# Brain Tumor Segmentation using UNET architecture

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# Outline

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# Introduction

1. A brain tumor is an abnormal growth of cells in the brain cells.
2. MRI scans are best for detecting brain tumors
3. An automated brain tumor segmentation will help to open new era in the treatment of brain tumor.

# 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 and IoU 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 (.nii) files.
3. **Segmentation Models 3D**: Libraries accessed for pre-built architectures and utilities tailored for 3D medical image segmentation and classification tasks.
4. **NumPy**, **Pandas**, **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**

# Methodology (Cont'd)

**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.

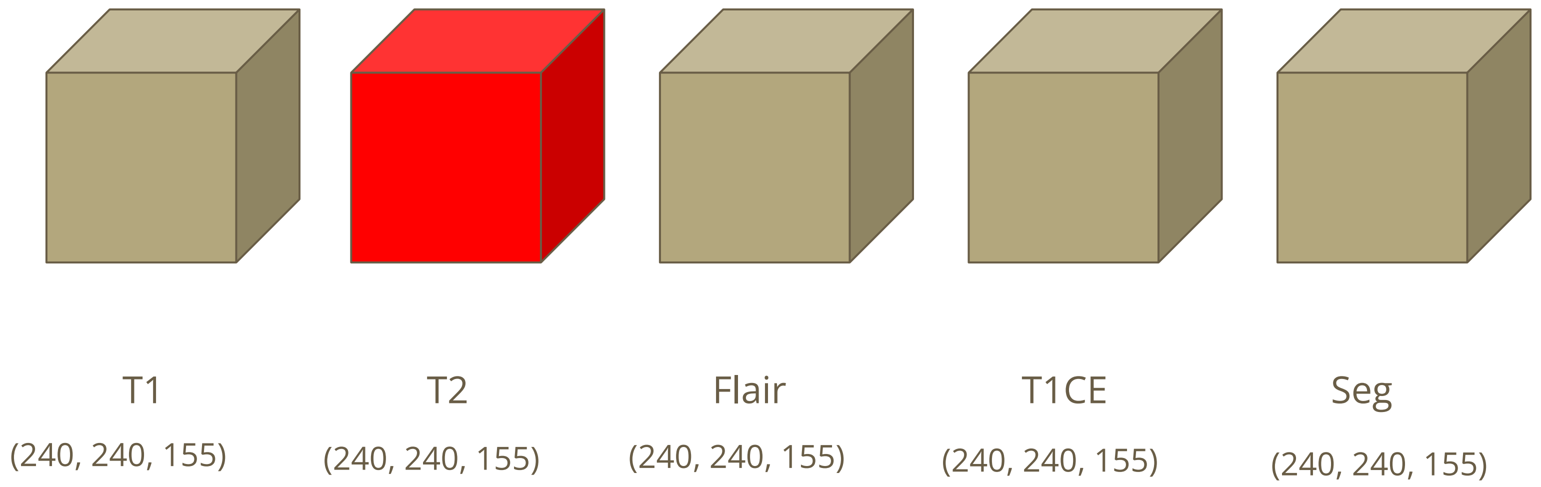
Segmentation file contains **3** types of annotations: **enhancing tumor**, **peritumoral edema**, and **tumor core**.

