Deep Learning-Based Multi-Compartment Brain Glioma Segmentation:Using U-Net, and Residual U-Net Architectures

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Introduction

Gliomas are among the most common and aggressive brain tumors, posing significant challenges for diagnosis and treatment due to their tendency to invade healthy brain tissue. After treatment, MRI scans play a crucial role in monitoring tumor progression. However, accurately identifying and segmenting the different parts of the tumor in these scans is often difficult because of the tumor's complex and irregular structure.

This project aims to tackle these challenges by focusing on the segmentation of key glioma regions in post-treatment MRI scans, including:

- **Enhancing Tissue (ET):** Active tumor areas that become visible after using a contrast agent.
- **Non-enhancing Tumor Core (NETC):** Necrotic or cystic parts of the tumor.
- **Surrounding Non-enhancing FLAIR Hyperintensity (SNFH):** Areas affected by tumor spread and associated swelling.
- **Resection Cavity (RC):** The space left after surgical removal of the tumor.

I and my team explored and compared deep learning models, such as U-Net and Residual U-Net, to evaluate their effectiveness in segmenting these regions using the BraTS 2024 dataset. By assessing model performance with metrics like the Dice coefficient, our goal is to contribute to the development of automated tools that can assist doctors in better understanding gliomas and planning more effective treatments for patients.

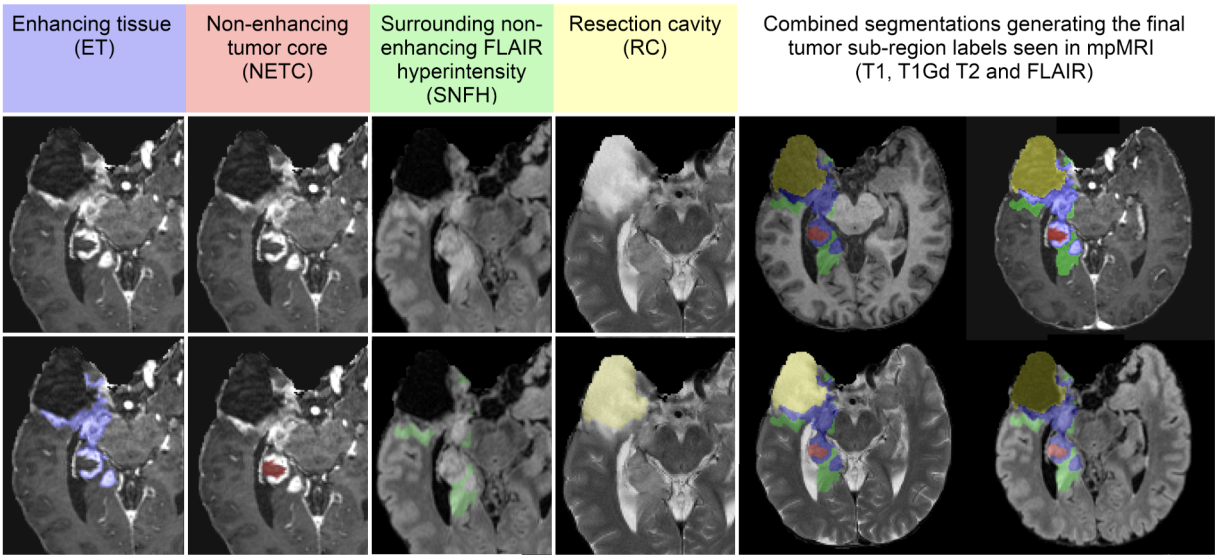


Fig 1.1 Multi-Compartment Glioma Segmentation in Post-Treatment MRI Scans

The image below shows the segmentation of tumor sub-regions in post-treatment MRI scans. Each region is color-coded for clarity: Enhancing Tissue (ET) is highlighted in blue, Non-enhancing Tumor Core (NETC) in red, Surrounding Non-enhancing FLAIR Hyperintensity (SNFH) in green, and Resection Cavity (RC) in yellow. The last column displays the combined segmentation of these regions across various multi-parametric MRI (mpMRI) images, including T1, T1Gd, T2, and FLAIR sequences.

