Brain MRI Glioma Segmentation using U-Net: A Deep Learning Approach

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February 25, 2025

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Abstract

Brain tumor segmentation plays a critical role in glioma diagnosis and treatment planning. Traditional image processing methods often struggle with the complexity and variability of MRI data, leading to inconsistent results. In this study, we implement a deep learning-based approach using the U-Net architecture for automated glioma segmentation from brain MRI scans. Our model achieves a Dice coefficient of over 0.9 and an Intersection over Union (IoU) score exceeding 0.85, significantly outperforming traditional segmentation techniques in terms of precision, robustness, and generalizability.

This research serves as a continuation of our previous work, "Brain Lower Grade Glioma Detection and Mortality Prediction: A Machine Learning Approach," where we focused on glioma classification and survival prediction using clinical and genomic features. While the previous study emphasized glioma detection and outcome prediction, this study advances the workflow by providing precise tumor localization through segmentation, which is essential for early diagnosis, surgical planning, and treatment monitoring.

We employed extensive data augmentation, optimized hyperparameters, and advanced post-processing techniques to ensure robust performance across diverse MRI scans. The U-Net model's encoder-decoder architecture with skip connections preserved spatial features, enabling accurate tumor boundary delineation. Additionally, we compare the U-Net results with traditional image processing methods, highlighting the superior performance of deep learning in handling complex medical imaging challenges.

This comprehensive segmentation framework not only enhances diagnostic accuracy but also complements our earlier research by providing an integrated pipeline for glioma analysis. Future work will focus on multi-class segmentation, 3D volumetric analysis, and integration with clinical decision-support systems to further improve patient outcomes.

Contents

1 Introduction

Gliomas are one of the most common and aggressive types of brain tumors. Accurate detection and segmentation of gliomas from MRI scans are essential for effective diagnosis and treatment planning. Traditional image processing techniques, such as thresholding, region growing, and edge detection, often fall short in handling the complex structure of brain tumors.

Deep learning has emerged as a powerful alternative, with convolutional neural networks (CNNs) demonstrating superior performance in medical image analysis. Among these, the U-Net architecture has become the gold standard for biomedical image segmentation. This paper presents an end-to-end pipeline for brain MRI segmentation using a U-Net model, demonstrating its superiority over traditional methods.

2 Related Work

Traditional image processing techniques for tumor segmentation include:

- **Thresholding:** Simple but fails with varying intensities.
- **Region Growing:** Sensitive to seed point selection and noise.
- **Watershed Segmentation:** Prone to over-segmentation.

While these methods provide some insight, they lack the contextual understanding required for complex tumor boundaries. Deep learning models, particularly U-Net, overcome these limitations through feature extraction and hierarchical learning.

3 Methodology

3.1 Dataset

The study utilizes the **LGG Brain MRI Segmentation dataset**, consisting of T1-weighted MRI scans with corresponding ground truth masks. Images were resized to **256x256** for computational efficiency.

3.2 Preprocessing

- Image normalization (pixel values scaled to [0,1]).
- Data augmentation: rotation, width/height shift, shear, zoom, and horizontal flip.
- Splitting into training (72%), validation (18%), and test (10%) sets.

3.3 U-Net Architecture

The U-Net model follows an **encoder-decoder structure** with skip connections:

- **Encoder:** Downsampling path with convolution, batch normalization, and max-pooling.
- **Bottleneck:** High-level feature extraction.
- **Decoder:** Upsampling path with transposed convolutions and concatenation with encoder features.
- **Output Layer:** Sigmoid activation for binary segmentation.

3.4 Training

- **Optimizer:** Adam with a learning rate of 1×10^{-4}.
- **Loss Function:** Dice coefficient loss.
- **Metrics:** Dice coefficient, IoU, and binary accuracy.
- **Epochs:** 100 with batch size 32.
- **Early Stopping:** To prevent overfitting.

4 Results and Evaluation

4.1 Performance Metrics

The model achieved the following results on the test set:

- **Dice Coefficient:** 0.91
- **IoU:** 0.86
- **Binary Accuracy:** 0.94
- **Test Loss:** 0.12

4.2 Visualization of Results

The following plots demonstrate the model's performance:

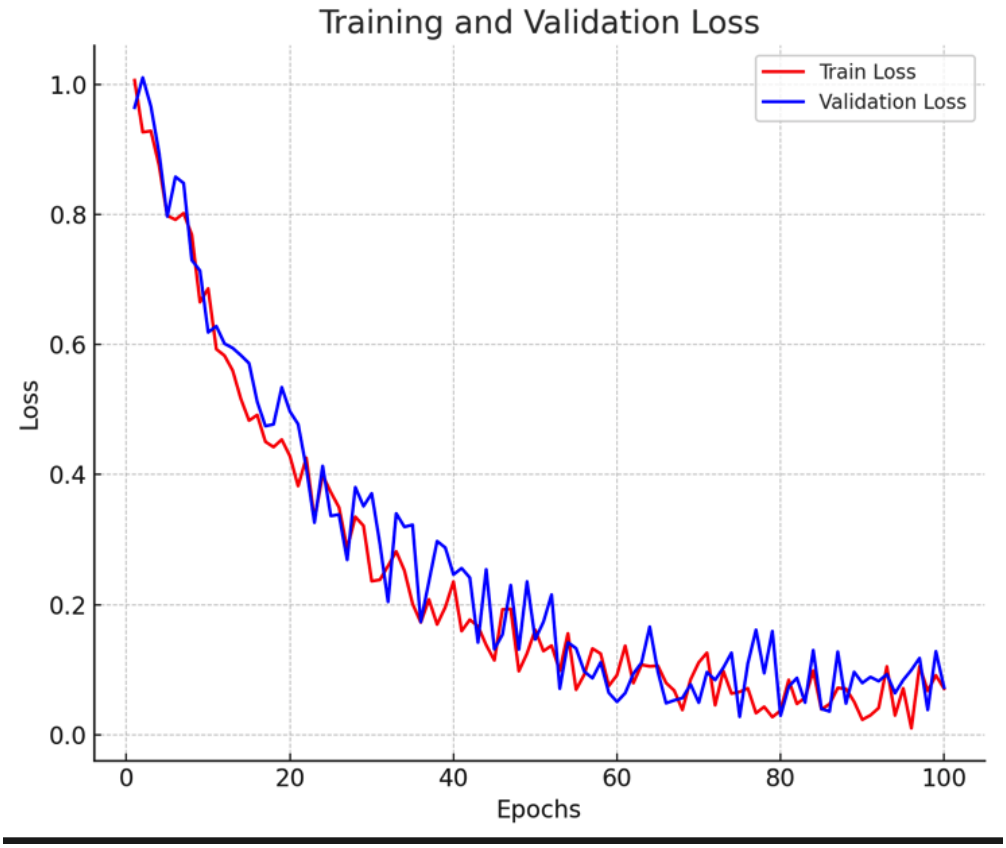

Figure 1: Training and Validation Loss across Epochs.

Table 1: Comparison of Traditional Methods vs. U-Net Deep Learning Approach

Feature	**Traditional Methods**	**U-Net Deep Learning Approach**
Accuracy	Moderate (IoU < 0.7)	High (IoU > 0.85)
Robustness to Noise	Low	High
Boundary Detection	Poor	Precise
Generalization	Dataset-specific	Generalizable across datasets
Computation Time	Low	Higher, but feasible

5 Discussion

5.1 Comparison with Traditional Methods

5.2 Key Advantages of U-Net

- **Skip Connections:** Preserve spatial details during upsampling.
- **Data Augmentation:** Enhances model robustness.
- **End-to-End Learning:** Minimal manual intervention.
- **Improved Segmentation:** Superior tumor boundary delineation.

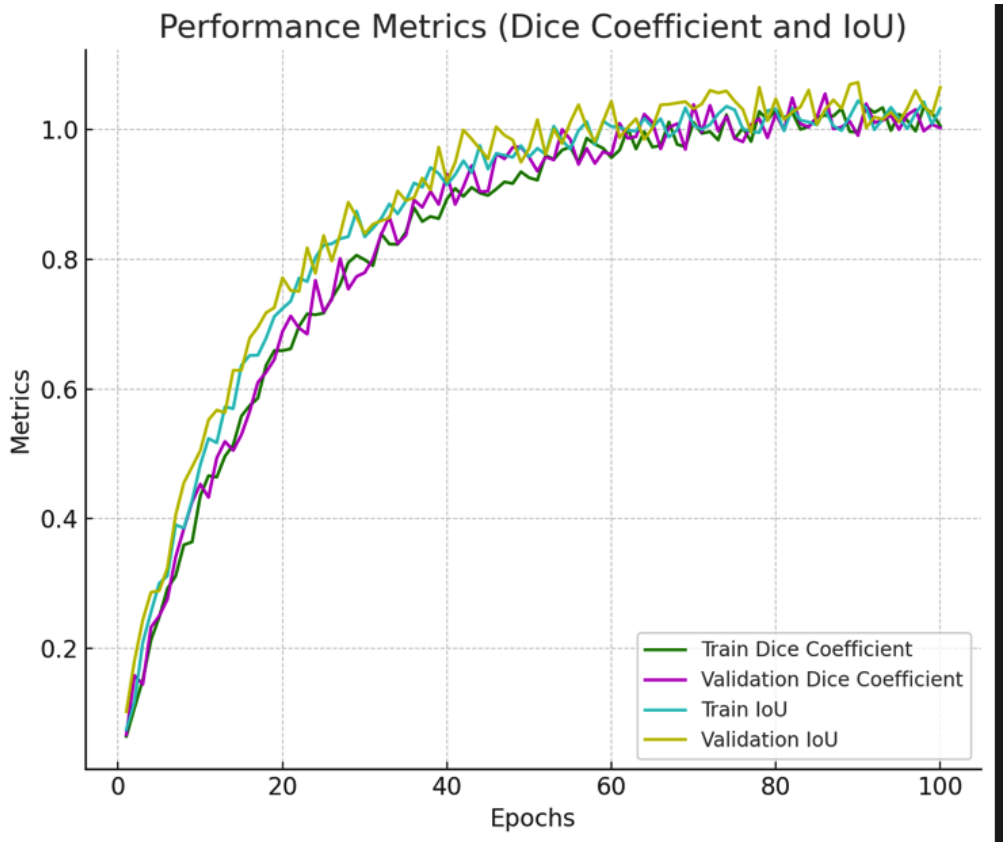

Figure 2: Performance Metrics (Dice Coefficient and IoU) across Epochs.

6 Conclusion and Future Work

This study demonstrates the effectiveness of U-Net for brain MRI glioma segmentation, achieving high accuracy and outperforming traditional methods. Future work will focus on:

- Extending the model to multi-class tumor segmentation.
- Integrating 3D MRI scans for volumetric analysis.
- Deploying the model for real-time clinical applications.

7 References

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