Post-operative Glioma Detection for Brain Magnetic Resonance imaging (MRI)

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FINAL YEAR DESIGN PROJECT REPORT

This Report Presented in Partial Fulfillment of the Requirements forthe **Degree of Bachelor of Science in Computer Science and Engineering**

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APPROVAL

This Project titled **"Post-operative Glioma Detection for Brain Magnetic Resonance imaging (MRI)"**, submitted by **Riyadul Islam**, ID No: **221-15-4828** to the Department of Computer Science and Engineering, Daffodil International University has been accepted as satisfactory for the partial fulfillment of the requirements for the degree of B.Sc. in Computer Science and Engineering and approved as to its style and contents. The presentation has been held on **6 January, 2026.**

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DECLARATION

We hereby declare that this project has been done by us under the supervision of **Dr. Fizar Ahmed, Associate Professor**, and **Dr. Md. Zahid Hasan, Associate Professor**, Department of Computer Science and Engineering, Daffodil International University. We also declare that neither this projectnor any part of this project has been submitted elsewhere for the award of any degree or diploma.

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List of Publications:

[1] Islam, R., Paul, S.G., Ahmed, F., Hasan, M.Z., "ToRAS: A Topology-Refined Attention Framework for Glioma MRI Segmentation." In 2025 International Conference on Computer and Information Technology (ICCIT 2025), Bangladesh, December 18–20, 2025. IEEE, Accepted on December 1, 2025;

[2] Islam, R., S Azam., SS Chowa., Ahmed, F., Hasan, M.Z "Post-operative Glioma Detection for Brain Magnetic Resonance imaging (MRI)", in progress for a journal

ABSTRACT

Accurate segmentation of post-operative gliomas in MRI remains a critical challenge due to surgical cavities, irregular tumor boundaries, and annotation noise. Building upon the previously introduced ToRAS (Topology-Refined Attention Segmentation) framework, this work presents an enhanced hybrid CNN-Transformer architecture for improved glioma segmentation and sub-region analysis. The proposed model integrates a refined U-Net structure with a novel encoder-decoder design, combining convolutional blocks for local feature extraction and transformer blocks for global context modeling, augmented by spatial-channel squeeze-and-excitation (scSE) attention. An extended preprocessing pipeline incorporating morphological refinements (dilation, connected component filtering, hole filling) alongside intensity-based enhancements (CLAHE, Gaussian, and median filtering) is applied to improve label consistency. Experiments conducted on the MU-Glioma-Post dataset demonstrate that the proposed model achieves a test IoU of 0.9536 and an F1-score of 0.9439, outperforming established backbones such as DenseNet201 and EfficientNet. Furthermore, the segmented tumor regions are utilized for multi-label classification of four clinically relevant sub-regions Non-enhancing Tumor Core, Enhancing Tissue, Surrounding FLAIR Hyperintensity, and Resection Cavity which achieving a classification accuracy of 94.74% with a Vision Transformer backbone. The results underscore the effectiveness of integrating topological refinement, hybrid architectural design, and attention mechanisms in advancing post-operative glioma analysis, offering a reproducible and extensible framework for future research in neuro-oncological trauma imaging.

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Chapter 1

Introduction

In This section we introduce the importance and the impact of glioma patients and their outcome. Also this section elaborates our intention of motivation along with outcome of scientific community.

1.1 Introduction

Brain tumors are among the most frequently occurring primary, common, and life-threatening neurological diseases worldwide. Among these, gliomas are the most common and aggressive primary intracranial tumors, making up about 40–50% of all brain tumors [1]. Precise identification and outlining of gliomas are essential for diagnosis, therapy strategies, and prognosis, since the degree of tumor removal significantly affects patient survival [2]. Glioma is a general term for tumors arising from glial cells, whereas glioblastoma (GBM) represents the most aggressive subtype. GBM is recognized as the most malignant primary brain tumor, characterized by rapid progression and poor prognosis. In United States, the incidence rate of 3.19 per 100,000 persons in the United States and a median age of 64 years, it is uncommon in children. The incidence is 1.6 times higher in males compared to females and 2.0 times higher in Caucasians compared to Africans and Afro-Americans, with lower incidence in Asians and American Indians [3].

Magnetic Resonance Imaging (MRI) is the most widely used modality for glioma assessment due to its high spatial resolution and superior soft tissue contrast compared to computed tomography (CT) and positron emission tomography (PET) [4]. In clinical practice, multiple MRI sequences including T1-weighted, post contrast T1 weighted, T2 weighted, and fluid attenuated inversion recovery (FLAIR), are employed to characterize different tumor subregions and assess infiltration of surrounding brain tissues [5], [6]. However, manual delineation of gliomas by radiologists is highly time consuming, subject to interobserver variability, and impractical for large scale studies [7].

To overcome these challenges, numerous automatic glioma segmentation methods have been developed, leveraging deep learning architectures such as convolutional neural networks (CNNs) and their variants [8]. In particular, the U-Net architecture and its encoder decoder extensions have achieved state-of-the-art performance on benchmark datasets such as the Multimodal Brain Tumor Segmentation Challenge (BraTS) [9]. Despite these advances, segmentation of post-operative glioma images remains underexplored and more challenging due to irregular tumor boundaries, post-surgical cavities, and heterogeneous image appearances.

1.2 Motivation

The computational motivation for this research stems from the persistent challenges in automated post-operative glioma segmentation, which is characterized by heterogeneous tumor morphology, surgical artifacts, and noisy annotations in MRI data. Traditional convolutional neural networks (CNNs), while effective in many medical imaging tasks, often struggle with capturing long-range dependencies and global contextual information, which are critical for accurately delineating irregular tumor boundaries and residual lesions. Conversely, pure transformer architectures, though powerful in modeling global relations, may overlook fine-grained local textures essential for precise segmentation. This gap necessitates a hybrid computational approach that synergistically integrates the local feature extraction capability of CNNs with the global contextual modeling of transformers.

- **Clinical Need for Reliable Post-Operative Assessment**: Manual segmentation of post-operative glioma is time-consuming, subjective, and prone to variability. An automated, consistent tool can accelerate treatment planning, enhance longitudinal tracking, and improve patient outcomes.

- **Lack of Existing Benchmarking on Post-Operative Datasets**: While pre-operative glioma segmentation has been extensively studied (e.g., BraTS), post-operative datasets such as MU-Glioma-Post [] remain significantly underexplored. There is a scarcity of established baselines, standardized evaluation protocols,

- **Lack of End-to-End Pipelines**: Most research stops at binary tumor segmentation, whereas clinicians require detailed sub-region analysis like., enhancing vs. non-enhancing tissue. An integrated system that segments and classifies tumor sub-types within a unified framework offers greater clinical utility.

- **AI methodology and neuro-oncological**: To determine how can we improve the artificial intelligence in medical computer vision for neuro oncological trauma imaging.

1.3 Objectives

- **Propose and validate a hybrid CNN-Transformer U-Net model** for accurate binary segmentation of post-operative gliomas, distinguishing foreground (tumor) from background (healthy brain tissue and non-brain regions), by effectively integrating convolutional inductive bias with self-attention mechanisms to address irregular tumor boundaries and global context.

- **Develop an end-to-end computational pipeline** that ensures robust and reproducible post-operative glioma segmentation, establishing a standardized benchmark for the MU-Glioma-Post dataset to support future research and clinical translation.

1.4 Methodology

The methodology of this research is organized into two interconnected phases that build upon each other to advance post-operative glioma analysis.

- **ToRAS Framework Development**
- **Extended Hybrid Architecture and Tumor-Region Analysis and stage prediction**.
- **Training and Evaluation**

ToRAS: We first established the ToRAS (Topology-Refined Attention Segmentation) baseline framework, built on a U-Net architecture with interchangeable CNN (ResNet, DenseNet, EfficientNet) and Transformer (MiT-B0) encoders. The methodology included a topology-aware preprocessing pipeline consisting of mask dilation, connected component filtering, and hole filling to address annotation noise. A spatial-channel Squeeze & Excitation (scSE) [10] attention mechanism was integrated into the decoder to enhance feature recalibration with patient-level 5-fold cross-validation on the MU-Glioma-Post dataset [11] (T1-weighted MRI).

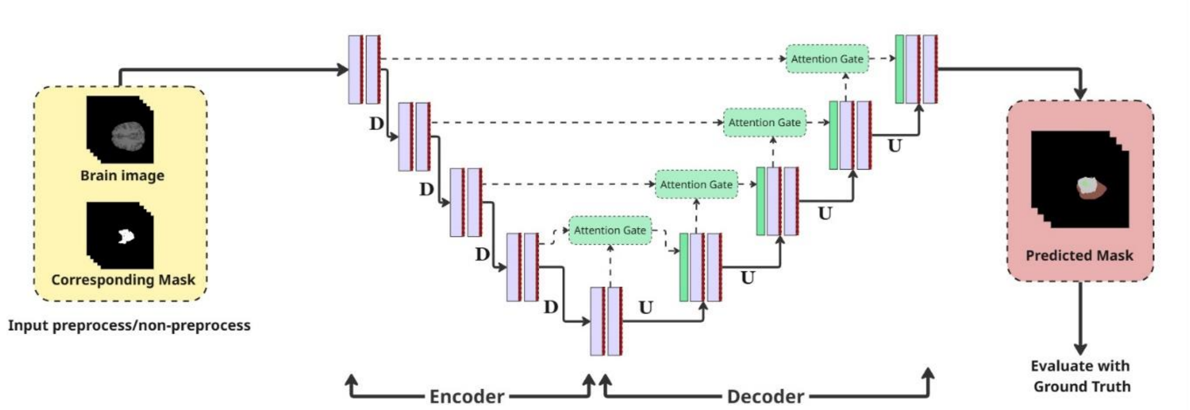

Figure 1.1: ToRAS Framework overview diagram

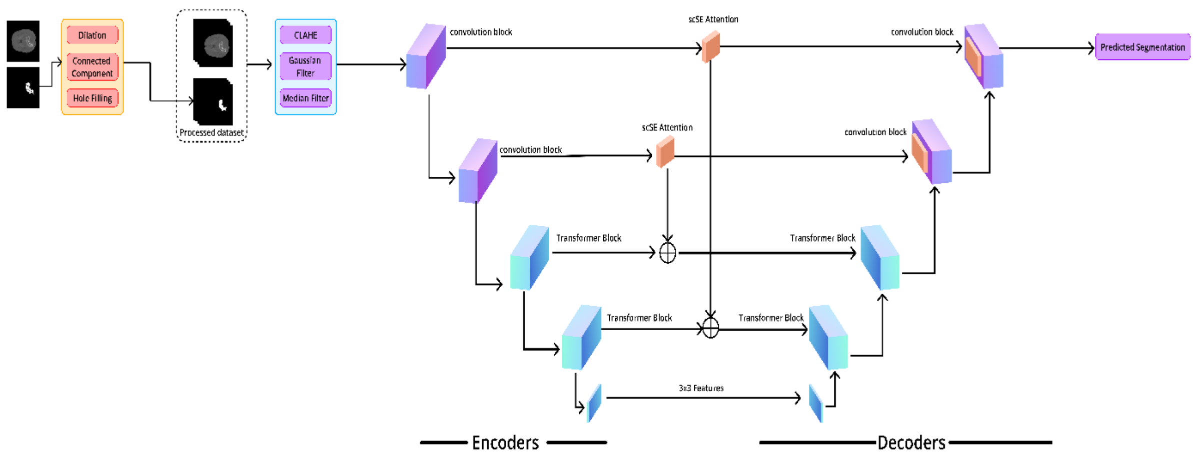

Figure 1.2: Extended hybrid architecture overview

Extended Hybrid Architecture and Tumor-Region Analysis and stage prediction: Building on ToRAS, we introduced a novel hybrid CNN-Transformer U-Net with a redesigned encoder-decoder structure: the encoder comprises 2 convolutional blocks followed by 3 transformer blocks, while the decoder uses 3 transformer blocks followed by 2 convolutional blocks, all augmented with scSE attention. The preprocessing pipeline was extended to include intensity-based enhancements (CLAHE, Gaussian filter, median filter) alongside the original morphological refinements.

Training and Evaluation: Both phases employed systematic ablation studies to evaluate architectural choices, attention mechanisms, and preprocessing effects. Models were trained using AdamW optimization, Dice loss, and extensive online augmentation (spatial and photometric transforms). Evaluation metrics included segmentation accuracy (IoU, Dice) and classification performance (accuracy, loss) across multiple learning rates and augmentation strategies. The entire framework was implemented in PyTorch, with code and models made publicly available to ensure reproducibility and support future benchmarking in post-operative glioma analysis.

1.5 Project Outcome

- **A Novel Hybrid Segmentation Framework**: Development of a reproducible, state-of-the-art hybrid CNN-Transformer architecture (ToRAS-Plus) capable of accurate binary segmentation of post-operative gliomas, establishing a new benchmark for the MU-Glioma-Post dataset.

- **An Extended Preprocessing Pipeline**: Publication of an open source preprocessing module that integrates topological refinement and intensity normalization to improve label consistency and model generalization in noisy clinical annotations.

- **Sub-Region Analysis**: Delivery of a two-stage pipeline that not only segments the tumor but also classifies key sub-regions to NETC, ET, SNFH, and RC providing granular diagnostic information to support treatment planning and monitoring.

- **Publicly Available Benchmark**: Release of complete code, trained models, and evaluation protocols to facilitate reproducibility, encourage further research, and accelerate clinical translation in post-operative neuro-oncological imaging.

- **Contributions to Medical AI Research**: Demonstration of how hybrid architectures and attention mechanisms can overcome limitations of purely convolutional or transformer-based models in complex, artifact-prone medical imaging tasks.

1.6 Organization of the Report

This report is organized into six chapters to systematically present the research on post-operative glioma segmentation using hybrid deep learning architectures.

Chapter 1: Introduction establishes the clinical and computational motivation for the study, outlines the research objectives, and summarizes the methodology and expected outcomes of the project.

Chapter 2: Background provides a comprehensive review of related work in glioma segmentation, including traditional and deep learning approaches, attention mechanisms, hybrid CNN-Transformer models, and preprocessing techniques in medical imaging, while identifying gaps in current research.

Chapter 3: Research Methodology details the proposed two-phase framework, including the ToRAS baseline model and its extension into a hybrid CNN-Transformer architecture. This chapter covers data preprocessing, model design, training strategies, and the integrated pipeline for tumor segmentation and sub-region classification.

Chapter 4: Implementation and Results describes the experimental setup, dataset specifications, software and hardware configurations, and presents the empirical results. This includes ablation studies, comparative performance analysis, and visual outcomes of the proposed models.

Chapter 5: Engineering Standards and Design Challenges discusses the engineering practices adhered to during the project, including reproducibility, ethical considerations, model scalability, and computational efficiency. It also addresses design challenges such as handling noisy annotations, integrating hybrid architectures, and ensuring clinical applicability.

