Project Design & Analysis Report

University/Department: CSUDH — Computer Science Department

Course/Thesis/Project Title: CSC 590/595 — Master's Project

Semester/Year: Fall 2025

Project Title: Brain Tumor Segmentation with U-Net & Fine-Tuned Foundation Models (MedSAM)

Student Name: Naushik Beladiya

Student ID: 212686840

Instructor / Committee Chair: Dr. Sahar Hooshmand

Date: October 12, 2025

Abstract

Accurate brain tumor segmentation from multi modal MRI is a critical step in neuro oncology, informing diagnosis, surgical planning, and therapy response assessment. This project investigates two complementary approaches: (1) a convolutional **U-Net** baseline trained end to end and (2) a **fine tuned foundation model (MedSAM)** adapted to the same data. Using the Medical Segmentation Decathlon Task01_BrainTumour dataset (FLAIR, T1, T1 contrast enhanced, T2), we target the standard subregions **whole tumor (WT), tumor core (TC)**, and **enhancing tumor (ET)** and evaluate performance with the **Dice similarity coefficient** and **95th percentile Hausdorff distance (HD95)**, alongside runtime and GPU memory footprint.

Our **objectives** are to (i) establish a reproducible U Net baseline, (ii) fine tune MedSAM for volumetric tumor delineation, and (iii) analyze accuracy efficiency trade offs and robustness under common clinical style perturbations (e.g., intensity shift, slice thickness variability). **Expected contributions** include a transparent pipeline (preprocessing, training, inference, post processing), an apples to apples comparison between a specialized CNN and a promptable foundation model, and practical guidance on when each approach is preferable under constrained compute. This work directly follows the Cedars Sinai brief emphasizing a U Net baseline and a fine tuned foundation model on Task01_BrainTumour and is structured to scale into the 40–50 page final report required by the course.

Keywords: Brain MRI, Tumor Segmentation, U Net, MedSAM, Dice, HD95, Foundation Models

Introduction

1.1 Background & Motivation

Primary and secondary brain tumors exhibit substantial heterogeneity in shape, location, and appearance across MRI modalities. Manual delineation of tumor subregions—edema/infiltration, necrotic/non enhancing core, and enhancing tumor—remains time consuming and operator dependent, impacting reproducibility and clinical throughput. Deep learning has delivered strong results in medical image segmentation through encoder–decoder architectures such as U Net, while **foundation models** (e.g., SAM variants and MedSAM) promise rapid adaptation and promptable segmentation with fewer labeled samples. For a graduate capstone setting, contrasting a purpose built CNN with a fine tuned foundation model offers both pedagogical value and clinically relevant insights. This project follows the Cedars Sinai topic specification to build a **U Net baseline** and then **fine tune a pre trained model (MedSAM)** on the Medical Segmentation Decathlon **Task01_BrainTumour** dataset.

1.2 Problem Statement

Given multi modal brain MRI volumes (FLAIR, T1, T1 contrast enhanced, T2), **automatically segment** three clinically meaningful subregions: **Whole Tumor (WT), Tumor Core (TC)**, and **Enhancing Tumor (ET)**. The model must generalize across patients and scans and output voxel wise labels suitable for volumetric analysis. We will quantify accuracy using **Dice** and **HD95** and report computational efficiency (inference time per volume, peak VRAM), enabling a rigorous **accuracy vs. efficiency** comparison between (i) a supervised **U Net** and (ii) a **fine tuned MedSAM**.

1.3 Objectives

1. Establish a U Net baseline: Implement a strong, reproducible baseline with standardized preprocessing (spacing/intensity normalization), patch based training (2D/2.5D or memory aware 3D), and post processing.

2. Fine-tune MedSAM : Adapt MedSAM to brain MRI segmentation via prompt design and lightweight parameter efficient fine tuning (e.g., adapters/LoRA), ensuring input/output compatibility with the baseline pipeline.

3. Evaluate rigorously : Use fixed data splits and report **Dice** and **HD95** per subregion, plus runtime and VRAM. Conduct paired statistics over cases to test significance of performance differences.

4. Analyze robustness : Stress test both models to modest domain shifts (e.g., intensity scaling, Gaussian noise) to examine generalization.

5. Report and release : Produce a clear write up and a minimal, reproducible codebase that can scale into the course's 40–50 page final report with code appendix and GitHub link, as required.

1.4 Scope & Limitations

Data scope : We focus on **MSD Task01_BrainTumour**; all experiments use only these labeled volumes to avoid data leakage.

Compute constraints : Training will respect a single GPU budget typical for graduate projects; we will prefer 2D or 2.5D training and memory aware 3D patches where feasible.

Model scope : We compare one representative CNN (U Net) with one representative foundation model (MedSAM). Broader architecture sweeps (e.g., Swin UNet, TransUNet) are noted for future work if time permits.

Clinical claims : The work is **research-oriented**; no diagnostic claims are made. External clinical deployment, regulatory validation, and prospective testing are **out of scope**.

