Brain Image Segmentation using Machine Learning

Ministry/Organisation Name: Dept. of Atomic Energy

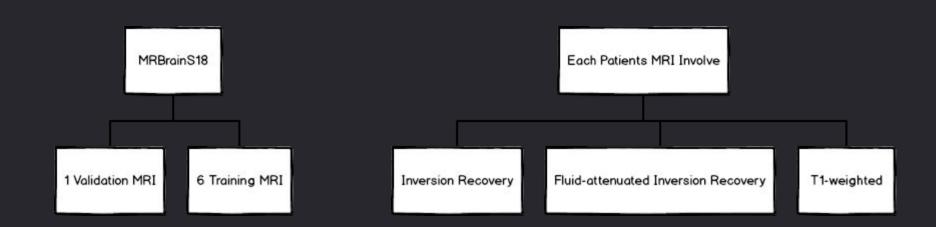
Problem Statement: Brain Image Segmentation using Machine Learning

Team Name: Defaulting

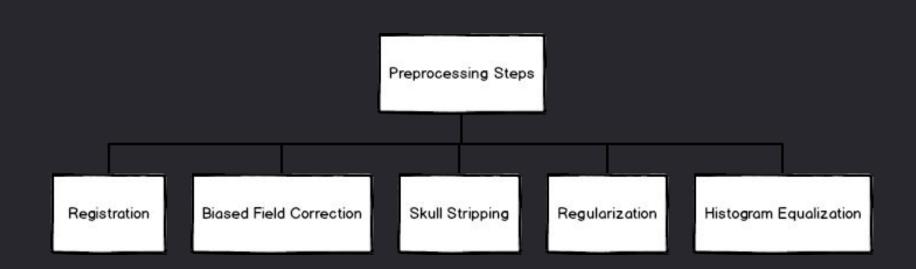
College Name: IIT (ISM) Dhanbad



Data Explanation



Preprocessing



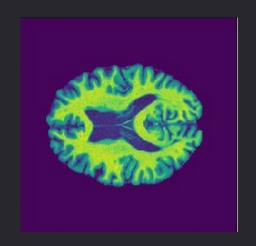
Preprocessing

- MRBrainS18 dataset came with Registered and Bias Field Corrected MRI's
- Skull Stripping:
 We performed skull stripping only for T1 weighted MRI using DeepBrain library
 which creates a mask for skull removal with the help of skimage. The main
 reason for skipping skull stipping for IR and FLAIR was that they predominantly
 contain lesions which may be lost during skull stripping
- Histogram Equalization:
 Performed on T1 weighted MRI to increase the contrast of Image

