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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

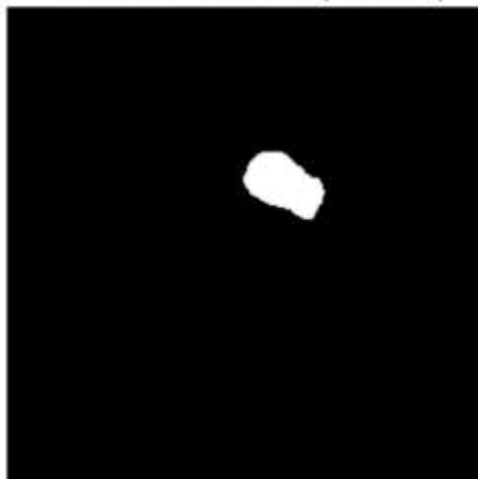
Middle Slice of Raw Label



Middle Slice - Tumor Core (Channel 0)



Middle Slice - Tumor Core (Channel 0)



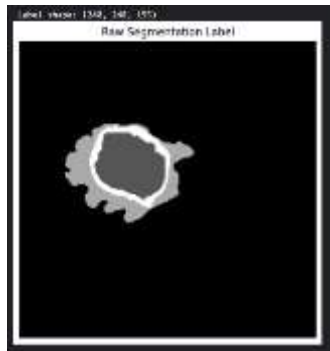
Middle Slice - Tumor Core (Channel 1)



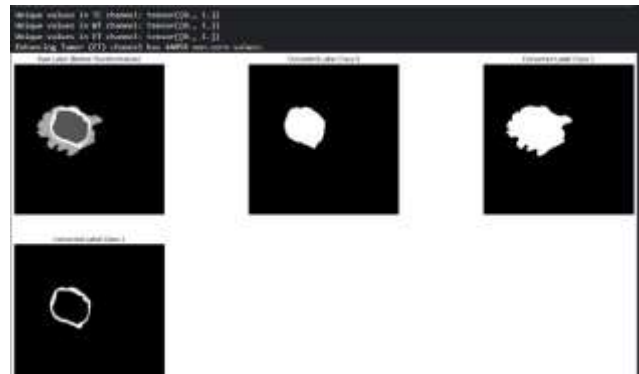
Middle Slice - Tumor Core (Channel 2)



Raw segmentation with labels as per dataset

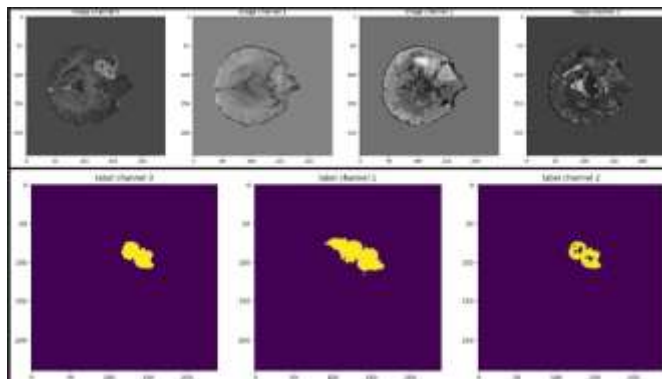
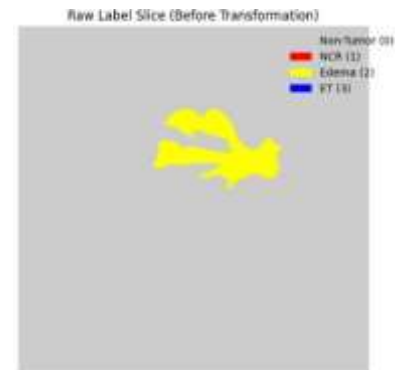
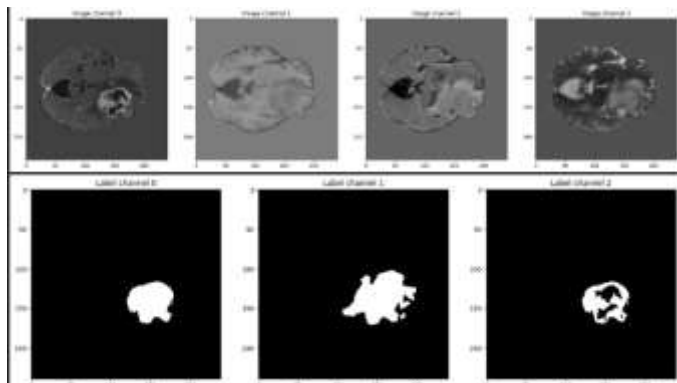