Timeline alignment : This **Design & Analysis** submission corresponds to the **Oct 12, 2025** milestone; subsequent progress reports and the in person final presentation will build on these foundations.

1.5 Contributions (This Stage)

• **Problem framing & requirements :** A precise segmentation objective with metrics (Dice, HD95) and compute constraints defined up front.

• **Design choices :** Justified selection of U Net baseline and MedSAM fine tuning consistent with the Cedars Sinai brief on Task01_BrainTumour.

• **Planned pipeline :** End to end plan for preprocessing, augmentation, training, inference, post processing, and evaluation—structured to scale into the **40–50 page** final report with a code appendix and GitHub link per course policy.

Literature Review

2.1 Public Datasets & Pre processing Norms

Datasets : We will use the **Medical Segmentation Decathlon (MSD) Task01_BrainTumour**, which reuses the BraTS multi site glioma MRI collection and labels (multimodal T1, contrast enhanced T1 (T1ce/T1Gd), T2, and FLAIR). MSD standardizes task definitions and evaluation across organs and includes a permissive license for research use. Medical Decathlon

The **BraTS** challenges distribute MRI volumes **pre processed** by the organizers: **co registered to a common anatomical atlas, resampled to 1 mm^3 isotropic resolution, and skull stripped** (typical volume shape ≈240×240×155). Labels target three sub regions which yield the common aggregates Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET). Perelman School of Medicine+2Perelman School of Medicine+2

Pre processing norms in the literature: Common steps (when not already provided) include **N4 bias field correction** to address intensity inhomogeneity, **brain extraction** (e.g., FSL BET or learned SynthStrip), and **rigid/affine registration + resampling** to harmonize spacing and orientation (SimpleITK/ITK pipelines). Intensities are then normalized per volume (e.g., z score inside brain mask).

All files use NIfTI; Python I/O through NiBabel is standard.

Implication for this project. Because MSD/BraTS already supply co registration, isotropic spacing, and skull stripping, our pipeline will mainly apply orientation harmonization and intensity normalization, with optional N4 for ablations.

2.2 CNN Architectures for Medical Segmentation

U Net (2D) : The seminal **U Net** couples a contracting path (context) with an expanding path (localization) via skip connections effective with limited annotations by heavy augmentation. Its locality and efficient inference made it the de facto baseline across modalities.

3D U Net : Extends U Net to volumetric convolutions for better through plane context, trading higher **GPU memory** and longer training for improved cross slice consistency.

U Net++ / Attention U Net : U Net++ narrows the semantic gap between encoder/decoder via **nested dense skip pathways** and deep supervision; Attention U Net inserts **attention gates** to highlight salient structures, often improving sensitivity for small lesions.

Strengths/weaknesses summary :

- **Strengths :** strong localization, data efficiency, simplicity, broad tooling support.
- **Weaknesses :** limited global context modeling (pure CNN locality), potential fragmentation in 2D (no z context), large memory for 3D on full volumes.

2.3 Transformer & Hybrid Models

To capture long range dependencies, **hybrids** combine CNN decoders with **Transformer encoders** (e.g., **TransUNet**), or adopt **pure Transformer U shapes** (e.g., **Swin-UNet** using shifted window self attention). These improve context aggregation but can demand more data/compute and careful optimization on 3D medical volumes.

2.4 Foundation/Promptable Models

Segment Anything (SAM) : introduced **promptable segmentation** (points/boxes/masks) trained on SA 1B (1B masks, 11M images) with strong **zero shot** transfer on natural images. However, **direct zero shot SAM on medical images underperforms** due to domain shift. **MedSAM :** addresses this by (1) curating >1.5M medical image–mask pairs across 10 modalities, and (2) **fine tuning** SAM to the medical domain, showing broad gains across 2D tasks; recent extensions explore **3D/temporal** cases (e.g., MedSAM 2/SAM 2).

Fine tuning strategies : Full fine tuning is costly; **parameter efficient fine tuning (PEFT)** such as **LoRA** inserts low rank adapters into attention/MLP layers, reducing trainable parameters while retaining performance—attractive for compute limited student projects and increasingly used with vision/medical foundation models.

2.5 Evaluation Standards

Primary metric : Dice Similarity Coefficient (overlap, 0–1). **Secondary: HD95** (95th percentile Hausdorff distance; boundary accuracy robust to outliers), plus sensitivity/specificity to detect over/under segmentation. BraTS/decathlon challenges canonicalized **Dice + HD95** as official metrics.

Caveat: HD95 **implementation details vary** across toolkits; report voxel spacing and code to ensure comparability. papers.miccai.org

Validation protocols: 5 fold cross validation enhances reliability on small datasets; hold out tests are simpler but risk higher variance—nnU Net popularized robust cross validated reporting with decathlon tasks.

2.6 Gap Analysis

1. **Label scarcity & cost** → motivates transfer and PEFT (e.g., LoRA) for **sample efficiency**.