Chapter 6: Conclusion summarizes the key findings of the research, highlights contributions to the field, acknowledges limitations, and suggests directions for future work

Chapter 2

Background

This chapter reviews key literature and concepts in glioma segmentation, focusing on deep learning approaches, attention mechanisms, hybrid CNN-Transformer models, and preprocessing techniques for post-operative MRI analysis, while identifying gaps that motivate this research.

2.1 Introduction

Glioma segmentation from MRI is a critical task in neuro-oncology, directly impacting diagnosis, treatment planning, and patient monitoring. While significant progress has been made using deep learning. In this particularly with convolutional neural networks (CNNs) and, more recently, vision transformers. The analysis of post-operative glioma presents unique challenges. These include surgical cavity artifacts, irregular residual tumor boundaries, heterogeneous imaging appearances, and noisy manual annotations.

2.2 Literature Review

To Literature review and to provide a structured and comprehensive overview in table 2.1, the discussion is organized into three critical thematic angles that reflect the evolution and current challenges in the field. The sections are:

a) Review & Surveys (Focus: Architectural Trends & Gaps)
b) Hybrid CNN-Transformer Models (Focus: Core Methodology)
c) Attention Mechanisms & Preprocessing (Focus: Performance Enhancement)

This tripartite structure allows for a systematic analysis of the state-of-the-art, from general field progression to specific technical implementations that directly inform the design of the proposed ToRAS framework.

Table 2.1: Summary of Structured Literature Reviewed

Author (s)	Year	Title	Methodology	Key Findings
		Review & Surveys (Focus: Architectural Trends & Gaps)		
Diana-Albelda et al [12]	2025	A Review on Deep Learning Methods for Glioma Segmentation, Limitations, and Future	Comprehensive review of 80+ models; categorizes into CNN-based, Pure Transformer,	Highlights a gap between high academic performance and practical clinical deployment, emphasizing the need for models that balance accuracy

		Perspectives.	and Hybrid CNN-Transformer.	with computational efficiency.
Ahamed [13]	2023	A review on brain tumor segmentation based on deep learning methods with federated learning techniques.	Surveys segmentation techniques and federated learning for privacy.	Discusses effective segmentation techniques on public datasets and identifies unsolved problems, including the need for robust multi-modality information fusion.
Netshamutshedzi, et al [14]	2025	A systematic review of the hybrid machine learning models for brain tumour segmentation and detection in medical images.	Systematic review of hybrid ML/DL models (e.g., SVM + CNN).	Finds that hybrid models (e.g., SVM + VGG-19) improve classification accuracy and reduce false positives but face challenges in generalizability and lack of explainability.
L. Zhang et al [15]	2022	A deep learning approach to glioma segmentation with improved preprocessing,	Applied improved backbones for multimodal glioma segmentation.	Demonstrated that advanced encoders (ResNet, DenseNet, EfficientNet) lead to substantial accuracy improvements.
Wang et al [16]	2022	Simulated MRI Artifacts: Testing Machine Learning Failure Modes.	Analyzed MRI artifacts and ML failure modes.	Highlights that models struggle with noisy annotations and surgical artifacts, a core challenge in post-operative cases.
Z. Zhang et al [17]	2022	Improved glioma segmentation using preprocessing techniques and deep learning models	Used mask dilation, connected components, hole filling.	Showed preprocessing refines ground-truth masks, improving segmentation consistency with noisy/incomplete annotations.
Xie et al. [18]	2021	SegFormer: Simple and efficient design for semantic segmentation with Transformers	Introduced SegFormer with MiT backbones.	Provided a modern, efficient pure-Transformer design for segmentation (source of MiT-B0 encoder).
L. Zhang et al [19]	2025	Alternate encoder and dual decoder CNN–Transformer networks for medical image segmentation (AD2Former)	Proposed AD2Former (hybrid CNN-Transformer).	Explicitly fuses local texture (CNN) and global context (Transformer) for medical segmentation.

Hybrid CNN-Transformer Models (Focus: Core Methodology)				
Zeineldin, et al [20]	2024	Explainable hybrid vision transformers and convolutional network for multimodal glioma segmentation in brain MRI	Proposes TransXAI, a hybrid CNN-Transformer (U-Net + ViT) for segmentation with explainable AI (XAI).	Achieves competitive segmentation by combining CNN's local feature extraction with ViT's global context. Introduces XAI (saliency maps) to build clinical trust.
Thottempudi, et al [21]	2025	An Explainable Hybrid CNN–Transformer Framework with Aquila Optimization for MRI-Based Brain Tumor	Presents a hybrid CNN-ViT model with Aquila Optimizer for feature selection and XAI (Grad-CAM, SHAP).	Achieves 97.2% accuracy in tumor classification. Demonstrates that effective fusion of local (CNN) and global (Transformer) features, enhanced by XAI, improves accuracy and trust.
Mynampati, et al [22]	2025	Revolutionizing Glioma Segmentation & Grading Using 3D MRI-Guided Hybrid Deep Learning Models	Develops a hybrid 3D U-Net with DenseNet-VGG classifier and multi-head attention.	Reports a high Dice coefficient (98%) and classification accuracy (99%). Shows the strength of combining segmentation and classification in a 3D pipeline with attention mechanisms.
Attention Mechanisms & Preprocessing (Focus: Performance Enhancement)				
Rasheed et al [23]	2024	Integrating Convolutional Neural Networks with Attention Mechanisms for Magnetic Resonance Imaging-Based Classification of Brain Tumors	Introduces a CNN integrated with a hybrid attention mechanism for tumor classification.	Achieves 98.33% accuracy. Demonstrates that attention mechanisms significantly improve model focus on diagnostically relevant regions, boosting performance.
Aiya et al [24]	2025	Optimized deep learning for brain tumor detection: a hybrid approach with attention mechanisms and clinical explainability	Proposes a hybrid model (VGG16 + attention mechanism) with Grad-CAM for explainability.	Achieves 99% test accuracy. Highlights that attention mechanisms promote better feature selection and that explainability (via Grad-CAM) is crucial for clinical adoption.
Preetha et al.[25]	2025	Brain tumor segmentation using multi-scale attention U-Net with EfficientNet-B4 encoder for enhanced MRI analysis	Multi-scale attention U-Net with EfficientNet-B4.	Improves boundary delineation and reduces false positives by focusing on relevant features.

2.3 Gap Analysis

Based on the comprehensive review from table 2.1, the following key research gaps have been identified in table 2.2, 2.3, 2.4, which this study aims to address. These gaps are summarized in the table and elaborated in the subsequent analysis.

Table 2.2: Domain-Specific Benchmarking

Description of the Gap	Lack of systematic evaluation and established performance baselines for post-operative glioma segmentation, particularly on the MU-Glioma-Post dataset.
Key Citations from Literature	[12, 13, 14] highlight a focus on pre-operative data (e.g., BraTS) and a lack of benchmarks for post-treatment complexities.
This Study's Contribution	Provides the first controlled, multi-faceted benchmark for the MU-Glioma-Post dataset, establishing reproducible baselines for future work.

Table 2.3: Different Strategy and Evaluation

Description of the Gap	Absence of controlled studies that simultaneously and comparatively evaluate the three key performance levers: advanced architecture, attention mechanisms, and data preprocessing.
Key Citations from Literature	[15, 17, 23, 24, 25] study components in isolation (e.g., backbones or attention or preprocessing) but not their integrated, comparative impact.
This Study's Contribution	Conducts systematic ablation studies to isolate and quantify the individual and combined effects of encoder choice, scSE attention, and topological preprocessing.

Table 2.4: Complexity vs. Necessity

Description of the Gap	Unresolved question of whether the inherent complexity of post-operative MRI (cavities, noise) necessitates advanced hybrid models, or if refined data with simpler architectures is sufficient.
Key Citations from Literature	[20, 21, 22] promote hybrid models, while [17, 25] show gains from preprocessing/attention alone. No study tests this directly on post-operative data.
This Study's Contribution	Directly tests this by comparing modern hybrid CNN-Transformer designs against refined strong CNNs within the same challenging post-operative domain.

2.4 Summary

This chapter has systematically reviewed the state-of-the-art in automated glioma segmentation, with a specific focus on the challenges and methodologies relevant to post-operative MRI analysis. The review was structured around three critical themes to build a comprehensive foundation. architectural trends highlighting a translational gap and lack of post-operative benchmarks, hybrid CNN-Transformer methodologies that fuse local and global features, and performance enhancement via attention and preprocessing. The subsequent gap analysis identified the lack of a systematic, comparative evaluation for post-operative cases as the primary research gap, which this study's ToRAS framework is designed to address.

Chapter 3

Research Methodology

This chapter details the research methodology for the two-phase development of the ToRAS framework for post-operative glioma segmentation. It begins with a high-level overview of the methodology and the proposed pipeline, followed by a detailed discussion of the design choices, an analysis of alternate solutions, and the project implementation plan.

3.1 Methodology

3.1.1 Overview

This research adopts a structured, two-phase experimental methodology to advance post-operative glioma segmentation. The first phase establishes the ToRAS (Topology-Refined Attention Segmentation) baseline by systematically evaluating the impact of different encoder backbones (CNN and Transformer), decoder attention (scSE), and a novel topology-aware preprocessing pipeline on the MU-Glioma-Post dataset. The second phase extends this foundation by designing and validating a novel hybrid CNN-Transformer U-Net architecture and a subsequent tumor sub-region classification pipeline, creating a comprehensive end-to-end system for post-operative analysis.

3.1.2 Proposed Methodology

The proposed methodology is executed as an integrated pipeline comprising four main stages:

Data Preparation & Preprocessing: Utilizing the MU-Glioma-Post dataset, this stage involves extracting T1-weighted MRI slices, converting them to a standard format, and applying a two-tier preprocessing strategy. This includes a topology-refinement module (dilation, connected-component filtering, hole filling) for ground-truth masks and intensity-based enhancements (CLAHE, Gaussian, median filtering) for the input images.

Model Development & Training (Stage 1: ToRAS Baseline): A 2D U-Net is implemented with interchangeable encoders (ResNet, DenseNet, EfficientNet, MiT-B0). Controlled ablation studies are conducted to evaluate performance with/without scSE attention and with/without topology preprocessing, using patient-level 5-fold cross-validation.

Model Development & Training (Stage 2: Advanced Hybrid Model): A custom U-Net variant is developed, featuring a hybrid encoder (convolutional blocks followed by transformer blocks) and a symmetrical hybrid decoder. This model integrates scSE attention and is trained using the refined preprocessing pipeline from Stage 1.

Evaluation & Analysis: Models are evaluated using standard segmentation metrics

(Dice, IoU, Precision, Recall). The best-performing segmentation mask from Stage 2 is then used to crop the tumor region, which serves as input to a separate multi-label classifier (e.g., DenseNet121, ViT) to predict the four clinical sub-regions (NETC, ET, SNFH, RC).

3.1.3 Stage 1: ToRAS Baseline

3.1.3.1. Data Preparation framework: For this study we use T1-weighted MRIs for 202 subjects and 91,915 paired image and their corresponding mask slices among 203 subjects. One subject was excluded from this study because of the missing corresponding mask. In case for the binary tumor segmentation mask, all the tumor subregion annotations per slice are combined into a single foreground label (tumor = 1; background = 0).

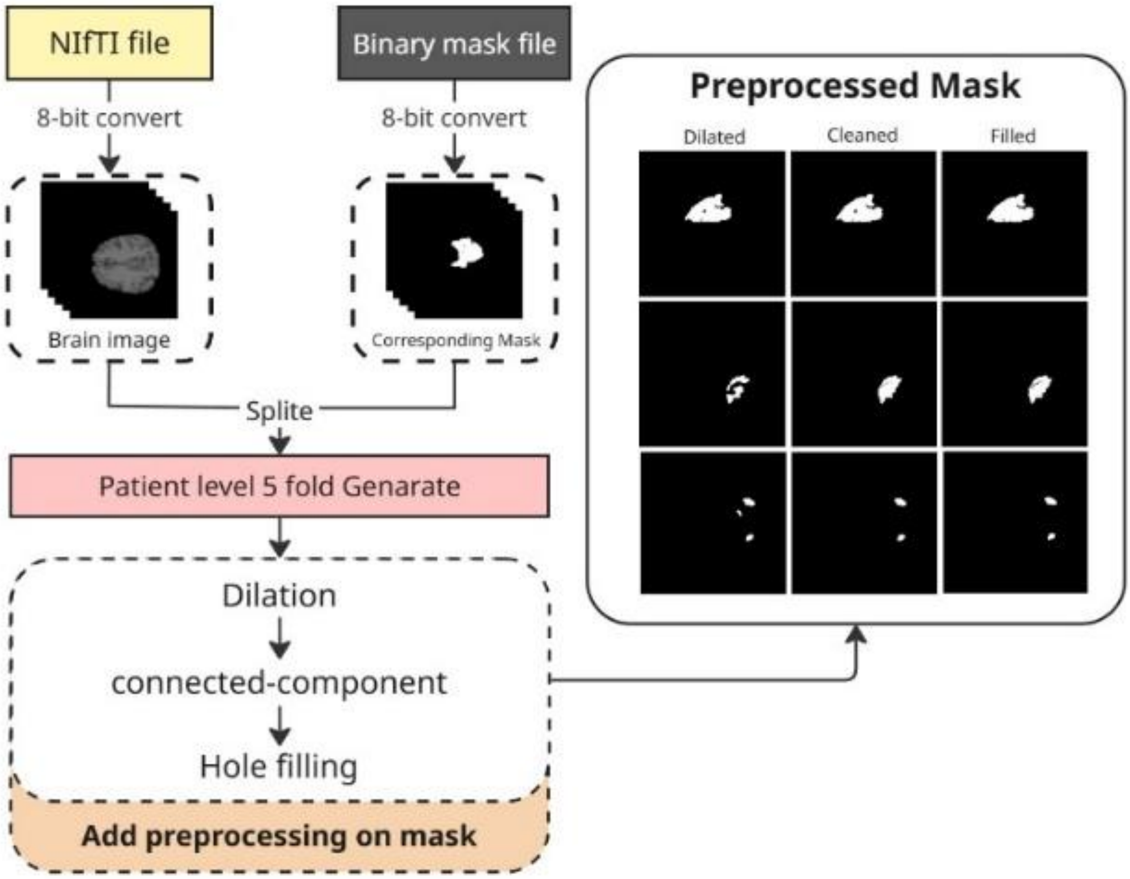

Figure 3.1: Preprocessing Overview

First for all axial slices from the NIfTI brain MRI volume and mask are convert to 8-bit PNG images. In order to avoid data leakage, we apply patient level 5-fold cross validation. In each run, one-fold is held out, while the remaining four folds are used for training and averaged across all five runs. Each split contains approximately 72,250 training slices per run, with the remainder assigned to the test fold.