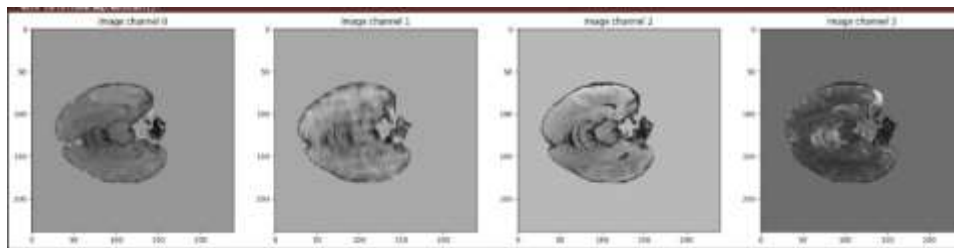
Conversion of labels into



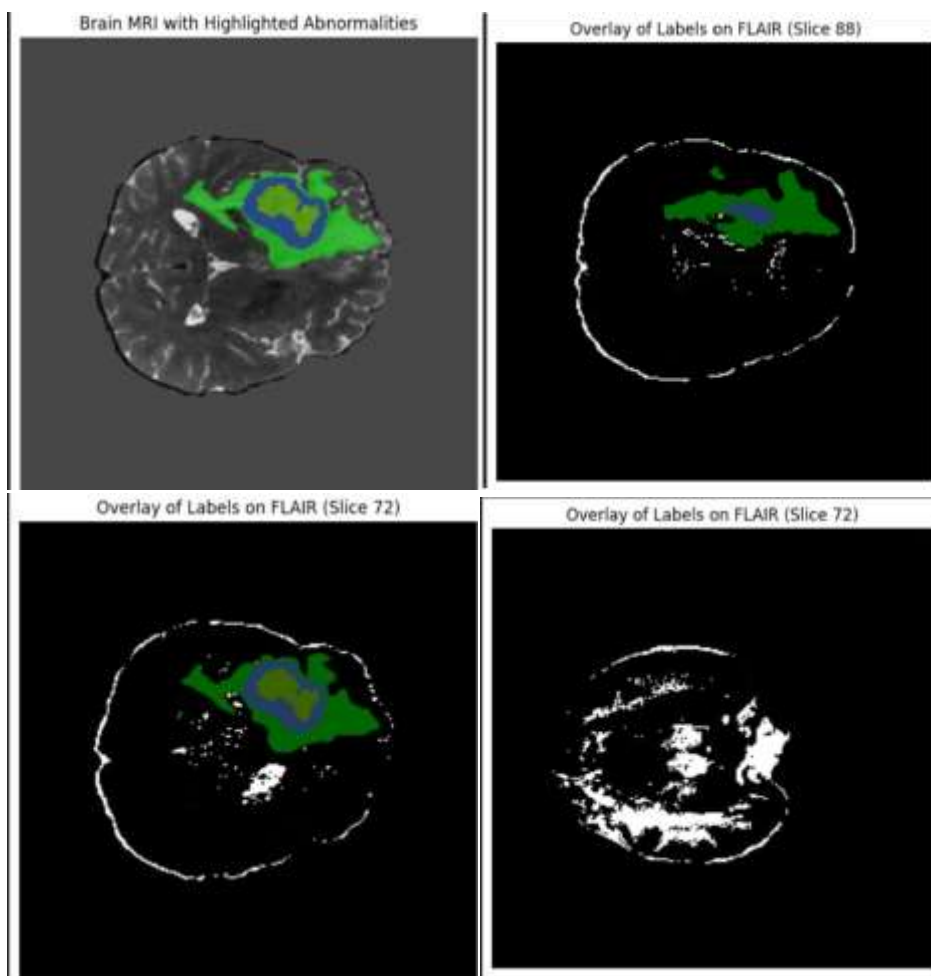
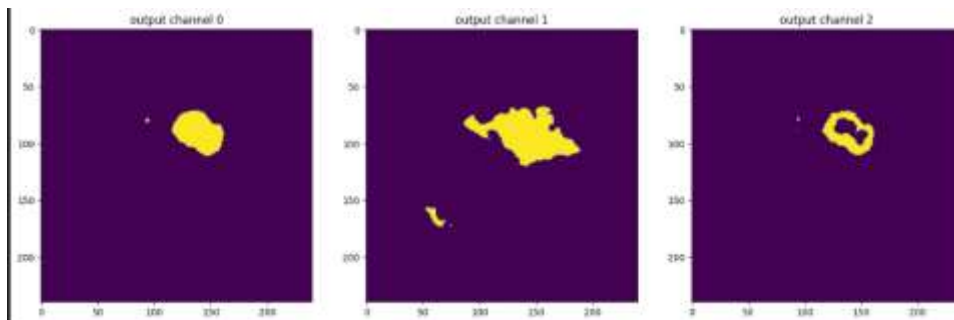
Transformed Label shape: torch.Size([3, 36, 96, 96])
Channel 0 (Tumor Core): tensor([0., 1.])
Channel 1 (Whole Tumor): tensor([0., 1.])
Channel 2 (Enhancing Tumor): tensor([0., 1.])