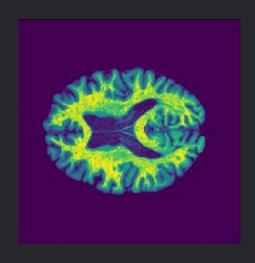
Preprocessing



Regularized Biased Field Corrected MRI

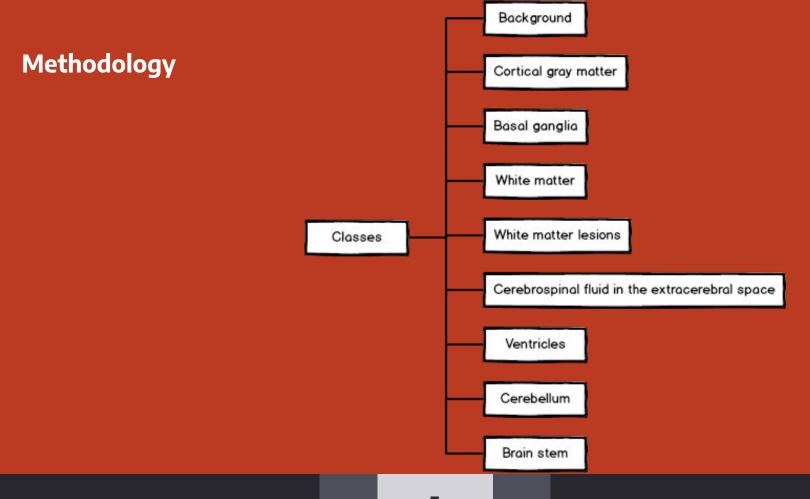


Removed Skull



Histogram equalization

Training

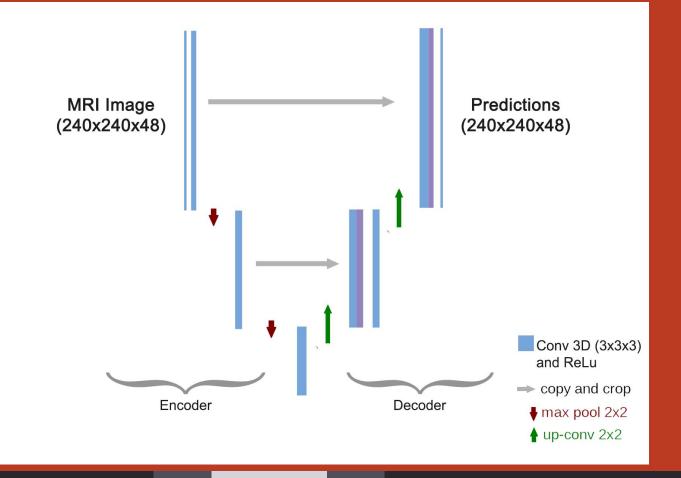


Methodology

We followed two different types of approaches for training

 Cortical gray matter, White matter, Cerebrospinal fluid in the extracerebral space can be easily reduced from T1- weighted MRI by applying threshold but the results were not good so we trained a small neural network to denoise the thresholding.

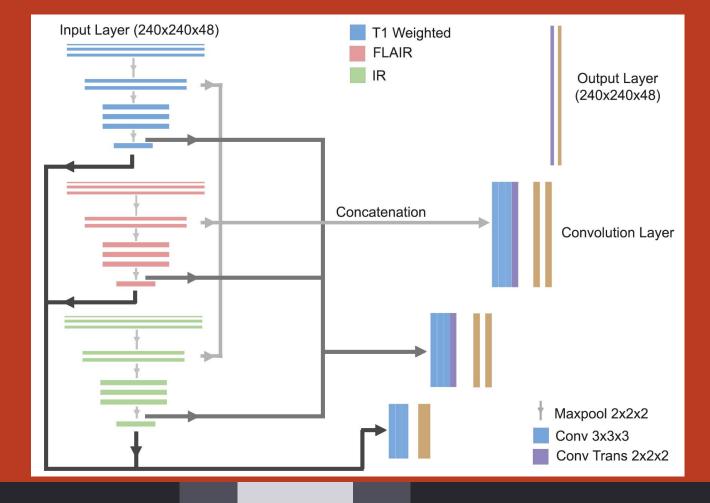
Network



Methodology cont...

For rest of the classes we trained a custom model inspired by Unet Architecture. The model has 3 encoders stacked together in bottleneck layer and then a single decoder. There are skip connections from encoder to decoder to enhance segmentation.

Network



Difference between Unet and our Architecture

Unet Architecture

- 1. Only one encoder and one decoder
- 2. Deep architecture with about 10 Million parameters
- Doesn't have dilated convolution layers

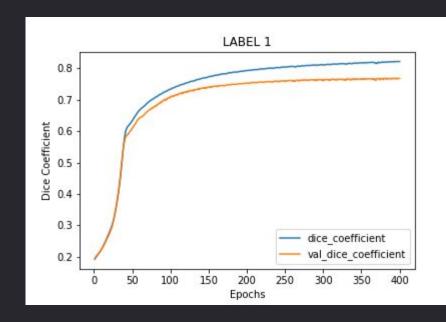
Our Architecture

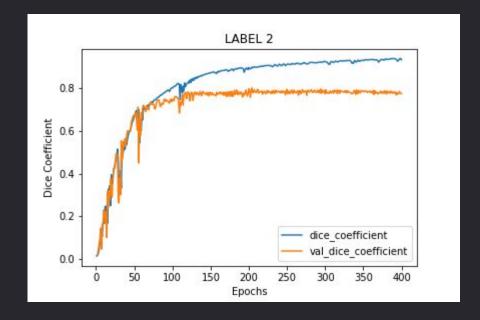
- 1. Three encoder and one decoder
- Shallow with about 600 Thousands parameters
- 3. Have dilated convolution layers

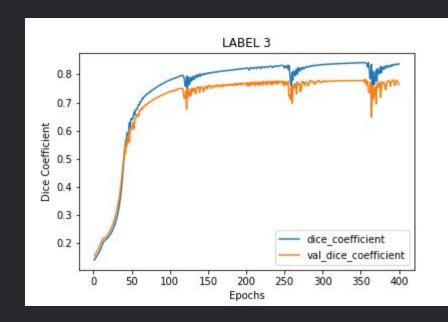
Loss Function

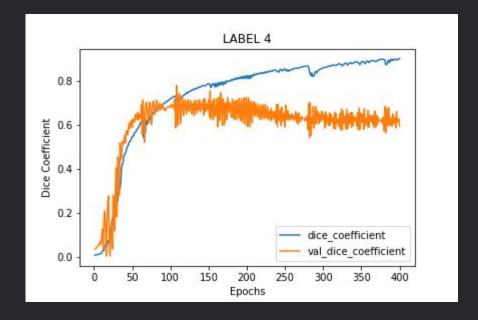
We took one minus dice coefficient as the loss function.

