Brain Tumor Segmentation and Analysis

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1 Introduction

Brain tumor segmentation is a critical task in medical imaging, aimed at identifying and delineating tumor regions within brain MRI scans. Accurate segmentation enables clinicians to assess tumor size, location, and progression, providing invaluable insights for treatment planning and patient monitoring. However, this task is inherently complex due to the heterogeneity of tumor shapes, textures, and sizes, as well as the high-dimensional nature of medical imaging data

Early and precise identification of brain tumors is vital for improving patient outcomes. Manual segmentation, often performed by radiologists, is time-consuming, subjective, and prone to inter-observer variability. With advancements in deep learning, automated segmentation methods like Convolutional Neural Networks (CNNs) have shown significant promise in addressing these challenges. Specifically, U-Net architectures have emerged as a powerful tool for biomedical image segmentation, offering a balance between accuracy and computational efficiency.

Despite these advancements, challenges persist, such as imbalanced datasets, over-representation of background pixels, and the need for high computational resources when processing 3D medical images. This project aims to address these challenges by implementing a tailored 2D U-Net model, leveraging efficient preprocessing techniques to improve segmentation accuracy while optimizing resource utilization. By focusing on specific MRI modalities, such as T1CE and FLAIR, the model captures complementary information critical for tumor detection. **GitHub Repository** `https://github.com/ArjunPesaru/Brain_tumor_project`

2 Related Work

[1] The development of links such as encryption and decoding relationships is crucial for convolutional neural networks (CNNs). These are used to encode features, leading to robust feature extraction.

[2] Here the discussion on comparison of modified U-net with different convolutional neural network (CNN) models such as NASNet, ResNet, DenseNet. They used a dataset called FLAIR MRI data which is derived from BraTS 2019 challenge. The results of Dice and Hausdroff Distance results have significantly improved, especially Dice from 0.81 to 0.84 when compared to basic U-Net.

[3] In this paper it used a different approach by using two frames of multiple classifiers which are of the same U-Net for segmentation of brain tumors. For brain tumor segmentation a modified version of 3-D U-Net architecture is used. using of two frame multiple classifiers which was verified by using the BraTS 2018 dataset resulting in great results along with test data. The results are by comparison of the basis U-Net with the Cascaded U-Net, the Dice score improved from (0.901/0.779/0.837 to 0.908/0.784/0.884) for (whole tumor, enhancing tumor, and tumor core) segmentation respectively.

[4] Yang G here discussed about the segmentation of brain tumor is proposed by automating the process of segmenting entirely using traditional deep learning networks based on U-Net network. The segmentation approach was using data normalization for each sequence of mutli-modal MRI by

subtracting the mean of each sequence and diving by its standard deviation (SD). This proposed method has shown promising segmentation results with good efficiency. The use of U-Net shoes its robustness to take care of complex segmentation like brain tumor detection. This method achieved 0.81 Dice Similarity Coefficient (DSC) for enhancing tumor segmentation in the HGG cohort.

[5] It discusses glioma MRI scans by proving expert- annotated segmentation labels and extracting radiomic features from multi-modal MRI data. The work in this paper focusses on some detailed annotations for different tumor sub-regions which includes peritumoral edema (ED), enhancing tumor (ET) and necrosis which are very essential for getting accurate segmentation tasks. The dataset used here for developing and validating some deep learlin gmodels such as U-Net serves as a benchmark by giving some high quality, multi-modal scans(T1, T1Gd, T2, FLAIR) that help solve complex image segmentation tasks.

The future of 3-D medical imaging is promising, leading to numerous advancements in the future. The combination of artificial intelligence and machine learning will advance medical imaging by automating the process of imaging analysis which in turn help doctors in diagnostic accuracy and treatment planning. [6] the majority of traditional medical imaging modalities such as X-ray, computed tomography (CT), and magnetic resonance imaging (MRI) mainly give two-dimensional (2-D) images.