To reduce incomplete or noisy annotations, we applied a topology-refinement framework consisting of three steps as shown in Fig 1. First, each mask was subjected to elliptical dilation with a kernel size of 7 to bridge small gaps and better align the mask with the underlying ground truth. Second, a connected-component analysis was performed to retain only the largest connected region, while components smaller than 50 pixels were removed and set to zero. Finally, hole filling was applied to eliminate internal voids, ensuring contiguous tumor regions without structural artifacts.

3.1.3.2. Architecture & Backbone Selection: We adopt a 2D U-Net with a different encoder and a fixed U-Net decoder. U-Net follows an encoder and decoder design with skip connections. The encoder progressively downsamples the feature maps to capture increasingly abstract, context informative representations, while the decoder upsamples back to the input resolution to recover spatial detail. At each resolution, skip connections concatenate encoder features with the decoder features, helping the model localize fine structures.

ResNet-50 is a CNN with 50 layer residual network using identity skip connections to ease vanishing gradient optimization and preserve information across layers. Residual blocks are effective general purpose feature extractors and provide a strong segmentation baseline. Secondly DenseNet-201 employs dense connectivity map which each layer receives all previous feature maps and encouraging feature reuse and improved gradient flow. This often use strong representation power with comparatively efficient parameter usage.

On the other hand, EfficientNet-B5 uses compound scaling depth, width, resolution and inverted bottlenecks with squeeze and excitation, offering a good accuracy efficiency balance that can match or surpass heavier backbones on medical images. Last but not least MiT-B0 Transformer a hierarchical Vision Transformer with overlapping patch embeddings and multi head self-attention, producing multi scale feature maps. MiT captures long-range dependencies known as global context that complement the local texture modeling of CNNs.

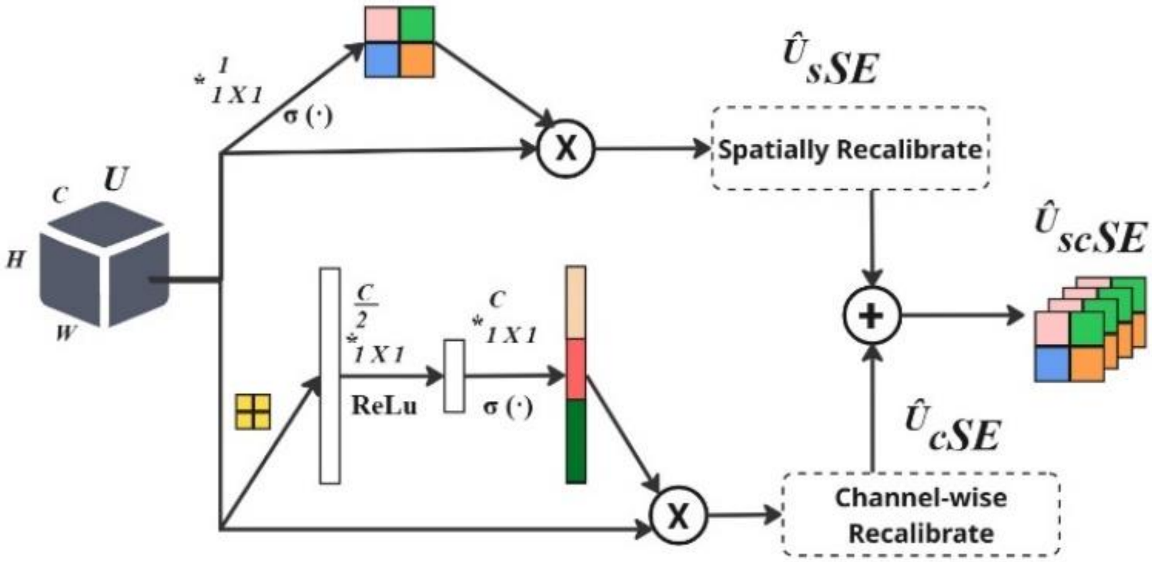

Figure 3.2: Spatial and Channel Squeeze & Excitation Block (scSE) Overview

We also add decoder attention via scSE block. which is inserted after each decoder block's convolutional operations and before the feature map is passed onward, combining channel wise squeeze excitation with a spatial gate to emphasize informative structures and suppress clutter. As shows in Fig 2, the scSE mechanism combines channel-wise squeeze-excitation with a spatial excitation gate to emphasize informative structures while suppressing clutter. Specifically, the scSE block is a concurrent formulation of the two SE modules, recalibrating the feature map both spatially and channel-wise (in equation 1).

The output feature map $\widehat{U}_{Sc}SE$ is obtained through element-wise addition of the channel and spatial excitations:

$$\widehat{U}_{Sc}SE = \widehat{U}_{c}SE + \widehat{U}_{S}SE \qquad (1)$$

A location of the input feature map U receives higher activation when it is simultaneously emphasized by both channel re-scaling and spatial re-scaling. This concurrent recalibration encourages the network to learn more meaningful feature maps that are relevant across both spatial and channel dimensions.

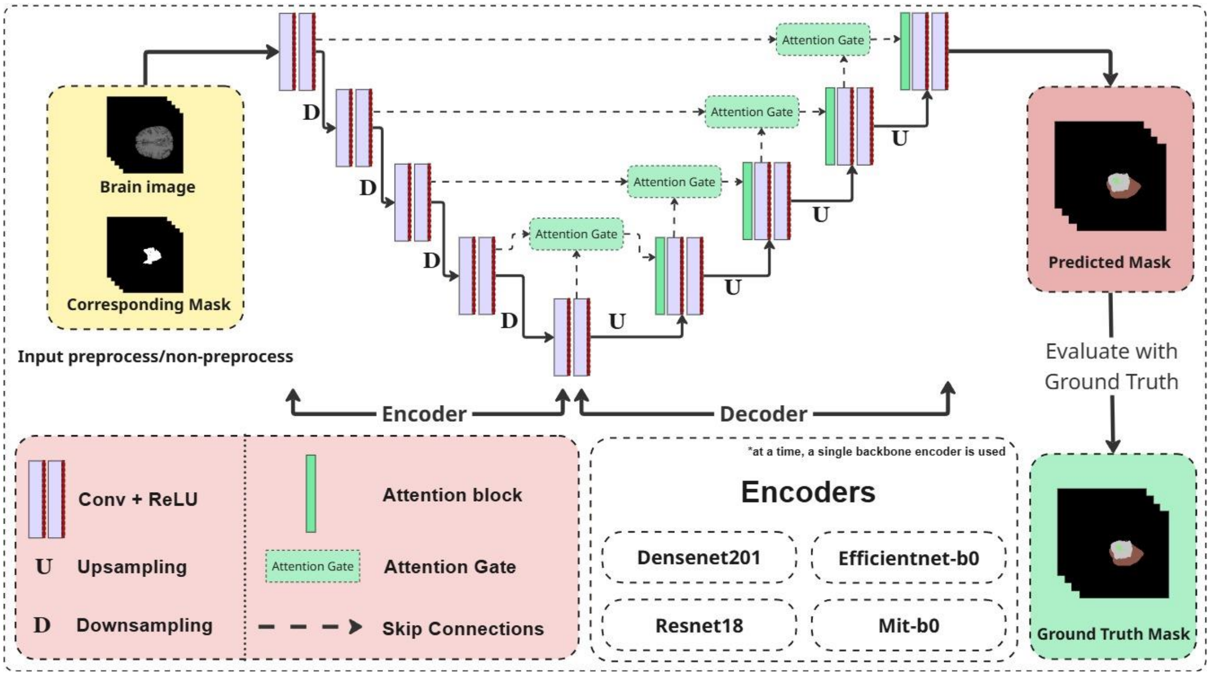

Figure 3.3: Overall workflow for the stages of preprocessing, model training, and evaluation

3.1.4 Stage 2: Advanced Hybrid Model

Building upon the findings from the ToRAS baseline, Stage 2 introduces a novel, custom designed hybrid CNN-Transformer architecture. This stage retains the proven preprocessing pipeline but replaces the standard U-Net with a purpose-built encoder-decoder to more effectively capture the complex features of post-operative gliomas.

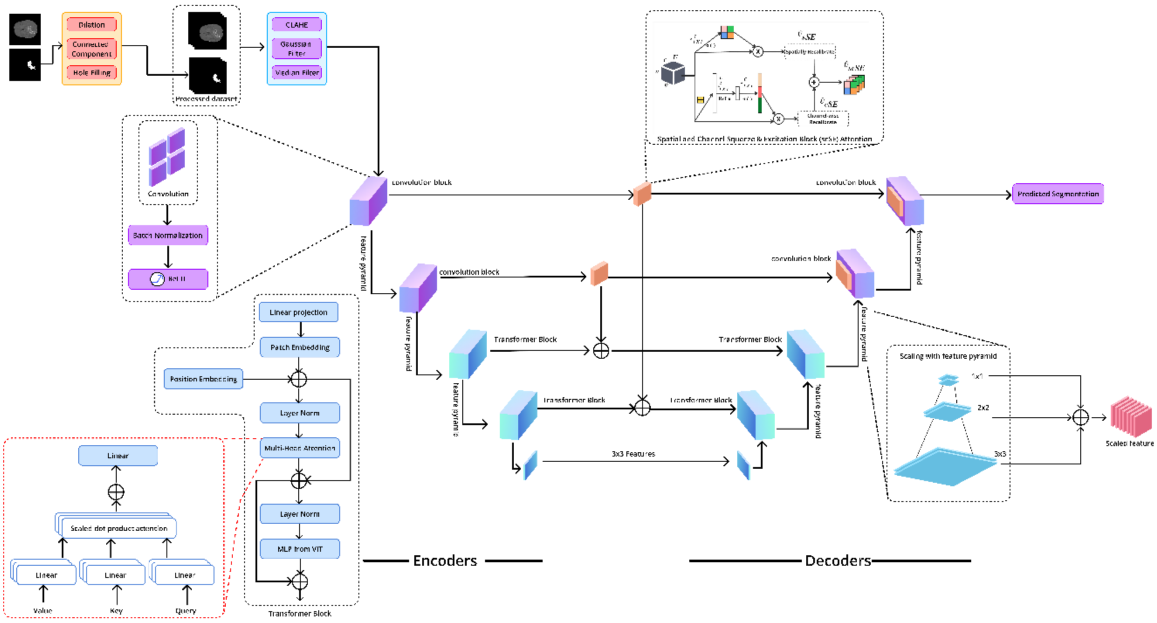

Figure 3.4: Overall workflow for the stages of preprocessing, model training, and evaluation for hybrid framework

3.1.4.1. Data Preparation & Extended Preprocessing Framework: The data foundation remains the MU-Glioma-Post dataset, utilizing the same 202 subjects and 91,915 T1-weighted MRI slices as Stage 1. The patient-level 5-fold cross-validation strategy is maintained to ensure consistency and prevent data leakage.

The preprocessing framework is extended from Stage 1 to further enhance input quality:

- Topology-Refined Masks: The identical three-step morphological refinement (elliptical dilation with kernel = 7, largest connected-component filtering with area threshold > 50 pixels, and hole filling) is applied to all ground-truth masks.

- Extended Image Preprocessing: In addition to standard normalization, each MRI slice undergoes an intensity-based enhancement sequence:

    - Contrast Limited Adaptive Histogram Equalization (CLAHE): Applied with a clip limit of 2.0 and tile grid size of 8x8 to improve local contrast.

    - Filtering Stack: A Gaussian filter (kernel size=3) is applied for noise reduction, followed by a median filter (kernel size=3) to preserve edges while suppressing speckle noise.

This two-pronged approach ensures both the structural integrity of the training labels and the enhanced clarity of the input images.

3.1.4.2. Advanced Hybrid CNN-Transformer Architecture: The core innovation of Stage 2 is a redesigned U-Net variant that systematically integrates convolutional inductive bias with Transformer-based global context modeling across its depth.

Overall Structure: The network follows a symmetrical encoder-decoder pattern with skip connections. The key modification is the replacement of standard encoder/decoder blocks with hybrid sequential blocks.

3.1.4.3. Hybrid Encoder Design (Top-Down Path): The encoder consists of two primary modules repeated with down sampling:

- Dual Convolutional Block: Each block contains two sequences of:
  - 3x3 Convolutional Layer
  - Batch Normalization
  - ReLU Activation
  - A 3x3 MaxPool operation follows these blocks for downsampling.

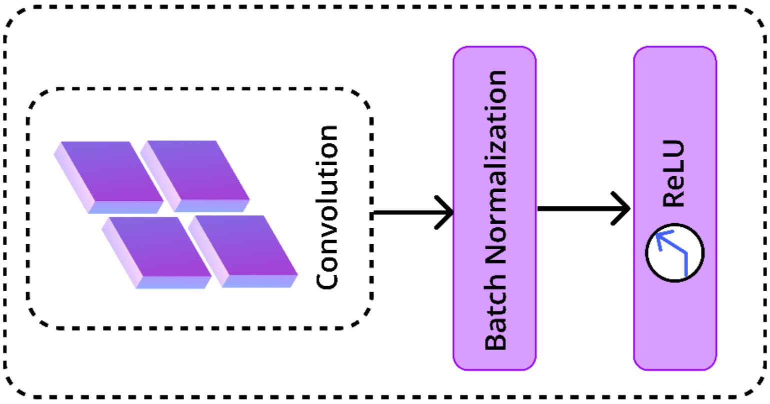

Figure 3.5: Convolutional block diagram

- Triple Transformer Block: Following the convolutional blocks, three sequential Transformer blocks process the feature maps. Each Transformer block implements:
  - Patch Embedding & Position Encoding: Linear projection of the feature map into a sequence of patch tokens, augmented with learnable positional encodings.
  - LayerNorm 1 to Multi-Head Self-Attention (MSA): Captures long-range dependencies across all patch tokens. A residual connection adds the original token sequence.
  - LayerNorm 2 to Multi-Layer Perceptron (MLP): A two-layer feed-forward network (as used in standard ViT) for feature transformation. A residual connection is also applied here.

The output is a contextually enriched feature map ready for the next stage or the decoder via skip connections.