2. **Domain shift (scanner, protocol, site)** continues to degrade generalization; active strands include domain adaptation/generalization and test time adaptation.

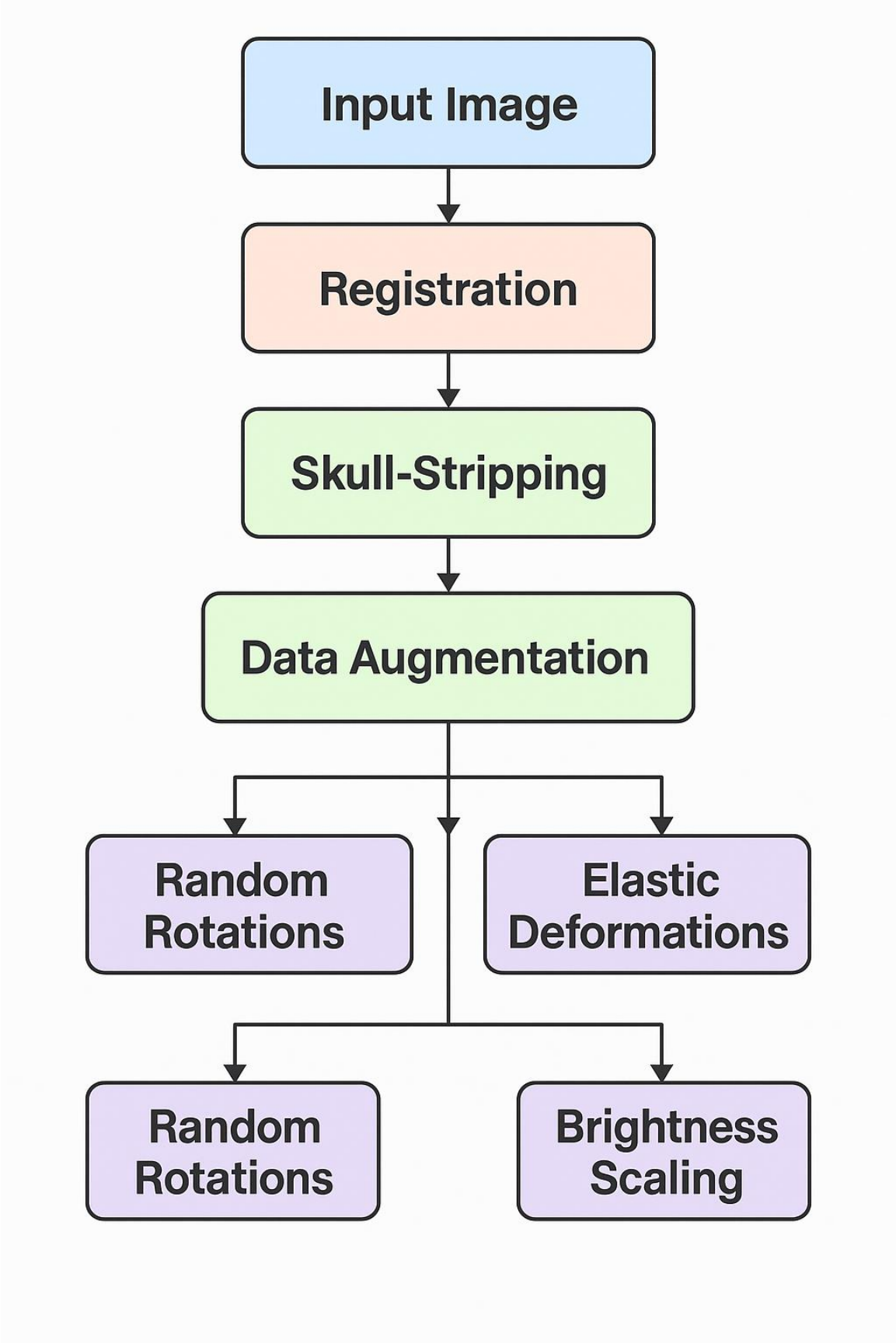
3. **Inference cost** for 3D/high capacity models → favors **2D/2.5D U Net baselines** and **adapter based MedSAM fine tuning** for practical deployment.

System Design

3.1 Overall Solution Overview

Pipeline: Data ingest → QC → Pre processing → Model training (baseline vs. MedSAM fine tune) → Validation/Test → Post processing → Reporting.

- **Data ingest/QC**: Verify modality presence/order (T1, T1ce, T2, FLAIR), header consistency, and spacing.
- **Pre processing**: Use **MONAI/ITK SimpleITK** for orientation (RAS/LPS), spacing confirmation, and z score normalization in brain mask; optional **N4** ablation.
- **Training**: U Net (2D/2.5D or patch based 3D) vs. **MedSAM + LoRA adapters**.
- **Evaluation**: Dice (per class + macro), HD95, sensitivity; runtime (ms/volume), VRAM footprint. Perelman School of Medicine
- **Reporting**: Tables/plots of metrics and qualitative overlays.


