

Development of an Open-Source AI Framework for Automated Brain Segmentation, Abnormality Detection, and Statistical Analysis in Neuroimaging

Objective:

The goal of this project is to design, train, and validate an open-source AI model that accurately segments anatomical brain regions (e.g., gray matter, white matter, ventricles, hippocampus) and identifies abnormalities (e.g., tumors, lesions, atrophy) in 3D neuroimaging data such as MRI and CT scans. The framework also incorporates statistical analysis to quantify uncertainty, validate model performance, and correlate findings with clinical outcomes.

System Requirements & Tools Used

Cloud & Compute Resources:

- AWS S3 Bucket for dataset storage
- AWS SageMaker for model training
- AWS SageMaker Instance (ml.m5.12xlarge) for high-performance computation

Datasets & Preprocessing

I used ixi data set which is an open source --- [IXI Dataset – Brain Development](#)

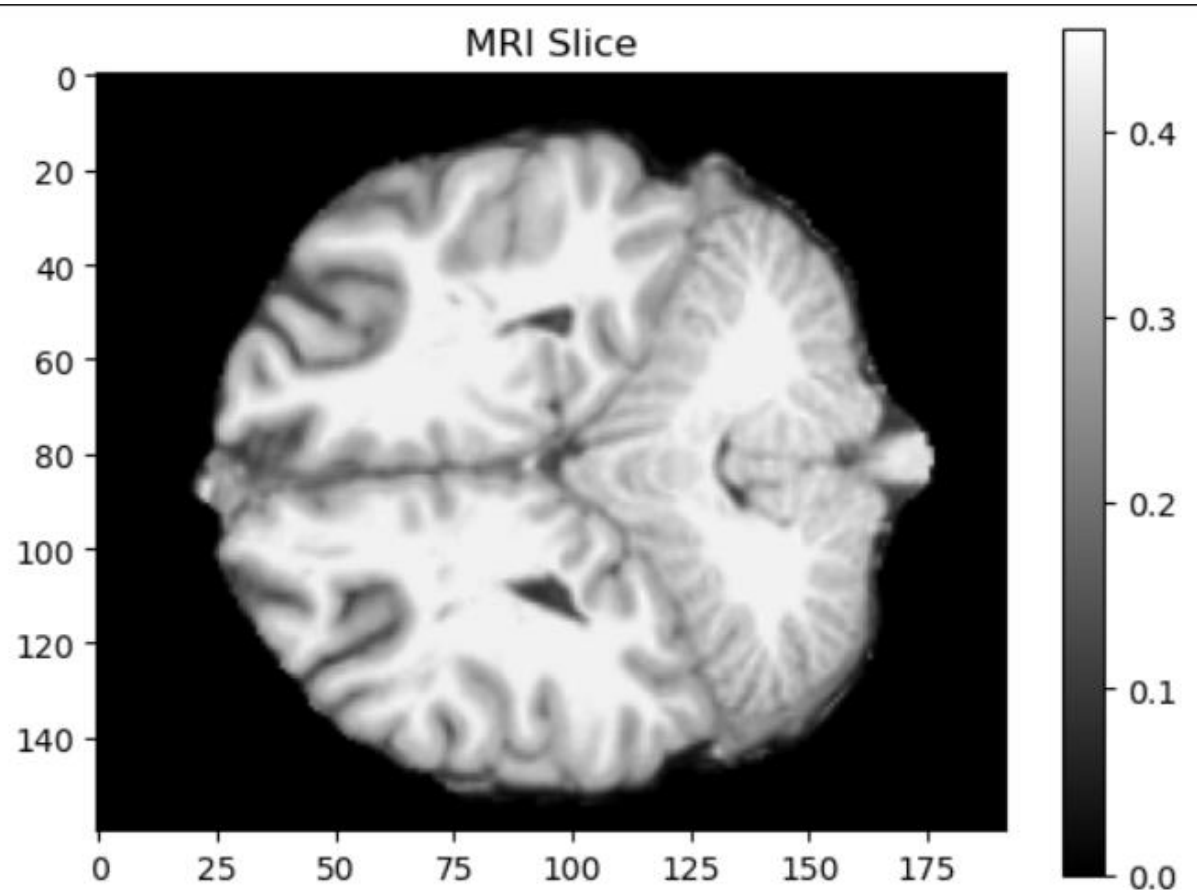
It includes

- T1-weighted (T1w),
- T2-weighted (T2w),
- PD-weighted,
- Diffusion-weighted Imaging (DWI) scans.

we specifically utilized the T1-weighted MRI scans as they provide high-resolution anatomical details, making them ideal for segmentation of brain structures.