Dataset:

The BraTS 2024 dataset is a collection of post-treatment MRI scans from glioma patients, designed to advance research in brain tumor segmentation. It supports understanding tumor progression and aids treatment planning by segmenting various tumor sub-regions. The dataset includes scans from 1,350 patients, with each case containing four types of MRI scans and segmented images for detailed analysis.

Types of MRI Scans:

- **T1c or T1-Gd (T1-weighted post-contrast):** Highlights Enhancing Tissue (ET), which appears bright, indicating active tumor areas and blood-brain barrier damage.
- **T1w or T1n (T1-weighted or native T1):** Identifies Non-enhancing Tumor Core (NETC), which appears dark and represents necrotic or cystic areas without contrast enhancement.
- **T2w (T2-weighted):** Detects Surrounding Non-enhancing FLAIR Hyperintensity (SNFH), showing bright areas linked to swelling, tumor growth, or treatment effects.
- **T2f (T2-weighted FLAIR):** Similar to T2w, it provides additional contrast to better distinguish tumor features.

Image Specifications:

The MRI scans are stored in NIfTI (.nii) format with the following dimensions:

- **Sagittal plane (182 slices):** Side view of the brain.
- **Coronal plane (216 slices):** Front view of the brain.
- **Axial plane (182 slices):** Top-down view of the brain.

Tissue Classification:

- **Enhancing Tissue (ET):** Bright on T1-Gd scans, representing active tumor regions.
- **Non-enhancing Tumor Core (NETC):** Dark on T1 and T1-Gd scans but brighter on T1w, indicating necrotic or cystic areas.
- **Surrounding Non-enhancing FLAIR Hyperintensity (SNFH):** Bright on T2 and T2f scans, showing swelling, tumor spread, or treatment effects.
- **Resection Cavity (RC):** Varies in appearance depending on its age; older cavities resemble cerebrospinal fluid, while newer ones may show air, blood, or proteins.

Data Preparation for Training:

To streamline the workflow, we organized the data into a structured directory and used a fixed random seed for reproducibility. The dataset was split into:

- **Training Set (80%)**
- **Validation Set (20%)**

For training, we created two primary folders:

- **train_images:** Contains image files (T1c, T1n, T2f, T2w) for each patient.
- **masks:** Holds the corresponding segmentation files.

A similar structure was set up for validation data with **val_images** and **val_masks**. A preprocessing pipeline was developed to process each patient's directory, verifying the presence of all required files before organizing them into the appropriate folders. This setup ensures the data is clean, accessible, and ready for training U-Net and Residual U-Net models, simplifying the loading process during both training and validation phases.

Preprocessing Techniques

I applied these preprocessing steps:

1. **Data Stacking:** Since MRI data is 3D, we combined all four types of scans (T1c, T1n, T2w, T2f) for each patient into a single dataset. This helped the model better understand spatial relationships and improved its ability to identify tumor-related features.
2. **Z-Score Normalization:** To standardize the pixel intensity values, we adjusted them so the mean was zero and the standard deviation was one. This step made the model training more stable and reduced sensitivity to input variations.
3. **Image Resizing:** The MRI images were resized to dimensions (132, 132, 116) to lower computational requirements while keeping important details intact. This made data processing more efficient without losing critical information for analysis.