Input Image
Registration
Skull-Stripping
Data Augmentation
Random Rotations
Elastic Deformations
Random Rotations
Brightness Scaling

3.2 Architecture Diagrams (to include as figures)

- **Fig. 1 — U Net baseline**. 4 level encoder–decoder with skip connections; 4 input channels (modalities); output logits for WT/TC/ET.

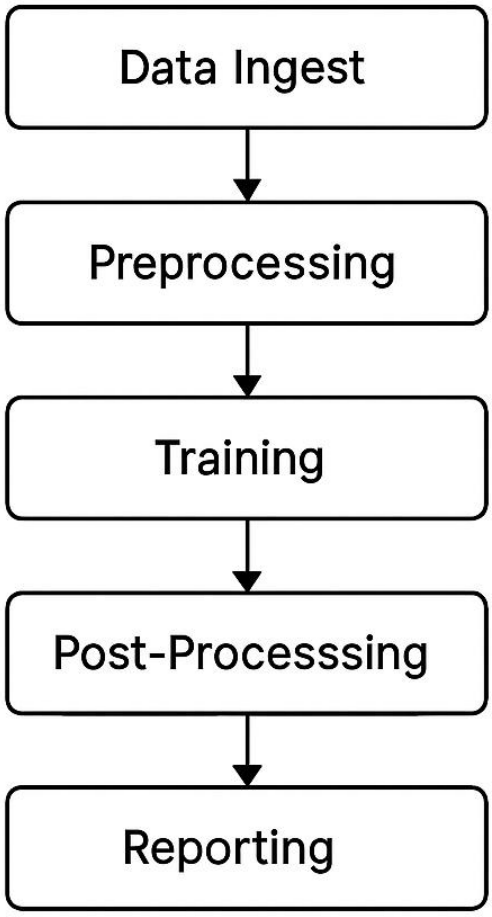


FIGURE 1 High-level pipeline

- **Fig. 2 — MedSAM fine tuning**. SAM image encoder + prompt encoder; **LoRA** adapters on attention blocks; **point/box prompts** formed from ground truth during training; inference with automatic box prompts from coarse proposals (optional).

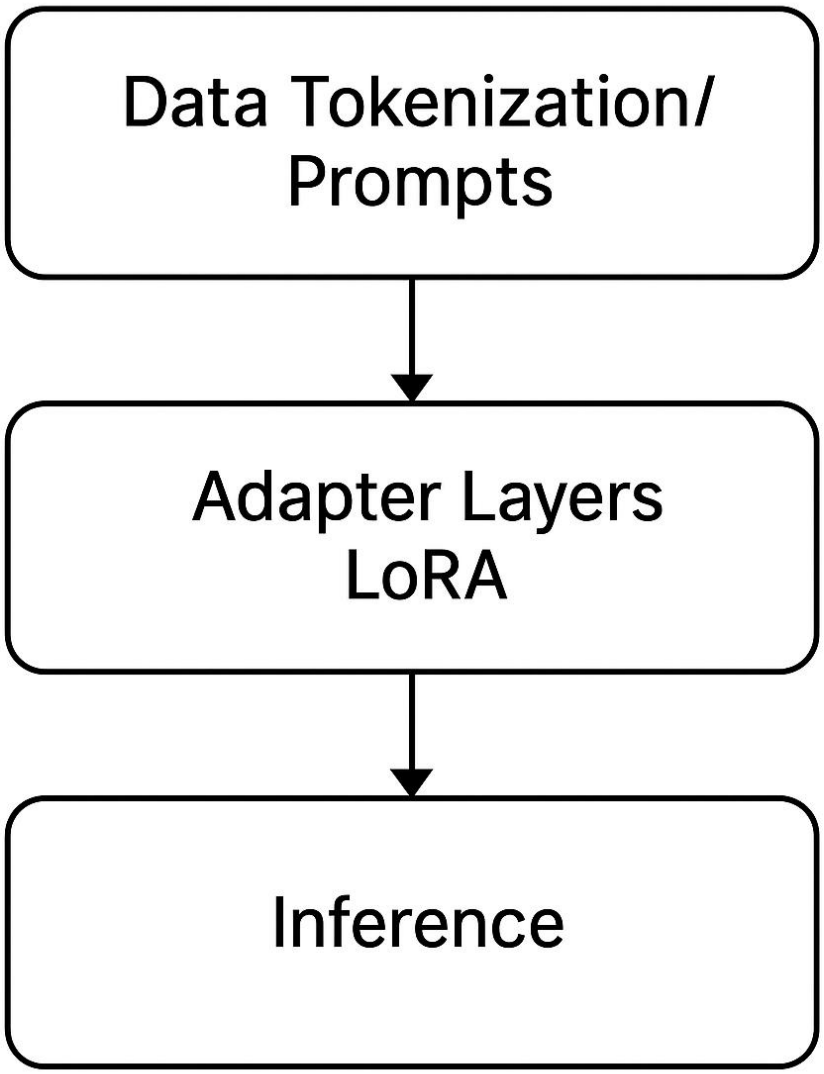


FIGURE 2 Fine-tuning workflow for MedSAM

3.3 Modules/Components

- **Data module :** NIfTI I/O (NiBabel), dataset registry, transforms (MONAI Spacingd, Orientationd, NormalizeIntensityd), class balanced patch sampling for 3D.