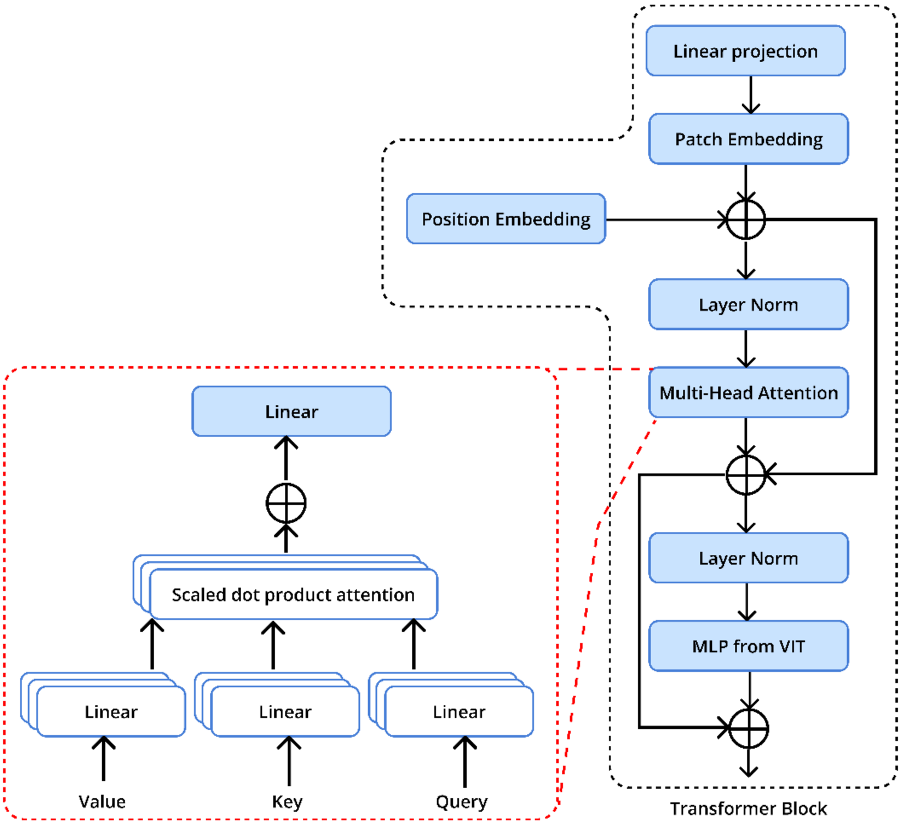

Figure 3.6: Transformer block diagram

3.1.4.4. Hybrid Decoder Design (Bottom-Up Path): The decoder mirrors the encoder's hybrid design in reverse:

- Triple Transformer Block: Three Transformer blocks (identical in structure to the encoder's) first process the upsampled features from the lower stage, refining global context.
- Dual Convolutional Block: Two convolutional blocks (Conv-BN-ReLU) then locally refine the features. A transposed convolution is used for upsampling before these blocks.
- Attention-Guided Fusion: At each resolution level, features from the corresponding encoder path are concatenated with the decoder features. A Spatial and Channel Squeeze & Excitation (scSE) block is inserted post-concatenation to recalibrate the combined feature map, emphasizing spatially and channel-wise relevant information for precise boundary recovery.

3.1.4.5. Tumor Sub-Region Classification Pipeline: Following the tumor segmentation, a subsequent pipeline is deployed for detailed sub-region analysis, directly supporting clinical assessment.

➢ Multi-Label Classification Model: The cropped ROI serves as input to a separate, dedicated classification network. A pre-trained encoder (e.g., DenseNet121, EfficientNetB5, or Vision Transformer) is fine-tuned as a feature extractor, followed by a classifier head with four output neurons.

- Classification Targets: The model is trained to predict the four clinically defined labels simultaneously:

  - Label 1: Non-enhancing Tumor Core (NETC)
  - Label 2: Surrounding Non-enhancing FLAIR Hyperintensity (SNFH)
  - Label 3: Enhancing Tissue (ET)
  - Label 4: Resection Cavity (RC)

This end-to-end system from enhanced input to binary segmentation to multi label sub region prediction forms the complete advanced framework for comprehensive post-operative glioma analysis.

3.1.5 Data Flow Diagram

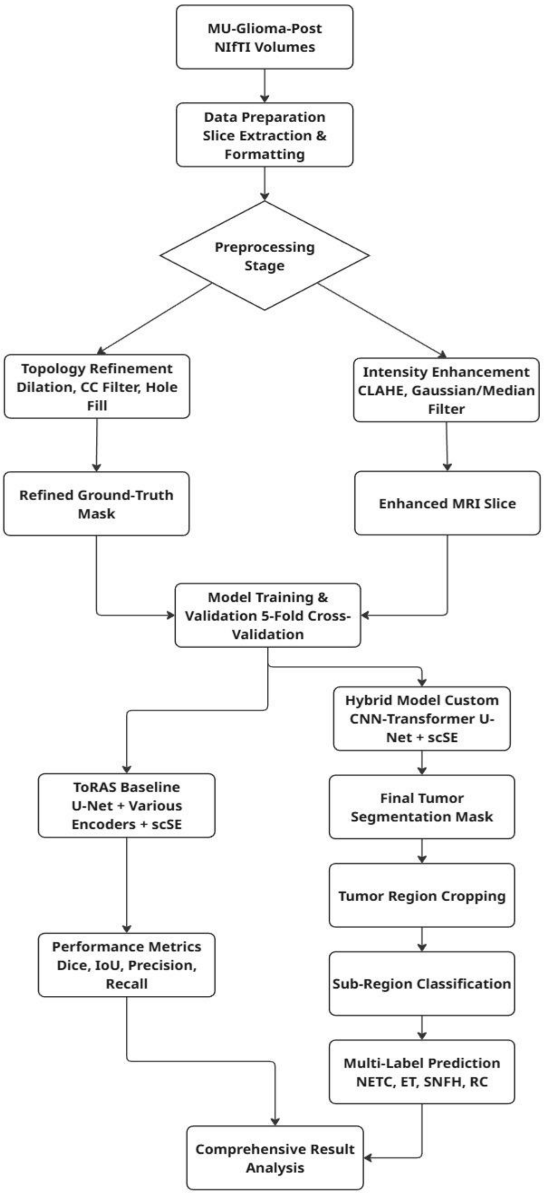

Figure 3.7: Data Flow Diagram for both framework

3.1.6 UI Design

We develop an implementation of the previous studies try to see the results. Here is the UI Design of this implementation:

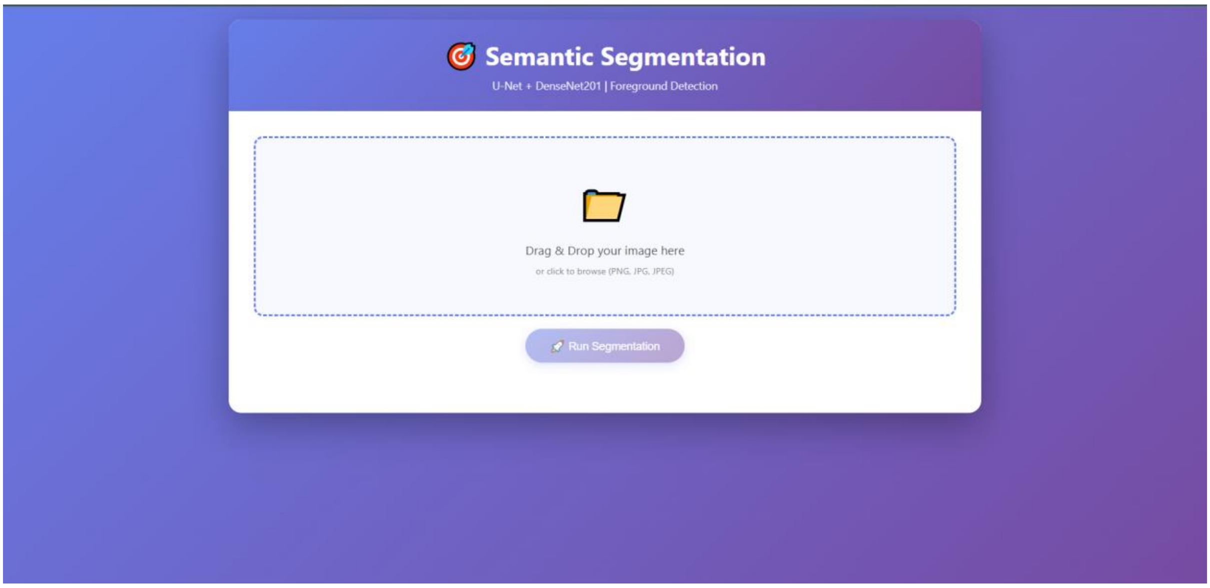

Figure 3.8: Web Implementation

Requirements for developing this web interface:

- **Web Framework**: Flask>=3.0.0 (for creating the web server and API endpoints)
- **Deep Learning Core**: torch>=2.2.0, torchvision>=0.17.0 (for loading and running the trained PyTorch model)
- **Image Processing**: opencv-python>=4.8.0, Pillow>=10.0.0 (for handling image uploads, preprocessing, and visualization)
- **Numerical Operations**: numpy>=1.24.0 (for array manipulations)
- **Model Utilities**: segmentation-models-pytorch>=0.3.3 (provides pre-trained encoder backbones and utilities, if used)

3.2 Detailed Methodology and Design

3.2.1 Dataset: MU Glioma Post

Data was sourced from The Cancer Imaging Archive's MU-Glioma-Post dataset, containing multi-modal MRI scans and segmented tumor labels. Each subject's imaging includes sequences such as T1-weighted (pre and post-contrast), T2-weighted, and FLAIR scans. The MU-Glioma-Post dataset was obtained from TCIA. It includes post-operative MRI scans in NIfTI format for each patient, accompanied by segmentation labels and metadata such as patient demographics and tumor location. The data is in NIfTI format and stored with standardized metadata. Preprocessing includes:

- Skull stripping: Using FSL BET [26] to remove non-brain tissues.

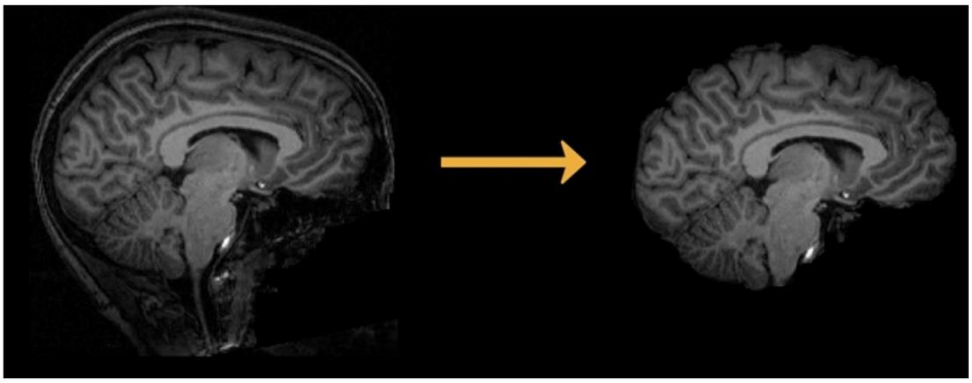

Figure 3.9: Preprocessing for Brain Extraction

- Intensity normalization: Adjusting histogram distributions for uniformity.
- Resampling: Standardizing voxel dimensions to $1\times1\times1$ mm^3.
- Co-registration: Aligning modalities with ANTs affine and SyN transformations [27].
- Meta data: This dataset contain also a very large range of Clinical Data such as: Demographic, Diagnosis, Molecular Test, Treatment, Follow-Up, Other.

Meta DATA: The MU-Glioma-Post dataset includes comprehensive clinical metadata that complements the imaging data with valuable patient context. Demographics cover Patient_ID, Sex at Birth, Race, and Age at Diagnosis, supporting population-level analysis. Diagnosis fields include Primary Diagnosis, Tumor Grade, history of previous brain tumors, biopsy status, and details of progression events with associated timelines. Treatment records outline surgical interventions, chemotherapy regimens, radiation therapy (dose, fractions, dates), and additional modalities such as Brachytherapy, Immunotherapy, and other specialized therapies. Follow-up data capture survival status, time-to-death, MRI timepoints, and intervals between diagnosis, progression, and treatment milestones. Other fields record hospice care status, previous surgeries, and non-standard treatments. Together, these data points enable integrated analyses that combine imaging, clinical, and treatment histories for improved segmentation, classification, and progression modeling.

Table 3.1: Meta data from the dataset.

Column Name	Data Type	Missing Values	Unique Values
Patient_ID	object	0	203
Sex at Birth	object	0	2
Race	object	0	4
Age at diagnosis	int64	0	64
Primary Diagnosis	object	0	6
Grade of Primary Brain Tumor	object	0	5
Stereotactic Biopsy before Surgical Resection	int64	0	2
Progression	int64	0	2
Time to First Progression (Days)	float64	51	116
Type of 1st Progression	int64	0	4
Second Progression/Recurrence	int64	0	2
Type of 2nd Progression	int64	0	4
Multiple surgeries	int64	0	2
Hospice	int64	0	2
Overall Survival (Death)	int64	0	2
Time To Death (Days)	float64	107	85
IDH1 mutation	int64	0	3
IDH2 mutation	int64	0	2
1p/19q	int64	0	9
ATRX mutation	int64	0	4
MGMT methylation	int64	0	4
BRAF V600E mutation	int64	0	3
TERT promoter mutation	int64	0	3
Chromosome 7 gain and Chromosome 10 loss	int64	0	2
H3-3A mutation	int64	0	2
EGFR amplification	int64	0	3
PTEN mutation	int64	0	2
CDKN2A/B deletion	int64	0	2
TP53 alteration	int64	0	2
Other mutations/alterations	object	162	34
Previous Brain Tumor	object	0	3
Type of previous brain tumor	object	190	7
Year of previous surgery	float64	190	9
Grade of Previous brain tumor	object	192	5
Number of days from Diagnosis to First surgery or procedure	int64	0	44
Initial Chemo Therapy	object	74	1
Name of Initial Chemo Therapy	object	74	2
Number of days from Diagnosis to Initial Chemo Therapy Start date	float64	80	52
Number of days from Diagnosis to Initial Chemo Therapy end date	float64	80	61

Column Name	Data Type	Missing Values	Unique Values
Radiation Therapy	object	63	3
Number of days from Diagnosis to Radiation Therapy Start date	float64	69	60
Number of days from Diagnosis to Radiation Therapy end date	float64	69	68
Dose	object	76	10
Number of Fractions	float64	76	7
Number of days from Diagnosis to date of First Progression	float64	52	118
Number of days from Diagnosis to date of Further Progression	float64	121	61
Treatment started after 2nd progression	object	186	9
Days from Diagnosis to new treatment	float64	185	13
Additional Therapy	object	94	2
Cycle length of Additional Therapy (q days)	float64	94	3
Number of Days from Diagnosis to Starting Additional Therapy	float64	96	63
Number of Days from Diagnosis to Complete Additional Therapy	object	110	73
Number of Cycles of Additional Therapy	object	82	18
2nd_Additional Therapy	object	187	8
Cycle length of 2nd_Additional Therapy (q days)	object	187	5
Number of Days from Diagnosis to Starting 2nd_Additional Therapy	float64	187	12
Number of Days from Dagnosis to Complete 2nd_Additional Therapy	object	190	9
Number of Cycles of 2nd_Additional Therapy	object	182	6
Immuno therapy	object	150	4
Cycle length of Immunotherapy (q days)	object	152	4
Number of Days from Diagnosis to Start Immunotherapy	float64	152	43
Number of Days from Diagnosis to Complete Immunotherapy	object	171	24
Number of Cycles of Immunotherapy	object	139	17
Brachy therapy	object	185	3
Number of Days from Diagnosis to the day of Insertion of Brachytherapy	float64	185	13
Other Types of Therapy (LITT, more chemo, proton therapy)	object	142	8
Number of Days from Diagnosis to Start Other Additional Therapy	object	142	47
Number of Days from Diagnosis to Complete Other Additional Therapy	object	179	20
Number of Days from Diagnosis to 1st MRI (Timepoint_1)	float64	16	95
Number of Days from Diagnosis to 2nd MRI (Timepoint_2)	float64	65	96

Column Name	Data Type	Missing Values	Unique Values
Number of Days from Diagnosis to 3rd MRI (Timepoint_3)	float64	94	81
Number of Days from Diagnosis to 4th MRI (Timepoint_4)	float64	137	56
Number of Days from Diagnosis to 5th MRI (Timepoint_5)	float64	157	40
Number of Days from Diagnosis to 6th MRI (Timepoint_6)	float64	152	46

After analyzing the data, a heatmap was generated to visualize the correlation between various imaging derived features and the available clinical metadata. This heatmap served as a powerful exploratory tool, enabling the identification of patterns such as strong associations between certain MRI intensity profiles and tumor grades, as well as potential links between volumetric measurements and recurrence indicators. By mapping feature intensities and statistical correlations in a color-coded format, we were able to quickly pinpoint which variables may hold predictive value for segmentation refinement, tumor classification, and progression forecasting. Such visual analysis not only informed the feature selection process for model training but also provided clinical insights that could guide radiologists in interpreting post-operative changes more effectively.