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

# Methodology (Cont'd)

## Preprocessing

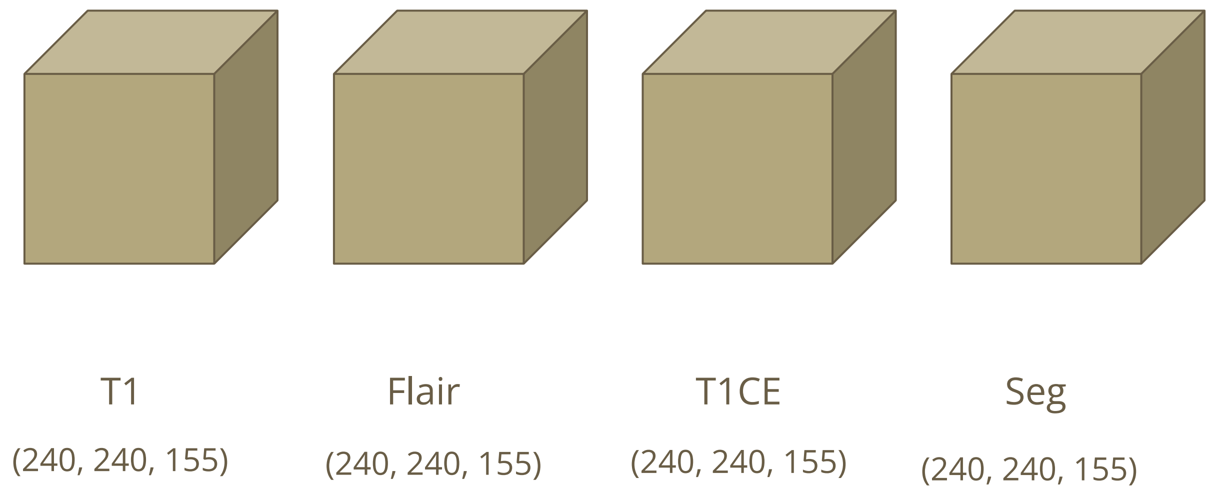
5 images in a single folder



# Methodology (Cont'd)

## Preprocessing

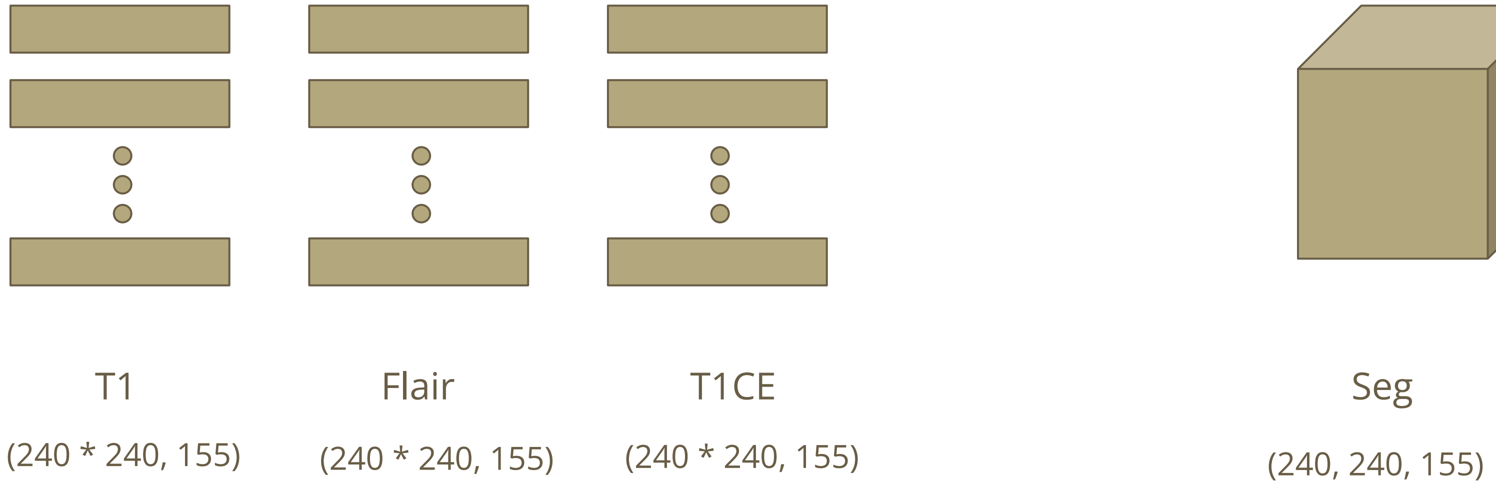
Removed T2 image



# Methodology (Cont'd)

## Preprocessing

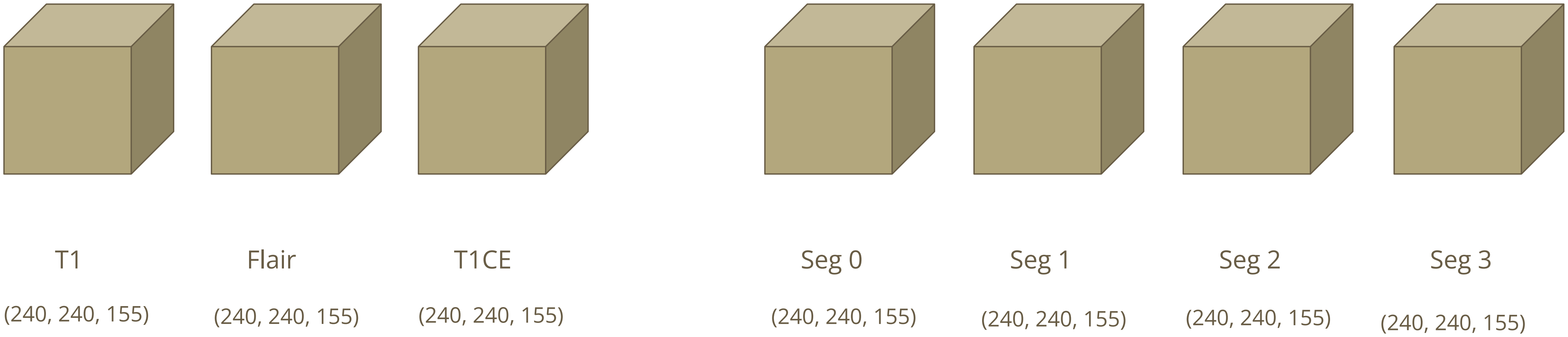
T1, Flair, T1CE were flatten on the first two axis. And MinMaxScalling were applied to them.



