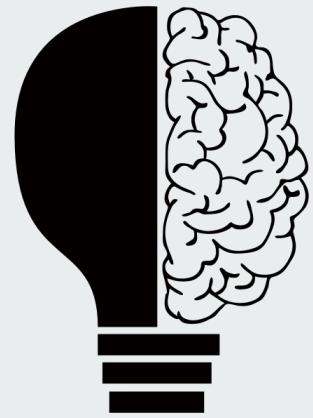


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# **Brain Tumor Segmentation using 3D MRI scans:**

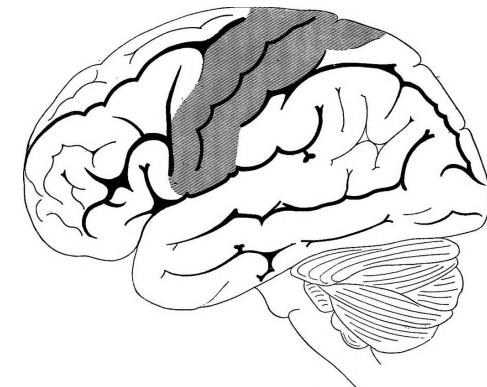


Name: Alimpan Barik  
M.Sc Big Data Analytics (BDA)  
Semester -2, First Year.  
Ramakrishna Mission Vivekananda Educational Research Institute.

## Brief Description of brain tumors- utility of this project:

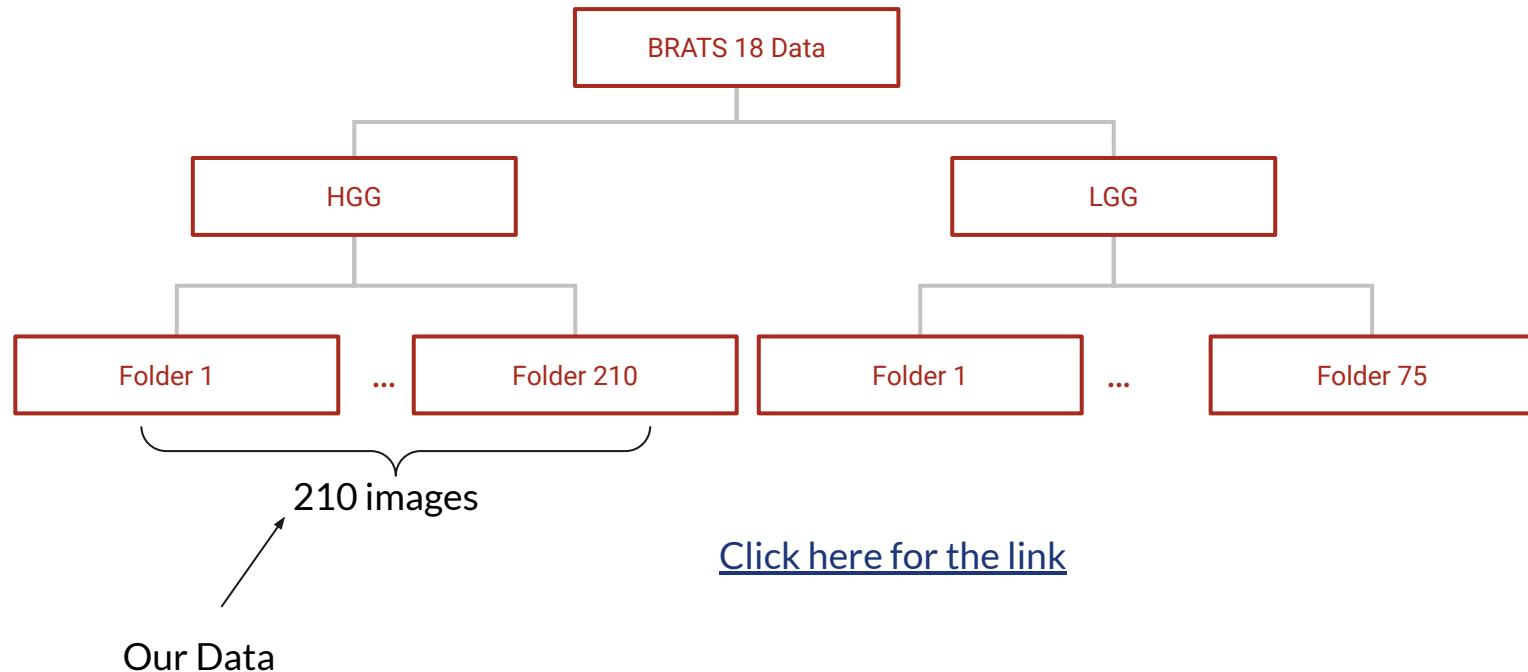
---

- ❖ **Brain tumors:** Growth of abnormal cells in the brain, that might be malignant or benign.
- ❖ **Segmentation task:** Separating the tumor tissues from the healthy tissues.
- ❖ Automation in extracting/ differentiating the tumor from the surrounding healthy tissue using CNNs help to detect the tumor both faster & more accurately.
- ❖ Helps to decide future treatment procedural and better results

