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CAP 5516

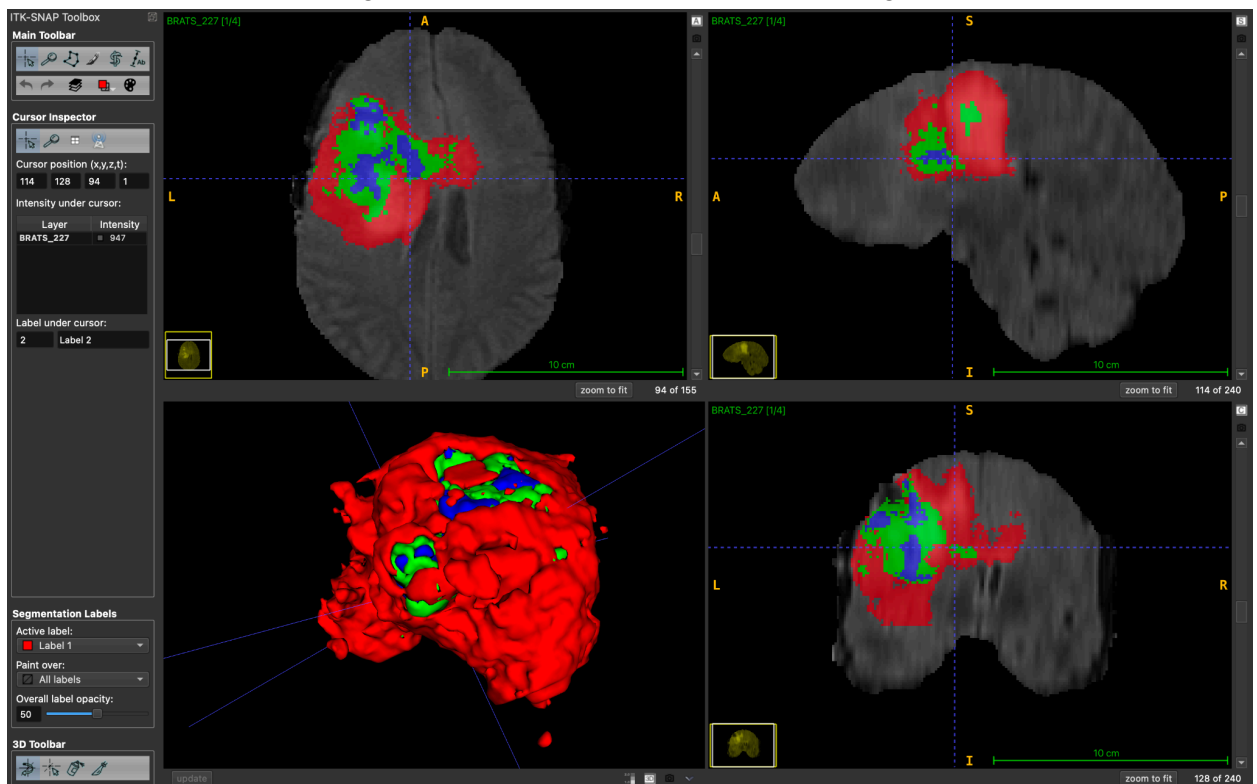
## PA2: Deep Learning-based Brain Tumor Segmentation Using MRI

### Introduction:

Segmentation is important for medical image analysis and the future of medical-AI. This assignment uses the BraTS dataset that includes high-quality MRI scans and their corresponding segmentation masks. U-Net was used to create a deep learning brain tumor segmentation model.

### Tasks:

- 1) Visualization of data and segmentation mask from BRATS\_227 using ITK\_SNAP:



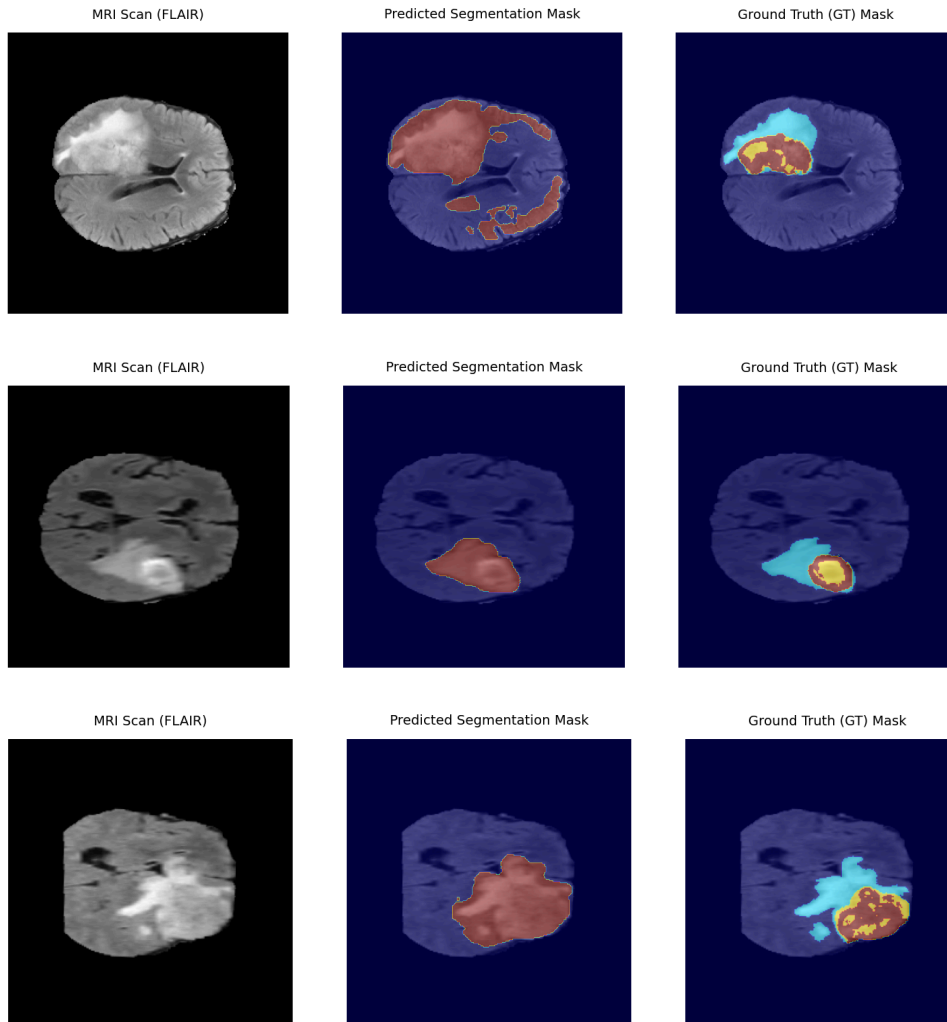
The segmentation mask includes different colors indicating subregions of the tumor. ITK-SNAP uses all the MRI slices and creates a 3D model of the tumor.

- 2) To implement the UNet model I used 3 files:
  - `unet_model.py`: First, I created the UNet model to be used in training and testing for the project. A 2D UNet architecture was implemented with a convolutional block, UNet encoder, and UNet decoder. In the convolutional block, images were preprocessed by normalizing pixel intensities. The encoder downsamples the images using convolution and max pooling and the decoder up samples with skip connections and convolution.

- `Train_unet.py`: Next, the model was trained using a 5-Fold cross-validation. Training was performed on GPU and each fold took approximately 45 minutes. I chose to use Cross Entropy Loss. For each fold, the Dice Score and Hausdorff distance were computed to evaluate the model's performance.
  - `test_unet.py`: Finally, the model will run the trained model on a test MRI scan and predict a segmentation mask. It will visualize the original MRI slice, predicted segmentation mask, and ground truth. It will compute the dice score and Hausdorff distance for this slice.
- 3) I did the 5 fold segmentation; the average dice score and Hausdorff distance suggest that the model is struggling to segment finer details and creating segmentation masks with rough edges. The variability in dice score may be due to differences in tumor intensity, shape or other factors.

Fold	Dice Score	Hausdorff Distance
1	0.5847	35.3651
2	0.6224	37.1108
3	0.6154	29.6093
4	0.6399	33.1249
5	0.5346	41.0441
<b>Average</b>	<b>0.5994</b>	<b>35.2508</b>

4)



As seen in the example images, the model effectively highlights the tumor region correctly, but most errors occur with over-segmenting the tumor area.

If I were to continue with this assignment, I would consider adding data augmentation to the model. This might help the model recognize finer features that it is currently struggling with.