# Methodology (Cont'd)

## Preprocessing

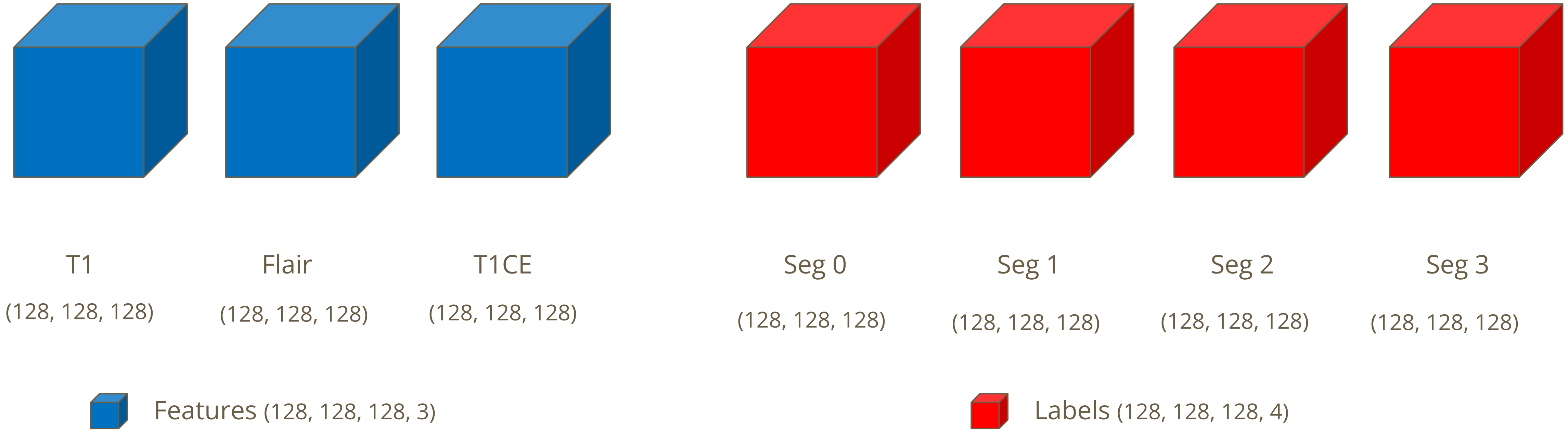
1. T1, Flair, T1CE were brought back to original shape.
2. One Hot Encoding were applied on Segmentation Image. Segmentation image had four unique pixel values 0 (Nothing), 1 (Non-enhancing tumor core), 2 (Edema), 3 (Not Specified), 4 (Enhancing tumor).
3. Label 3 was replaced by label 4.