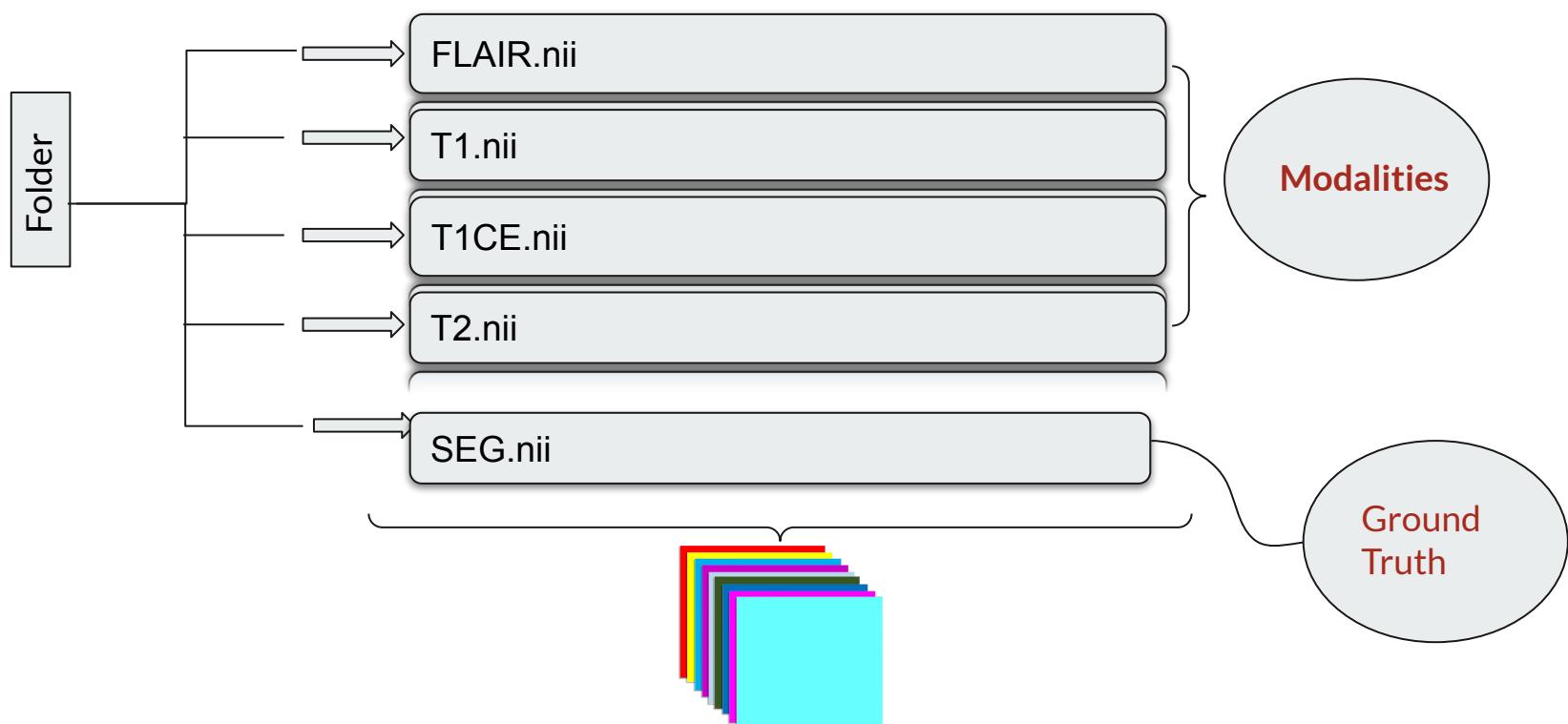


# Dataset description:

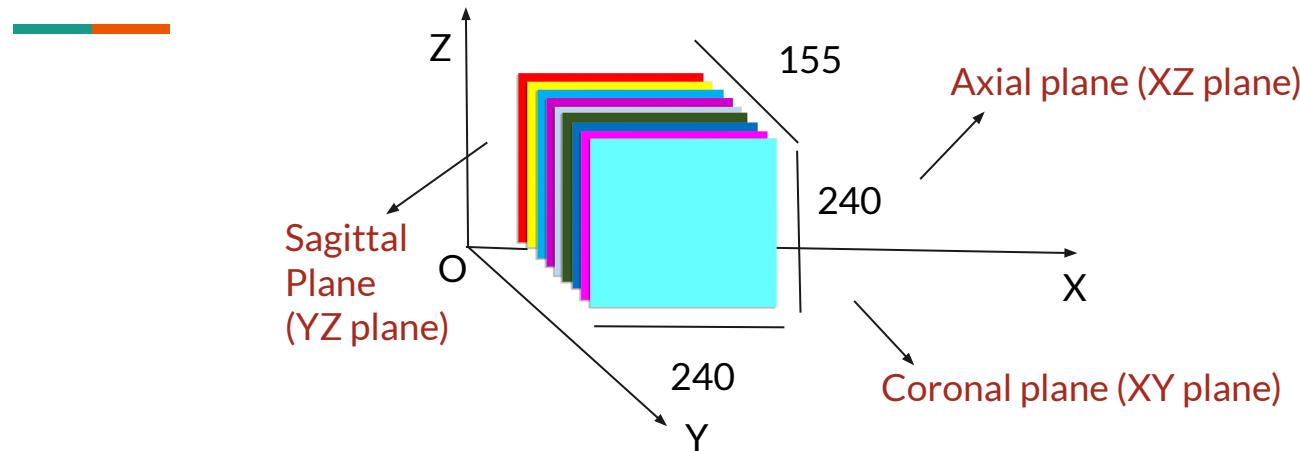
- ❖ Dataset: MICCAI BRATS 2018 Dataset (Downloaded from Kaggle)



