Automated Brain Tumor Segmentation and Classification using Attention U-Net on BRISC2025 Dataset

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***Abstract*—Brain tumor diagnosis requires precise segmentation and classification of magnetic resonance imaging (MRI) scans to assist medical professionals in treatment planning. This paper presents a comprehensive analysis and implementation of deep learning models for the BRISC2025 dataset. We perform an Exploratory Data Analysis (EDA) to understand class distributions and intensity profiles. Subsequently, we propose a multi-task framework utilizing U-Net and Attention U-Net architectures for semantic segmentation, alongside a parallel classification network. Our experiments demonstrate robust performance, achieving a segmentation Intersection over Union (IoU) of 0.7525 and a classification accuracy of 97.30%. The Attention U-Net mechanism specifically enhances the model's ability to focus on relevant tumor regions, effectively handling the inherent complexity of MRI data.**

***Index Terms*—Brain Tumor Segmentation, Attention U-Net, Deep Learning, MRI, Classification, Medical Imaging.**

I. Introduction

The automated analysis of brain MRI is critical for the early detection and treatment of gliomas, meningiomas, and pituitary tumors. Manual segmentation is time-consuming and subject to inter-observer variability. Deep learning, particularly Convolutional Neural Networks (CNNs), has revolutionized this field by providing tools for both pixel-level segmentation and image-level classification.

This study focuses on the BRISC2025 dataset, employing rigorous Exploratory Data Analysis (EDA) to guide model design. We implement and evaluate an Attention U-Net architecture, which integrates attention gates into the standard U-Net skip connections. This allows the model to suppress irrelevant regions in the input image (background noise) while highlighting salient features useful for the specific task. We further evaluate a classification backbone to categorize the tumor type, providing a holistic diagnostic tool.

II. Dataset and Exploratory Data Analysis

A. Dataset Overview

The study utilizes the BRISC2025 dataset. The data is organized into two primary tasks:

- **Segmentation Task:** Contains MRI images and their corresponding binary ground truth masks.
- **Classification Task:** Organized into four subdirectories corresponding to the classes: Glioma, Meningioma, Pituitary, and No Tumor.

B. Data Distribution

Our EDA revealed the following distribution for the training set (3,933 images) and test set (860 images) utilized in the segmentation task:

TABLE I
Class Distribution (Segmentation Task)

Class	**Train Samples**	**Percentage**
Glioma	1147	29.16%
Meningioma	1329	33.79%
Pituitary	1457	37.05%

A critical finding from the EDA is that the segmentation dataset consists exclusively of samples containing tumors (100% tumor presence). The "No Tumor" class is excluded from the segmentation training pipeline to prevent class imbalance issues, as these images result in blank masks which can hinder convergence during segmentation training.

C. Preprocessing

Images were preprocessed using the following pipeline to ensure model stability:

1) **Grayscale Conversion:** All MRI scans were converted to single-channel grayscale to standardize input depth.
2) **Resizing:** Images were resized to a fixed dimension of 256×256 pixels.
3) **Normalization:** Pixel intensities were scaled to the range $[0, 1]$ by dividing by 255.0.
4) **Mask Binarization:** Segmentation masks were thresholded (> 0) to create binary ground truth maps (Tumor vs. Background).

III. Methodology

A. Model Architectures

We implemented and compared two primary architectures for the segmentation task:

1) Standard U-Net: A symmetric encoder-decoder structure with skip connections. The encoder captures contextual information via downsampling, while the decoder constructs the segmentation map through upsampling.

2) Attention U-Net: To improve upon the standard U-Net, we integrated Attention Gates (AGs) at the skip connections. The AGs use the gating signal from a coarser scale to filter the features from the skip connection before concatenation. This effectively suppresses background noise and focuses the model's activation on the target tumor regions without requiring explicit localization modules.

B. Classification Model

A separate CNN-based classifier was trained to categorize the input MRI into one of four classes: Glioma, Meningioma, Pituitary, or No Tumor.

C. Training Configuration

- **Loss Function:** A hybrid loss function was employed to address the class imbalance between background and tumor pixels:

$$L_{total} = 0.2 \cdot L_{BCE} + 0.8 \cdot L_{Dice} \tag{1}$$

where L_{BCE} is Binary Cross Entropy and L_{Dice} is the Dice Loss.
- **Optimizer:** AdamW with a learning rate of 1×10^{-4}.
- **Device:** Training was conducted on an NVIDIA Tesla T4 GPU.
- **Epochs:** 25 epochs.

IV. Experiments and Results

A. Segmentation Performance

The Attention U-Net model showed consistent convergence over 25 epochs. The training logs indicate a steady decrease in BCE and Dice loss, with the Intersection over Union (IoU) metric improving significantly.

TABLE II
Segmentation Results (Test Set)

Metric	Value
BCE Loss	0.0301
Dice Loss	0.1415
IoU	**0.7525**

The final test IoU of 0.7525 demonstrates that the Attention U-Net is highly effective at delineating tumor boundaries, even with the complex morphological variations present in the BRISC2025 dataset.

B. Classification Performance

The classification model was evaluated on the test set comprising 63 batches. The model achieved a high overall accuracy of 97.3%.

TABLE III
Classification Metrics (Test Set)

Metric	Value
Test Loss	0.1006
Accuracy	**97.30%**
Precision	0.9731
Recall	0.9730
F1-Score	0.9729

C. Per-Class Analysis

To understand the classifier's performance across different tumor types, we analyzed the Precision, Recall, and F1-Scores for each class:

- **Glioma:** Precision 98.78%, F1-Score 96.99%.
- **Meningioma:** Precision 95.75%, F1-Score 95.75%.
- **Pituitary:** Precision 97.90%, F1-Score 98.94%.
- **No Tumor:** Precision 97.39%, F1-Score 98.35%.

The results indicate that the Pituitary class was the easiest to classify (F1 $\approx$ 99%), while Meningioma presented slightly more challenge, likely due to visual similarities with Gliomas in certain MRI contrasts.

V. Conclusion

In this work, we presented a robust pipeline for Brain Tumor MRI analysis using the BRISC2025 dataset. Through detailed EDA, we identified the class imbalance and dataset characteristics. Our implementation of the Attention U-Net yielded a segmentation IoU of 0.75, while our classification model achieved 97.3% accuracy.

The combination of Dice-weighted loss and attention mechanisms proved effective in handling the medical imaging segmentation task. Future work will explore 3D segmentation techniques and ensemble methods to further boost the Intersection over Union scores.

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References