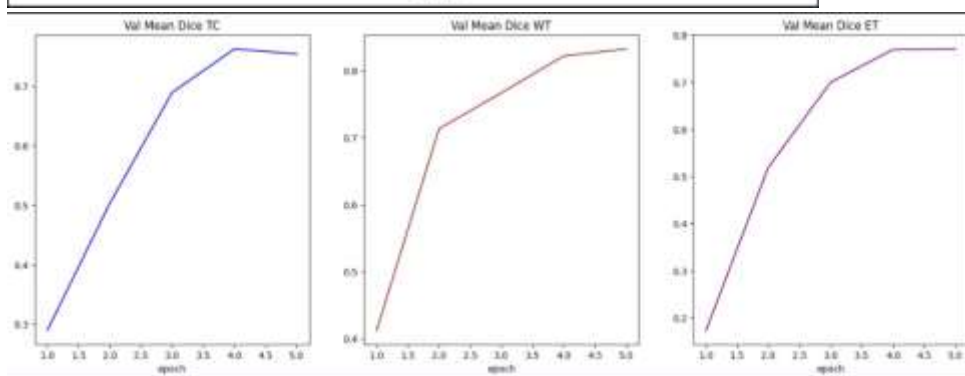
image shape: torch.Size([4, 240, 240, 155])
Label shape: torch.Size([3, 240, 240, 155])

