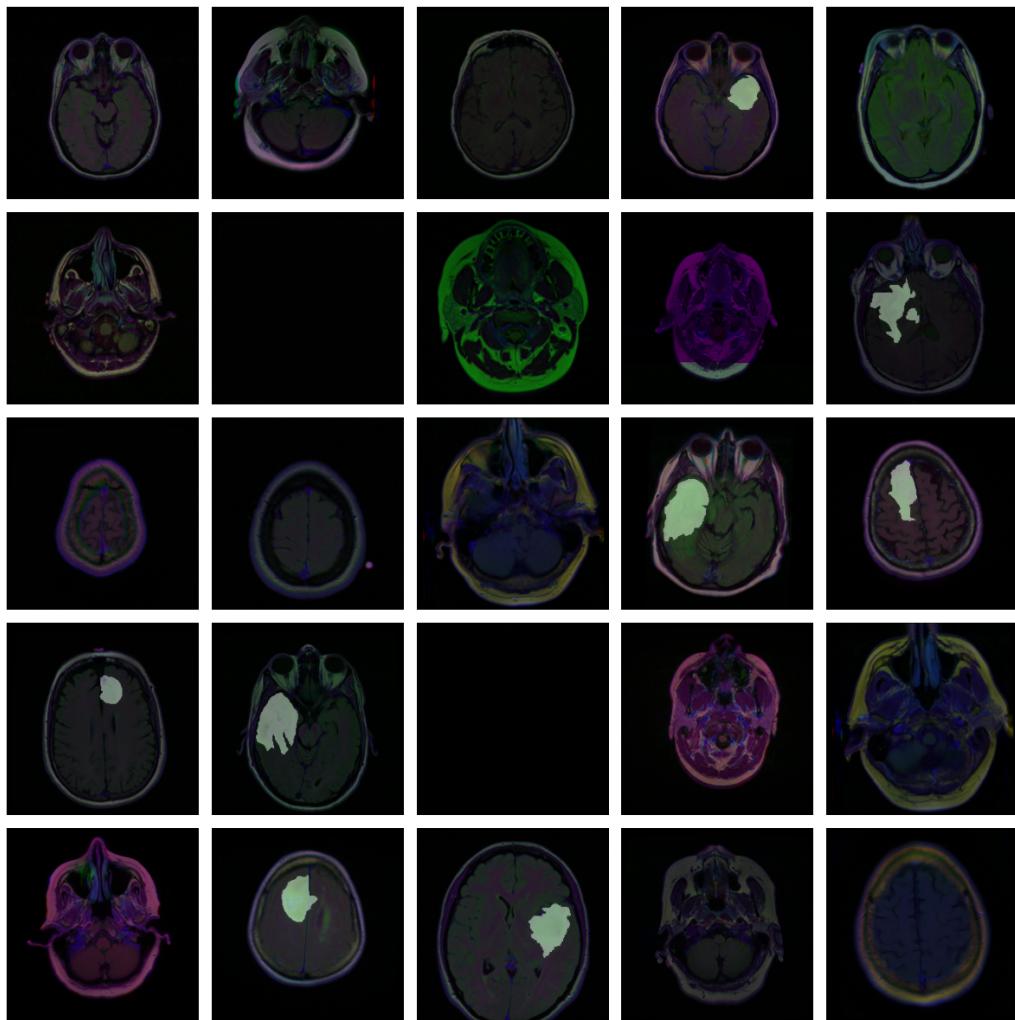
Overview of the Swin UNETR architecture. The input to our model is 3D multi-modal MRI images with 4 channels. The Swin UNETR creates non-overlapping patches of the input data and uses a patch partition layer to create windows with a desired size for computing the self-attention. The encoded feature representations in the Swin transformer are fed to a CNN-decoder via skip connection at multiple resolutions. Final segmentation output consists of 3 output channels corresponding to ET,WT and TC sub-regions.