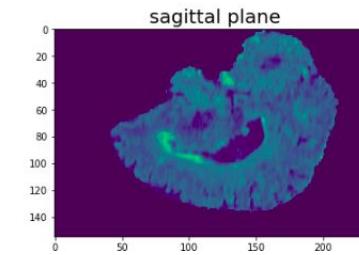
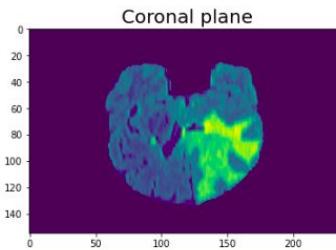
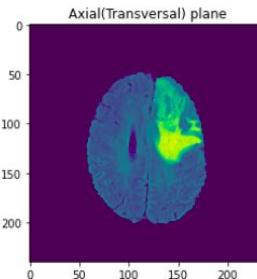
# Dataset description:



# Data Visualization:

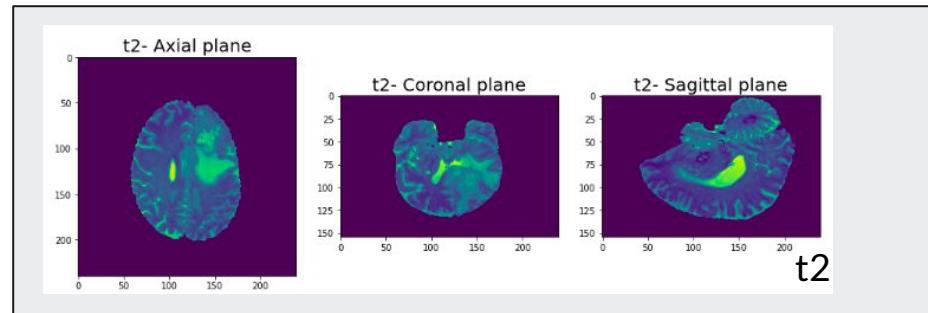
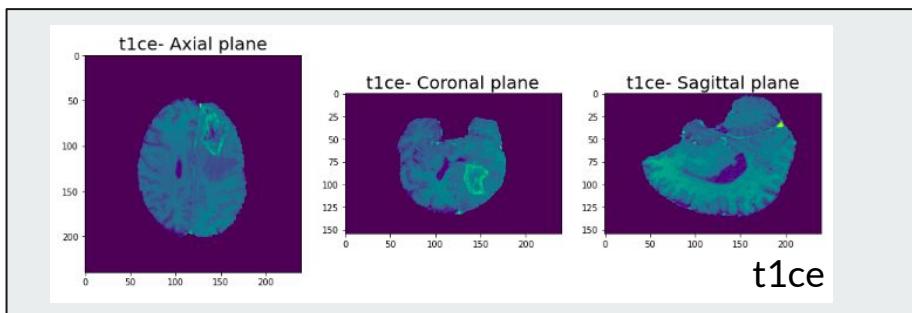
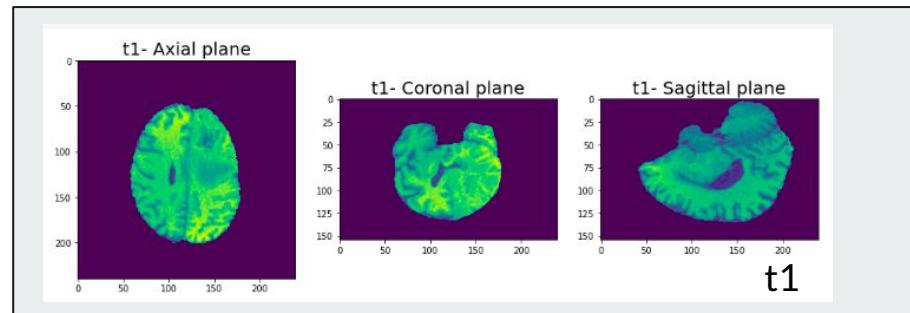
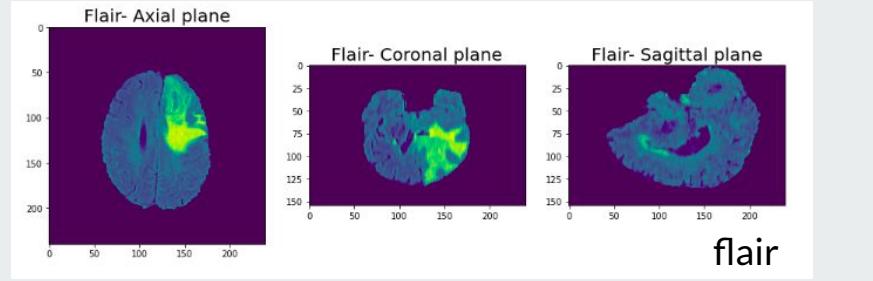