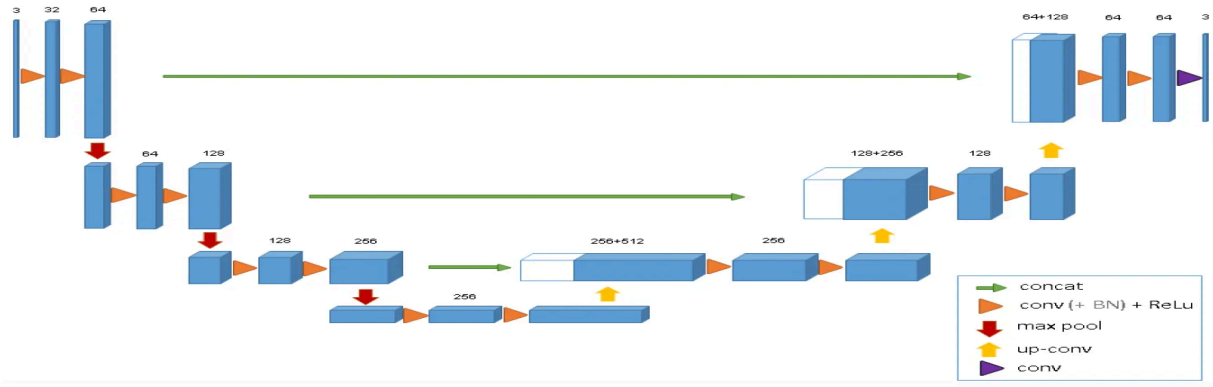
Model Architecture

U-Net (3D):

This is the base model we have used.The U-Net architecture is specifically built for medical image segmentation, like glioma segmentation. It uses an encoder-decoder structure with skip connections to keep important spatial details for accurate localization. Here's an overview of the 3D U-Net model used in this project:

Model Structure:

- **Encoder:** This part extracts features using convolutional layers and reduces the image size through max pooling, focusing on important details while increasing feature complexity.
- **Bottleneck:** The central layer where the model learns the most abstract and detailed features.
- **Decoder(Expansive Path):** Upsamples the feature maps using transposed convolutions and combines them with features from the encoder using skip connections to restore spatial resolution.
- **Final Output Layer:** A 1x1 convolution layer that generates segmentation maps for different tumor sub-regions.



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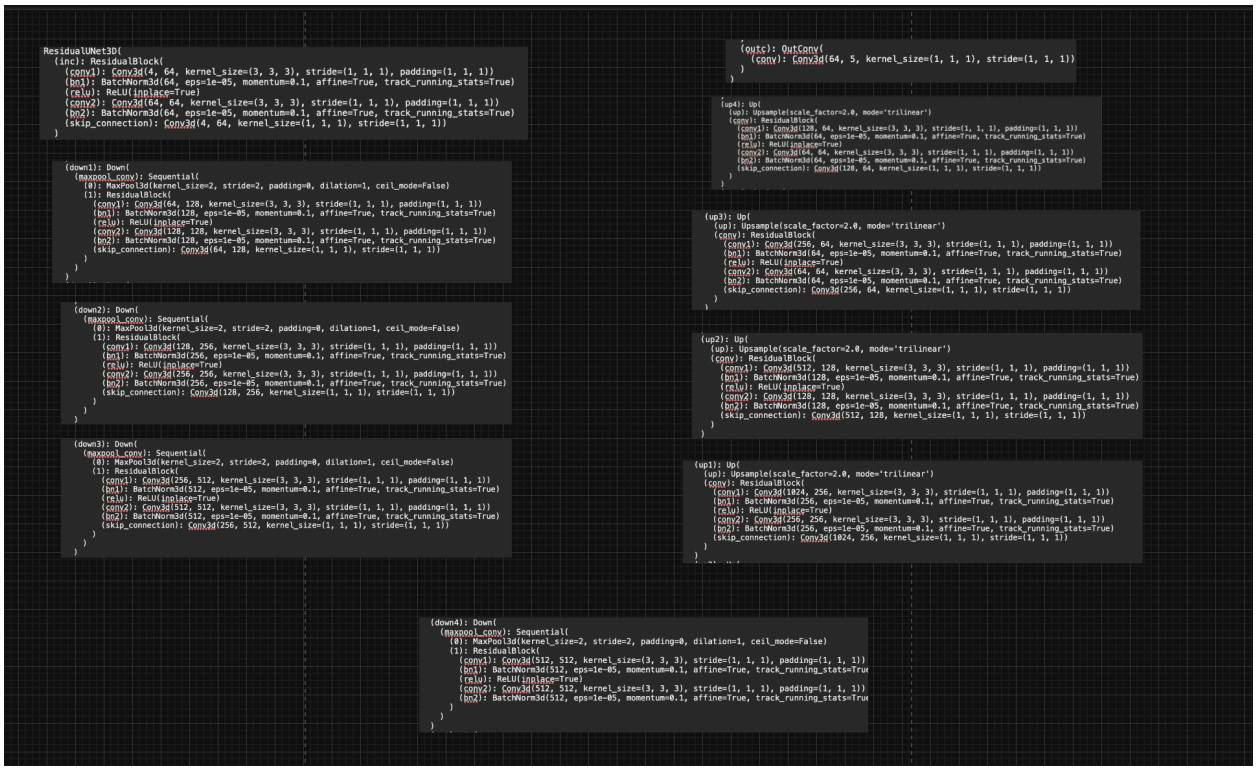
Residual 3D U-Net summary Architecture



