Brain Tumor Segmentation using UNET architecture

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Outline

- 1. Introduction
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Introduction

- 1. BraTS 2020: Focuses on brain tumor segmentation in MRI scans
- 2. Evaluation of methods for glioma segmentation, patient survival prediction, progression status assessment, and segmentation uncertainty estimation
- 3. Data includes multi-institutional MRI scans with manual tumor segmentations and clinical information
- 4. Scans cover native, post-contrast, T2-weighted, and T2-FLAIR volumes
- 5. Annotations include enhancing tumor, peritumoral edema, and tumor core
- 6. Job: Automation of segmentation process using U-NET

Objectives

- 1. Creating a UNET architecture that can generate segmented 3D mask images containing 3 types of annotations i.e. enhancing tumor, peritumoral edema, and tumor core.
- 2. Enhancing Dice Coefficient, IoU score, precision, recall, and F1-score.
- 3. Surpass related works on it.

Functions

From any 3D MRI of the brain, this trained model can generate segmentation containing 3 types of annotations i.e. **enhancing tumor**, **peritumoral edema**, and **tumor core**.

Language & Tools with justification

- 1. **Python**: Programming language used for the project.
- 2. **Nilearn**: Library utilized for handling and visualizing neuroimaging data, especially NIfTI files.
- 3. **Segmentation Models 3D**: Libraries accessed for pre-built architectures and utilities tailored for 3D medical image segmentation and classification tasks.
- 4. **Visualkeras**: Tool employed for visualizing the architecture of neural network models.
- 5. **NumPy**, **scikit-learn**, **Matplotlib**: Standard libraries used for data preprocessing, model evaluation, and result visualization.

Methodology

I will describe the following topics under methodology in the next slides:

- 1. Dataset
- 2. Preprocessing
- 3. Model Creation
- 4. Experimental Set Up

Dataset

Dataset name: BraTS2020

Dataset Size: 369 items for training and 125 items for validating

(Only worked with the training part of the dataset for both training and validation)

Each item has **5** .nii type files.

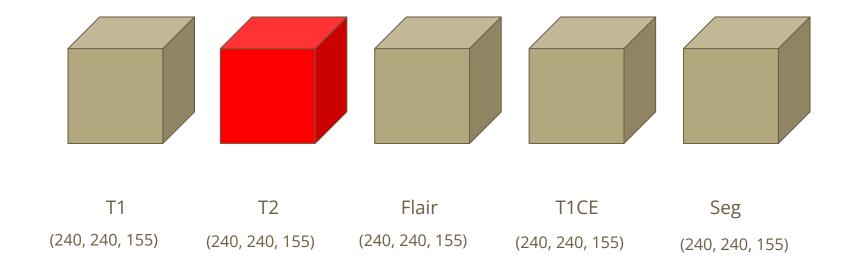
They contain **native**, **post-contrast**, **T2-weighted**, **T2-FLAIR** volumes and one **segmentation** file.

Segmentation file contains **3** types of annotations: **enhancing tumor**, **peritumoral edema**, and **tumor core**.

Each .nii file has a shape of **(240, 240, 155)**.

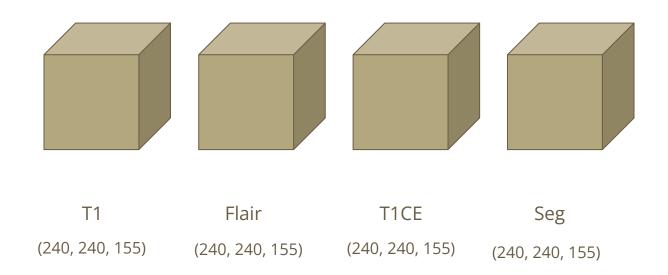
Preprocessing

5 images in a single folder



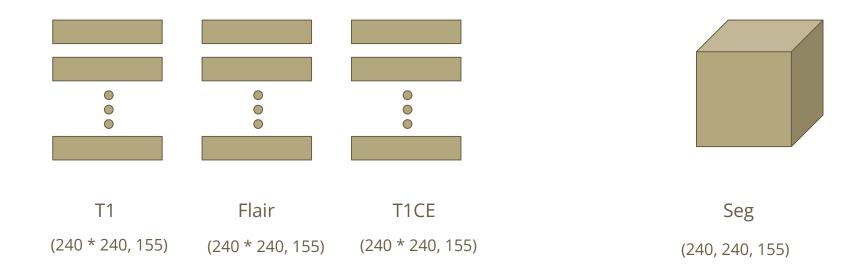
Preprocessing

Removed T2 image



Preprocessing

T1, Flair, T1CE were flatten on the first two axis. And MinMaxScalling were applied to them.



