

BrainScan
- AI -

BrainScan AI

Brain Tumor Segmentation

*Done by: Ahmad AbuDyak, Moayad Rabaa,
Mohammad Ali, Abdullah Abdelhamid*

Supervisors:
Dr. Tamam Al-Sarhan - Dr. Ali Al-Rodan

What is brain tumor?

A brain tumor is an abnormal and uncontrolled growth of cells in the brain that potentially causes various neurological symptoms and health issues.

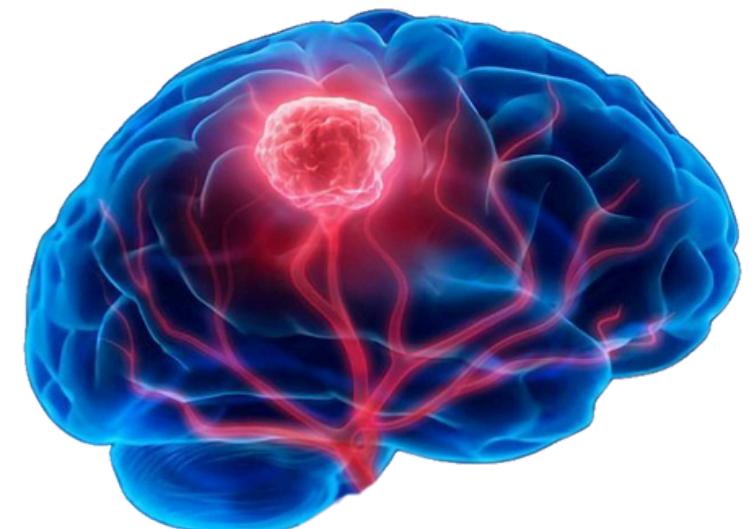
Brain tumors can be either benign (non-cancerous) or malignant (cancerous)

Primary brain tumors originate in the brain, while secondary tumors metastasize from other organs.

Common primary brain tumors include gliomas, which are classified into low-grade (LGG) and high-grade (HGG) subtypes.

Early detection is crucial for proper treatment.

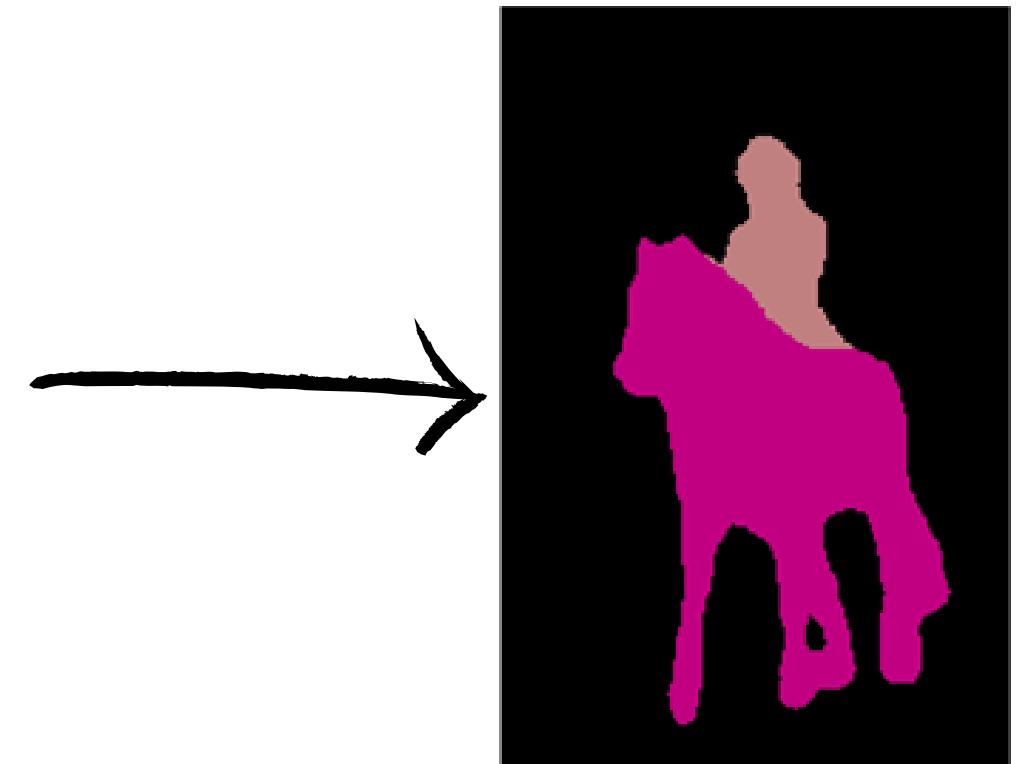
MRI is essential for brain tumor monitoring and surgical planning.



