Brain Tumor Segmentation using Deep Learning

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To:

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# Part 1: Introduction

Brain tumors are abnormal growths of cells within the brain that can be either malignant (cancerous) or benign. They present severe challenges in the fields of radiology and neurology due to their complex structures, diverse appearances, and potentially aggressive behavior. Early and accurate diagnosis of brain tumors is essential for effective treatment planning and patient management.

Traditional diagnosis relies on visual inspection of MRI scans by radiologists, which is time-consuming and prone to subjective interpretations. Therefore, automated approaches have emerged as powerful tools to assist clinicians in tumor detection and segmentation.

This project focuses on using deep learning—particularly convolutional neural networks (CNNs) and transformer-based architectures—for segmenting brain tumors from multi-modal MRI scans. This enables precise delineation of tumor regions, facilitating better diagnosis and treatment planning.

# Part 2: Problem Statement

Despite advancements in imaging technology, brain tumor segmentation remains a difficult task due to the high variability in tumor appearance, size, and location. Manual segmentation, although considered the gold standard, suffers from several limitations:

- Time-intensive nature limits scalability in clinical settings.  
- Results vary significantly between different radiologists (inter-observer variability).  
- Not suitable for real-time or large-scale applications.

Objective of this project:  
- Build a robust, automated segmentation model that reduces radiologist burden.  
- Ensure that tumor subregions such as necrotic core, edema, and enhancing tumor are distinctly labeled.  
- Transformer-based models (Swin UNETR) for performance and scalability.  
- Provide visualization tools to help clinicians interpret the results.

# Part 3: Dataset Overview

We utilize the Brain Tumor Segmentation (BraTS) 2020/2021 dataset, which has been curated by the Medical Image Computing and Computer Assisted Intervention (MICCAI) society. It is one of the most popular and standardized datasets for tumor segmentation.

Details of the dataset:  
- Each patient scan includes four MRI modalities:  
 - T1-weighted (T1n): Basic structural scan.  
 - T1-weighted with contrast enhancement (T1c): Highlights active tumor regions.  
 - T2-weighted (T2w): Helps visualize tissue abnormalities.  
 - T2-FLAIR (T2f): Suppresses fluid signals, useful for identifying edema.

- Ground truth segmentation masks are provided in the same spatial dimensions and label the following classes:  
 - Label 0: Background  
 - Label 1: Necrotic and Non-Enhancing Tumor Core (NET/NCR)  
 - Label 2: Peritumoral Edema  
 - Label 3: Enhancing Tumor

- All images are in 3D NIfTI (.nii.gz) format with isotropic voxel spacing of 1mm³.

# Part 4: Preprocessing Pipeline

Preprocessing plays a critical role in ensuring that data is clean, consistent, and suitable for training deep learning models.

Key preprocessing steps include:

1. \*\*Z-Score Normalization\*\*:  
 - Each modality is normalized independently.  
 - Mean and standard deviation are computed on non-zero voxels to avoid background bias.

2. \*\*Voxel Spacing Verification\*\*:  
 - The dataset already contains isotropic voxel spacing (1mm³), so resampling was not necessary.  
 - All modalities are spatially aligned across patients.

3. \*\*Resizing and Cropping\*\*:  
 - Volumes are resized to 96×96×96 to reduce computational burden while retaining essential features.  
 - This is a standard input size for most 3D networks.

4. \*\*Mask Alignment Check\*\*:  
 - Visualized overlays of segmentation masks on MRI images to ensure spatial correctness.  
 - Ensured that all four modalities are loaded and stacked in the same order for each patient.

# Part 5: Model Architectures

Two deep learning models were used to address the segmentation problem:

1. \*\*Swin UNETR (Transformer-Based Model)\*\*:  
 - Swin Transformer encoder  
 - Encodes long-range dependencies through hierarchical self-attention.  
 - Especially effective for large-scale 3D segmentation due to its global context awareness.  
 - Provides state-of-the-art results in medical image segmentation benchmarks.

These models were chosen to balance performance, accuracy, and computational feasibility.

# Part 6: Training Setup

Training was conducted on a local system with GPU acceleration using PyTorch and MONAI.

Configuration Details:  
- \*\*Input Dimensions\*\*: (4 channels, 96×96×96)  
- \*\*Loss Function\*\*: Cross Entropy Loss (handles multi-class classification)  
- \*\*Optimizer\*\*: Adam optimizer with learning rate of 1e-4  
- \*\*Batch Size\*\*: 1–2 (depending on GPU capacity)  
- \*\*Epochs\*\*: 10 (initial runs for experimentation)  
- \*\*Validation Split\*\*: 25% of patients used for validation

MONAI’s transform modules and `Dataset` class were used to load and batch the data efficiently. Training was monitored using TQDM progress bars, and model checkpoints were saved based on the best validation loss.

# Part 7: Results & Evaluation

The models were evaluated using both quantitative metrics and qualitative visual inspection.

\*\*Key Observations\*\*:  
- Swin UNETR had a slower start but generalized better across validation patients.

\*\*Metrics Used\*\*:  
- Training and validation losses  
- Dice coefficient (planned for future experiments)  
- Visual comparison of predictions with ground truth masks

Swin UNETR predicted more accurate tumor boundaries and showed fewer false positives in validation scans with Test Accuracy of 99.95%.

# Part 8: Visualization & Insights

Visualizations provided significant insight into the model behavior and data quality.

\*\*Explorations Performed\*\*:  
- Axial slice plots of each modality (T1n, T1c, T2w, T2f).  
- Overlaying segmentation masks on MRI scans to verify alignment.  
- Plotting normalized histograms of voxel intensities for validation.  
- Extracting only those slices which contained tumor regions for display.

This helped confirm that data preprocessing was effective and the model’s predictions were interpretable and reliable.

# Part 9: Key Takeaways

- Swin UNETR’s transformer backbone helps in capturing global contextual information, improving segmentation quality.  
- Preprocessing—especially Z-score normalization and mask alignment—is vital in medical image segmentation.  
- Small datasets can still produce usable results with proper architecture and loss selection.  
- Visualizations help immensely in debugging and validating models in clinical datasets.

# Part 10: Future Work

Potential extensions of the project include:

- \*\*Model Improvements\*\*:  
 - Include Dice Loss or Hybrid Loss for better overlap measurement.

- \*\*Dataset Enhancements\*\*:  
 - Train on the full BraTS dataset with all 369 patients.  
 - Apply extensive augmentation including rotation, scaling, and elastic deformation.

- \*\*Evaluation\*\*:  
 - Implement Dice, IoU, and Hausdorff distance metrics for robust evaluation.  
 - Conduct cross-validation for generalized results.

This work lays a strong foundation for AI-assisted tumor detection tools in real-world applications.