- **Model zoo :** U Net (2D/3D), MedSAM (checkpoint loader), LoRA injection.
- **Trainer :** Mixed precision, gradient clipping, early stopping, checkpointing; TensorBoard/W&B logging.
- **Evaluator :** Per case metrics (Dice/HD95); ensure consistent HD95 implementation. papers.miccai.org
- **Visualizer :** Slice and 3D orthoview overlays; error maps (FP/FN).

3.4 Algorithms/Techniques Considered

- **Losses : DiceCE** (Dice + Cross Entropy), Focal for class imbalance, **Tversky** for recall favoring, and **Boundary loss** to sharpen contours—evaluated per task.
- **Augmentations :** Spatial (flip/rotate/elastic), intensity (gamma, bias field), modality dropout; implemented via MONAI transforms.
- **Post processing :** Connected component filtering, small island removal, and optional **DenseCRF** refinement to reduce spurious edges.

Data Analysis & Requirements

4.1 Data Sources

Primary : MSD Task01_BrainTumour/BraTS derived volumes with expert labels for tumor sub regions; standardized NIfTI imaging and evaluation protocol (Dice/HD95).

4.2 Collection/Cleaning & Pre processing

- **Integrity checks:** modality files per case, affine/spacing, non empty masks.
- **Normalization:** z score inside brain mask; keep modality channels aligned.
- **Resampling/orientation:** confirm isotropic 1 mm^3 (BraTS preprocessed) and consistent orientation (RAS/LPS) for our pipeline.
- **Optionals (for ablations): N4 bias correction; brain extraction** if testing external data; registration with SimpleITK if needed.

4.3 Tools/Libraries/Frameworks

PyTorch + MONAI for medical transforms/loaders; **NiBabel** for NIfTI; **SimpleITK/ITK** for registration/resampling; experiment tracking via TensorBoard/W&B.

4.4 Hardware/Software Requirements

- **Compute:** For **2D/2.5D U Net**, ≥12 GB VRAM suffices for batch sizes ≥8 (mixed precision). For **3D patch based** (e.g., 128^3), ≥16–24 GB is preferable.

- **Storage**: ~10–20 GB for dataset + ~5–10 GB for checkpoints and logs (varies with runs).

- **OS/Env**: Linux, CUDA enabled GPU, Python 3.10+, PyTorch/MONAI latest stable.

4.5 Ethics, Privacy, Governance

The dataset is **de-identified** and curated for research; decathlon tasks are distributed under a permissive **CC-BY-SA** license. No PHI is collected or processed. Medical Decathlon

Methodology

5.1 Workflow

1. **Freeze splits :** (train/val/test) to ensure fair comparison.

2. **Baseline first:** train **U-Net** to convergence under the finalized pipeline.

3. **Foundation model:** fine tune **MedSAM** with **LoRA** adapters using identical pre/post processing and splits; evaluate with/without prompts.

4. **Hold out test + (optional) 5 fold CV** to bound variance.

5.2 Models Considered

- **U Net:** start with **2D (2.5D)** using all four modalities as channels (optionally stack k neighboring slices = 2.5D for context); then, if time permits, compare a **3D patch based** variant for TC/ET improvements.

- **MedSAM:** initialize from public MedSAM weights; **PEFT (LoRA)** on attention blocks; prompts: box/points derived from ground truth during training, and at inference from a learned proposal (or a single center point) to study prompt sensitivity.

5.3 Training Setup

- **Optimizer:** AdamW; **LR schedule**: cosine decay with warmup; **epochs:** 200 (early stop on val Dice); **batch size:** tuned to VRAM; **AMP** mixed precision; **augmentation:** elastic, rotate, gamma, bias field.

- **Regularization:** weight decay; stochastic depth (if using Transformer blocks).

- **Checkpointing:** top k by mean Dice (WT/TC/ET).

5.4 Evaluation Criteria

- **Primary:** Dice per class and macro averaged.

- **Secondary: HD95, sensitivity/specificity, inference latency** per volume, **VRAM** peak, and **#params/trainable params**. Report **confidence intervals** via bootstrapping across cases; publish the **metric implementation** used (HD95).

5.5 Statistical Testing & Ablations

- **Significance tests: paired** Wilcoxon (non parametric) or paired t test on per case Dice.

- **Ablations:** (i) augmentation on/off; (ii) 2D vs. 2.5D vs. 3D; (iii) MedSAM **prompt type/number**; (iv) **LoRA rank** and which layers are adapted.