What is Segmentation?

Segmentation in deep learning refers to the process of partitioning an image into multiple segments, or regions, to simplify or change the representation of the image into something more meaningful and easier to analyze.

This is a crucial task in various computer vision applications, such as medical imaging, autonomous driving, and object recognition.

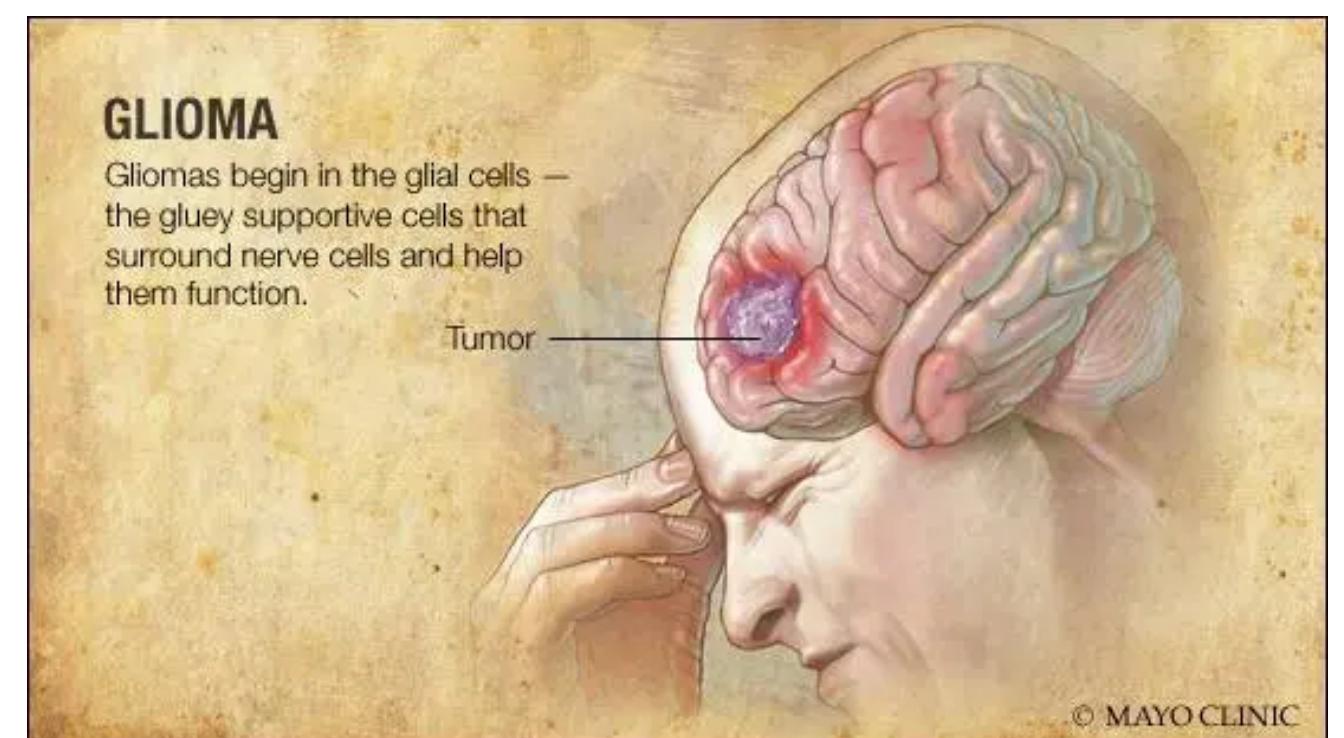


Brain Tumor Segmentation

Brain Tumor Segmentation involves the partitioning of brain MRI scans into different regions to identify and classify tumor tissues.

Glioma:

- A type of tumor that arises from glial cells in the brain.
- One of the most common and aggressive types of primary brain tumors.
- Comprises about 30% of all brain tumors and 80% of malignant brain tumors.
- Segmentation of gliomas is crucial for accurate diagnosis, treatment planning, and monitoring.