5 | Details of the Models

1. On training the BraTS21 Dataset on UNet Model, promising results were observed with great accuracy.

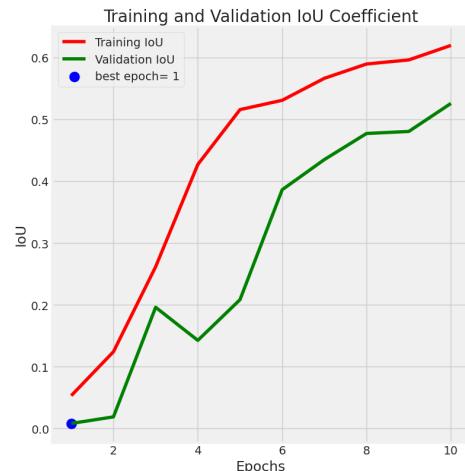
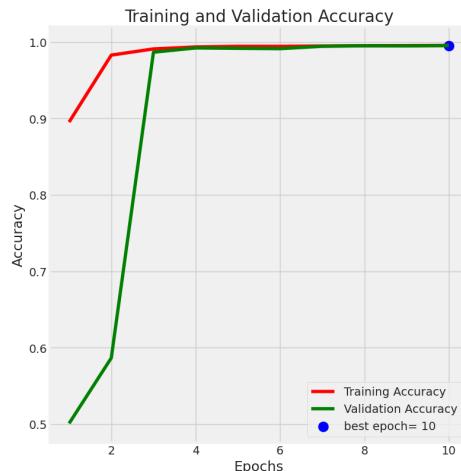
The structure of the attached model included:

- Functions to create data frame from dataset :
 - *create_df* : Function to create data frame
 - *split_df* : Function to split data frame into train, valid, test
- Function to create image generators and augmentation : *create_gens*
- Functions that have UNet Structure: *unet*
- Functions for coefficients and loss :
 - *dice_coef* : function to create dice coefficient
 - *dice_loss* : function to create dice loss
 - *iou_coef* : function to create iou coefficient
- Function to show images sample : *show_images*
- Function to display training history : *plot_training*

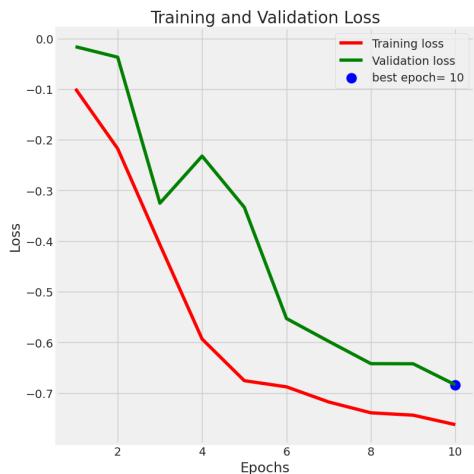
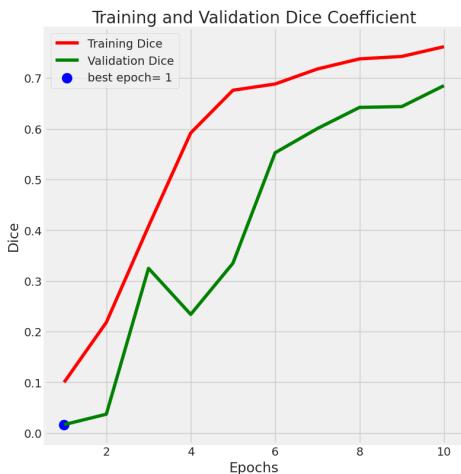


Input Images from BraTS21 Dataset

All BraTS mpMRI scans are available as NIfTI files (.nii.gz) and describe a) native (T1) and b) post-contrast T1-weighted (T1Gd), c) T2-weighted (T2), and d) T2 Fluid Attenuated Inversion Recovery (T2-FLAIR) volumes, and were acquired with different clinical protocols and various scanners from multiple data contributing institutions.