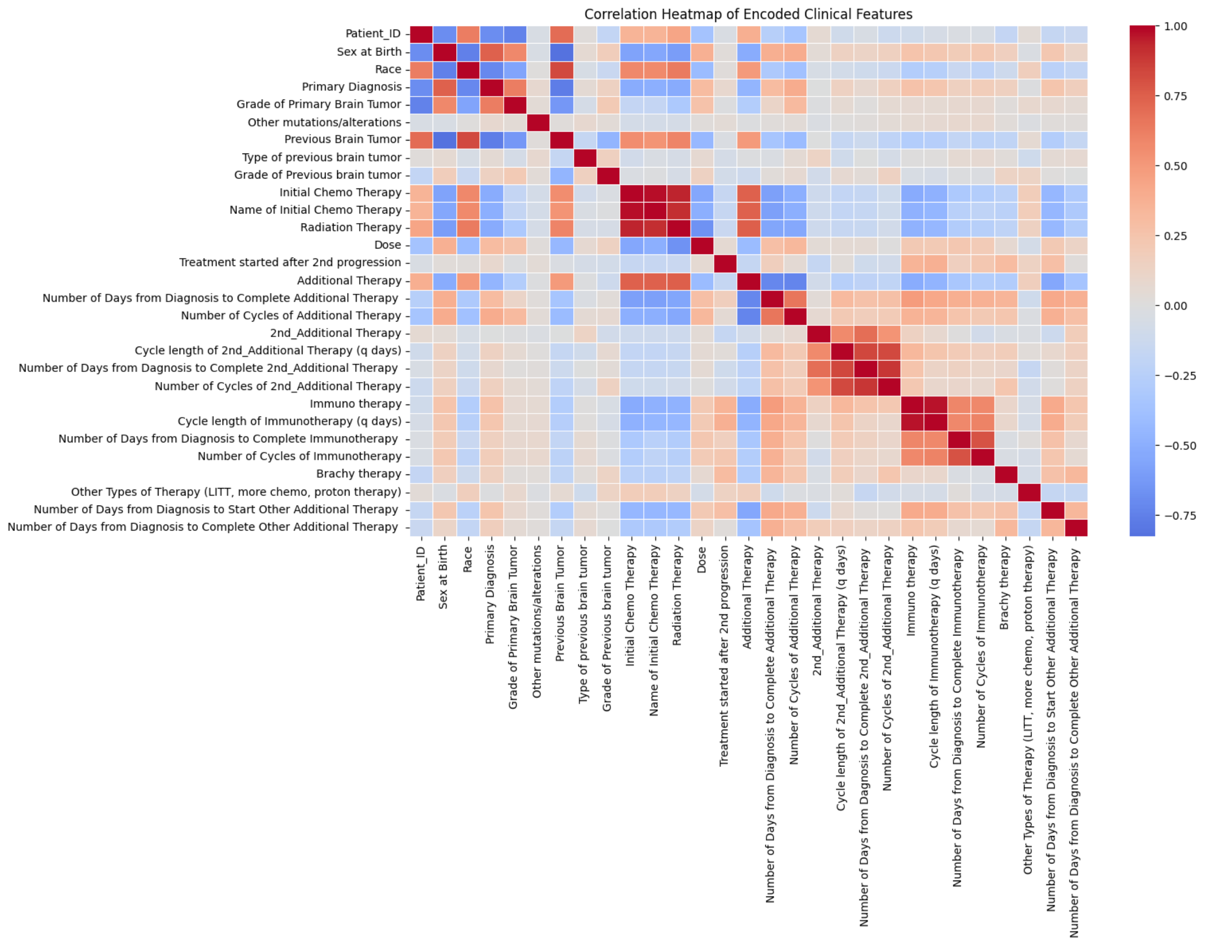

Figure 3.10: Find Co-relation heatmap from the data

3.2.2 Visualization of every angle of metadata

A comprehensive, slice-level inspection of the NIfTI volumes was performed alongside an analysis of the associated clinical metadata to understand data heterogeneity and potential confounders. The dataset provides detailed treatment history, including fields such as 'Name of Initial Chemotherapy', 'Additional Therapy', 'Immunotherapy', and 'Treatment started after 2nd progression'. Here is some visualization of given metadata:

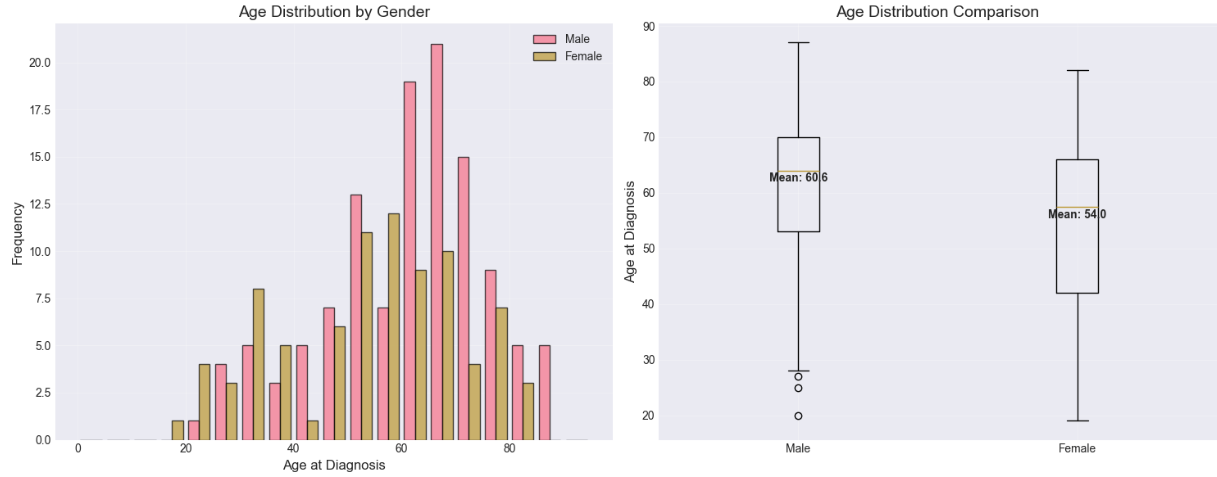

Figure 3.11: Age distribution by gender

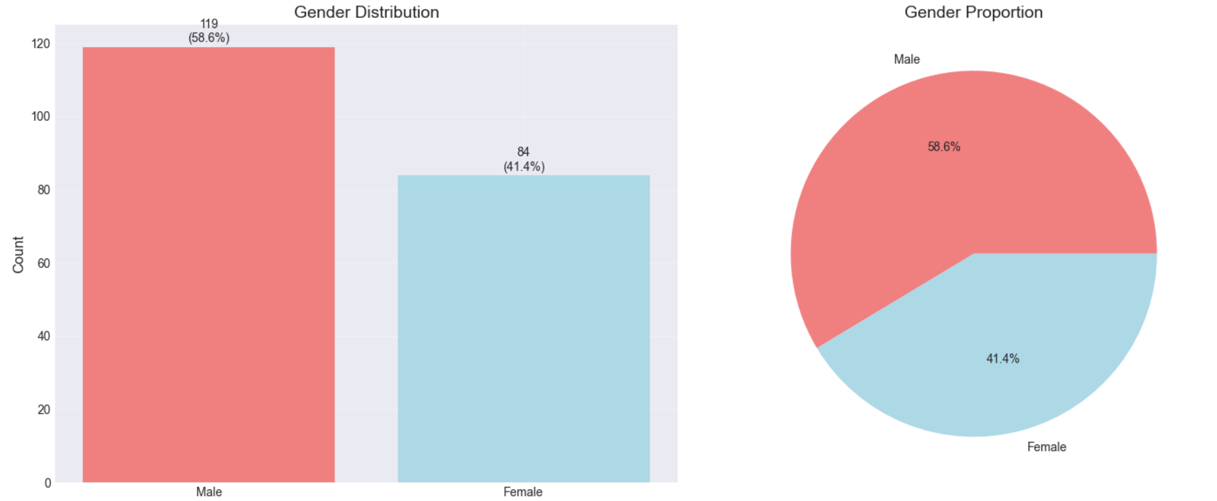

Figure 3.12: Gender distribution from the data

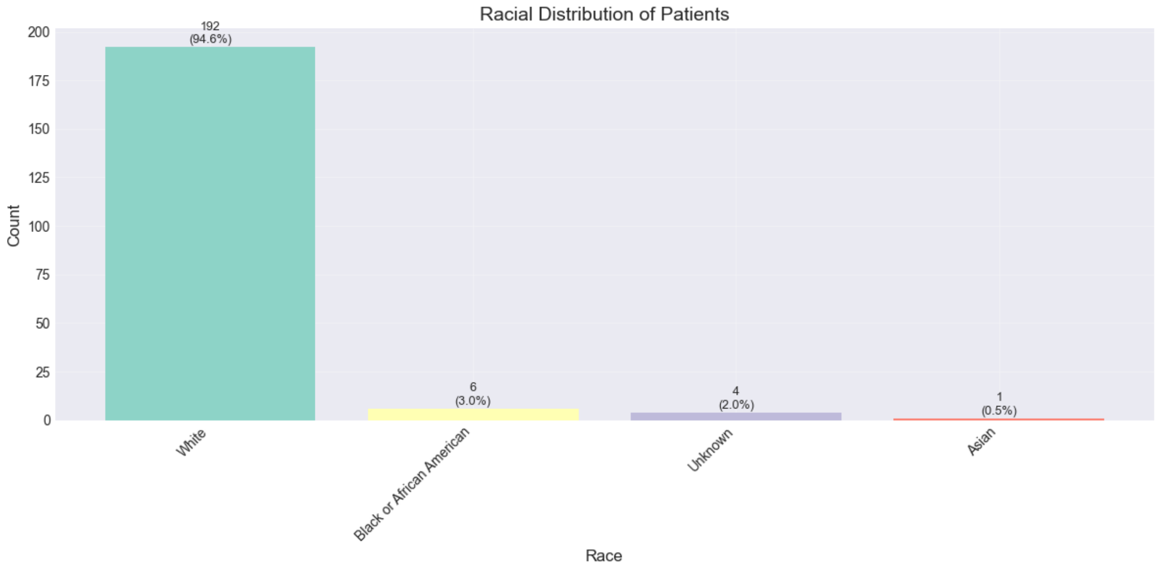

Figure 3.13 Race distribution from the data.