- **Robustness:** simulate **domain shift** via style/intensity transforms; test on held out sites if available.

Project Plan

6.1 Milestones & Timeline

Your course schedule specifies graded checkpoints and the **Final Report (40–50 pages) + in person presentation**. Map our milestones to the syllabus dates:

- **By Oct 12:** Report 0 – Design & Analysis (this document).

- **By Oct 26:** Progress Report 1 — U Net baseline trained; initial Dice/HD95 and sample overlays.

- **By Nov 09:** Progress Report 2 — MedSAM+LoRA implemented; early comparison to baseline.

- **By Nov 23:** Progress Report 3 — Full evaluation, ablations, robustness study; draft figures/tables.

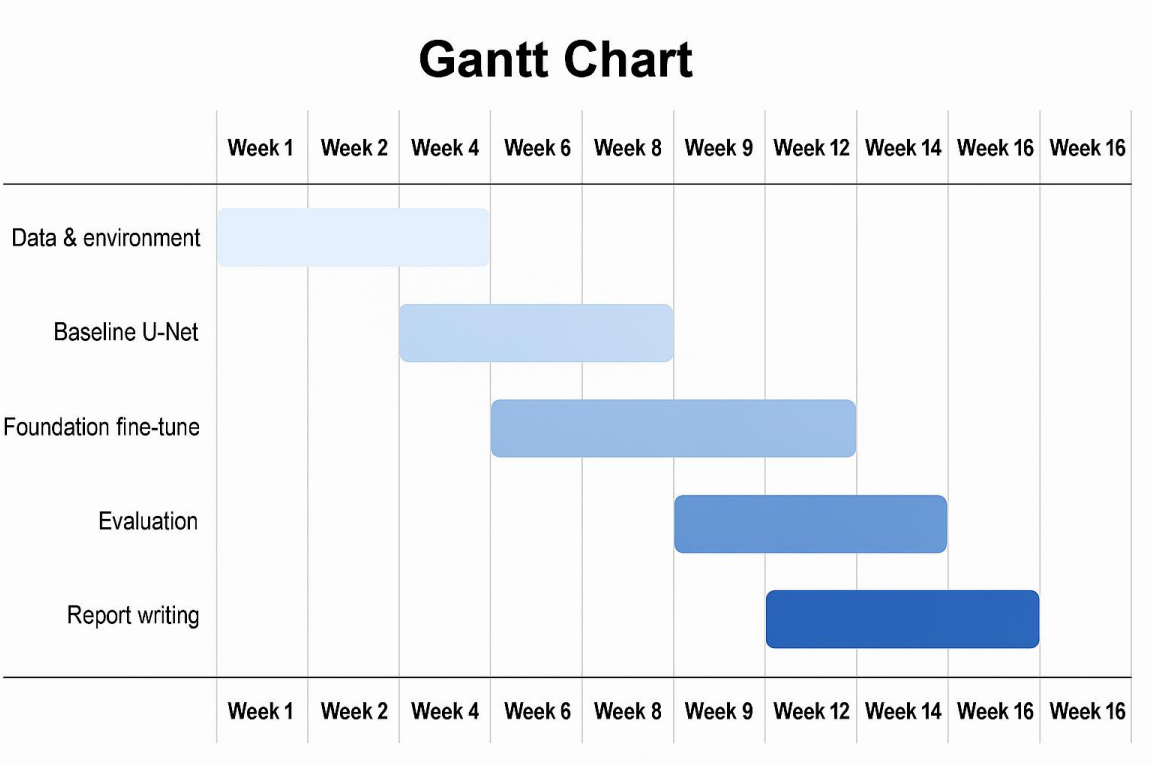
- **By Dec 07:** Final Report & Presentation — complete write up (40–50 pp, 10 pt), code appendix + GitHub link.

6.2 Risk Management

- **GPU memory/time limits**: prefer **2.5D** or **3D patches**, mixed precision, gradient accumulation.

- **Training instability (Transformer/PEFT):** learning rate sweeps; scale LoRA rank; freeze more layers.

- **Dataset quirks:** enforce rigorous QC; lock splits; document metric code to avoid HD95 inconsistencies.



Expected Outcomes

Technical: A reproducible pipeline with **quantified performance deltas** between a **from-scratch U-Net** and **MedSAM+LoRA**, including accuracy (Dice/HD95), efficiency (latency/VRAM), and robustness under basic domain shifts.

Practical: Clear guidance on when a conventional U Net suffices vs. when **foundation model fine tuning** pays off for brain MRI segmentation (compute/data budgets).

Challenges: Sensitivity to scanner differences, small enhancing lesions (ET), and prompt design for foundation models (quality/number of prompts).

References

[1] O. Ronneberger, P. Fischer, and T. Brox, "U Net: Convolutional Networks for Biomedical Image Segmentation," MICCAI, 2015.