Visualizing a sample image in these 3 planes:



# Data Visualization (Contd.):

Visualizing the four modalities in 3 planes:



# Data Visualization (Contd.):

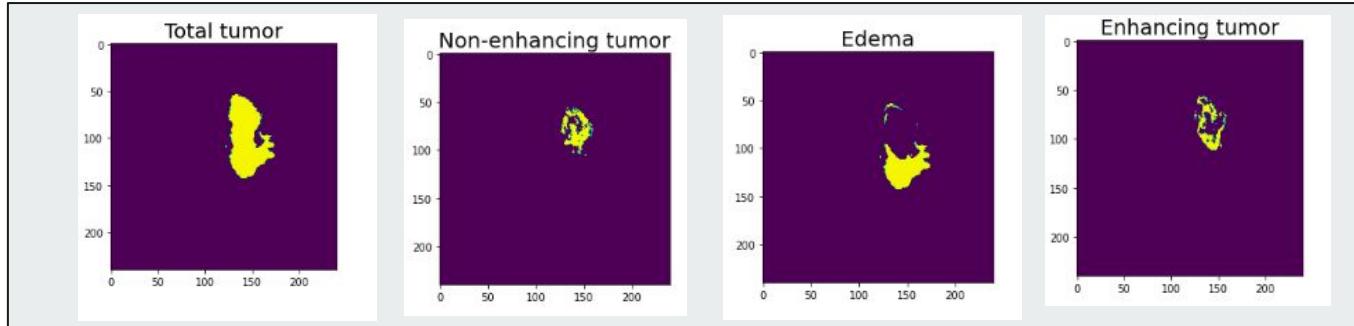
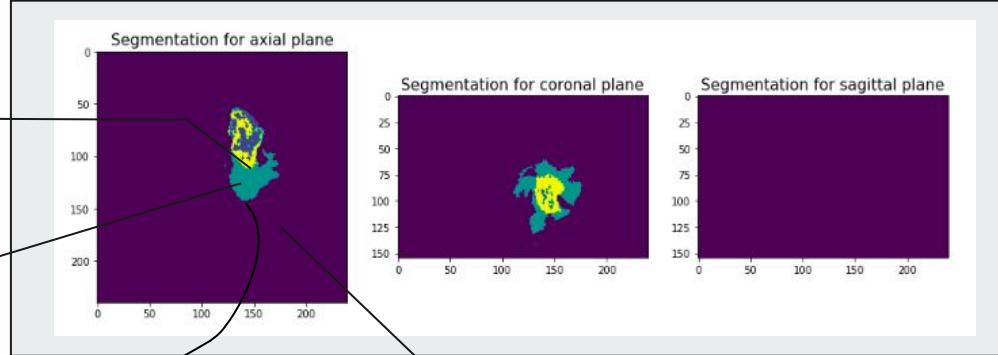
The Segmented image- Exploring different labels:

Non-enhancing  
Tumor (label 1)

Enhancing tumor  
(Label 4)

Edema(label 2)

Healthy tissue(Label 0)



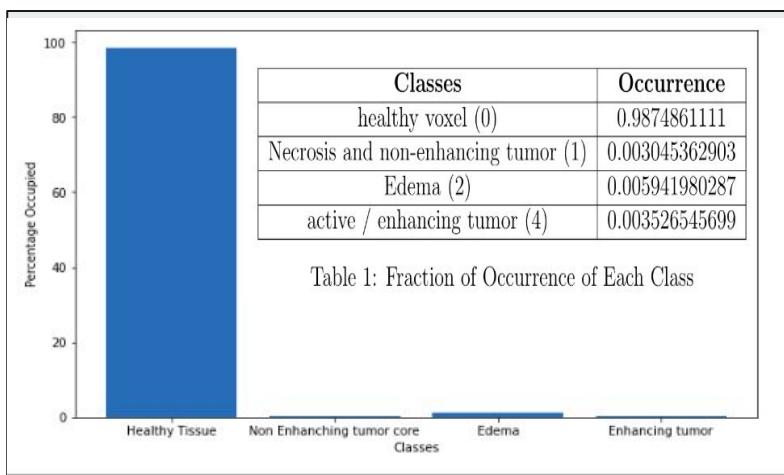
# Class imbalance problem:

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- ❖ What is class imbalance problem?

When there is an unequal distribution of **classes** in the training dataset.