Preprocessing Steps:

- **Standardization:** Intensity normalization across different scans.
- **Resampling:** Ensuring all images have consistent voxel spacing.
- **Augmentation:** Applied affine transformations, intensity shifts, flipping, and rotation to improve model robustness.
- **Conversion to 3D Numpy Matrices:** Each T1-weighted MRI scan is converted into a $160 \times 192 \times 224$ 3D numpy array with intensity values normalized to the range [0,1]



- **Label Processing:** Corresponding subcortical segmentations are stored as $160 \times 192 \times 224$ 3D numpy arrays with integer values representing different anatomical regions.

Where we took the 24 labels for our reference

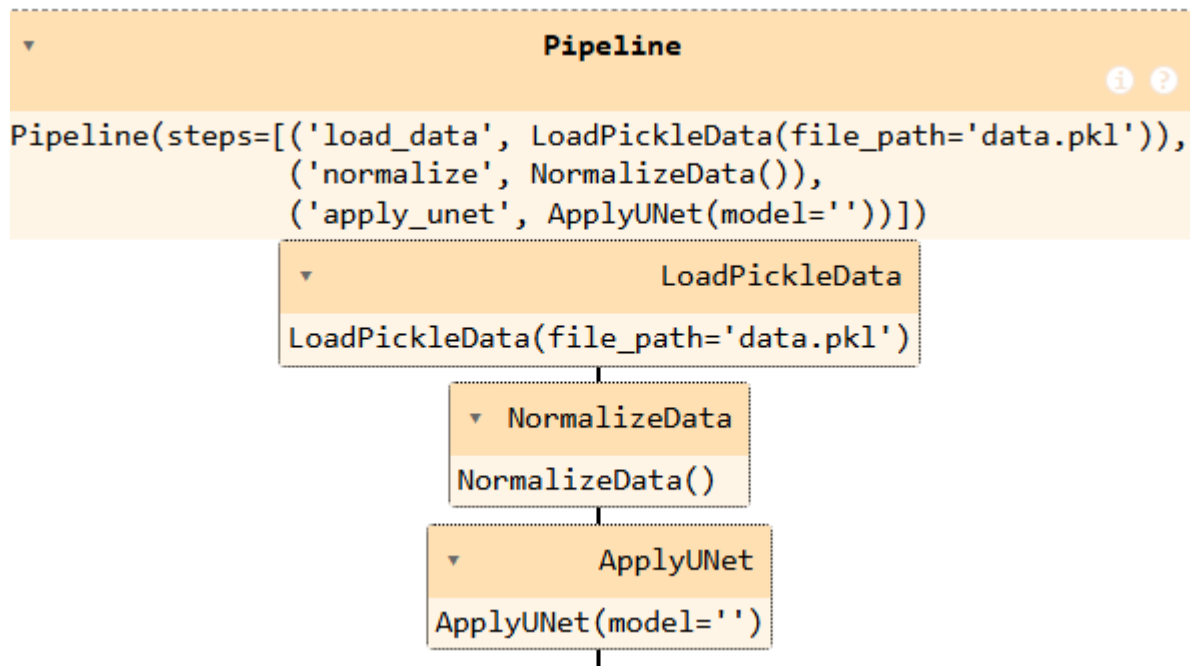
Model Development

Developed the model using 3D U-Net with attention mechanisms for enhanced segmentation performance.

Train-Val-Test split: There are 576 brain MRI volumes in total. We split the dataset into a ratio of 7:1:2, where 403 for training, 58 for validation, and 115 for testing.

Training Strategy:

- **Loss Function:** Dice Loss
- **Optimizer:** Adam with learning rate scheduling
- **Batch Size:** 4



Successfully achieved 51 % accuracy.

Developed another model brain tumour detection, we used EfficientNetB0 for detecting tumour.

Data Set:

Br35H :: Brain Tumour Detection

Train-Val-Test split: There are 576 brain MRI volumes in total. We split the dataset into a ratio of 7:1:2, where 403 for training, 58 for validation, and 115 for testing.