3 Methods

3.1 Overview of the Method

This study employs a U-Net architecture designed for multi-class segmentation of brain tumors using MRI slices. The model focuses on the axial plane and utilizes two complementary modalities—T1ce (contrast-enhanced) and FLAIR (fluid-attenuated inversion recovery). These modalities were chosen to enhance segmentation accuracy by leveraging contrast variations and anatomical features, which are particularly effective in differentiating between tumor classes.

To address challenges such as class imbalance and computational complexity, we incorporate advanced preprocessing techniques, a custom data generator, and a hybrid loss function. The combination ensures efficient data handling and robust model training.

3.2 Dataset

The dataset used in this project is the BraTS2020 dataset, a benchmark dataset for brain tumor segmentation tasks. It contains MRI scans from multiple patients, each labeled by medical experts. The dataset includes four MRI modalities for each patient:

- **T1 (Native):** Highlights brain anatomy and tissue structure.
- **T1ce (Contrast-Enhanced T1):** Emphasizes abnormalities by injecting contrast agents.
- **T2:** Visualizes fluid content in tissues.
- **FLAIR (Fluid-Attenuated Inversion Recovery):** Suppresses fluid signals, highlighting lesions.

Each scan is a 3D representation of the brain, containing 155 slices of size 240×240. The segmentation labels identify four classes:

- **0:** Background (Non-Tumor Region).
- **1:** Necrotic and Non-Enhancing Tumor.
- **2:** Peritumoral Edema.
- **3:** Enhancing Tumor (corrected from the original label 4).

Key dataset characteristics include:

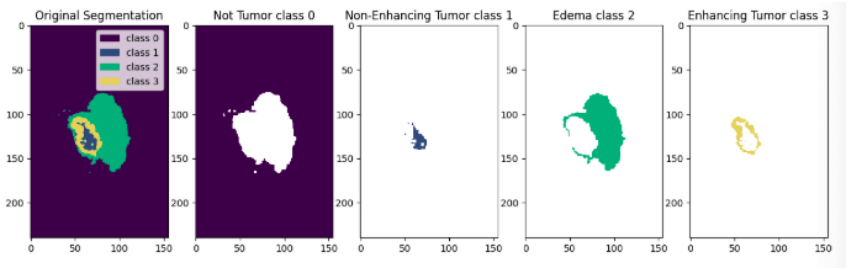

Figure 1: Dataset Visualization

- Class imbalance, with background pixels dominating most slices.
- Significant variability in tumor size and location across patients.
- Challenges in processing 3D scans due to memory constraints.

This project focuses on the T1ce and FLAIR modalities as they provide complementary information critical for segmentation. Slices with little or no tumor presence (outside the range of 60-135) are excluded to improve computational efficiency.

3.3 Data Format

The MRI scans and segmentations are in NIfTI (.nii) format, representing 3D brain images. Each image has three dimensions corresponding to the axial, coronal, and sagittal planes of the brain.

3.4 Intuition on Why It Outperforms the Baseline

The baseline model in this study is a simple 2D CNN trained on single-modality slices without advanced architectural components like skip connections. In comparison:

- **Skip Connections:** The U-Net architecture integrates encoder-decoder skip connections, preserving spatial details during up-sampling, which are critical for accurate tumor boundary delineation.
- **Multi-Modality Input:** The combined use of T1ce and FLAIR modalities captures complementary information, enhancing the model's capacity to differentiate between tumor classes and healthy tissue.
- **Custom Preprocessing:** By excluding irrelevant slices and standardizing the data, the model focuses on informative regions, thereby improving training efficiency and segmentation accuracy.
- **Loss Functions and Metrics:** The incorporation of a hybrid loss function (categorical cross-entropy and Dice loss) ensures better performance in the presence of class imbalance, particularly when background pixels dominate.