In our project, I created a 3D Residual U-Net designed for segmenting volumetric images. For the Residual U-Net model, we improved the traditional U-Net by adding residual connections, making it better at learning features and handling gradients. Here's how it works:

Key Enhancements:

1. **Residual Blocks:**

- Instead of regular convolutional blocks, we used residual blocks. Each block has two 3D convolutional layers, batch normalization, and ReLU activation.
- We added a skip connection within each block to directly pass the input or use a 1x1 convolution to match dimensions if needed. This prevents vanishing gradient problems and helps the network learn both basic and complex patterns more effectively.

2. **Network Architecture:**

    - **Encoder (Downsampling):** Reduces image size using max pooling, followed by a residual block to capture important features.
    - **Decoder (Upsampling):** Increases image size with upsampling layers and combines features from the encoder using skip connections, followed by a residual block.
    - **Final Layer:** A 1x1x1 convolution maps the features to the desired output classes.

3. **Input and Output:**

    - The model takes 4 input channels (different MRI scans) and outputs 5 classes (background and tumor subregions).

The residual connections improve gradient flow during training, making it easier to train deeper networks. This allows the model to capture both simple and complex features, which is essential for accurately segmenting intricate structures like brain tumors. By addressing some of the limitations of the original U-Net, this enhanced Residual U-Net is more reliable and effective for our brain tumor segmentation task.

Loss and Dice Plots:

CrossEntropyLoss

We used CrossEntropyLoss for our segmentation task.