- ❖ How it affects our dataset:

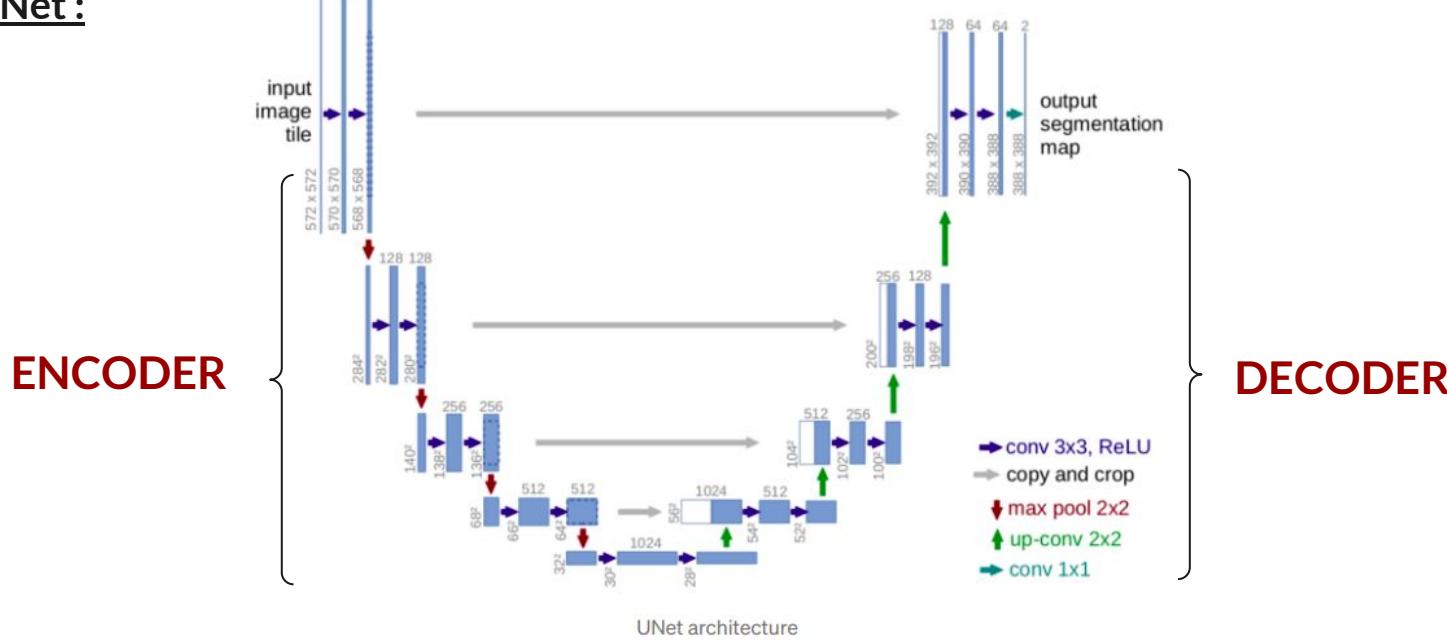


- ❖ Strategies to cope up class imbalance:

- Use multi class Dice loss
- Different weights to penalize labels.

# Architecture of our model:

UNet:



# Training Details:

Trained on 200 HGG images with validation split of 0.25, i.e. 150 images for training and 50 images for validation.  
Epochs=50, lr=1e-4, drop out=0.25

➤ Loss function:- Dice loss

$$1 - \frac{2 \sum_{pixels} y_{true} y_{pred}}{\sum_{pixels} y_{true}^2 + \sum_{pixels} y_{pred}^2}$$

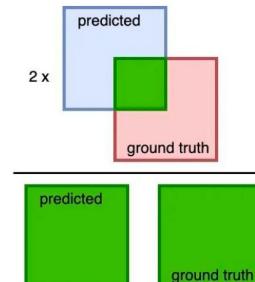
This scoring is  
repeated over all  
**classes** and averaged

$y_{true}$  = ground truth

$y_{pred}$  = output

➤ Metric to measure accuracy: Dice coefficient:

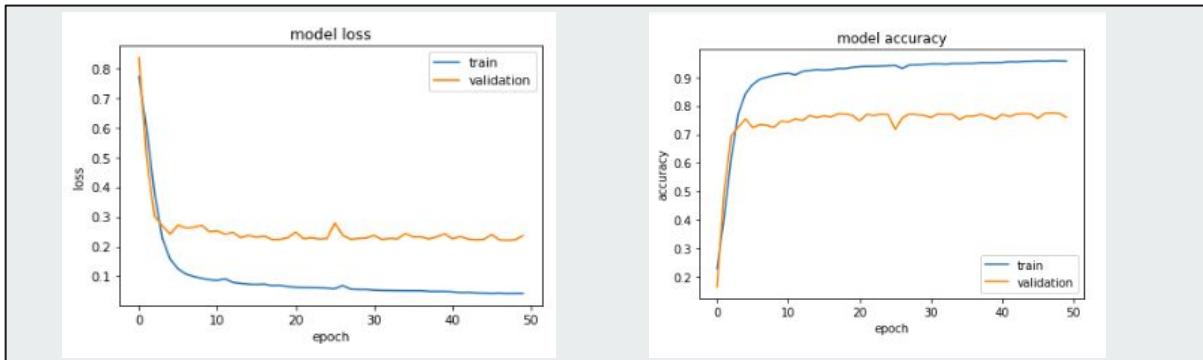
$$\text{Dice co-eff} = 1 - \text{Dice loss} =$$