# Methodology (Cont'd)

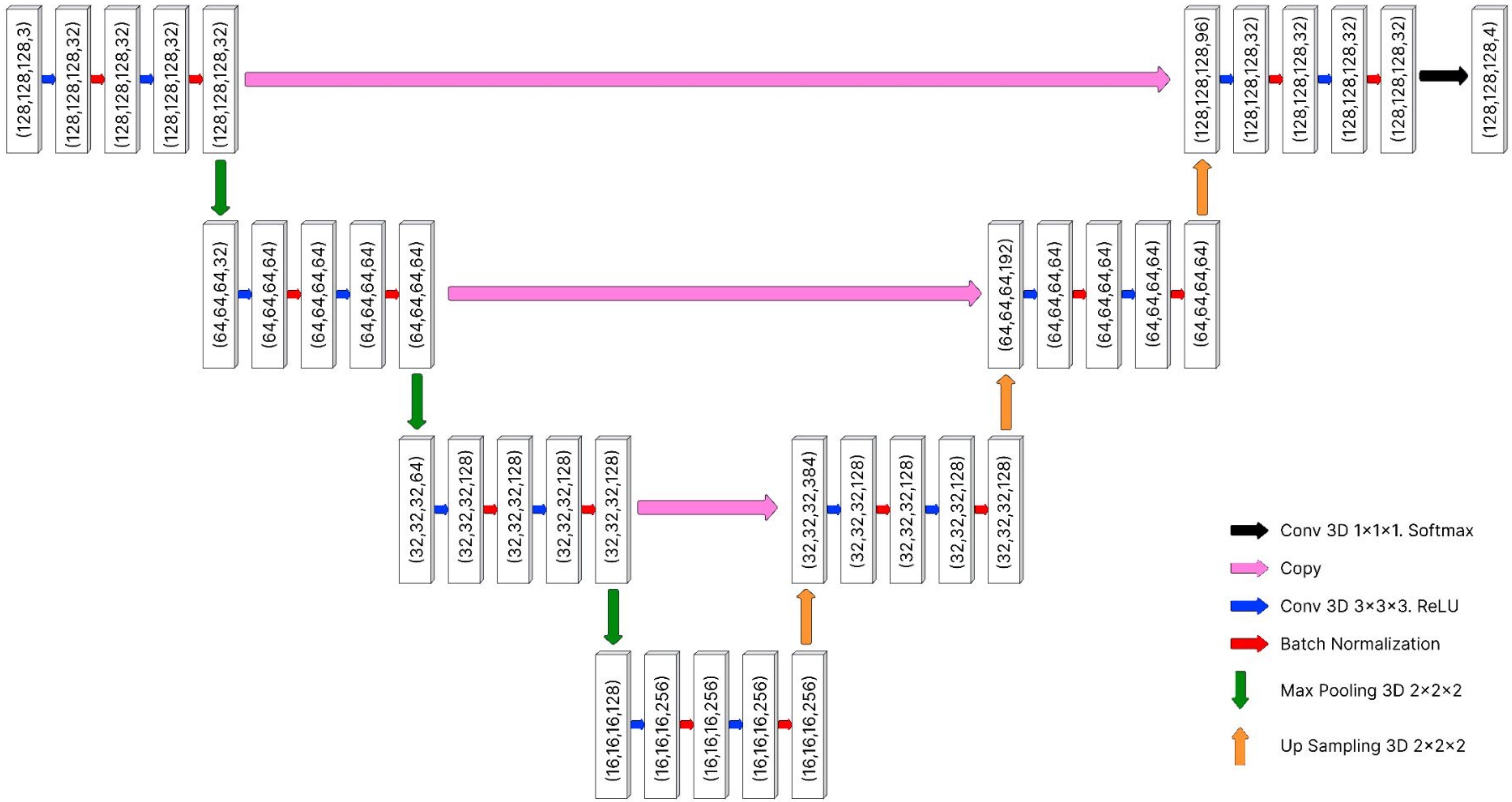
## Preprocessing

T1, Flair, T1CE and segmentations were cropped to (128, 128, 128)
Cropped Image = Original Image [56:184,56:184,13:141]