$$\text{Loss} = -\sum_{c=1}^{C} y_c \cdot \log(\hat{y}_c)$$

C: Total number of classes

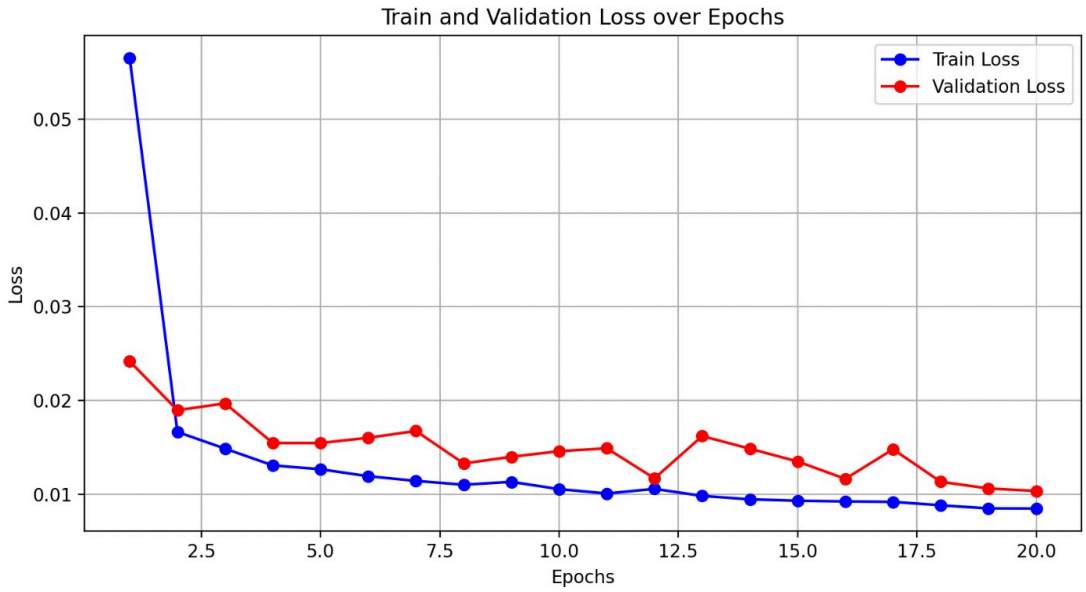
y_c: Ground truth label

$\hat{y}_c$: Predicted probability

I used CrossEntropyLoss as the loss function for training the 3D U-Net model. This loss measures the difference between the predicted probabilities and the true class labels, making it ideal for multi-class segmentation tasks such as brain tumor segmentation.

Train and Validation Loss:

1. The blue line shows the training loss, which gradually decreases over the epochs.
2. The red line represents the validation loss, which also decreases overall but has some ups and downs in the middle, which is normal during training.
3. Both losses appear to converge towards the lower end, indicating good model performance and generalization.



Dice coefficient:

For our segmentation task we implemented the Dice coefficient as a performance metric. The Dice coefficient measures the overlap between the predicted segmentation and the ground truth, providing a value between 0 and 1, where 1 indicates perfect overlap.

Our Dice coefficient formula is calculated as follows:

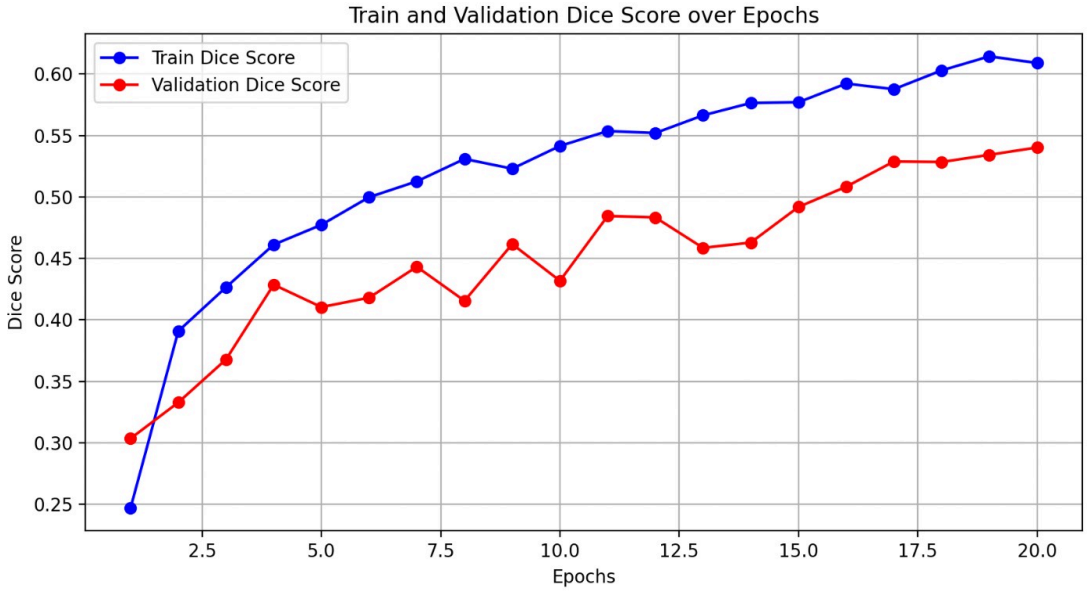
$$\text{Dice} = \frac{1}{C-1} \sum_{c=1}^{C-1} \frac{2|\text{Pred}_c \cap \text{Target}_c|}{|\text{Pred}_c| + |\text{Target}_c| + \epsilon}$$

- C is the number of classes
- Pred_c is the predicted segmentation for class c
- Target_c is the ground truth segmentation for class c
- ε is a small constant (1e-6) added for numerical stability

We calculate the Dice coefficient for each class separately (excluding the background class) and then average the results.