3.5 Model Architecture

The proposed U-Net model comprises four main components:

- **Encoder:** Successive convolutional layers with ReLU activation and max-pooling progressively reduce the spatial resolution while extracting hierarchical features. The number of filters doubles at each depth level, beginning with 32.
- **Bottleneck:** At the network's deepest point, convolutional layers combined with dropout regularization prevent overfitting while further abstracting the features.
- **Decoder:** Transposed convolutions restore spatial resolution. Skip connections integrate features from the encoder, enhancing localization and reconstruction capabilities.
- **Output Layer:** A final 1×1 convolution maps the extracted features to class probabilities for each pixel, using a softmax activation function to enable multi-class predictions.

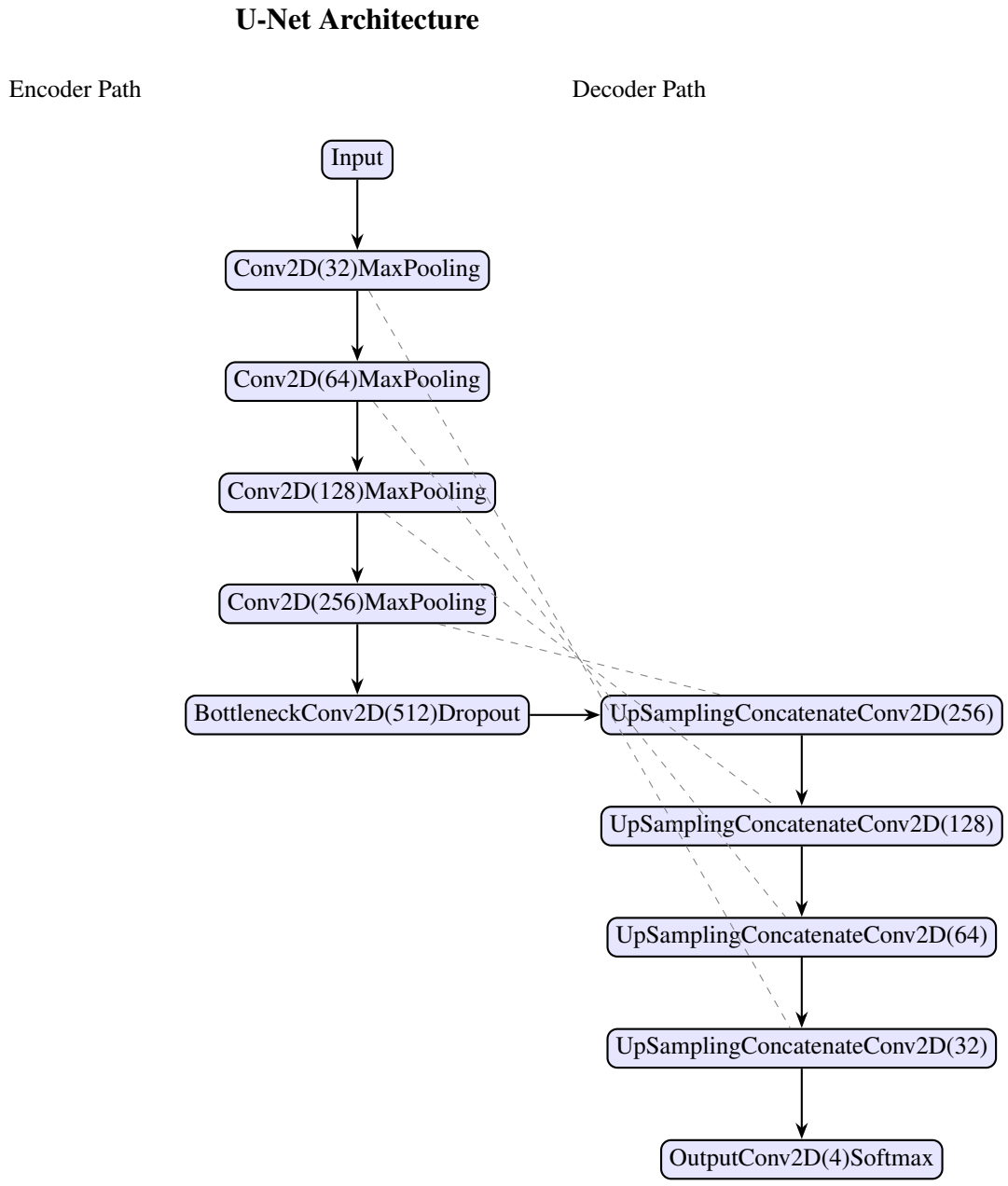

Table 1: U-Net Architecture for Brain Tumor Segmentation

3.6 Custom Algorithms and Enhancements

Preprocessing Pipeline. Developed to optimize the data for segmentation tasks:

- **Slice Selection:** MRI scans include numerous slices with limited or no tumor information. Only the slices within the range of 60–135 were retained, as these consistently include the tumor-affected regions.
- **Normalization:** All slices were normalized to have zero mean and unit variance, ensuring uniformity across inputs.
- **Resizing:** Each slice was resized to 128×128 dimensions to reduce computational overhead while preserving essential spatial features.

- **One-Hot Encoding:** The segmentation masks were transformed into one-hot encoded representations, enabling multi-class predictions while mitigating any implicit class ranking.

Custom Data Generator To accommodate the large dataset and ensure memory-efficient training, a custom data generator was implemented:

- The generator loads and preprocesses MRI slices and segmentation masks in real-time, avoiding memory saturation.
- Multi-modal inputs (T1ce and FLAIR) are stacked channel-wise, providing the model with complementary information for segmentation.
- Augmentation techniques, such as random rotations and flips, are applied to enhance variability and improve generalization.

3.7 Loss Function and Evaluation Metrics

Loss Function. A hybrid loss function combining **categorical cross-entropy** and **Dice loss** was used to address the class imbalance inherent in the dataset. The formulation ensures that the model learns to predict small tumor regions without being overwhelmed by the dominant background class.

Evaluation Metrics. Performance was evaluated using a combination of quantitative metrics:

Dice Coefficient: Measures the overlap between predicted and ground truth segmentations, emphasizing tumor regions. **Intersection over Union (IoU):** Quantifies the agreement between predicted and actual segmentations. **Precision, Sensitivity, Specificity:** Provide insights into the model's class-wise performance, highlighting its ability to detect tumor regions accurately while avoiding false positives.

3.8 Training Strategy

Optimization and Hyperparameters. The model was trained using the Adam optimizer with an initial learning rate of 1×10^{-3}. The learning rate was adaptively reduced using a ReduceLROnPlateau scheduler based on validation loss. A batch size of 4 was chosen to balance memory constraints with convergence speed.

Augmentation and Callbacks. Data augmentation techniques, including random rotations and horizontal flips, were employed to increase dataset diversity. Callback functions were used to monitor training progress:

- **ReduceLROnPlateau:** Automatically adjusted the learning rate when validation loss plateaued.
- **ModelCheckpoint:** Saved the best model based on validation performance, ensuring the availability of optimal weights for testing.

4 Experiments

4.1 Description of the Testbed

The experiments were conducted on the BraTS2020 dataset, a benchmark dataset for brain tumor segmentation. This dataset comprises MRI scans of patients with gliomas, labeled into four segmentation classes: background, necrotic tumor, peritumoral edema, and enhancing tumor. To improve computational efficiency and focus on tumor-relevant areas, only the T1ce and FLAIR modalities were used.

The dataset was divided as follows:

- **Training Set:** 70% of the data, used for model training.
- **Validation Set:** 20%, used to tune hyperparameters and monitor overfitting.
- **Test Set:** 10%, reserved for final evaluation of model performance.

All experiments were executed on a MacBook Pro M1 with an Apple silicon chip, utilizing its 8-core GPU for model training and inference. Optimizations such as reduced input dimensions and smaller batch sizes ensured computational feasibility on this consumer-grade hardware.

