

Name: Bommala Deepak Kumar

Output Images

Here are the label wise segmentation images according to the BraTs dataset, which mainly focuses on tumors

Label	Abbreviation	Full Form	Description
0	NA	Background / Non-tumor	Healthy tissue or non-labeled area
1	NCR	Necrotic Core Region	Dead/necrotic tissue at tumor center
2	ED	Edema	Swelling or inflammation around tumor
3	ET	Enhancing Tumor	Actively growing tumor, contrast-enhanced

There are three main channels here

Channel 0: Tumor Core (TC) = labels 1 (NCR) + 3 (ET)

Channel 1: Whole Tumor (WT) = labels 1 (NCR) + 2 (ED) + 3 (ET)

Channel 2: Enhancing Tumor (ET) = label 3 only

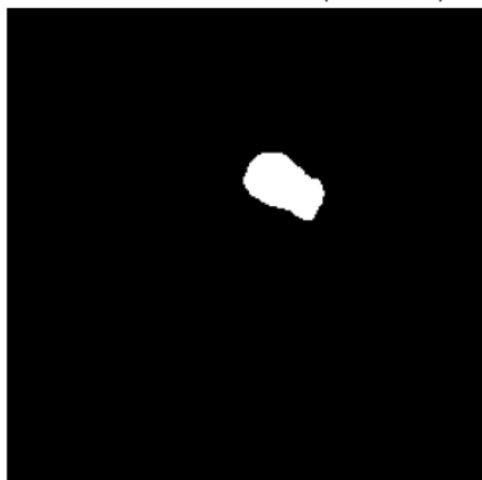
Middle Slice of Raw Label



Middle Slice - Tumor Core (Channel 0)



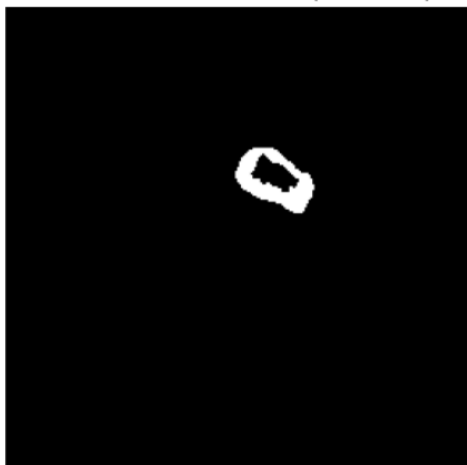
Middle Slice - Tumor Core (Channel 0)



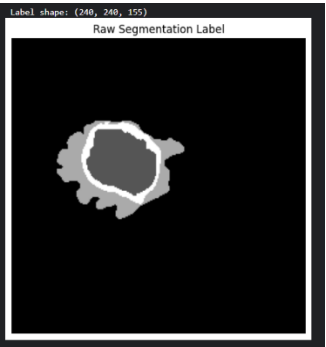
Middle Slice - Tumor Core (Channel 1)



Middle Slice - Tumor Core (Channel 2)



Raw segmentation with labels as per dataset classes

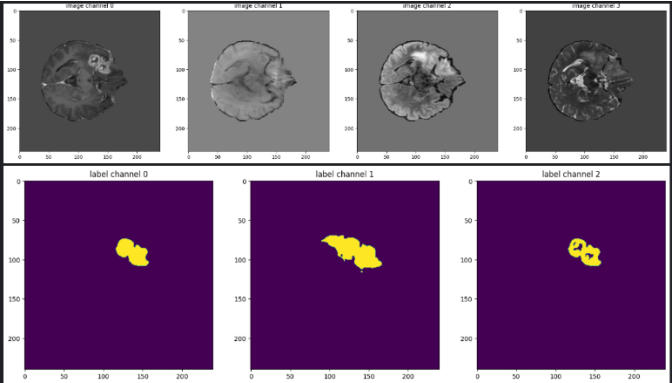
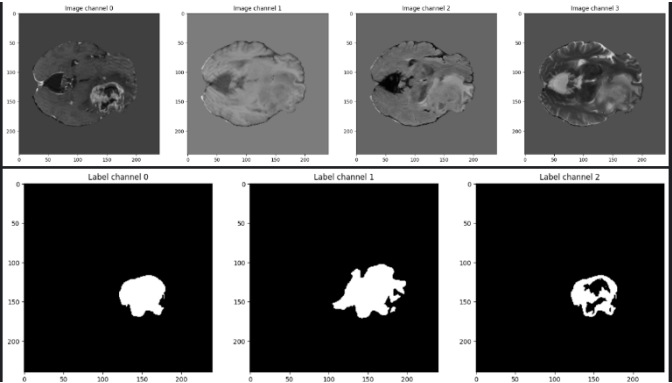