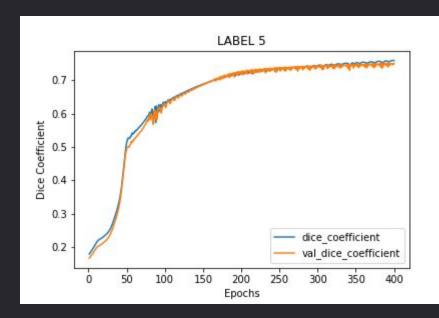
$$1-rac{2*|X\cap Y|}{|X|+|Y|}$$

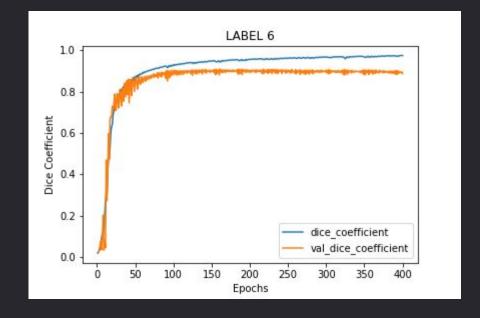


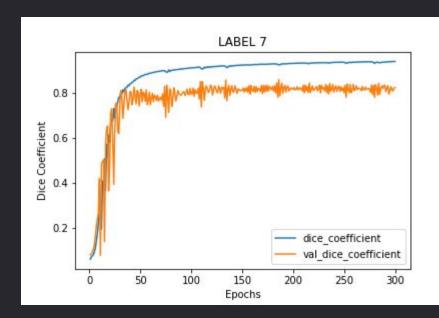


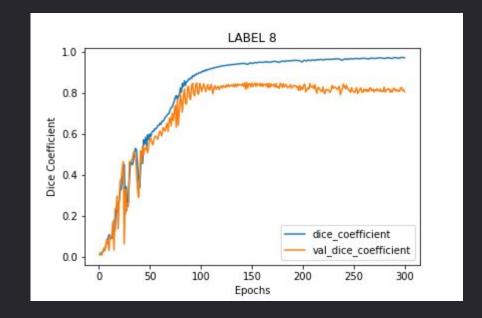












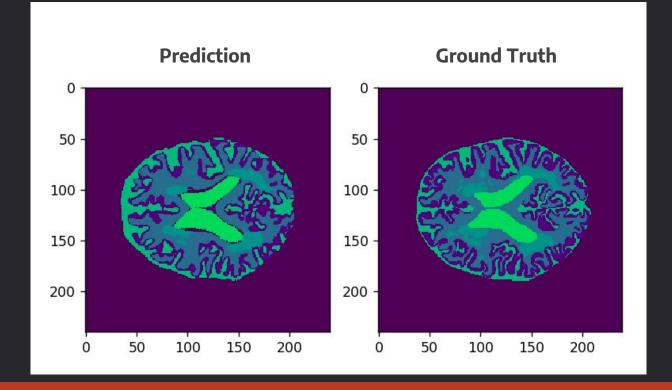
Findings

- Large network seems to overfit the data
- Skull removal improve dice's coefficient
- Thresholding works better for label 1,3 and 5

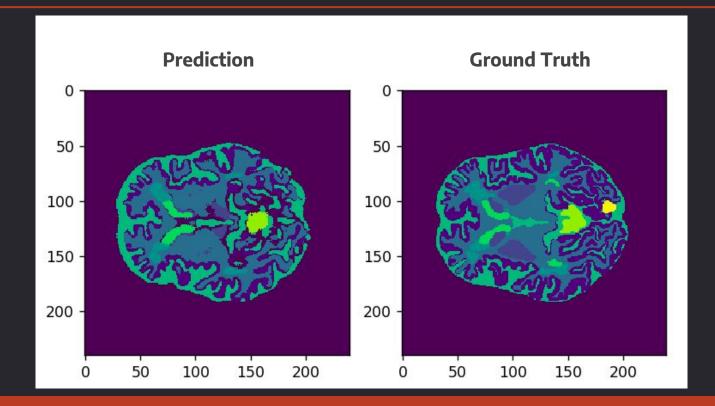
Problems

- Edge of tissue boundary is not clear
- Some small labels are difficult to segment
- There are many neighbour between different labels
- Lack of computation power

Results



Results



Evaluation

Class	Dice Score	Hausdorff Distance	Volume Similarity
1	0.7027	2.999	0.84702
2	0.7582	5.463	0.9835
3	0.7702	3.149	0.988
4	0.7463	9.054	0.8385
5	0.7043	3.149	0.986
6	0.8825	3.030	0.9955
7	0.8879	5.160	0.9207
8	0.8551	4.281	0.998

BraTS 2018 Dataset

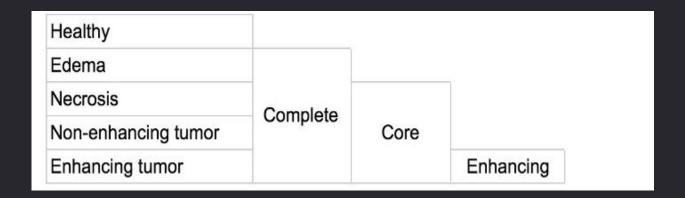
A more common dataset used in brain tumor segmentation is the BraTS Challenge 2018 dataset (Brain Tumor Segmentation Challenge).