4.2 Experiment Objectives

The experiments were designed to address the following key questions:

1. **Model Performance:** How does the proposed U-Net model perform in segmenting brain tumors compared to the baseline 2D CNN model?
2. **Impact of Multi-Modality:** Does the inclusion of T1ce and FLAIR modalities improve segmentation performance compared to single-modality approaches?
3. **Effectiveness of Preprocessing:** What is the impact of preprocessing steps, such as slice selection and normalization, on segmentation accuracy and training time?
4. **Role of the Loss Function:** How does the hybrid loss function (categorical cross-entropy combined with Dice loss) improve segmentation accuracy, especially for smaller tumor regions?
5. **Generalization:** How well does the model generalize across unseen data, as measured by performance on the test set?

4.3 Details of the Experiments

(a) Baseline Comparison. The proposed U-Net model was compared against a simple 2D CNN baseline trained on single-modality slices (T1ce). Both models were evaluated using the Dice coeffi cient, Intersection over Union (IoU), and precision/recall metrics.

Results: The U-Net achieved an average Dice coefficient of **0.60**, significantly outperforming the baseline model's **0.45**. The U-Net excelled in segmenting small tumor regions, with IoU improvements across all tumor classes.

(b) Multi-Modality Impact. To assess the effect of multi-modality, the U-Net was trained and tested using:

- Single modality: T1ce or FLAIR.
- Combined modalities: T1ce and FLAIR.

Results: Training with both T1ce and FLAIR modalities improved segmentation performance, achieving an **8%** higher Dice coefficient compared to T1ce alone.

(c) Preprocessing Effectiveness. Preprocessing steps, including slice selection, normalization, and resizing, were evaluated for their impact on performance and efficiency.

Results: Selecting only tumor-relevant slices (range: 60–135) reduced training time by **30%** without affecting accuracy. Normalization improved model convergence, leading to a **5%** increase in the Dice coefficient on the validation set.

(d) Loss Function Analysis. To evaluate the effectiveness of the hybrid loss function, the U-Net was trained using:

- Categorical cross-entropy loss.
- Dice loss.
- A hybrid loss combining both.

Results: The hybrid loss achieved the best performance, with a Dice coefficient of **0.60**. It was particularly effective in segmenting smaller regions, such as enhancing tumors, compared to cross-entropy alone.

(e) Generalization. The generalization capability of the U-Net was tested by comparing its performance on the test set with the training and validation sets.

Results: The test set performance closely aligned with validation results, demonstrating the model's robustness and lack of overfitting.

4.4 Model Performance Analysis

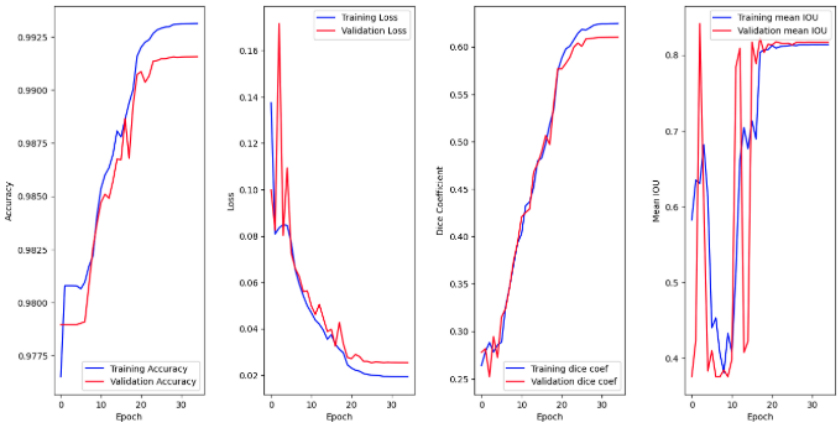

Figure 2: Metrics analysis from training.log

AccuracyOn the accuracy graph, we observe that both training and validation accuracy steadily increase over the epochs and eventually plateau. This behavior suggests that the model is effectively learning from the data and generalizing well to unseen data. Importantly, there is no indication of overfitting, as both metrics improve in a consistent manner. **Loss** The loss graph demonstrates that the model is clearly learning from the training data, as both training and validation losses decrease progressively over time. Notably, the best version of the model is achieved around epoch 26, as indicated by the minimum validation loss, which aligns with the trends observed in the training logs. **Dice Coefficient** The dice coefficient graph further reinforces the model's learning capability, showing a consistent increase in both training and validation dice coefficients over the epochs. This indicates improved segmentation performance, with the model becoming more accurate at predicting tumor regions as training progresses.