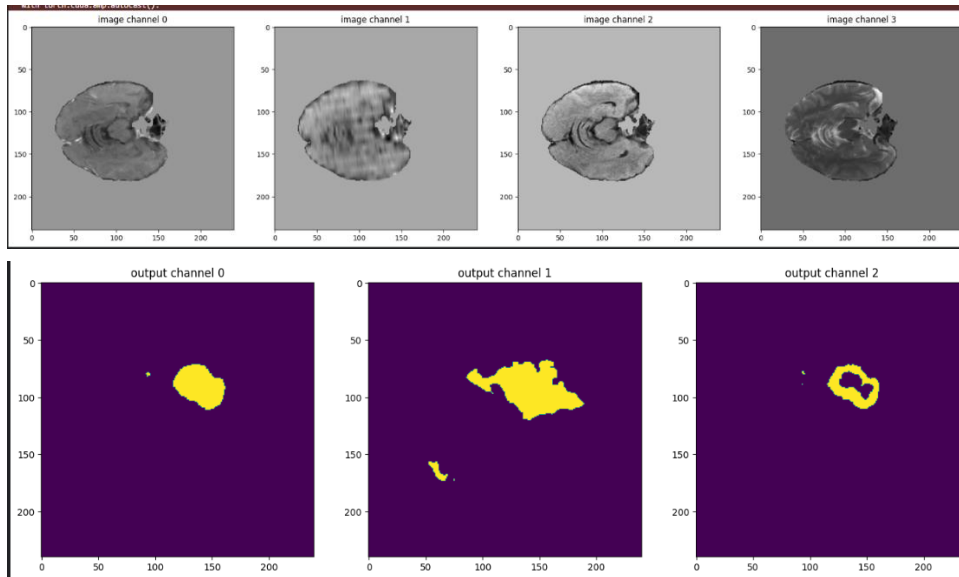
Conversion of labels into



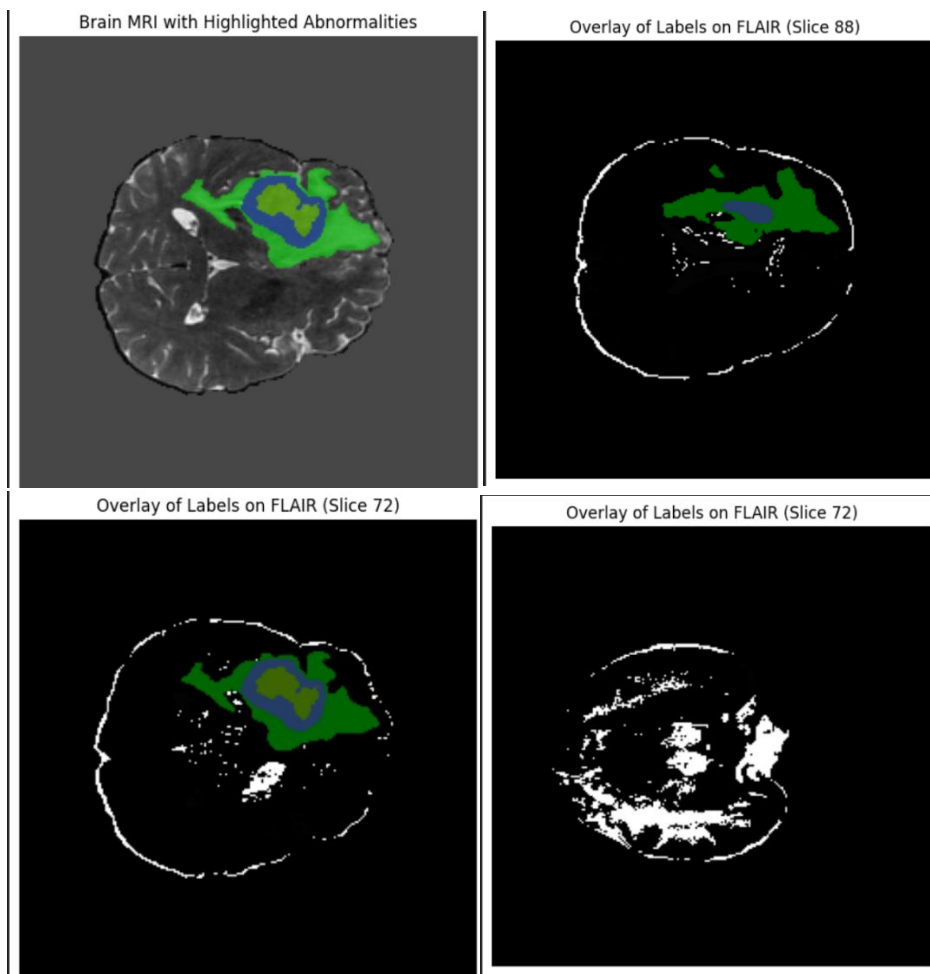
Transformed Label shape: torch.Size([3, 3, 96, 96, 96])
Channel 0 (Tumor Core): tensor([0., 1.])
Channel 1 (Whole Tumor): tensor([0., 1.])
Channel 2 (Enhancing Tumor): tensor([0., 1.])

Image shape: torch.Size([4, 240, 240, 155])
Label shape: torch.Size([3, 240, 240, 155])