# Results: (for whole tumor segmentation)

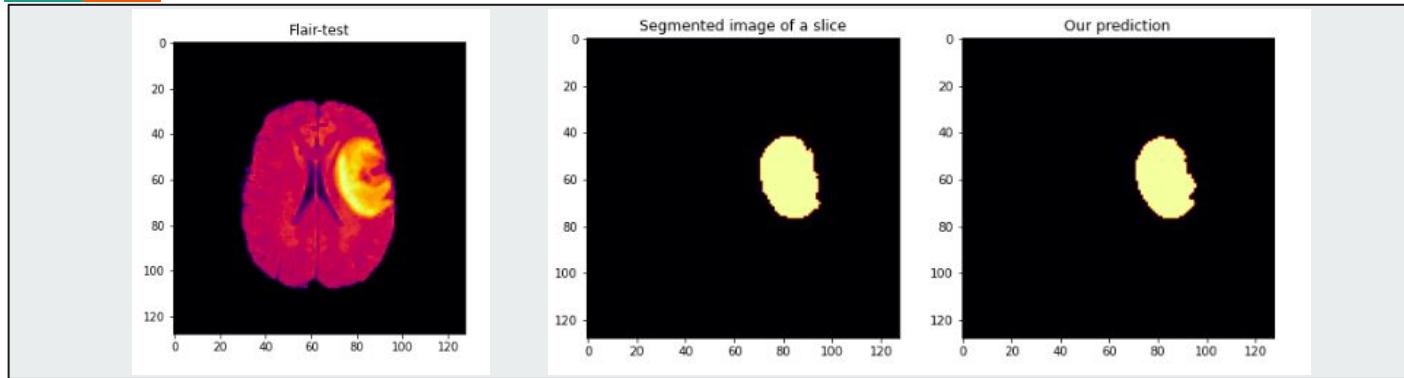
Validation\_loss=0.25, Validation dice coefficient=0.75

Model loss & accuracy:

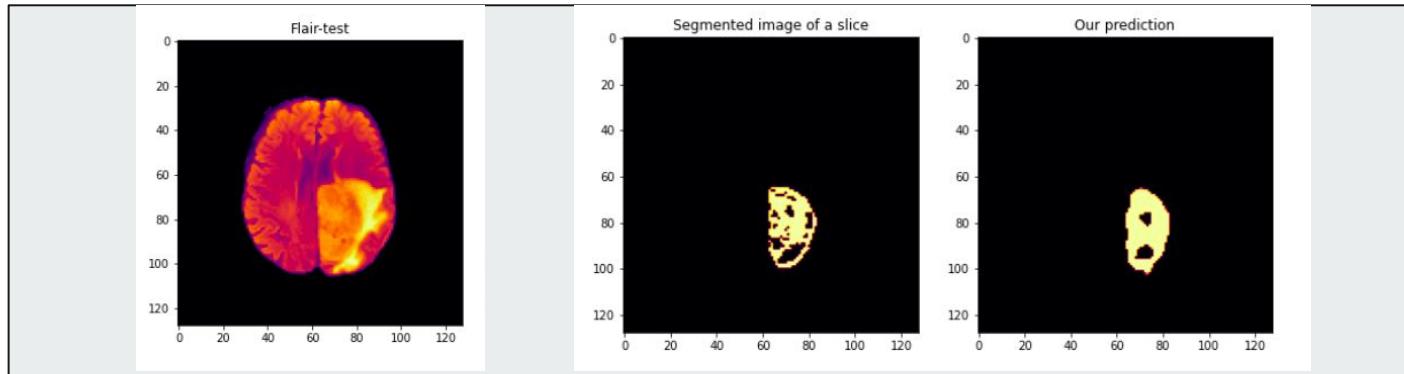


# Predictions:

For whole tumor:



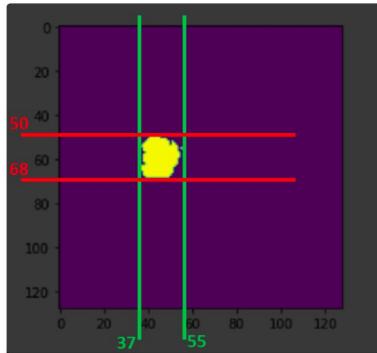
For enhancing tumor only: Validation dice coeff=0.3 :(