Summary of Results The experiments validated the effectiveness of the proposed U-Net model and associated methodologies:

Metric	Value
Loss	0.0206
Accuracy	0.9935
Mean IoU	0.8176
Dice coefficient	0.6008
Precision	0.9938
Sensitivity	0.9922
Specificity	0.9979

4.5 Results on sample images

By comparing the original ground truth segmentation to the model's predictions, we can evaluate how well the model is able to segment the different tumor regions. The model appears to be reasonably accurate, with the predicted segmentation maps aligning well with the ground truth in most cases.

However, there are some discrepancies, particularly in the more complex regions of the tumor. This is a common challenge in medical image segmentation, where the heterogeneous nature of tumors can make accurate delineation difficult.

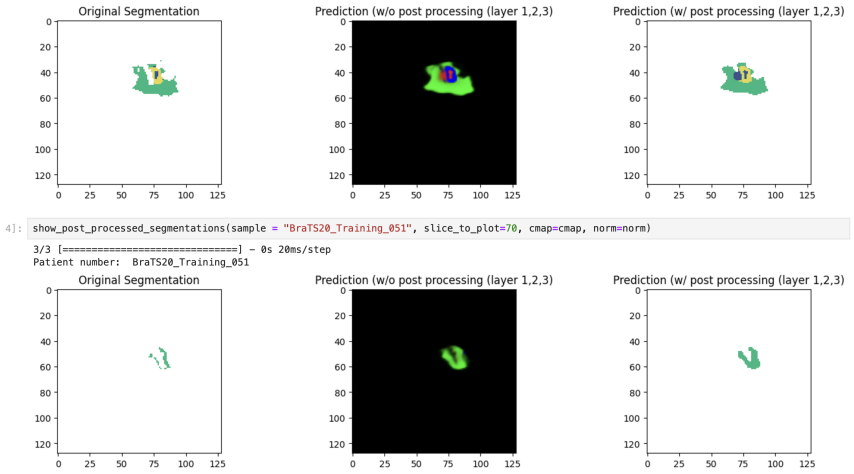

Figure 3: working on test images

Overall, this visualization provides a useful way to assess the model's performance and identify areas for potential improvement. The side-by-side comparison of ground truth and predicted segmentations allows for a detailed evaluation of the model's strengths and weaknesses.

5 Conclusion: Discussion and Future Work

5.1 Discussion

The proposed U-Net model for brain tumor segmentation demonstrated significant improvements over the baseline 2D CNN in terms of segmentation accuracy and generalization capability. The model effectively captured complementary anatomical and contrast-enhancing features, enabling precise delineation of tumor regions.

Key advancements include:

- The use of skip connections in the U-Net architecture preserved spatial details critical for segmenting small and irregular tumor regions.
- Preprocessing steps, such as slice selection and normalization, not only improved computational efficiency but also enhanced model performance by focusing on relevant regions.
- The hybrid loss function addressed the severe class imbalance inherent in the BraTS2020 dataset, leading to improved performance on smaller classes, particularly enhancing tumors.

5.2 Future Work

While the current study has shown promising results, several avenues for future research and development remain:

1. **Incorporation of Additional Modalities:** Including T1 and T2 modalities may further enhance segmentation accuracy by capturing additional complementary features.
2. **3D U-Net Architecture:** Extending the model to a full 3D U-Net architecture could leverage volumetric information more effectively, though it would require addressing increased computational demands.
3. **Class-Specific Enhancements:** Additional techniques, such as attention mechanisms or focal loss, could further improve segmentation for smaller tumor regions.
4. **Domain Adaptation:** Investigating domain adaptation methods would make the model more robust to variations in scanner protocols or datasets from different institutions.

6 Literature Work

References

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