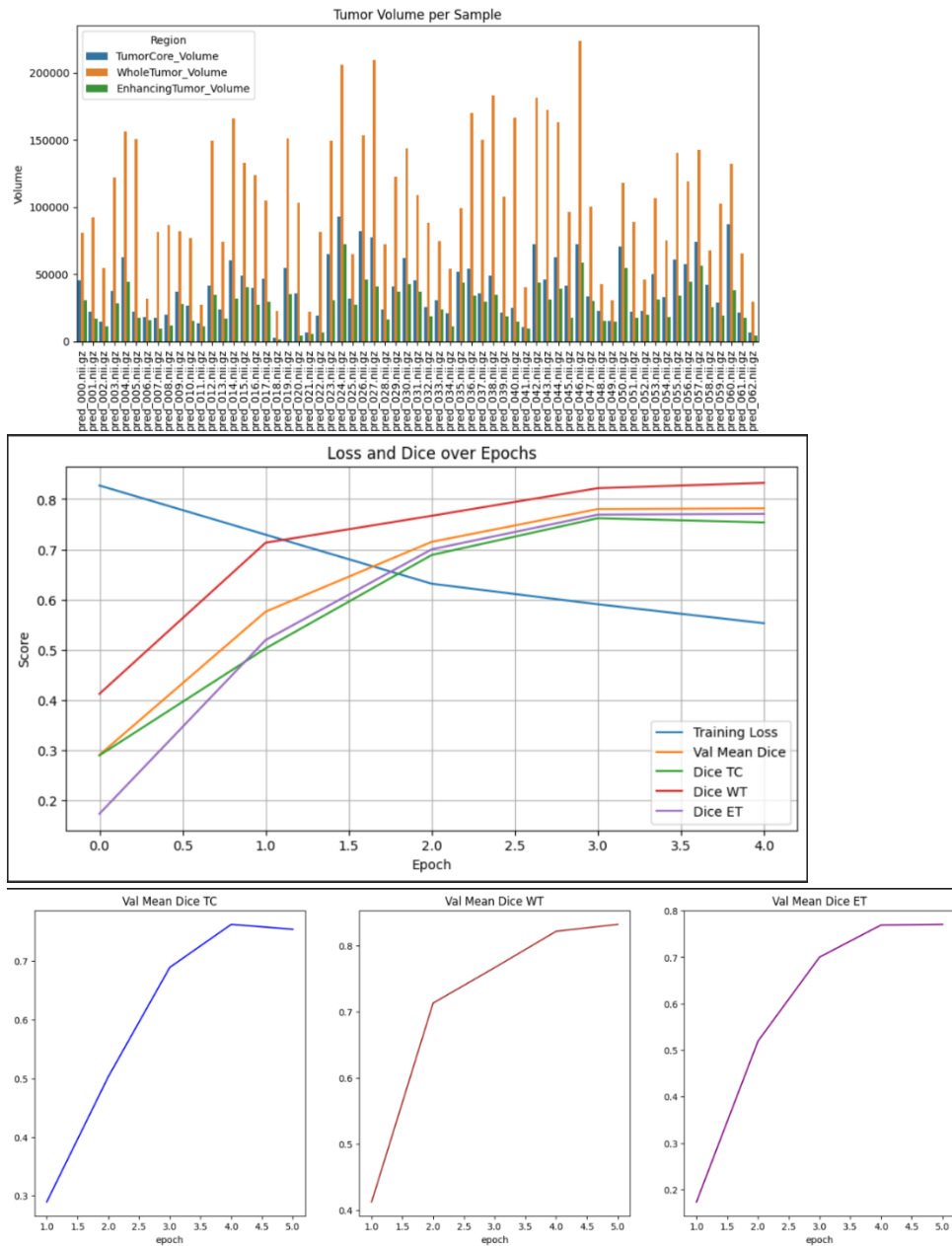
Predicted masks

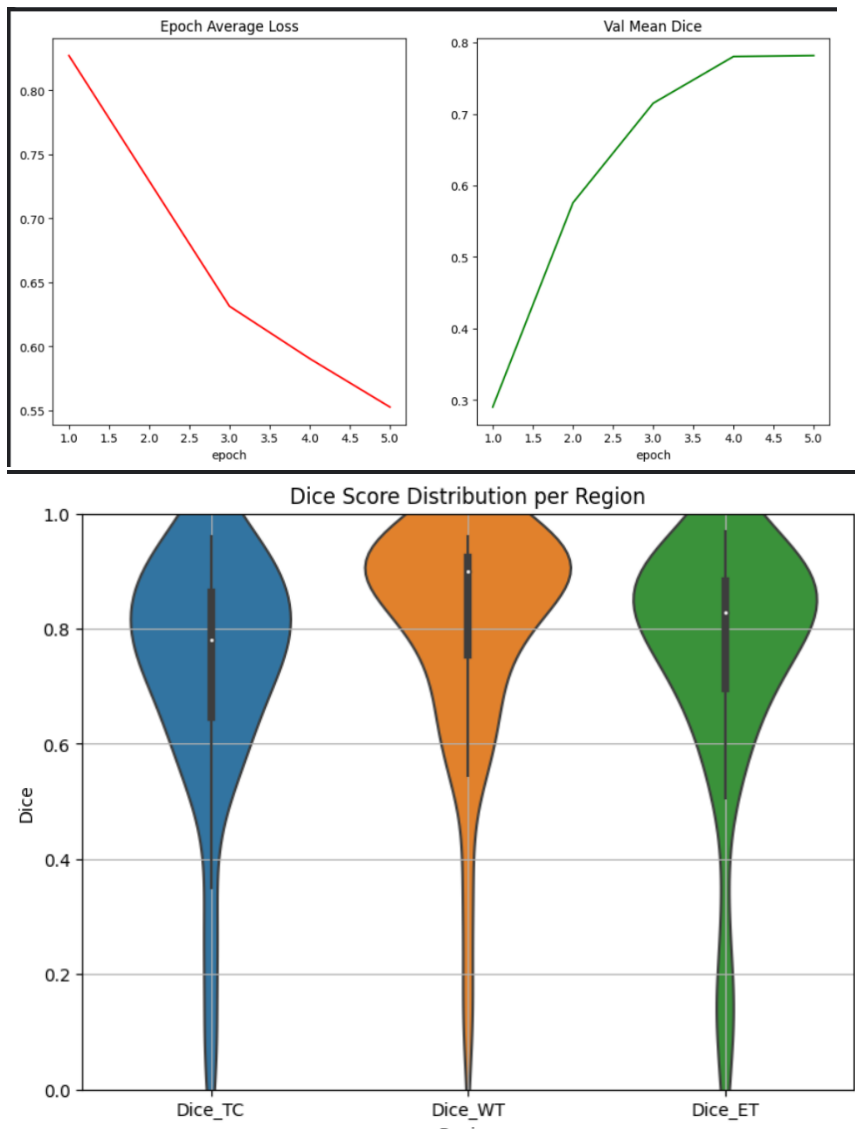


Above images are after training where abnormalities are highlighted with different