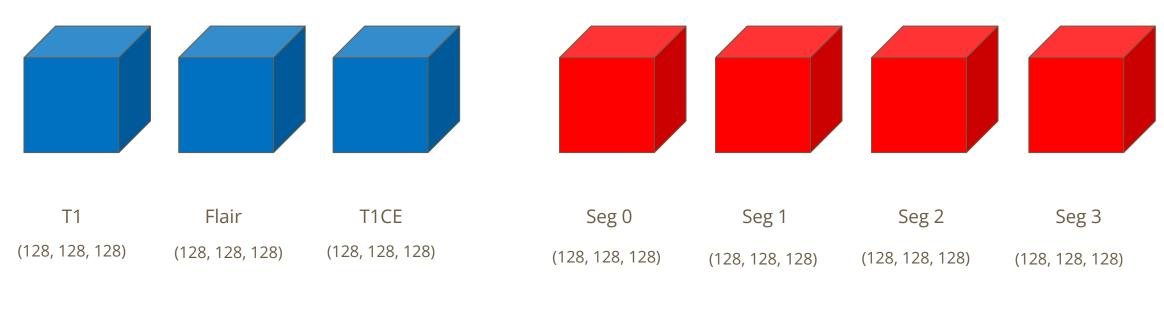
Preprocessing

- 1. T1, Flair, T1CE were brought back to original shape.
- 2. One Hot Encoding were applied on Segmentation Image. Segmentation image had four unique pixel values 0 (Nothing), 1 (Non-enhancing tumor core), 2 (Edema), 3 (Not Specified), 4 (Enhancing tumor).
- 3. Label 3 was replaced by label 4.



Preprocessing

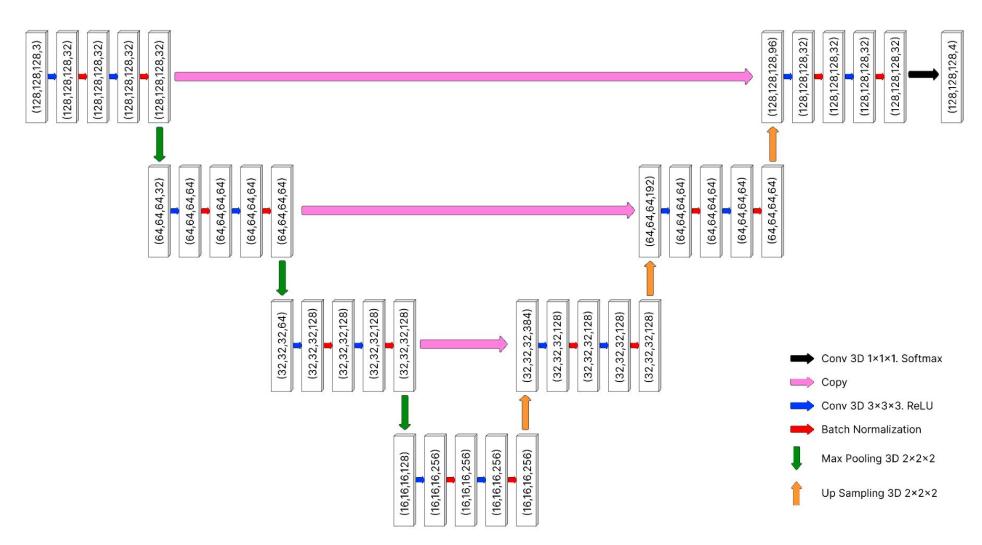
T1, Flair, T1CE and segmentations were cropped to (128, 128, 128)







Model Creation



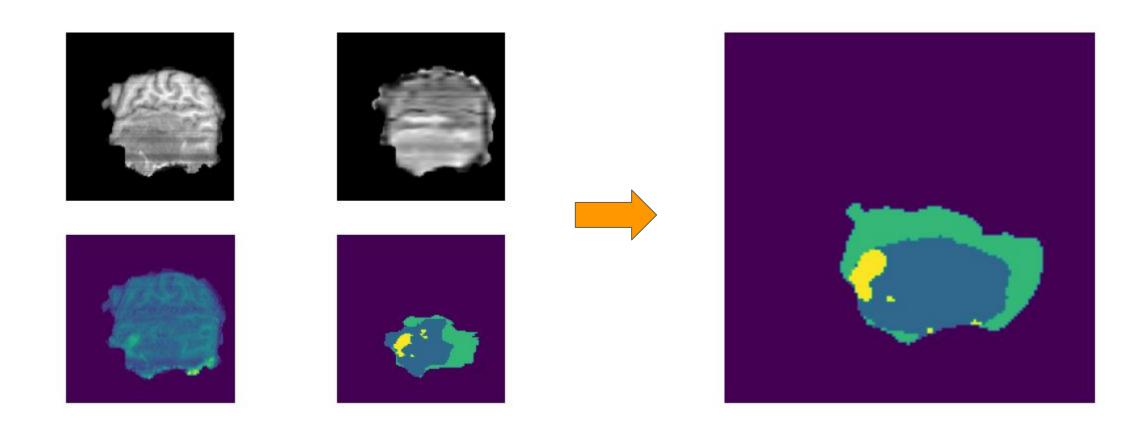
Environmental Set Up

- 1. I split the Training Folder into train(80%) and test(20%).
- 2. I further split the train set into train(80%) and validation(20%).
- 3. I trained the model for 50 epochs with a batch size of 1.
- 4. Loss function was totalloss=diceloss+(1*focalloss).
- 5. Learning rate was 0.001.
- 6. Optimizer was Adam.
- 7. Early Stopping was applied with patience 5 on validation loss.
- 8. For evaluation metrics I used Dice Coefficient, Intersection over Union,

Scores

| Label | Dice-Coefficient (%) | IoU (%) |
|-------|----------------------|---------|
| 0 | 98.97 | 98.05 |
| 1 | 55.20 | 44.59 |
| 2 | 62.26 | 49.98 |
| 3 | 62.17 | 51.94 |

Scores (Cont'd)



Thank You