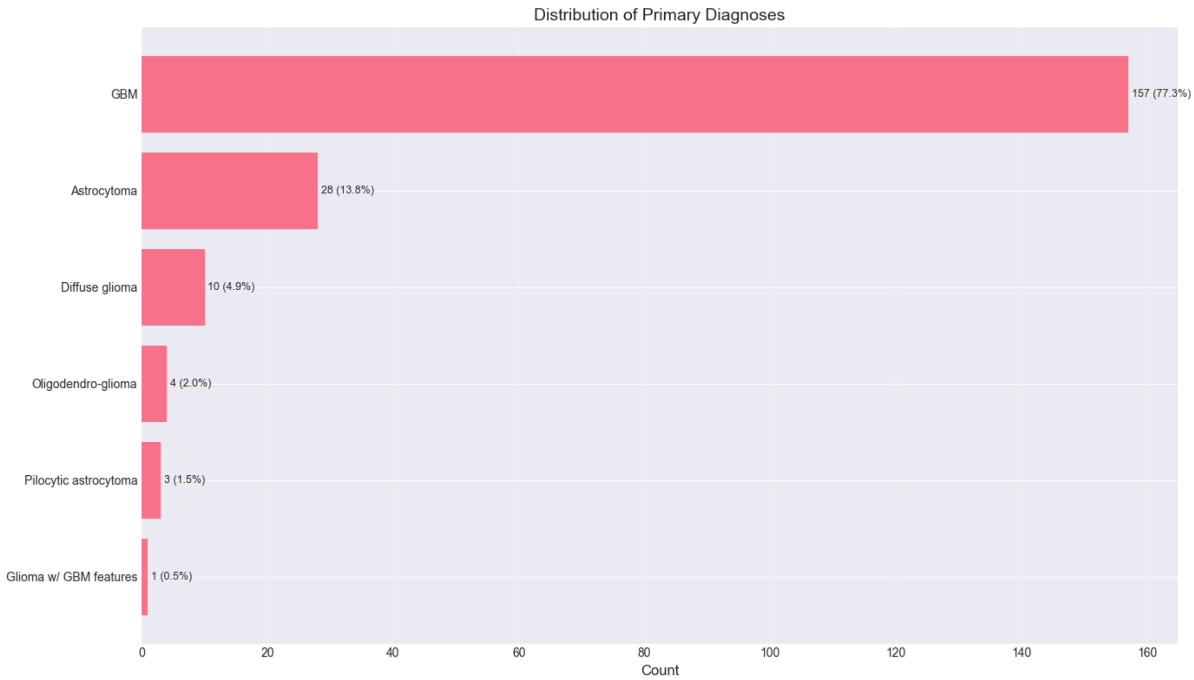

Figure 3.14: Distribution of primary diagnoses from the data

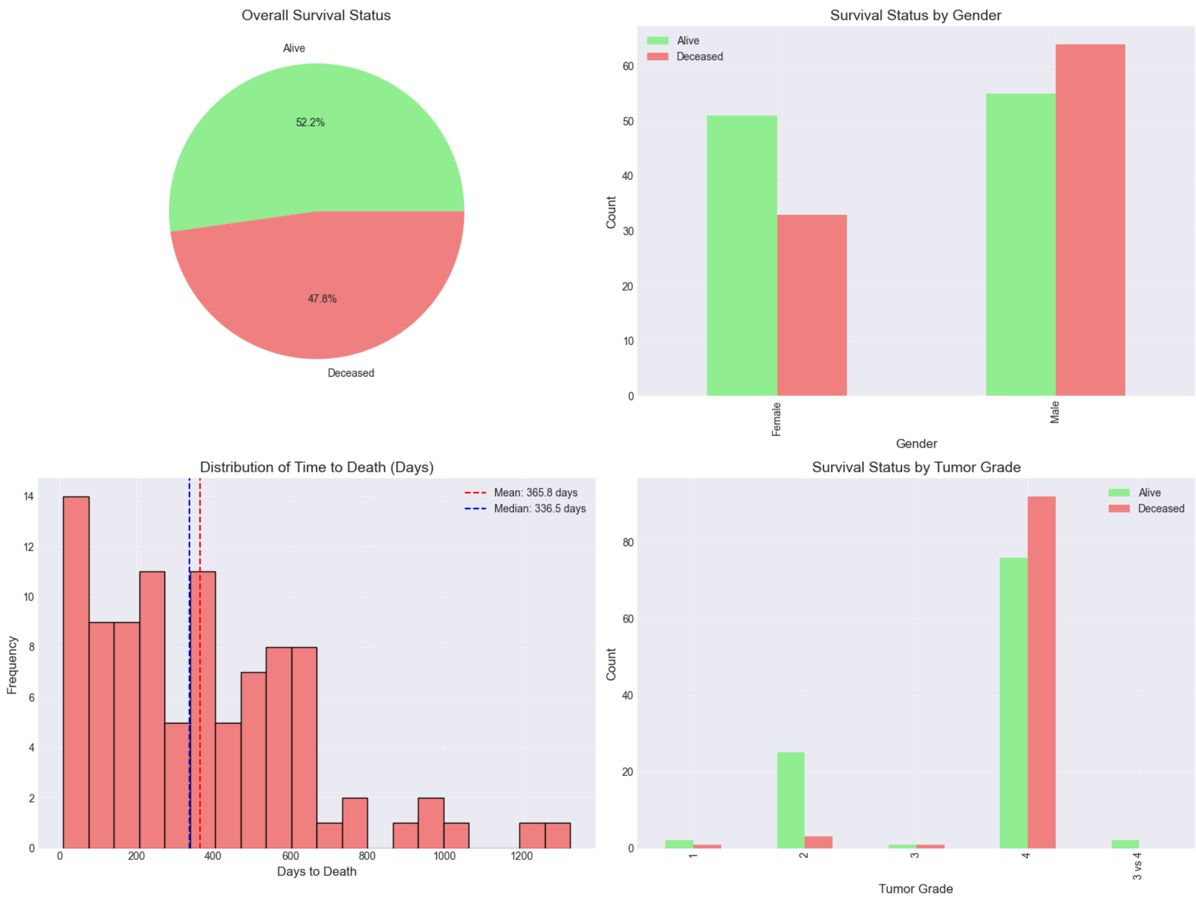

Figure 3.15: Survival analysis

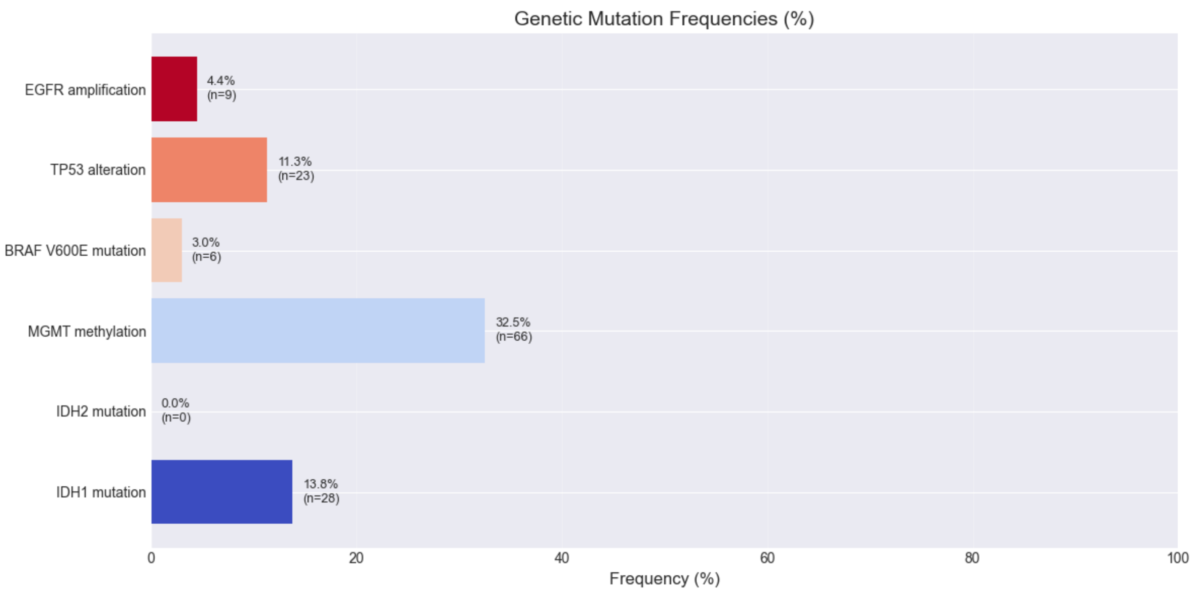

Figure 3.16: Genetic mutations of the data

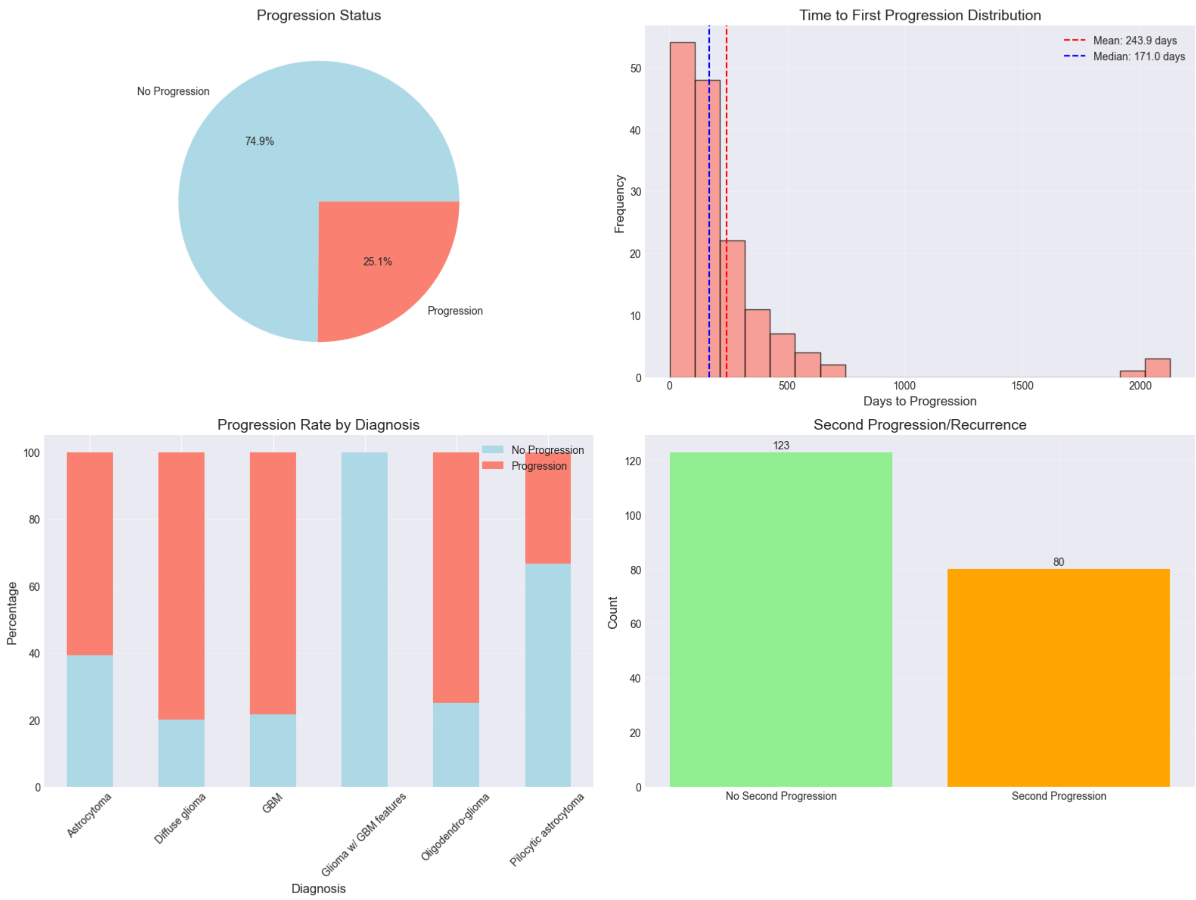

Figure 3.17: Progression of entire dataset's subjects

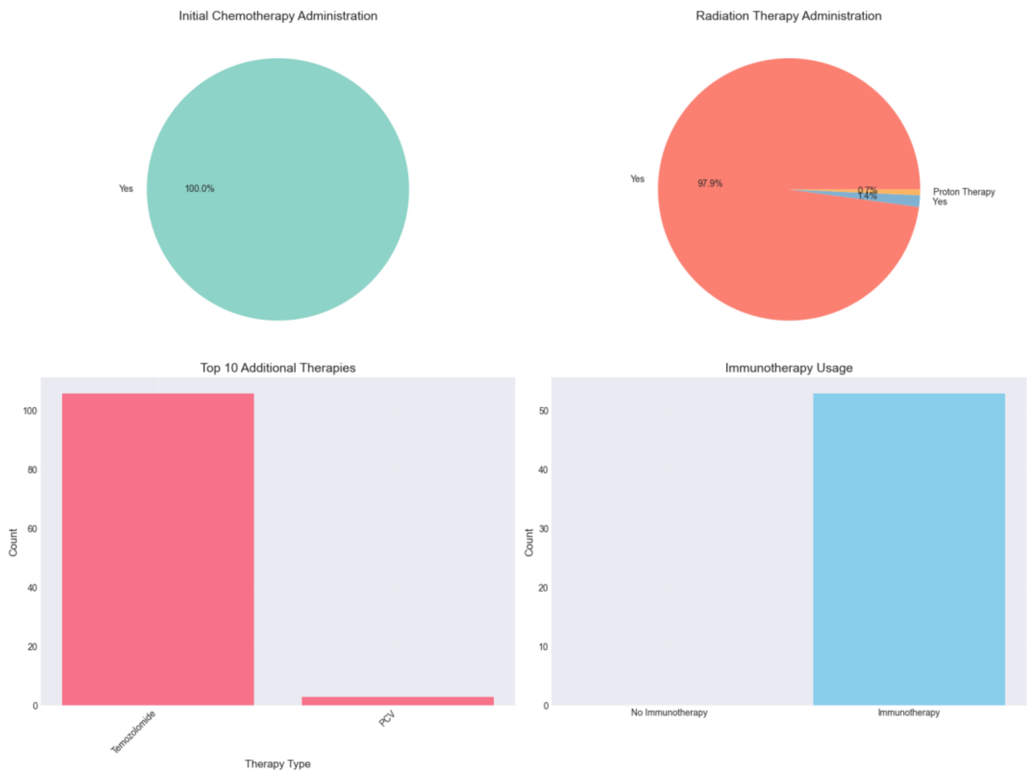

Figure 3.18: Therapy type.

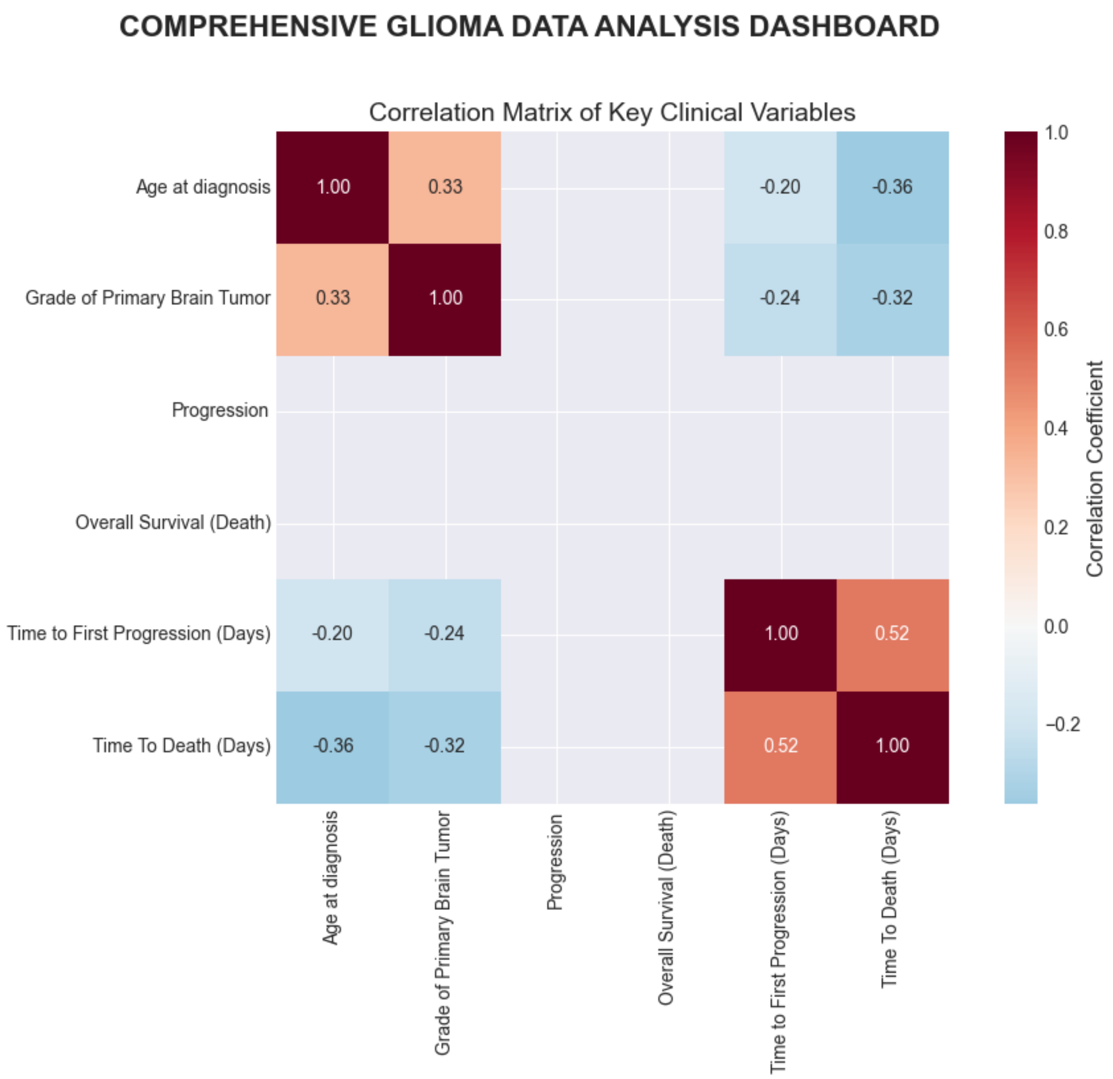

Figure 3.19: Comprehensive Glioma Data Analysis

3.2.3 Architectural Design Choices

The U-Net architecture, a fully convolutional network, is specifically engineered for biomedical image segmentation, characterized by a symmetric encoder-decoder structure. The encoder path performs progressive down-sampling through convolutional and pooling operations to extract hierarchical contextual features and increase the receptive field. The decoder path utilizes up-sampling and transposed convolutions to restore spatial resolution for precise pixel-wise localization. Crucially, skip connections directly link corresponding feature maps from the encoder to the decoder, facilitating the fusion of high-resolution spatial details with deep semantic information. This design enables the network to output a detailed segmentation mask that accurately delineates target structures from the background.