GLIOIMA

Gliomas begin in the glial cells — the gluey supportive cells that surround nerve cells and help them function.

Tumor

AI and Our Solution

The use of AI in healthcare has become a necessity.

Our work focuses on deep learning for effective and accurate brain tumor segmentation.

Existing Systems:

- CNN-based methods like U-Net struggle with long-range dependencies and global context.
- Enhancements such as dense skip connections increase model complexity and computational demands.

Our Solution: Swin-Unet:

- Integrates strengths of both CNNs and Transformers.
- Swin Transformer-based encoder captures long-range dependencies and fine details.
- CNN-based decoder ensures computational efficiency and effective reconstruction of high-resolution segmentation maps.
- Skip connections help preserve detailed spatial information.

Methodology

Model Architecture

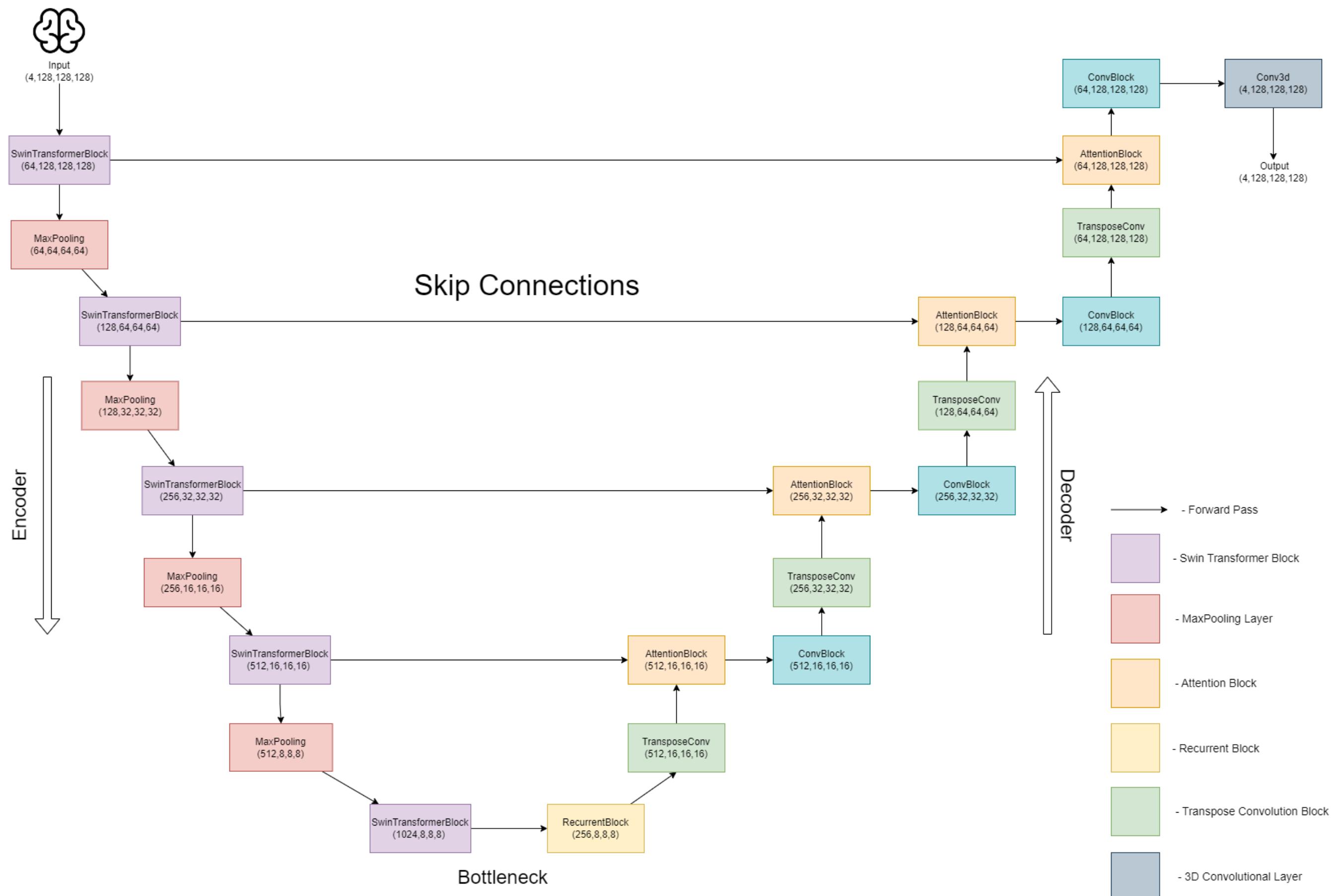
Input: Multimodal MRI image with 4 channels ($T1$, $T1c$, $T2$, $FLAIR$).