[2] Ö. Çiçek et al., "3D U Net: Learning Dense Volumetric Segmentation from Sparse Annotation," MICCAI, 2016.

[3] Z. Zhou et al., “UNet++: A Nested U Net Architecture for Medical Image Segmentation,” MICCAI, 2018.

[4] O. Oktay et al., “Attention U Net: Learning Where to Look for the Pancreas,” arXiv:1804.03999, 2018.

[5] J. Chen et al., “TransUNet: Transformers Make Strong Encoders for Medical Image Segmentation,” arXiv:2102.04306, 2021.

[6] H. Cao et al., “Swin UNet: Unet like Pure Transformer for Medical Image Segmentation,” arXiv:2105.05537, 2021 / ECCV W 2022.

[7] A. Kirillov et al., “Segment Anything,” ICCV 2023.

[8] J. Ma et al., “Segment Anything in Medical Images (MedSAM),” arXiv:2304.12306, 2023.

[9] E. Tustison et al., “N4ITK: Improved N3 Bias Correction,” ISBI, 2010.

[10] S. M. Smith, “Fast Robust Automated Brain Extraction (BET),” Hum. Brain Mapp., 2002.

[11] SimpleITK documentation: Resample/Registration.

[12] NiBabel documentation: Working with NIfTI images.

[13] S. Bakas et al., “Advancing the TCGA Glioma MRI Collections with Expert Segmentation Labels,” Scientific Data, 2017.

[14] BraTS evaluation: Dice and HD95.

[15] F. Milletari et al., “V Net” (Dice Loss). arXiv:1606.04797, 2016.

[16] S. S. M. Salehi et al., “Tversky Loss,” MICCAI MLMI, 2017.

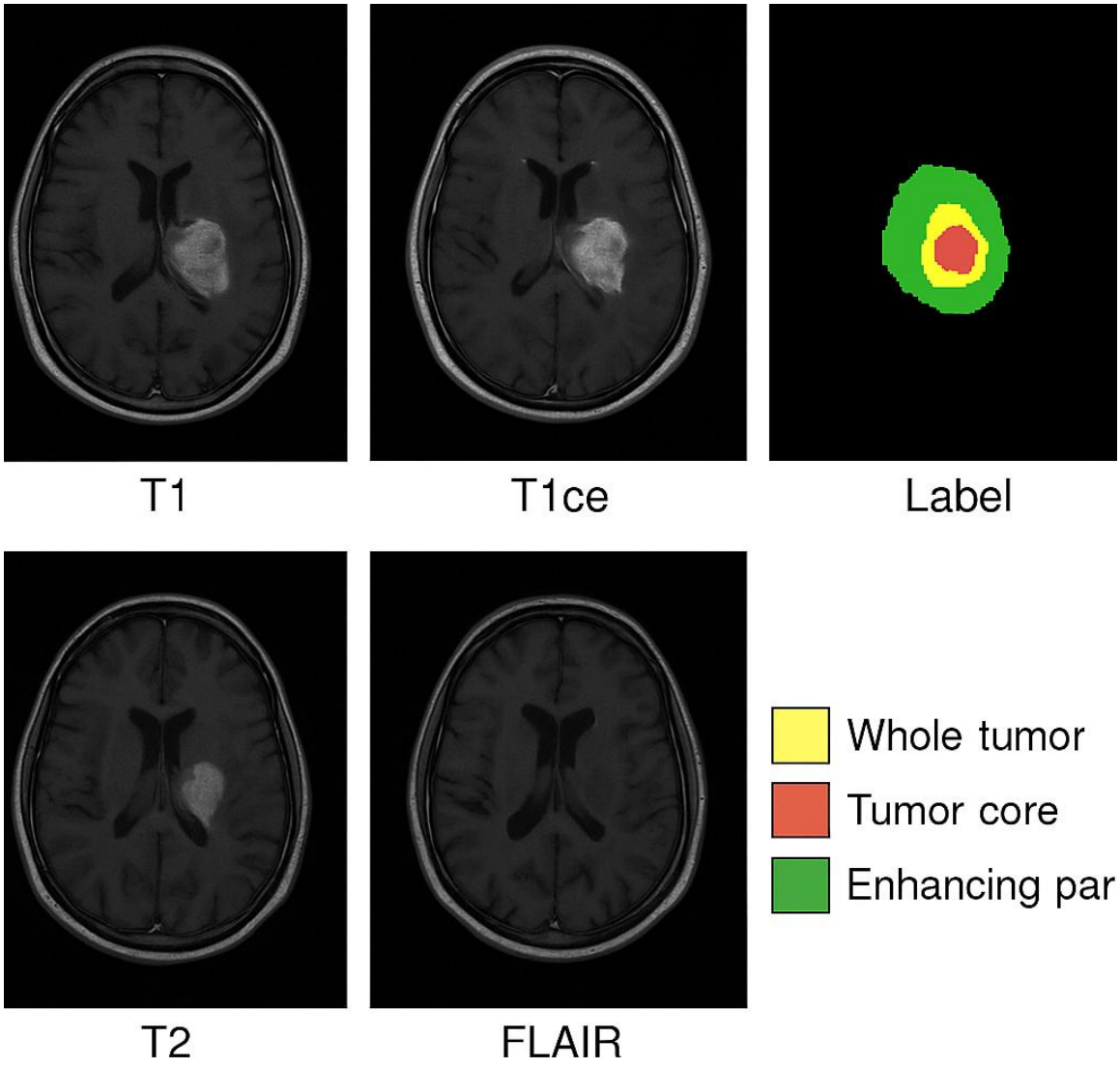
[17] H. Kervadec et al., “Boundary Loss,” MIDL/MedIA, 2019–2020.