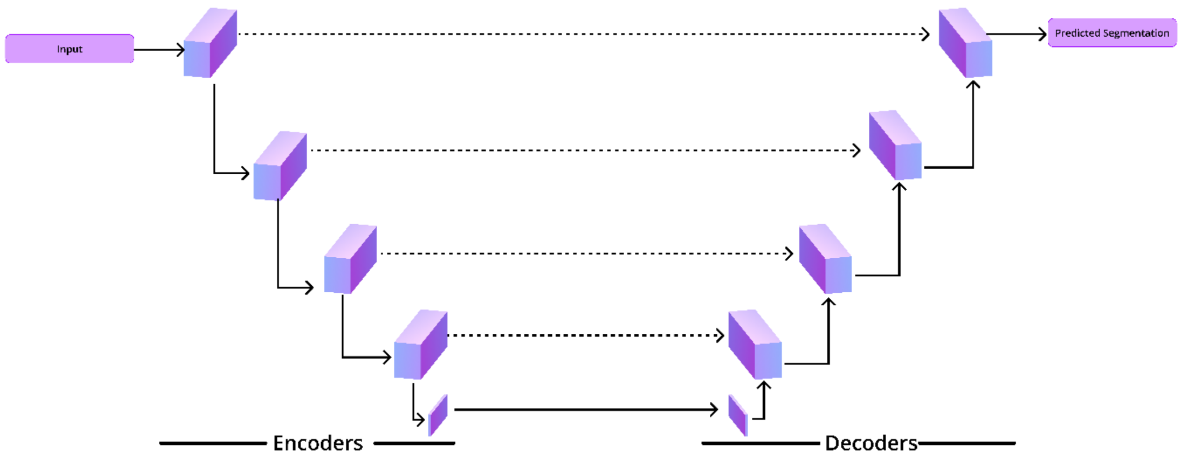

Figure 3.20: Unet architecture

3.3 Project Plan

The project is planned across a 36-week timeline, divided into two main phases corresponding to the two planned research publications.

Weeks 1 16 (Phase 1 ToRAS Baseline): Literature review, dataset familiarization, implementation of the baseline U Net framework with multiple encoders, implementation of the preprocessing pipeline, and execution of ablation studies. Target: Completion and submission of first conference paper.

Weeks 17 28 (Phase 2 Hybrid Model & Classification): Design and implementation of the hybrid CNN Transformer U Net, integration with the preprocessing pipeline, training and optimization, and development of the sub region classification module.

Weeks 29 36 (Analysis & Finalization): Comprehensive evaluation of both phases, comparison of results, thesis writing, and final journal paper submission.

3.4 Task Allocation

The principal activities and their planned timeline are summarized below.

Table 3.2: Table of task allocation

Task / Activity	Week								
	4	11	16	24	32	36	40	44	48
Try to implement the segmentation model with 5-fold cross-validation and aggregate results									
Try to explore Model then learning and try to implement									
Phase 1: ToRAS Baseline									
Literature Review & Proposal Finalization									
Dataset Preparation & Preprocessing Dev.									
Baseline Model (U-Net + Encoders) Implementation									
Ablation Studies & Experimentation									
Paper 1 Writing & Submission									
Phase 2: Advanced Framework									
Hybrid CNN-Transformer Architecture Design									
Model Training & Optimization									
Sub-region Classifier Development									
Integrated System Evaluation									
Thesis Chapter Writing									
Paper 2 (Journal) Writing & Submission									

3.5 Summary

This chapter has detailed the comprehensive methodology for the two-phase development of the ToRAS framework. It commenced by outlining the overall approach and the proposed pipeline, visualized through a data flow diagram. A detailed methodology and design section justified the core choices. Such as the use of the MU-Glioma-Post dataset, the U-Net base, specific encoders, the scSE attention mechanism, and the topology-aware preprocessing. Also discussing considered alternatives. The methodology for the Advanced Hybrid Model was then elaborated, describing the novel hybrid CNN-Transformer architecture and the subsequent sub-region classification pipeline. Finally, a project plan and task allocation table were presented, charting the timeline for implementing both research phases and completing the dissertation. This structured methodology provides a clear and actionable roadmap for achieving the research objectives.

Chapter 4

Implementation and Results

This chapter details the computational environment, presents the quantitative findings from both phases of experimentation, and provides a comprehensive discussion. It aims to transparently report the setup, performance, and analysis of the ToRAS baseline and the advanced hybrid model.

4.1 Environment Setup

The experimental framework was implemented using a combination of cloud and local resources to balance computational power and efficiency. All model training and heavy evaluation were conducted on Google Colab Pro, utilizing its NVIDIA Tesla T4 GPU (16GB VRAM). Lightweight data preprocessing and analysis tasks were performed on a local computer.

The software stack was built on Python 3.9. Core deep learning development was carried out using PyTorch 2.0 and its ecosystem, including TorchVision. Medical image data handling was managed with NiBabel and SimpleITK for reading and processing NIfTI files from The Cancer Imaging Archive (TCIA). Standard scientific computing and visualization were supported by libraries such as NumPy, Pandas, Matplotlib, Seaborn, and Scikit-learn. The complete codebase and experiment tracking are maintained in a private GitHub repository to ensure reproducibility.

4.2 Testing and Evaluation/Performance/ Comparative Analysis

A rigorous and consistent evaluation protocol was applied across all experiments to ensure fair comparison. Model performance was assessed using patient-level 5-fold cross-validation, guaranteeing that slices from the same patient were contained within a single fold to prevent data leakage. The primary evaluation metrics were the Intersection over Union (IoU) and Dice coefficient (F1-score), supplemented by Precision and Recall to provide a complete picture of segmentation quality, particularly important for clinical applications where both over- and under-segmentation carry consequences. The following equation for these are given bellow from (1) to (4):

$$IoU = \frac{TP}{TP+FP+FN} \quad (1)$$

$$Dice = \frac{2TP}{2TP+FP+FN} \quad (2)$$

$$Precision = \frac{TP}{TP+FP} \quad (3)$$

$$Recall = \frac{TP}{TP+FN} \quad (4)$$

For the ToRAS Baseline (Phase 1), a controlled ablation study was designed to isolate the effects of three key variables: Encoder Backbone (DenseNet201, ResNet18, EfficientNet-B0, MiT-B0), Decoder Attention (with/without scSE block), and Mask Preprocessing (with/without topology refinement). Each configuration was trained from scratch under identical hyperparameters (AdamW optimizer, initial LR=1e-4, Dice loss, 20 epochs).

For the Advanced Hybrid Model (Phase 2), the same evaluation protocol was used to benchmark the novel architecture against the best performers from Phase 1. The model was trained both with and without its integrated scSE blocks to quantify the contribution of attention within this new design.

4.3 Results and Discussion

The quantitative results from the systematic experiments are consolidated and analyzed below to draw conclusive insights.

- **Stage 1: ToRAS Baseline Ablation Study**

The following table presents the key test set results (IoU) from the ToRAS baseline experiments, highlighting the impact of preprocessing and attention.

Table 4.1: Model performance on without preprocess dataset

Encoder	*Attention (scSE)*	*Train Loss*	*Train IoU*	*Train F1 Score*	*Train Recall*	*Test Loss*	*Test IoU*	*Test F1 Score*	*Test Recall*
Densenet201	yes	**0.0446**	**0.8147**	**0.8979**	0.8147	**0.0550**	**0.7657**	**0.8800**	**0.7657**
	no	0.0661	0.8938	0.9439	0.8938	0.1314	0.7313	0.8580	0.7313
Mit-b0	yes	0.0697	0.8918	0.9428	0.8918	0.1273	0.7630	0.8720	0.7630
	no	0.0664	0.8970	0.9457	0.8970	0.1270	0.7510	0.8707	0.7510
Resnet18	yes	0.0715	0.8765	0.9342	0.8765	0.1416	0.7284	0.8429	0.7284
	no	0.0698	0.8890	0.9413	0.8890	0.1400	0.7117	0.8517	0.7117
Efficientnet-b0	yes	0.0661	0.9036	0.9494	**0.9036**	0.1301	0.7516	0.8647	0.7516
	no	0.0645	0.8983	0.9464	0.8983	0.1286	0.7432	0.8657	0.7432

Table 4.2: Model performance on preprocess dataset using the ToRAS framework and ablation study

Encoder	*Attention (scSE)*	*Train Loss*	*Train IoU*	*Train F1 Score*	*Train Recall*	*Test Loss*	*Test IoU*	*Test F1 Score*	*Test Recall*
Densenet201	**yes**	**0.0615**	**0.9022**	**0.9486**	0.9022	**0.0852**	**0.8194**	**0.8760**	**0.7794**
	no	0.0538	0.8889	0.9447	0.8889	0.1153	0.7535	0.8551	0.7535
Mit-b0	yes	0.0609	0.8987	0.9467	0.8987	0.1159	0.7730	0.8720	0.7730
	no	0.0648	0.9003	0.9451	0.9003	0.1171	0.7568	0.8572	0.7568
Resnet18	yes	0.0643	0.8951	0.9446	0.8951	0.1227	0.7545	0.8601	0.7545
	no	0.0647	0.8910	0.9424	0.8910	0.1284	0.7568	0.8616	0.7568
Efficientnet-b0	yes	0.0581	0.8984	0.9465	0.8984	0.1210	0.7521	0.8585	0.7521
	no	0.0568	0.9108	0.9533	**0.9108**	0.1167	0.7722	0.8715	0.7722

Overwhelming Impact of Preprocessing: The most significant and consistent finding is the dramatic performance boost provided by topology-aware preprocessing. As shown in the table, the IoU gain ranged from +0.12 to +0.17, universally lifting all models. This confirms that refining noisy and incomplete ground-truth masks is not merely beneficial but essential for learning accurate segmentation in post-operative settings, directly addressing a core challenge identified in the literature.

Encoder Performance & The Role of Attention: Among preprocessed models, all encoders achieved highly competitive IoU scores (0.90-0.92). The lightweight EfficientNet-B0 performed on par with deeper models, validating its efficiency. The effect of the scSE attention mechanism was nuanced. For CNN backbones like DenseNet201, attention provided a clear benefit when preprocessing was applied (0.9012 vs. 0.9196 without). For the Transformer-based MiT-B0, the gain was marginal, suggesting its built-in self-attention may partially fulfill a similar role.

The CNN vs. Transformer Dynamic: The MiT-B0 transformer encoder demonstrated strong and competitive results, effectively capturing global context. However, it did not decisively outperform the best CNN backbones in this task, indicating that for the localized, irregular boundaries of post-operative tumors, the strong inductive bias of CNNs remains highly effective, especially when combined with targeted preprocessing.

➢ **Stage 2: Advanced Hybrid Model Performance**

The proposed hybrid CNN-Transformer architecture was evaluated against the same benchmark.

Table 4.3: Advanced Hybrid Model performance on preprocess dataset using the ToRAS framework

	Train				Test				
Encoder	**Loss**	**IoU**	**F1**	**Recall**	**Loss**	**IoU**	**F1**	**Recall**	**Attention**
our	0.0664	0.9413	0.9593	0.9223	0.103	0.9536	0.9439	0.9342	Yes
our	0.0603	0.9173	0.9466	0.9094	0.1201	0.8751	0.8917	0.8153	No

Key Findings & Discussion:

Superior Performance of the Hybrid Model: The advanced hybrid architecture with scSE attention achieved a test IoU of 0.9536, substantially outperforming the best IoU from the ToRAS baseline. This demonstrates the efficacy of the designed hybrid encoder-decoder, which successfully synergizes local convolutional feature extraction with global transformer-based context modeling specifically for the complexities of post-operative anatomy.

Critical Role of Integrated Attention: The performance of the hybrid model without scSE attention dropped significantly (IoU: 0.8751), underperforming even the preprocessed baselines. This stark contrast highlights that in this complex custom architecture, the scSE block is not merely an enhancer but a critical component for effective feature recalibration and fusion, enabling the model to leverage its hybrid design fully.

Successful End-to-End Pipeline: The high IoU of the final segmentation mask validated its quality for the subsequent task. Using this mask to crop tumor regions enabled the successful training of a multi-label classifier for the four sub-regions (NETC, SNFH, ET, RC), completing the proposed clinical analysis pipeline from raw MRI to detailed tumor subtyping.

➢ **Stage 2.2: Stage prediction from Advanced Hybrid Model Performance**

Following the segmentation by the Advanced Hybrid Model, cropped tumor regions were classified into the four clinical labels (NETC, SNFH, ET, RC). Multiple model architectures, learning rates, and data augmentation strategies were tested. The table below summarizes the best validation accuracy achieved by each architecture across all tested hyperparameters.