Train and Validation Dice Score:

- The blue curve (train Dice score) steadily increases, indicating improving performance on the training set.
- The red curve (validation Dice score) also increases but with more fluctuation compared to the training score. This suggests that while the model is improving, some adjustments or regularization might be needed to stabilize the validation performance.



Validation Results Summary-3d residual Unet:

metric	value
Validation Loss	0.0104
Dice Scores	
Enhancing Tumor (ET)	0.325
Non-enhancing Tumor Core (NETC)	0.422
Surrounding Non-enhancing FLAIR Hyperintensity (SNFH)	0.797
Resection Cavity (RC)	0.61

The validation loss was 0.0104, indicating a low overall error in predictions. The Dice scores for individual tumor regions showed that the model performed well in segmenting

the surrounding non-enhancing FLAIR hyperintensity with a score of 0.797 and the resection cavity with a score of 0.61. The non-enhancing tumor core achieved a score of 0.422, while the enhancing tumor had a lower score of 0.325. These results show that the model is effective in segmenting certain tumor regions compared with U net.

Model Performance Visualization:

The following images display an example of model performance for segmentation:

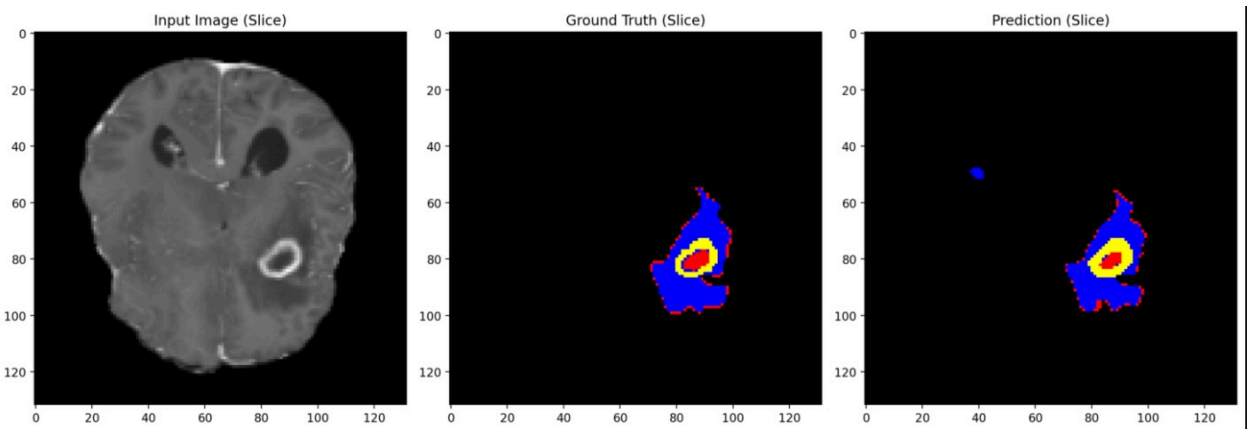
- **Input Image**: The original MRI scan of the brain.
- **Ground Truth**: The manually annotated segmentation for the tumor sub-regions, including **Enhancing Tumor (blue)**, **Necrotic/Core (red)**, **Edema (Green)**, and **Resection Cavity (Yellow)**.
- **Prediction**: The segmentation predicted by the model.

Example 1: Tumor Segmentation

- **Ground Truth and Prediction Comparison**:

  This image shows a **slice of the MRI input**, with the corresponding **ground truth** (middle) and **predicted segmentation** (right).