(a) Training and Validation Accuracy a



(b) Training and Validation Accuracy b

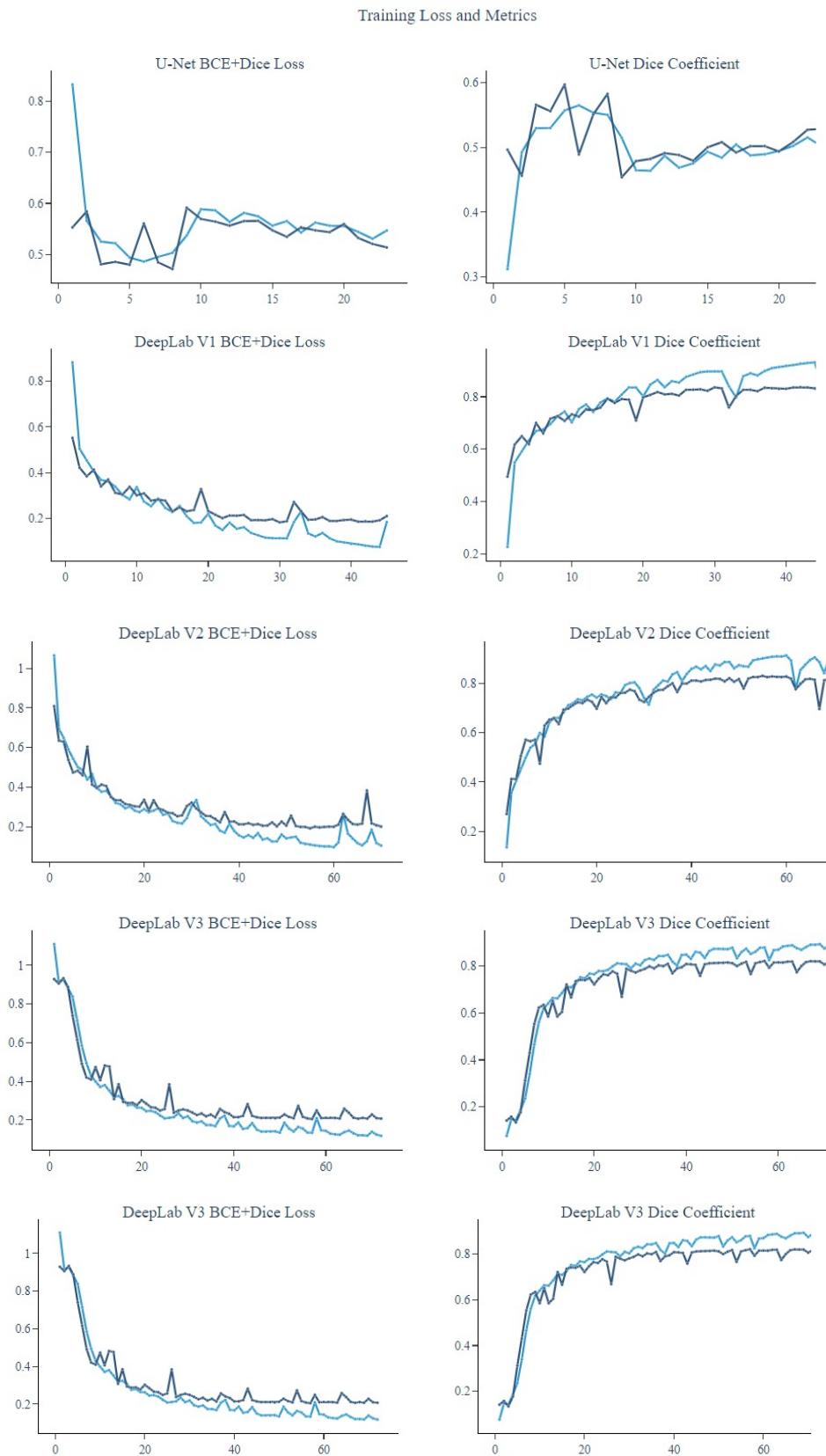
2. To test the accuracy of various deep learning models in order to develop a better model, we tested various models and simultaneously compared them as well.