colors and overlays are shown as segmentation masks

Results

graphs





The first image is the tumor value calculated while doing the predictions, next graphs are the loss, dice score while training the data

Summary

Best Dice Score: 0.7816 at Epoch: 5

Total Training Time: 10371.49 sec

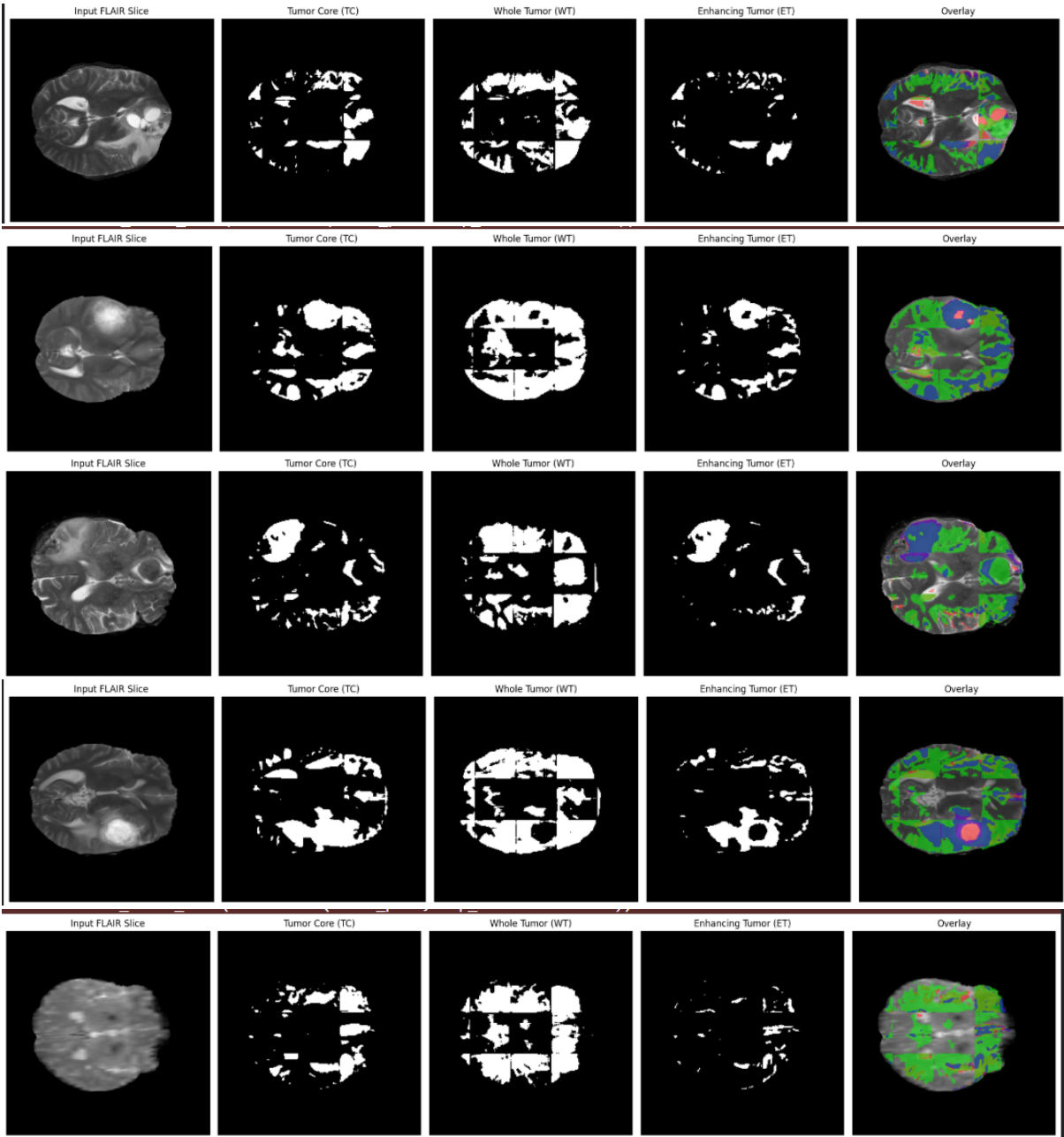
Average Dice Scores Per Class:

Tumor Core (TC): 0.5993

Whole Tumor (WT): 0.7094

Enhancing Tumor (ET): 0.5865

Final Automated results with an MRI data as input and colour graded brain abnormality highlighted as output



The predicted tumor values for 50 predictions

A	B	C	D
Sample	TumorCore_Volume	WholeTumor_Volume	EnhancingTumor_Volume
pred_000.nii.gz	45437	81203	30843
pred_001.nii.gz	22382	92508	17003
pred_002.nii.gz	14942	54903	11397
pred_003.nii.gz	37576	122037	28489
pred_004.nii.gz	62991	156607	44540
pred_005.nii.gz	22133	150826	17896
pred_006.nii.gz	18277	31852	15929
pred_007.nii.gz	Nan	0	Nan
pred_008.nii.gz	20016	86698	11969
pred_009.nii.gz	36820	82027	27851
pred_010.nii.gz	26599	77115	15393
pred_011.nii.gz	13965	27610	11659
pred_012.nii.gz	41896	149517	34833
pred_013.nii.gz	23744	73948	17301
pred_014.nii.gz	60481	166301	31838
pred_015.nii.gz	49298	132958	40745
pred_016.nii.gz	39913	124034	27168
pred_017.nii.gz	46772	105157	29933
pred_018.nii.gz	2835	22766	1581

DICE scores recorded at the time of Inferencing/Prediction

A	B	C	D
Sample	Dice_TC	Dice_WT	Dice_ET
sample_000	0.95778126	0.93379796	0.8775542
sample_001	0.8958127	0.9446344	0.8837947
sample_002	0.8115655	0.81846946	0.88255525
sample_003	0.960001	0.92872727	0.9222021
sample_004	0.79216564	0.9064579	0.8994001
sample_005	0.27421924	0.18813723	0.13350402
sample_006	0.5622667	0.57492065	0.63953334
sample_007	0.75975126	0.7750833	0.82733136
sample_008	0.77965844	0.9433505	0.8764209
sample_009	0.5792088	0.9324844	0.7484186
sample_010	0.92008317	0.9199392	0.8476307
sample_011	0.85111105	0.90111464	0.8046354
sample_012	0.5940302	0.92453885	0.7475891
sample_013	0.6469786	0.78472435	0.5608924
sample_014		0.68359494	
sample_015	0.5689542	0.6612549	0.58887196
sample_016	0.6025687	0.31157902	0.6963851
sample_017	0.9089242	0.822336	0.9302071
sample_018	0.092447884	0.89964324	0.15592356
sample_019	0.9293307	0.95930344	0.9185769

3D representation of Abnormality/ tumor region