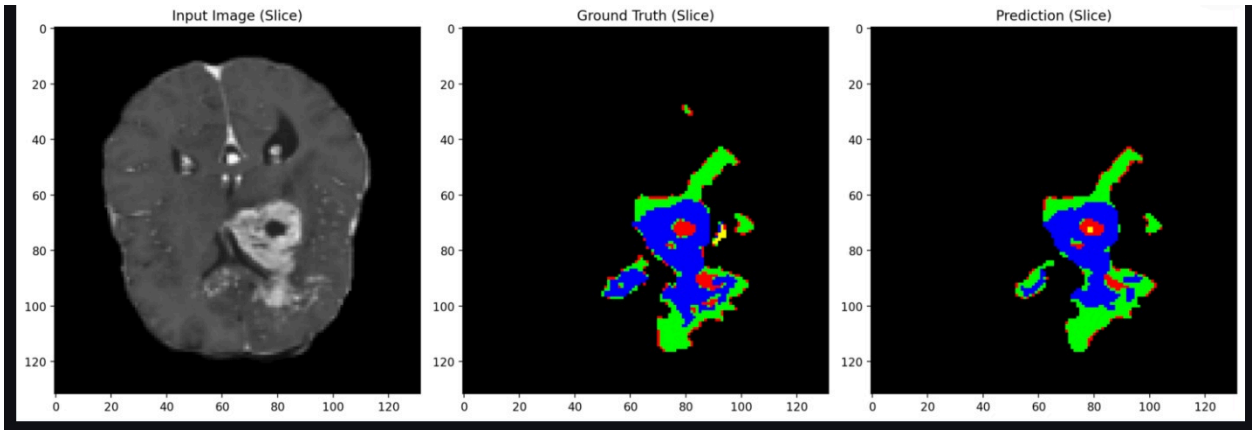
  The **model successfully predicts the Enhancing Tumor (blue)**and **Resection Cavity (Yellow)** ,**Necrotic/Core (Red)**sub-regions, which appear almost clear.



Example 2: Tumor Segmentation

Ground Truth and Prediction Comparison:

- This image shows a **slice of the MRI input**, with the corresponding **ground truth** (middle) and **predicted segmentation** (right).
- The **model successfully predicts the almost Enhancing Tumor (blue)**and edema (green) ,sub-regions, which appear almost clear. There is partial prediction **Necrotic/Core (Red),Resection Cavity (Yellow)** .



Summary and conclusion:

In this project,I implemented the 3D Residual U-Net model and I and my team prepared the BraTS 2024 dataset for training and validation by formatting the data into structured directories. This involved separating MRI modalities (T1c, T1n, T2w, and T2f) and corresponding segmentation masks into folders for training (`train_images` and `masks`) and validation (`val_images` and `val_masks`). This organization ensured seamless integration of the dataset into the model training pipeline and made the data easily accessible for processing and evaluation.

I implemented the 3D Residual U-Net model, which enhances the traditional U-Net architecture by incorporating residual blocks to improve gradient flow and feature learning. The model was designed with 4 input channels (for different MRI modalities) and 5 output classes (background and tumor subregions). It used a series of

downsampling and upsampling layers, with skip connections to retain spatial resolution. Residual blocks consisted of 3D convolutions, batch normalization, and ReLU activations, along with identity mapping to enhance performance. I trained the model for 20 epochs using a batch size of 2 and Adam optimizer with a learning rate of 0.0001.

The post-training analysis of the 3D Residual U-Net model showed promising results, with a validation loss of 0.0104. The Dice scores for different tumor regions were 0.325 for Enhancing Tumor (ET), 0.422 for Non-enhancing Tumor Core (NETC), 0.797 for Surrounding Non-enhancing FLAIR Hyperintensity (SNFH), and 0.61 for Resection Cavity (RC). The model performed especially well in segmenting SNFH and RC regions, which are important for understanding tumor progression and treatment effects. While there is room for improvement in segmenting ET and NETC, the overall results show that the model is effective at handling the complexity of brain tumor segmentation.

Percentage of code used from other sources:

I used 60% of my own code and relied on chat gpt for 40% to get ideas and optimize the code. I did not use any other resources apart from chat gpt.

References :

- https://arxiv.org/pdf/1606.06650
- https://ieeexplore.ieee.org/stamp/stamp.jsp?tp=&arnumber=10635180&tag=1
- https://www.sciencedirect.com/science/article/pii/S1361841524002056