Dataset size: 220 subjects with high grade tumors. 54 subjects with low grade tumors.

Input: For each subject we are given four MR images, i.e four three-dimensional volumes (FLAIR, T1W, T1C and T2).

Results

Labels: Each example has been segmented and labelled by 5 raters (certified doctors). Each voxel are labelled, (1) Healthy, (2) Edema, (3) Necrosis, (4) Non Enhancing tumour, (5) Enhancing tumour.



Approach

We used the same methods taken in the previous dataset .Images were regularized and histogram equalization was done to make the features appear more prominent. Finally skull stripping was done to the images to remove the skull borders from the images.

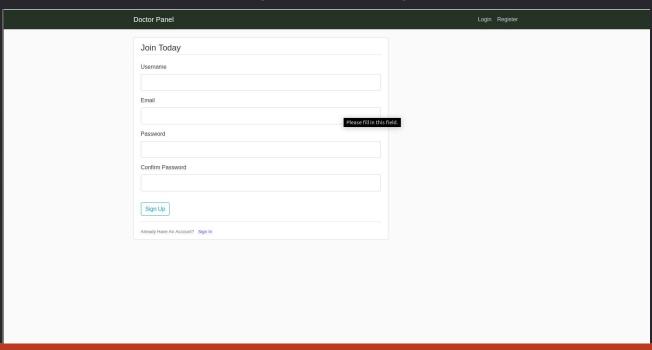
The same model consisting of a 3 Encoder U-Net Based architecture was used to train the data with the Loss function being **1 - Dice Coefficient.**

Challenges Faced

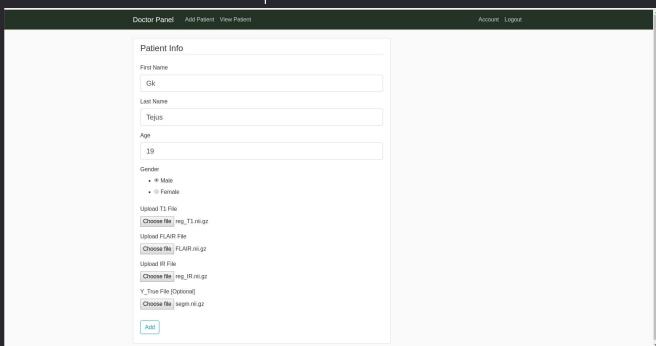
Since the dataset was a very large one, so the lack of time and computing resources made it very difficult for us to train the model in a short period of time.

To tackle this we instead of training on the whole dataset, we took the train and validation sample size of that equivalent to the MRBrainS18 dataset. This posed another problem to us that not all the samples that we took contained all the labels that we intended to predict

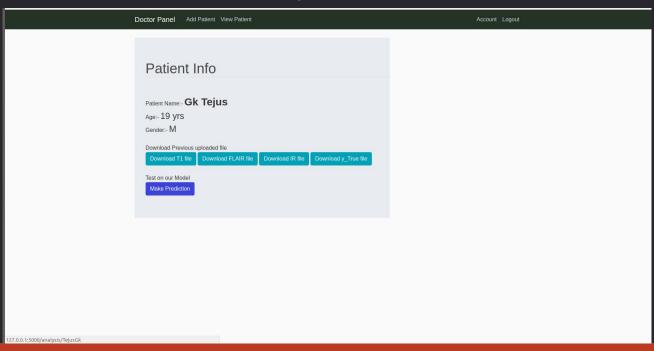
Registration page



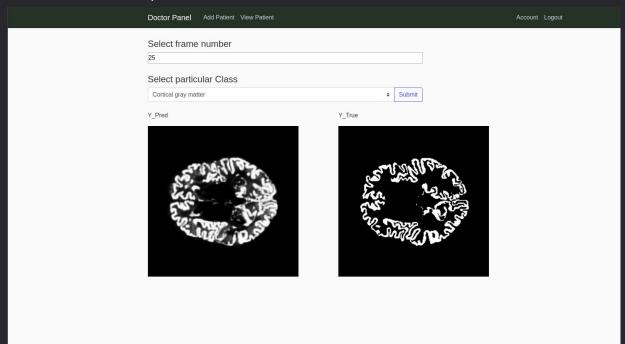
Fill patients Details



View existing patients details



Compare Predictions to Ground truths



Technology Stack