# Methodology (Cont'd)

## Model Creation



# Methodology (Cont'd)

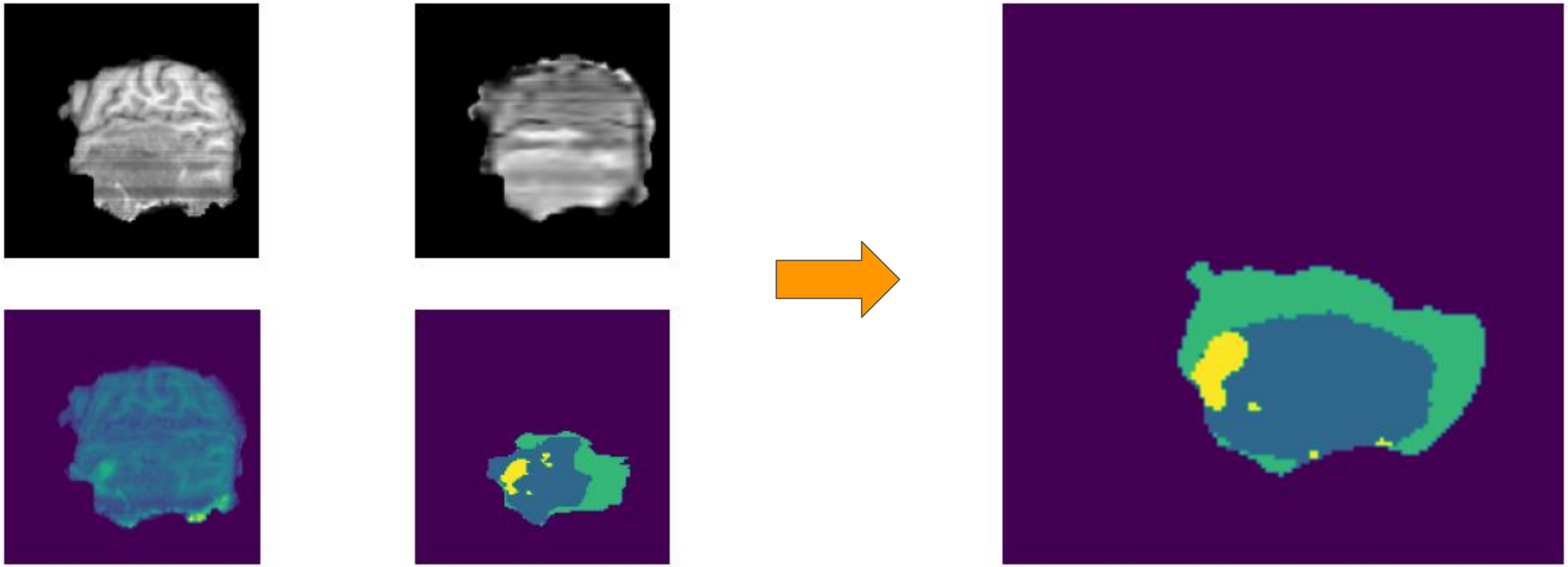
**Environmental Set Up**

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