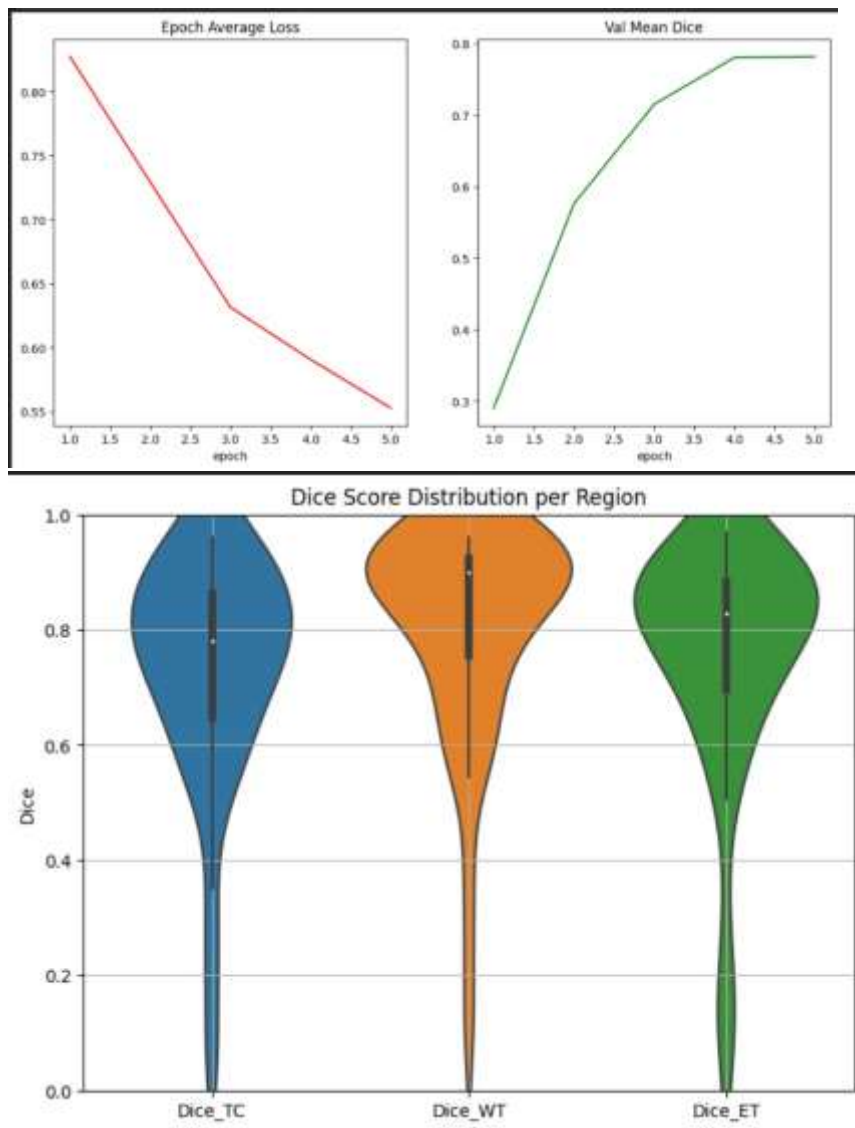




Predicted masks







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

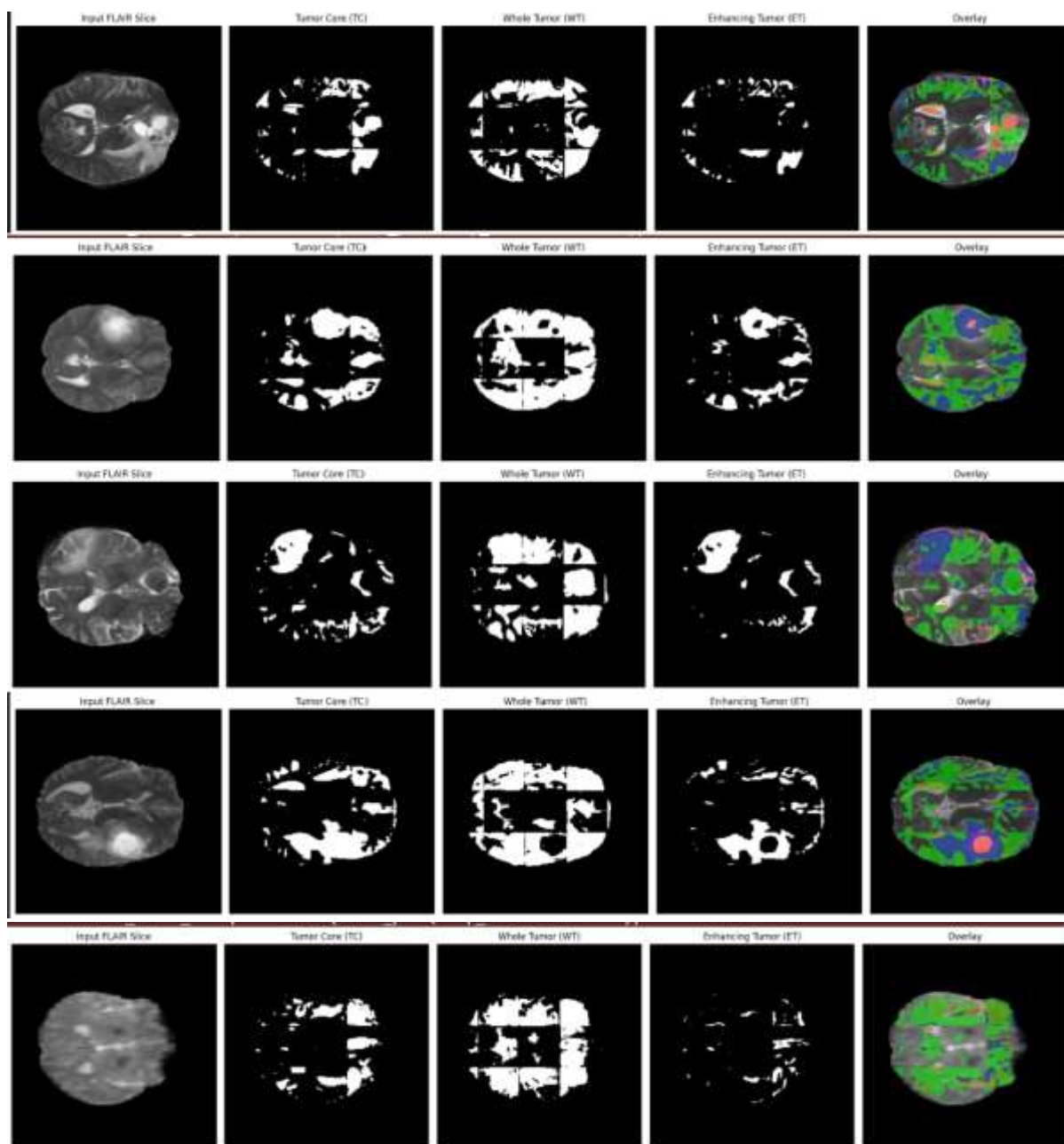
Average Dice Scores Per Class:

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