Encoder: Swin Transformer blocks with MaxPooling layers for down-sampling.

Recurrent Block: Enhances temporal dependency handling.

Decoder: Employs transposed convolutions and attention blocks to refine features.

Skip Connections: Ensure detailed spatial information is preserved.



Methodology

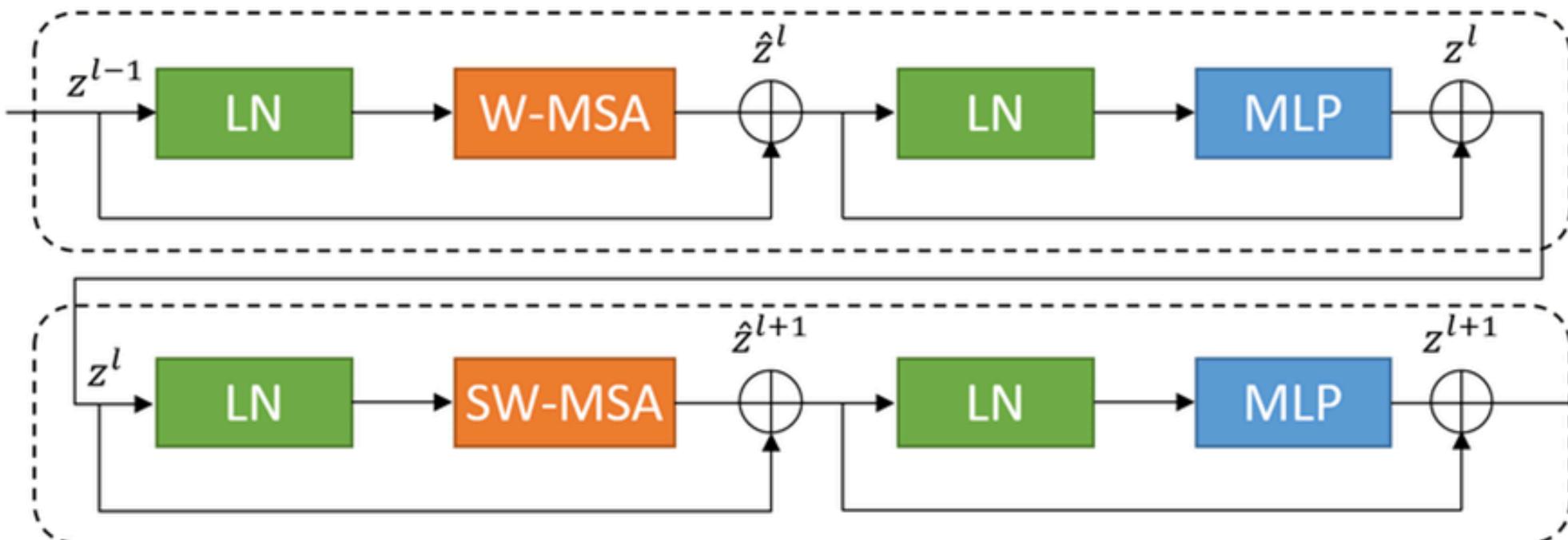
Swin Transformer block

Shifted Window Partitioning:

Efficiently captures both local and global features by alternating between W-MSA and SW-MSA.

Components:

- **LayerNorm (LN):** Normalizes input features.
- **Multi-head Self Attention (MSA):** Captures dependencies across different parts of the image.
- **Residual Connection:** Ensures gradient flow and stabilizes training.
- **2-layer MLP with GELU Non-linearity:** Enhances learning capability.