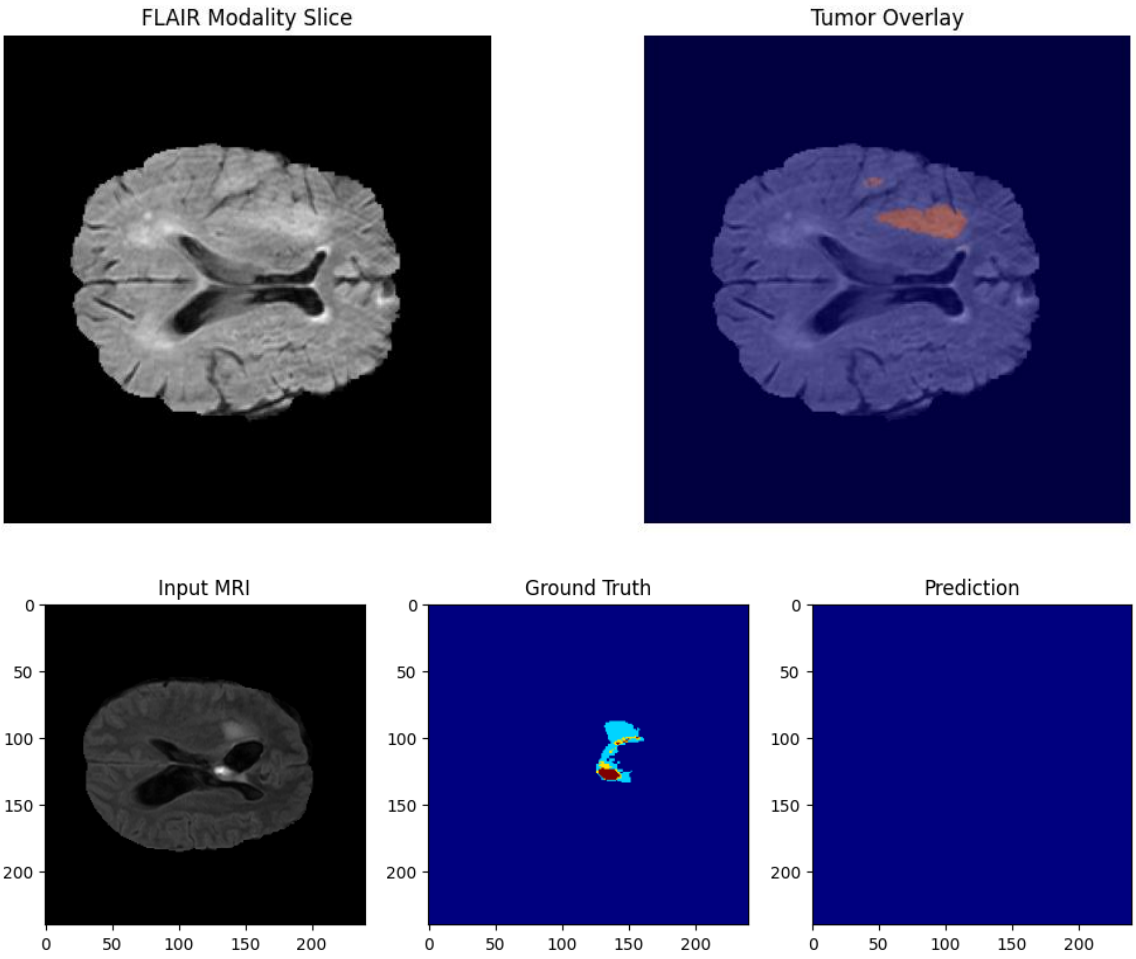
[18] P. Krähenbühl and V. Koltun, “Efficient Inference in Fully Connected CRFs,” NeurIPS, 2011/2012.

[19] F. Isensee et al., “nnU Net: A Self Configuring Method,” Nature Methods, 2021.

[20] B. A. Reinke et al., “Towards a guideline for evaluation metrics in medical image segmentation,” BMC Res Notes, 2022; and HD dilemma (implementation variability).

Appendix- If any: In later stages you will have more to put here




FLAIR Modality Slice
Tumor Overlay
Input MRI
Ground Truth
Prediction
0
50
100
150
200