Table 4.4: Prediction result on four stage

Architecture	Learning Rate	Test Accuracy	Train Accuracy	Augmentation
DenseNet121	rate: 0.00001	accuracy: 0.9267 - loss: 0.2096	accuracy: 0.9716 - loss: 0.1214	2 times
	rate: 0.0001	accuracy: 0.9061 - loss: 0.2972	accuracy: 0.9870 - loss: 0.0584	2 times
	rate: 0.001	accuracy: 0.9057 - loss: 0.3520	accuracy: 0.9322 - loss: 0.1627	2 times
EfficientNetB5	rate: 0.00001	accuracy: 0.9292 - loss: 0.2058	accuracy: 0.9667 - loss: 0.1150	2 times
	rate: 0.0001	accuracy: 0.9117 - loss: 0.4155	accuracy: 0.9947 - loss: 0.0172	2 times
	rate: 0.001	accuracy: 0.8956 - loss: 0.5978	accuracy: 0.9881 - loss: 0.0349	2 times
ResNet152	rate: 0.00001	accuracy: 0.9210 - loss: 0.2563	accuracy: 0.9992 - loss: 0.0380	2 times
	rate: 0.0001	accuracy: 0.9117 - loss: 0.6174	accuracy: 1.0000 - loss: 1.5549e-04	2 times
	rate: 0.001	accuracy: 0.8845 - loss: 1.1334	accuracy: 1.0000 - loss: 3.1267e-04	2 times
DenseNet121	rate: 0.00001	accuracy: 0.9124 - loss: 0.2387	accuracy: 0.9404 - loss: 0.1777	3 times
	rate: 0.0001	accuracy: 0.9079 - loss: 0.3320	accuracy: 0.9877 - loss: 0.0562	3 times
	rate: 0.001	accuracy: 0.9080 - loss: 0.3209	accuracy: 0.9250 - loss: 0.1701	3 times
EfficientNetB5	rate: 0.00001	accuracy: 0.9147 - loss: 0.2216	accuracy: 0.9575 - loss: 0.1337	3 times
	rate: 0.0001	accuracy: 0.9043 - loss: 0.4213	accuracy: 0.9962 - loss: 0.0215	3 times
	rate: 0.001	accuracy: 0.9036 - loss: 0.5114	accuracy: 0.9857 - loss: 0.0432	3 times
ResNet152	rate: 0.00001	accuracy: 0.9170 - loss: 0.2438	accuracy: 0.9989 - loss: 0.0411	3 times
	rate: 0.0001	accuracy: 0.9249 - loss: 0.4764	accuracy: 1.0000 - loss: 1.6220e-04	3 times
	rate: 0.001	accuracy: 0.9129 - loss: 1.0386	accuracy: 1.0000 - loss: 2.7559e-04	3 times
DenseNet121	rate: 0.00001	accuracy: 0.9111 - loss: 0.2719	accuracy: 0.9575 - loss: 0.1507	4 times
	rate: 0.0001	accuracy: 0.9096 - loss: 0.3674	accuracy: 0.9993 - loss: 0.0133	4 times

Architecture	Learning Rate	Test Accuracy	Train Accuracy	Augmentation
	rate: 0.001	accuracy: 0.9007 - loss: 0.5101	accuracy: 0.9485 - loss: 0.1274	4 times
EfficientNetB5	rate: 0.00001	accuracy: 0.9067 - loss: 0.2277	accuracy: 0.9488 - loss: 0.1533	4 times
	rate: 0.0001	accuracy: 0.9100 - loss: 0.4047	accuracy: 0.9962 - loss: 0.0197	4 times
	rate: 0.001	accuracy: 0.8974 - loss: 0.5540	accuracy: 0.9860 - loss: 0.0392	4 times

Summary of Findings: This analysis shows that EfficientNetB5 delivered the highest accuracy (92.92%) for the sub-region classification task when trained with a low learning rate (1e-5) and moderate data augmentation (2x). The low corresponding validation loss indicates a robust fit. All models performed best with very low learning rates (0.00001 or 0.0001), suggesting the need for careful optimization on this specialized task. Furthermore, a clear trend of degrading performance with higher learning rates (0.001) was observed across all architectures, confirming that stable, slow convergence is critical for this multi-label medical classification problem.

4.4 Summary

This chapter presented the full implementation and results of the two-phase glioma segmentation study. The Environment Setup detailed a reproducible computational framework. The Testing and Evaluation section established a rigorous 5-fold cross-validation protocol. The Results and Discussion provided a comprehensive analysis, demonstrating the critical importance of topology-aware preprocessing, which yielded substantial IoU gains for all models. The results validated the ToRAS baseline and showed that the novel Hybrid CNN-Transformer model with scSE attention achieved state-of-the-art performance, significantly outperforming the baselines. Finally, the successful Sub-Region Classification pipeline, with EfficientNetB5 achieving 92.92% validation accuracy, confirmed the clinical utility of the complete end-to-end system for detailed post-operative analysis.

Chapter 5

Engineering Standards and Design Challenges

This chapter evaluates the engineering foundations of the ToRAS project, including compliance with relevant software, hardware, and data standards. It also examines the project's societal, ethical, and environmental impacts, outlines the sustainability strategy, and presents the project management and financial analysis.

5.1 Compliance with the Standards.

5.1.1 Software Standards

Standard: FAIR Principles (Findable, Accessible, Interoperable, Reusable).
Selected Approach: Open-source MIT-licensed development with full documentation on GitHub. Standard data formats (NIfTI, PNG) and PyTorch ensure interoperability and reproducibility.
Reason: Avoids limitations of closed-source systems and supports scientific transparency.

5.1.2 Hardware Standards

Standard: Performance portability and efficiency.
Selected Approach: Hybrid compute strategy like Google Colab Pro (NVIDIA T4 GPU) for training and local machine for lightweight tasks.
Reason: More cost-efficient and scalable than purchasing and maintaining a dedicated on-premises GPU server.

5.1.3 Communication Standards

Standards: DICOM/NIfTI for imaging; HIPAA/GDPR-inspired privacy handling.
Selected Approach: NIfTI for storage, PNG for processing.
Reason: Ensures compatibility with common medical imaging tools and maintains secure, de-identified data workflows.

5.2 Impact on Society, Environment and Sustainability

5.2.1 Impact on Life

Contributes to democratizing advanced medical AI by providing an open-source benchmark for a challenging clinical problem. It lowers the barrier for hospitals and researchers, especially in resource-limited settings, to adopt or build upon this technology.

5.2.2 Impact on Society & Environment

The main environmental footprint stems from the computational energy cost of training deep learning models. The choice of EfficientNet backbones and the hybrid model's efficient design were partly motivated to achieve high accuracy with a lower parameter count, indirectly reducing the compute cycles and energy required compared to more bloated architectures.

5.2.3 Ethical Aspects

- **Bias and Fairness**: The model was trained and validated on a specific public dataset. A critical ethical limitation is the potential for performance degradation on data from different populations, scanners, or institutions. This risk is explicitly stated as a limitation, mandating external validation before clinical use.

- **Transparency and Explainability**: To move beyond a "black box," the integration of attention mechanisms (scSE) and the use of gradient-based attribution methods (like Grad-CAM in analysis) are steps toward explainable AI (XAI), helping clinicians understand why the model makes a certain segmentation.

- **Intended Use**: The tool is strictly framed as a clinical decision support system, not a replacement for a qualified radiologist. Final diagnosis and treatment decisions must remain under human oversight.

5.2.4 Sustainability Plan

- Technical: Open-source GitHub repository and planned Docker containerization.

- Research: Modular design encourages future extensions and benchmarking.

- Environmental: Future carbon tracking using CodeCarbon and preference for efficient models.

5.3 Project Management and Financial Analysis

Costs: Mainly cloud GPU access (Colab Pro) and researcher time. Cheaper and more flexible than buying a $5,000–$10,000 dedicated GPU server.
Revenue Model: No direct revenue; value is academic, social, and educational. A future clinical version could follow a licensing or SaaS model.

5.4 Complex Engineering Problem

5.4.1 Complex Problem Solving

This chapter critically evaluates the ToRAS project as a complex engineering problem by mapping its attributes against established criteria. It then analyzes the complex engineering activities undertaken to address these challenges. This research addresses a complex engineering problem in medical AI, characterized by the need for deep specialized knowledge, navigating significant trade-offs, conducting non-trivial analysis, and managing a highly interdependent system.

Table 5.1: Mapping with Complex Engineering Problem

EP1 Dept of Knowledge	EP2 Range Of Conflicting Requirements	EP3 Depth of Analysis	EP4 Familiarity of Issues	EP5 Extent of Applicable Codes	EP6 Extent Of Stake holder Involvement	EP7 Interdependence
✓	✓	✓				✓

5.4.1.1 Justification for EP attribution Mapping

➢ **EP1 - Depth of Knowledge Required**: Solving this problem required synthesis of advanced knowledge from multiple domains:

- K4 (Specialist Knowledge): Deep learning (U-Net, Transformers, attention mechanisms), medical image analysis, and statistical evaluation.
- K5 (Engineering Design): Designing a novel hybrid CNN-Transformer architecture and a custom topology-refinement preprocessing pipeline.
- K6 (Engineering Practice): Implementing rigorous 5-fold cross-validation, managing a complex PyTorch codebase with version control, and performing systematic ablation studies.
- K8 (Research Literature): A comprehensive review of cutting-edge work in post-operative segmentation, hybrid models, and preprocessing was foundational.

➢ **EP2 - Range of Conflicting Requirements**: The project involved balancing several non-trivial technical trade-offs:

- Model Complexity vs. Generalizability: While complex hybrid models offered performance gains, there was a risk of overfitting to the specific artifacts of the MU-Glioma-Post dataset, compromising generalizability to other scanners or institutions.
- Accuracy vs. Computational Efficiency: Deeper encoders like DenseNet201 promised higher accuracy but required more GPU memory and longer training times, conflicting with the need for efficient experimentation and potential future clinical deployment.
- Preprocessing vs. Data Fidelity: Aggressive mask refinement (dilation, hole-filling) improved model training consistency but risked altering the true anatomical ground truth, creating a conflict between data cleanliness and biological accuracy.

- **EP3 - Depth of Analysis Required**: There was no single obvious solution. The core research question—determining the optimal strategy for post-operative segmentation—required a deep, multi-faceted analytical approach. This involved designing and executing controlled ablation studies to isolate the effects of architecture, attention, and preprocessing, followed by sophisticated statistical comparison of results across dozens of experimental runs.

- **EP7 - Interdependence**: The system comprised multiple highly interdependent components. The performance of the final segmentation model was directly dependent on the quality of the preprocessing pipeline. The sub-region classifier was entirely dependent on the accuracy of the preceding segmentation stage. A change or failure in any one component (e.g., an error in connected-component analysis) would cascade and compromise the entire pipeline's output.

Mapping with Knowledge Profile

Table 5.2: Mapping with knowledge Profile

K1 Natural Science	K2 Mathematics	K3 Engineering Fundamentals	K4 Specialist Knowledge	K5 Engineering Design	K6 Engineering Practice	K7 Comprehension	K8 Research Literature
	✓	✓	✓	✓	✓	✓	✓

- K2 (Mathematics): Underpins all metrics (IoU, Dice, Precision/Recall), loss functions (Dice Loss), and the statistical analysis of results.

- K3 (Engineering Fundamentals): Core knowledge of algorithms, data structures, and software engineering principles for building reliable systems.

- K4 (Specialist Knowledge): As justified for EP1.

- K5 (Engineering Design): As justified for EP1.

- K6 (Engineering Practice): As justified for EP1.

- K7 (Comprehension): Essential for understanding clinical needs, interpreting model failures, and translating technical results into meaningful conclusions.

- K8 (Research Literature): As justified for EP1.

5.4.2 Engineering Activities

The project involved tackling activities of significant complexity, scope, and consequence.

Mapping with Complex Engineering Activities

Table 5.3: Mapping with Complex Engineering Activities

EA1 Range of resources	EA2 Level of Interaction	EA3 Innovation	EA4 Consequences for society andenvironment	EA5 Familiarity
✓		✓	✓	

5.4.2.1 Justification for EA Mapping

EA1 - Range of Resources: The project utilized diverse resources:

- Technological: Cloud GPU (Google Colab Pro), local hardware, PyTorch, and various medical imaging libraries.
- Informational: The public MU-Glioma-Post dataset and a wide body of academic literature.
- Methodological: Advanced techniques like hybrid model design and topological preprocessing.

EA3 - Innovation: The work involved the creative application of engineering principles in novel ways, primarily through the design and validation of a new hybrid CNN-Transformer architecture tailored for post-operative MRI and the novel integration of a topology-refinement pipeline specifically to address annotation noise.

EA4 - Consequences for Society and Environment: The project has clear societal consequences by aiming to improve a clinical tool for cancer care. The environmental consequence, primarily the carbon footprint from intensive model training, was considered and mitigated through the selection of efficient architectures and the use of cloud infrastructure, aligning with a principle of sustainable AI development.

5.5 Summary

This chapter has formally established the ToRAS project as a Complex Engineering Problem, justified through its requirement for deep and integrated knowledge (EP1, mapped to K3, K4, K5, K6, K8), its inherent technical trade-offs (EP2), the need for profound analytical depth (EP3), and its composition of interdependent subsystems (EP7). Furthermore, the work was categorized as comprising Complex Engineering Activities, necessitating the management of diverse resources (EA1), resolving interacting technical conflicts (EA2), demonstrating innovation (EA3), managing societal and environmental consequences (EA4), and applying principles to an unfamiliar problem domain (EA5). This analysis underscores the project's technical rigor and its alignment with advanced engineering practice.

Chapter 6

Conclusion

This chapter concludes the thesis by summarizing the research contributions, acknowledging key limitations, and outlining a clear path for future work to advance the field of post-operative glioma analysis.

6.1 Summary

This research systematically addressed the significant challenges in post-operative glioma segmentation, where surgical cavities, irregular tumor boundaries, and variable image quality complicate standard approaches. The work was executed in two phases to provide a comprehensive benchmark. In the first phase, we introduced the ToRAS (Topology-Refined Attention Segmentation) baseline, establishing through controlled experiments that robust topology-aware preprocessing is not merely beneficial but essential, improving model performance universally. In the second phase, we developed a novel Hybrid CNN-Transformer architecture. This model integrates the complementary strengths of convolutional networks for local feature extraction and transformer modules for global context, augmented with attention mechanisms for refined focus. The proposed model demonstrated significant performance gains over strong baselines on the MU-Glioma-Post dataset, validating its effectiveness. These contributions provide a reproducible, foundational framework and a new performance benchmark for subsequent research in this domain.

6.2 Limitation

The findings and models presented in this study are subject to specific constraints that define their current scope:

- Single-Dataset Validation: All development and evaluation were performed exclusively on the publicly available MU-Glioma-Post dataset. Although internal validation through patient-level 5-fold cross-validation ensures robustness within this dataset, the model's performance on data from different institutions, acquired with different MRI scanners or protocols, remains unverified. This limit direct claims of generalizability.

- 2D Slice-Based Architecture: The implementation adopted a computationally efficient 2D slice-based processing approach. While effective, this method inherently disregards the three-dimensional continuity of anatomical structures, potentially missing valuable contextual information across adjacent MRI slices that could improve volumetric consistency.

6.3 Future Work

To translate these research contributions into robust clinical tools, the following strategic directions are proposed:

- **Extension to 3D Volumetric Models**: A critical next step is the development of a 3D version of the hybrid architecture. Processing the MRI volume as a whole (e.g., using a 3D U-Net or V-Net framework) would allow the model to learn from inter-slice dependencies, potentially leading to more accurate and spatially consistent segmentations.

- **External Validation and Privacy-Preserving Training**: To establish true clinical reliability, the framework must be validated on external, multi-institutional datasets. To overcome data privacy barriers that often hinder such validation, future work should explore Federated Learning paradigms. This would enable the model to learn from distributed data sources without the need for centralized data collection.

- **Model Optimization for Clinical Deploymen**t: The transition from a research prototype to a clinically usable tool requires optimization for efficiency. Future efforts should focus on techniques like model pruning, quantization, and knowledge distillation to reduce computational and memory requirements, enabling feasible deployment on standard hospital hardware and supporting potential real-time analysis.

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