Dataset

BraTS 2023 Dataset

Description: Multimodal MRI scans

File Extension: NIfTI files (.nii.gz)

Image Size: 240x240x155 Voxels

Number of Samples: 1251

Training Set: 80% Training, 10% Validation, 10% Testing

Image Modalities: T1, T1c, T2, FLAIR

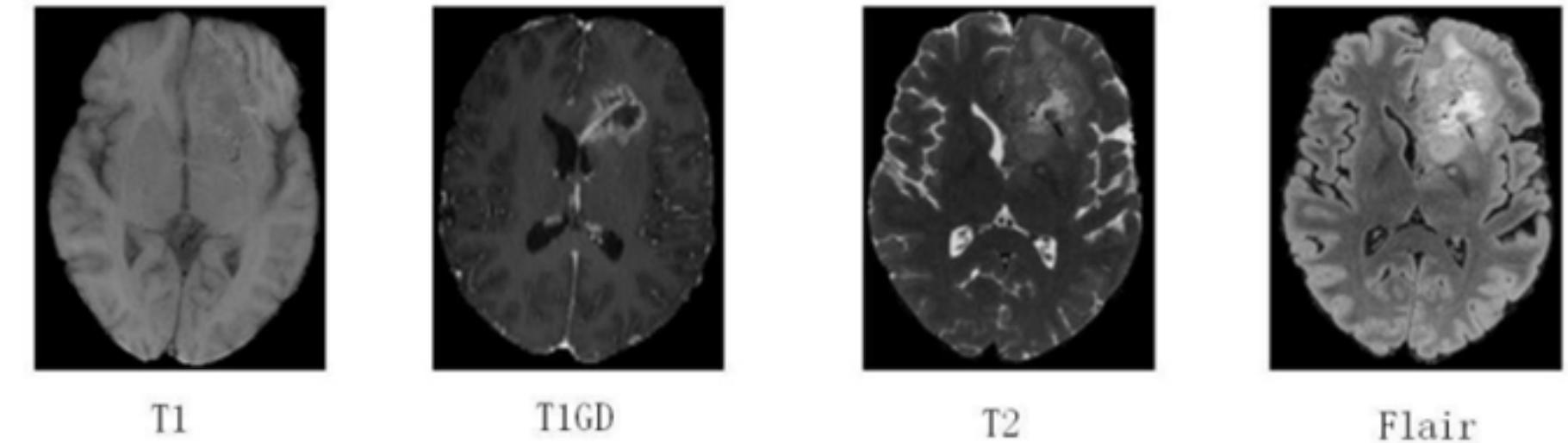
Labels: Necrotic/non-enhancing tumors, peritumoral edema, enhancing tumors



Dataset

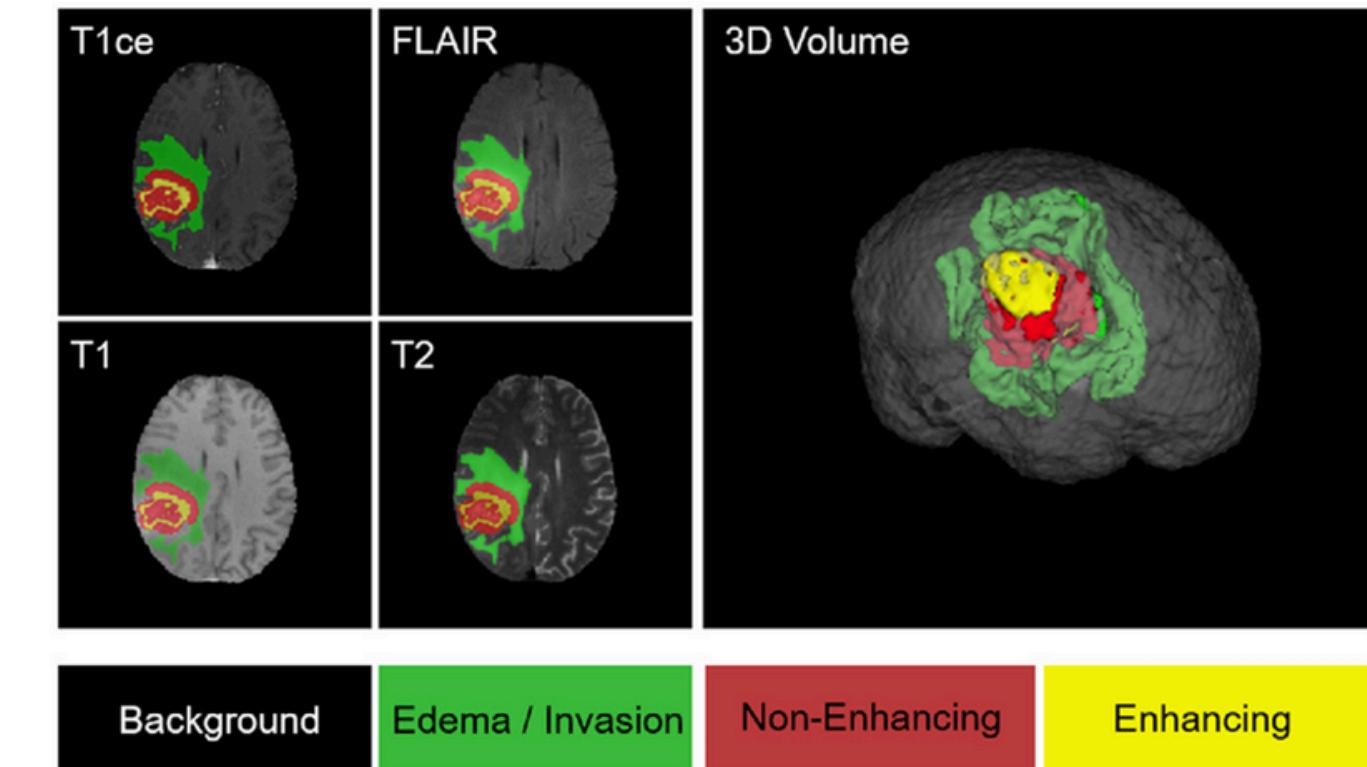
Image Modalities (4 Channels):