# Why so!!

May be because in the whole image the enhancing tumor occupies too little space

**Strategy:** removing the useless area and center the images by cropping and train using cropped images.



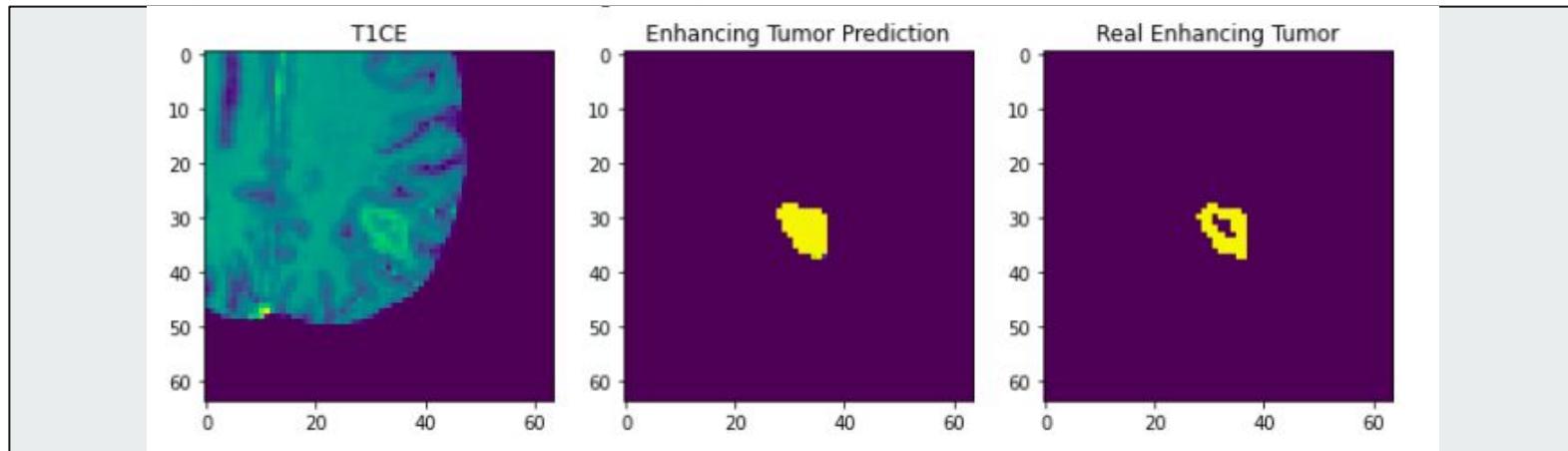
makes the tumor clearer!!!

**Training:**

40 images to train, 10 images for validation.

With SAME ARCHITECTURE

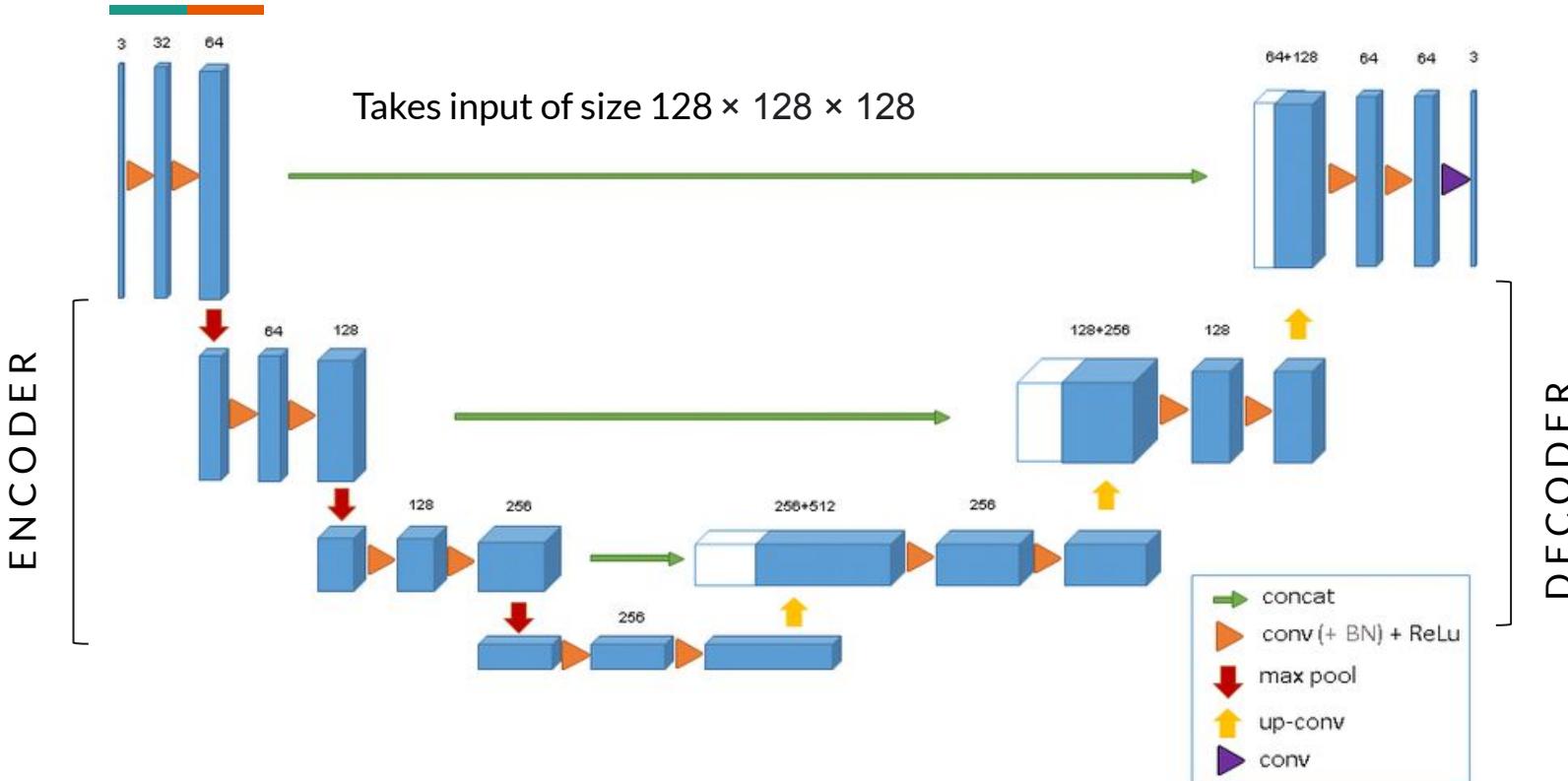
# Results after cropping:



Validation dice coeff=0.6 !!!

Clear improvement :)

# Another architecture: UNet 3D



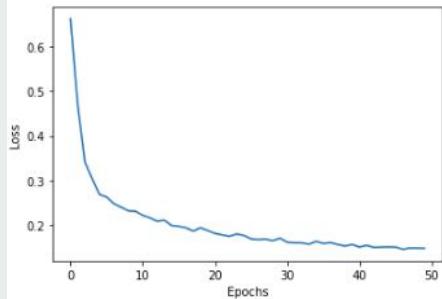
# Training:



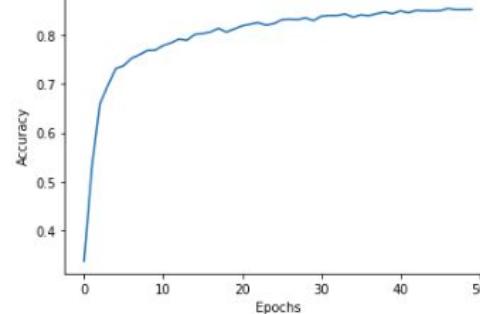
- 180 images for training, 30 images for validation
- epochs=60
- learning\_rate=0.001, decay\_rate=0.0000001
- Optimizer: Adam
- Loss: Dice Loss
- Metric: Dice Co efficient

# Results:

Training Loss



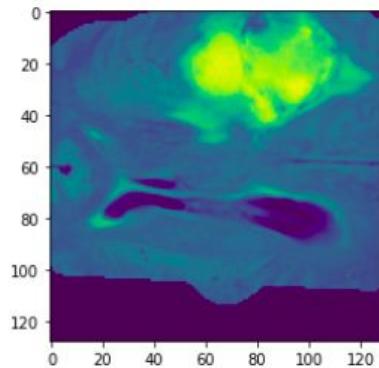
Training Accuracy



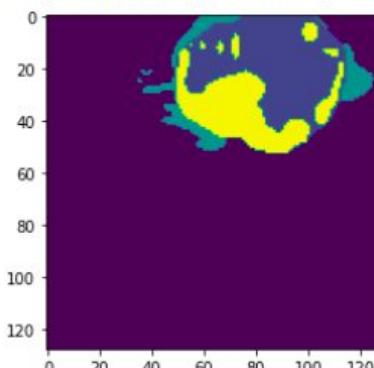
However Validation dice coeff=0.05 !! A disaster :(

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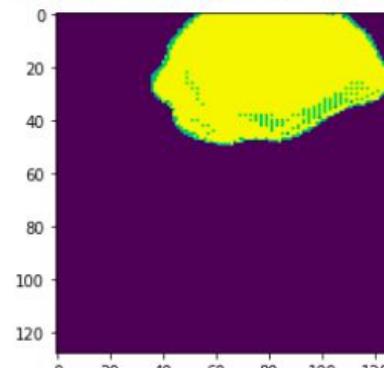
## Very poor predictions:



Flair modality of test image



Ground Truth



Prediction

TO BE IMPROVED...

# Summary of the results:

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Name of the method	Number of training images	Number of Validation images	Loss function	Metric	Validation Loss	Validation Accuracy
UNet 2D	150	50	Dice Loss	Dice Coefficient	0.25	0.75
UNet 2D with cropped images	40	10	Dice Loss	Dice Coefficient	0.4	0.6
UNet 3D	180	30	Dice Loss	Dice Coefficient	0.95	0.05

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## Citations:

- <https://www.cse.iitb.ac.in/~shalabhgupta/Report.pdf>
- <https://arxiv.org/pdf/2011.01118.pdf>
- <https://www.jeremyjordan.me/semantic-segmentation/>
- <https://arxiv.org/pdf/1802.10508v1.pdf>

## Link to dataset:

[Click here for the dataset](#)

OR, paste the below link in your browser

[https://drive.google.com/file/d/1gfLZlHaqTDeSKt7zDEIIWJydt\\_eR7uay/view?usp=sharing](https://drive.google.com/file/d/1gfLZlHaqTDeSKt7zDEIIWJydt_eR7uay/view?usp=sharing)

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**THANK YOU FOR YOUR PATIENCE !**