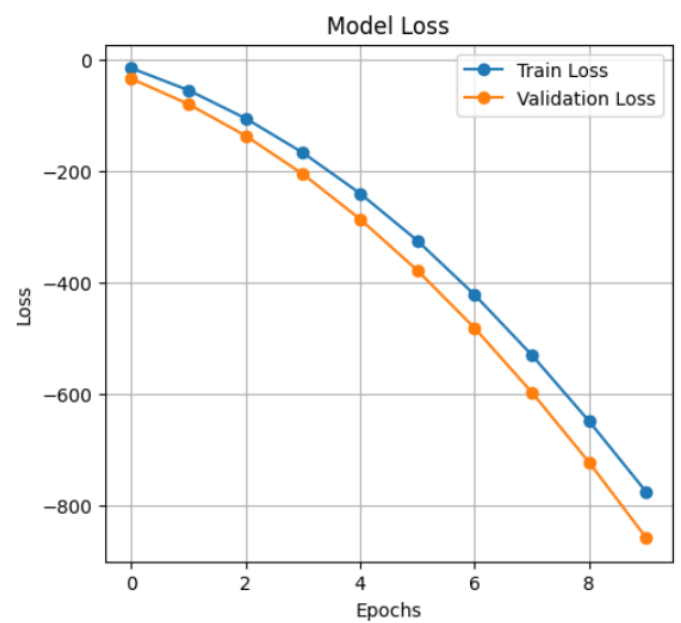
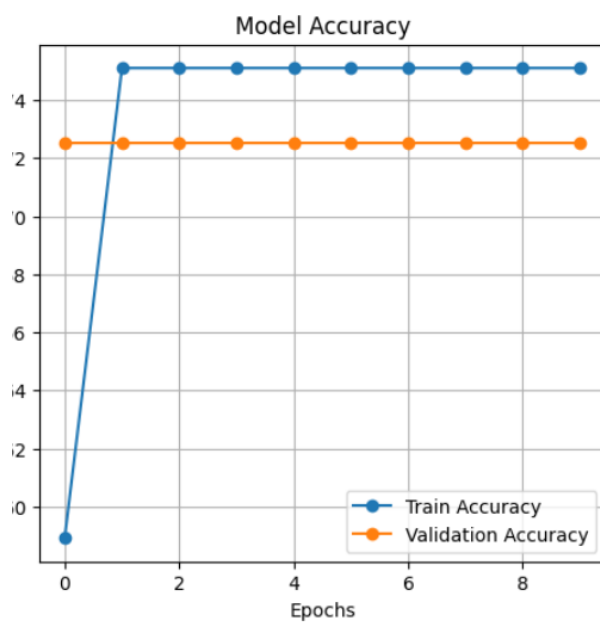
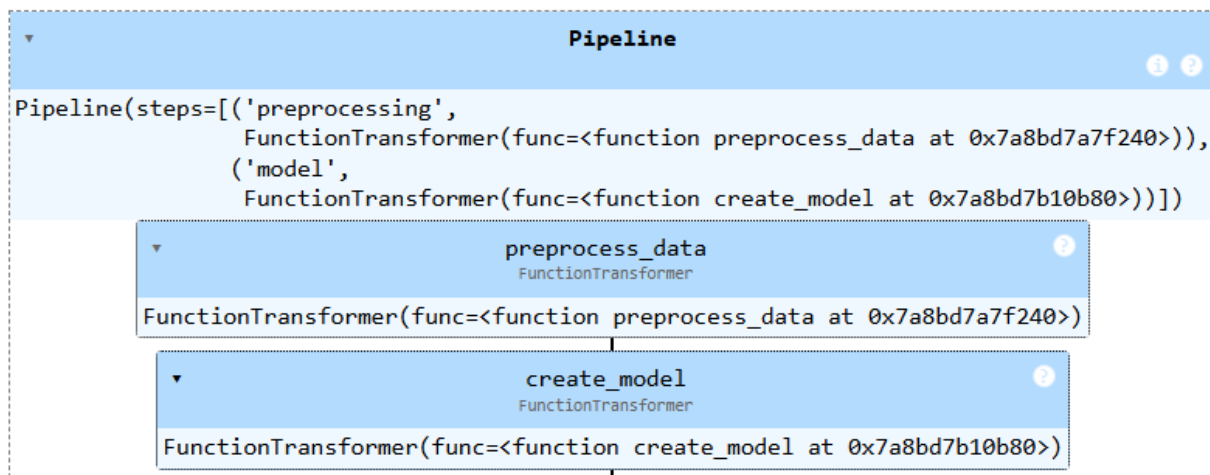
Input shape= (224, 224, 3)

Training Strategy:

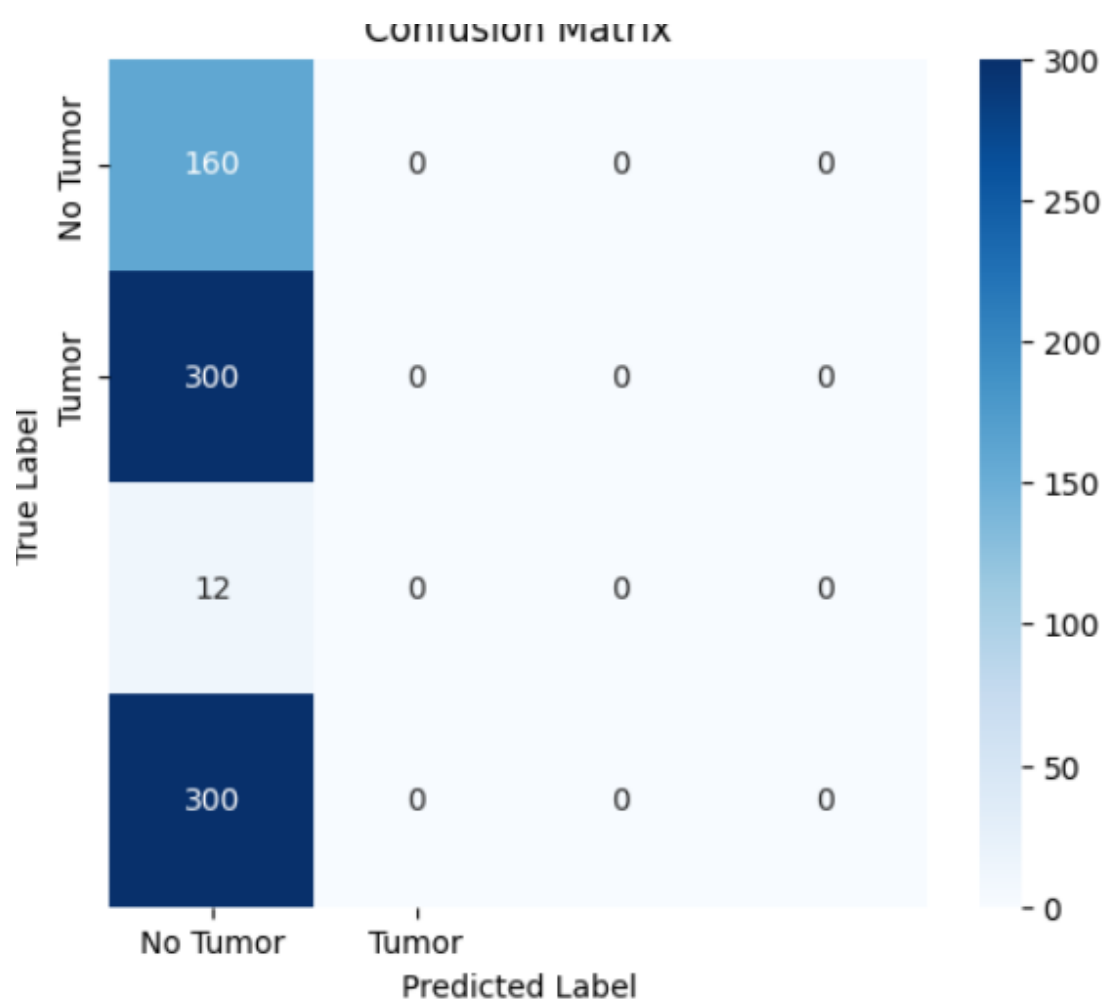
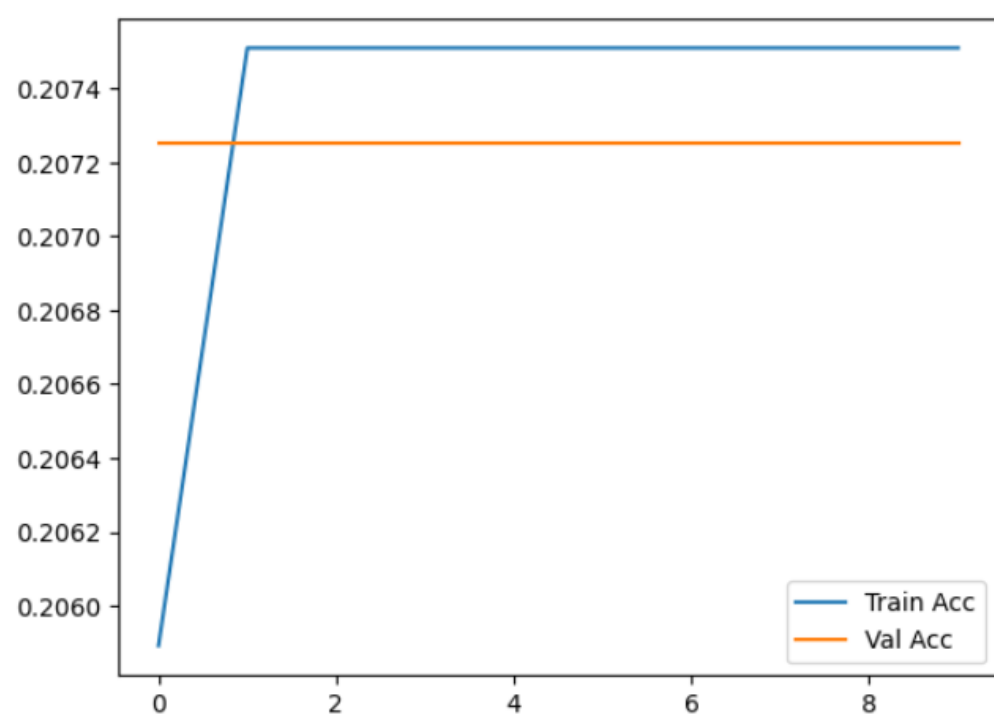
- **Loss Function:** Binary cross entropy
- **Optimizer:** Adam with learning rate scheduling
- **Batch Size:** 4