- Weighted ($T1$)
- Post-contrast $T1$ -Weighted ($T1c$)
- $T2$ -Weighted ($T2$)
- $T2$ Fluid Attenuated Inversion Recovery ($T2$ -FLAIR)



Original Labels: 4

- Background – Label 0
- NCR/NET – label 1: Necrotic and Non-enhancing tumor core
- ED – label 2: Peritumoral Edema
- ET – label 4: Enhancing tumor



Data Preprocessing

Normalization: Min-Max normalization to scale the input images consistently.

Cropping: From size (240x240x155) to (128x128x128) to reduce volume and speed up training.

Conversion: Converting preprocessed data to ".npy" format for efficient loading during training and testing.

Implementation Details

Framework: PyTorch.

Hardware: NVIDIA Tesla T4 GPU.

Optimizer: Adam with a learning rate of 0.00005.

Batch Size: 1.

Training Epochs: 150.

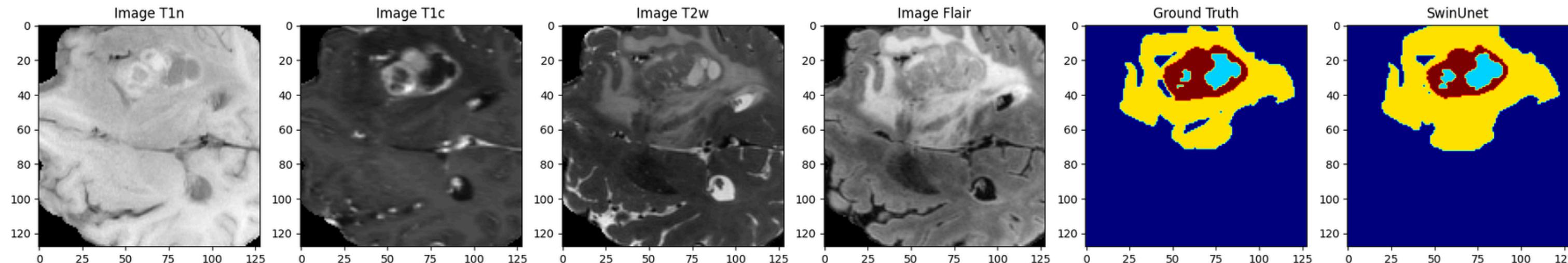
Results

Swin-Unet shows superior performance with Dice scores of 0.807 (ET), 0.839 (TC), and 0.864 (WT). Comparison with other models like U-Net and ReFuSeg.