The structure of the attached DeepLab model has following dependencies included:

- sklearn.model_selection
- Tensorflow
- Keras package: keras.utils, keras.preprocessing, keras.models, keras.optimizers, keras.layers

The structure of the attached model Deeplabv3+ is as follows On checking the metrics and results, we implemented DeepLab V3+.

- Preparation
- Data Processing
- Image Segmentation
 - Helper Functions
 - Deeplabv3+
- Result : Training Loss and Metrics
- Image Results



(a) Plots of Training Metrics for the Compared Deep Learning Models

- 3.** On training the BraTS21 Dataset on SWIN UNeTR Model, promising results were observed with great accuracy.

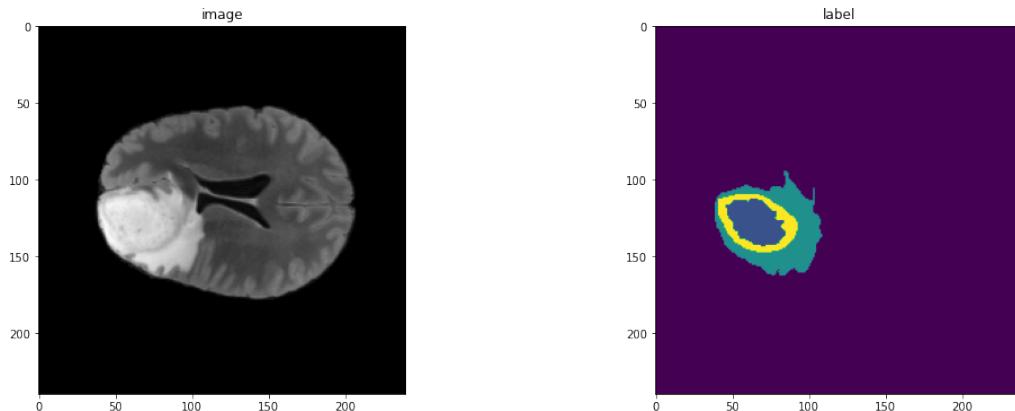
The structure of the attached SWIN UNetR model has following dependencies included:



- MONAI version: 0.9.0rc3
- Numpy version: 1.22.2
- Pytorch version: 1.10.0

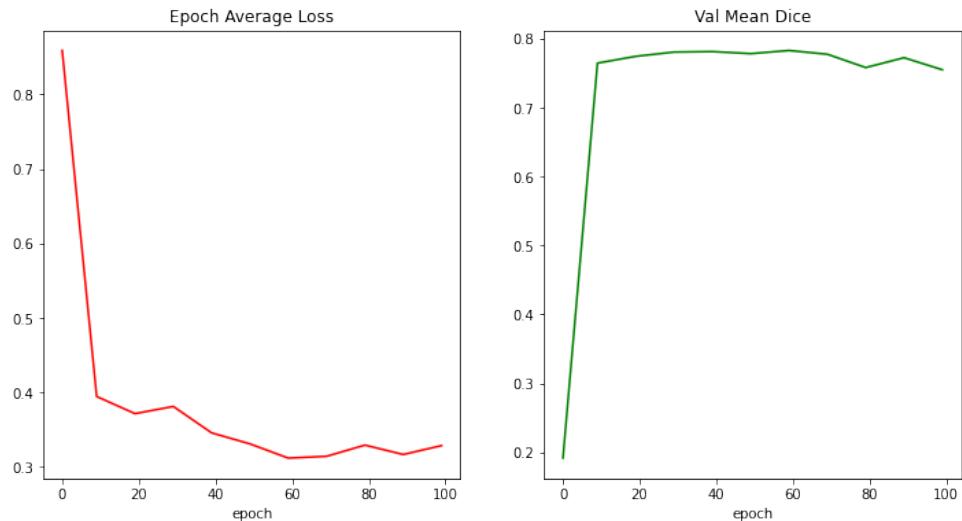
The structure of the attached model included:

- Setup average meter, fold reader, checkpoint saver : Class AverageMeter
 - *datafold_read*
 - *save_checkpoint*
- Setup dataloader : *get_loader*
- Set dataset root directory hyperparameters
- Checking data shape and visualize
- Creating SWIN UNetR Model
- Optimizer and Loss Functions

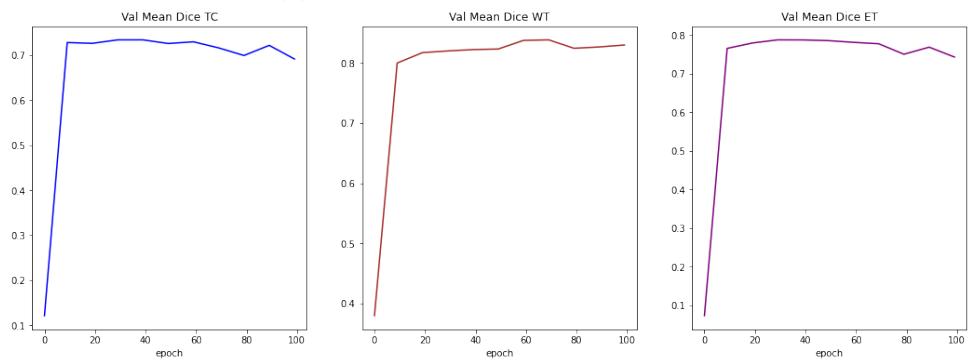


Input Images from BraTS21 Dataset as read by SWIN Model

All BraTS mpMRI scans are available as NIfTI files (.nii.gz) and describe a) native (T1) and b) post-contrast T1-weighted (T1Gd), c) T2-weighted (T2), and d) T2 Fluid Attenuated Inversion Recovery (T2-FLAIR) volumes, and were acquired with different clinical protocols and various scanners from multiple data contributing institutions.



(a) Training and Validation Accuracy a



(b) Training and Validation Accuracy b



6 | Results

Here are the results of the tested UNet model:



Figure 6.1: Output 1 of UNetR Model



Figure 6.2: Output 2 of UNetR Model



Figure 6.3: Output 3 of UNetR Model



Here are the results of the tested DeepLab V3 model:

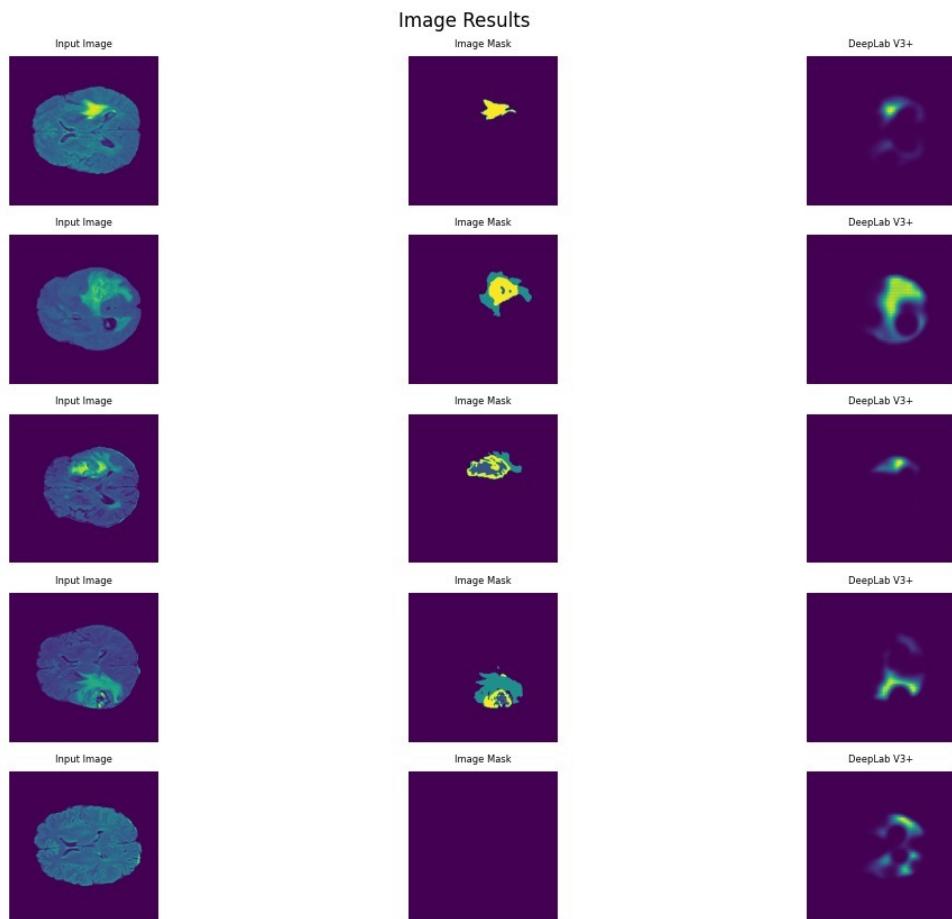


Figure 6.4: Sub-Region Segmentation using DeepLabV3+ Model

Here are the results of the tested SWIN UNetR model:

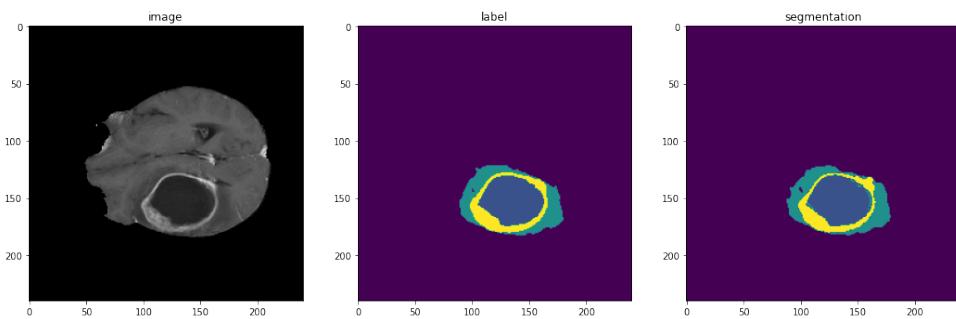


Figure 6.5: Sub-Region Segmentation using SWIN UNetR Model



7 | Learning Outcomes

In this project we tried to develop a model to solve one of the prominent medical problems, which is Brain Tumor Sub-region segmentation.

Starting from a simple model based on simple thresholding and morphological operations.

Further, we explored UNet model, with which we could segment simply the tumor region.

On obtaining the testing metrics, we implemented the DeepLabV3+ Model for the sub-region segmentation

Finally, we explored a transformer based model, SWIN UNetR model, with which we could segment the subregions to a great accuracy.

8 | References

- 1.** Hatamizadeh, A., Nath, V., Tang, Y., Yang, D., Roth, H., Xu, D. (2022). Swin UNETR: Swin Transformers for Semantic Segmentation of Brain Tumors in MRI Images. ArXiv. [/abs/2201.01266](https://arxiv.org/abs/2201.01266)
- 2.** Nasim, M. A., Munem, A. A., Islam, M., Palash, M. A., Haque, M. M., Shah, F. M. (2022). Brain Tumor Segmentation using Enhanced U-Net Model with Empirical Analysis. ArXiv. [/abs/2210.13336](https://arxiv.org/abs/2210.13336)
- 3.** Chen, L., Papandreou, G., Schroff, F., Adam, H. (2017). Rethinking Atrous Convolution for Semantic Image Segmentation. ArXiv. [/abs/1706.05587](https://arxiv.org/abs/1706.05587)