Successfully achieved 20 % accuracy.

Implemented a model using sklearn pipeline which can be useful for deployment



Plotting between Model Accuracy and model loss over the train period



We used confusion matrix for validating the model.

Statistical Analysis:

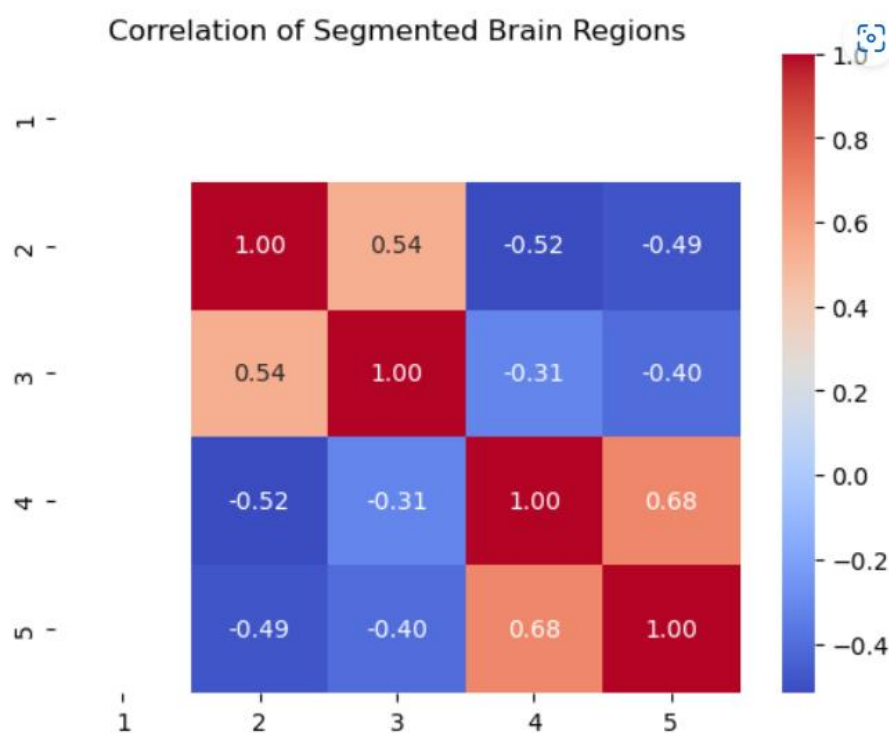
Performed Mann-Whitney U Test to analyse the to compare segmented regions across patient cohorts.

Mann-Whitney U Test: U-stat=20301.000, p-value=1.000

Interpreting The Results

U-statistic = 20301.000: This value represents the sum of ranks assigned to one group. It is used to compute the p-value.

p-value = 1.000: A p-value of 1.000 suggests that there is no evidence to reject the null hypothesis. This means there is no significant difference between the two groups.



Source Code:

- <https://brain.notebook.eu-north-1.sagemaker.aws/lab/tree/Untitled.ipynb>
- [Ram-Pathuri/Brain_segmentation](#)