Models	Dice			
	ET	TC	WT	Avg.
Optimized U-Net	0.752	0.774	0.825	0.783
ReFuSeg	0.786	0.832	0.910	0.842
Our U-net	0.718	0.743	0.775	0.745
Our Swin-Unet	0.807	0.839	0.864	0.836

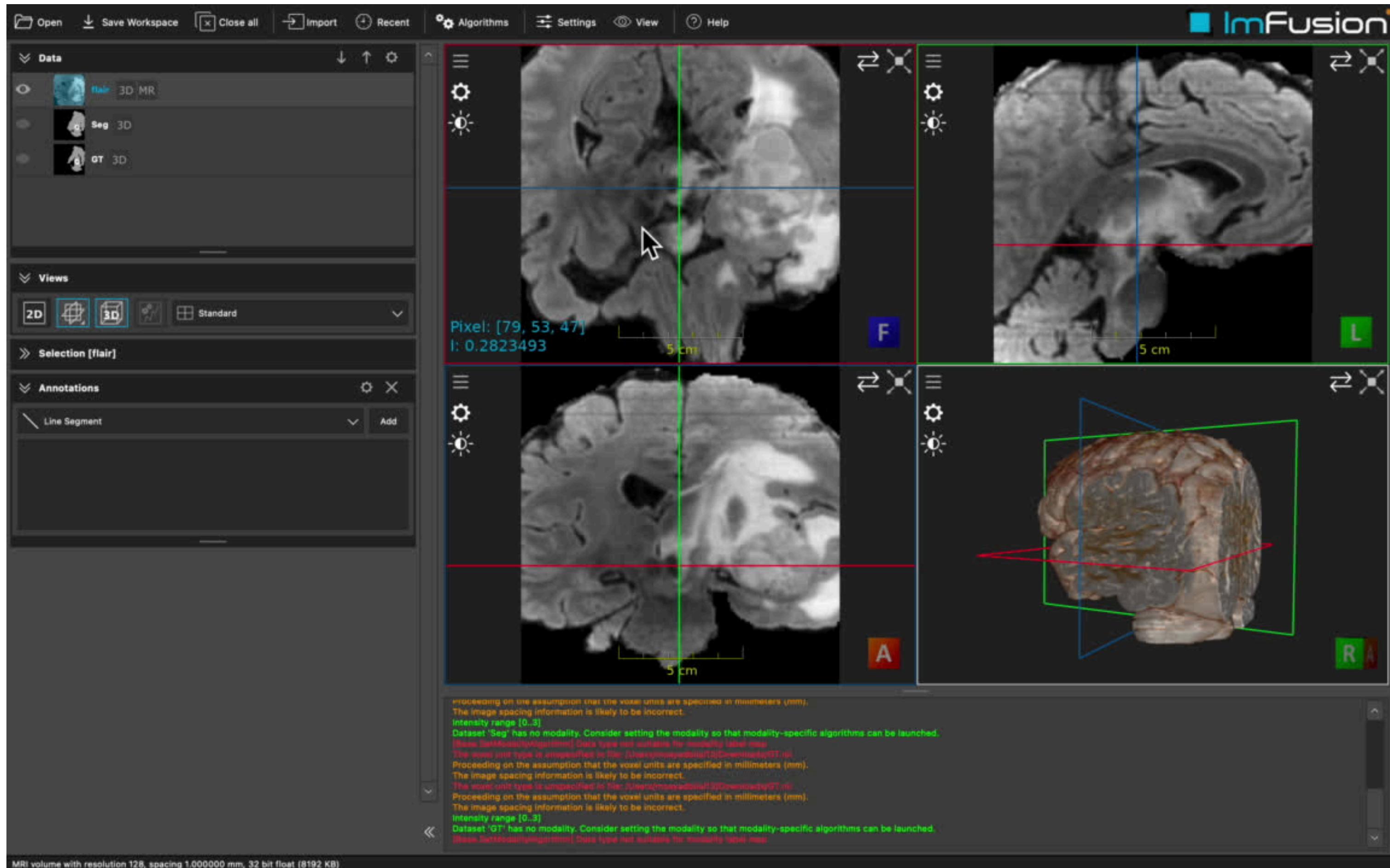
Sample outputs from Swin-Unet.

Image and Mask Visualization



Output visualized using GUI

GUI from ImFusion



Discussion

Limitations

- *Limited GPU access*
- *Financial constraints*
- *Model Complexity.*

Future work

- *Expand dataset*
- *Implement data augmentation*
- *Reduce model complexity*
- *Develop custom GUI*

THANK YOU