Galala University
Faculty of Computer Science and Engineering
Artificial Intelligence Science Program and Big Data Program

B.Sc. Final Year Project

Deep Learning-Driven Liver Tumor Diagnosis: An MRI-Based Detection Pipeline Integrating SVM Classifier & Feature Extraction, U-Net Feature Selection, and MONAI for Enhanced Clinical Intelligence

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DEDICATION

We sincerely dedicate this project to our families, whose belief in us never wavered and whose support gave us strength, to each other, for the patience, collaboration, determination that kept us moving forward, and continuously supporting each other.

And above all, to God, for granting us the ability and perseverance to reach this milestone.

ACKNOWLEDGEMENTS

This project was completed in partial fulfillment of the requirements for the Bachelor's degree at Galala University, Faculty of Computer Science and Engineering. Throughout our academic journey, we benefit from the instruction, efforts, and dedication of the faculty members, whose teaching over the past years provided the essential foundation needed to undertake this work.

Building on the knowledge and skills acquired during our studies, we were able to apply theoretical principles to practical challenges encountered during the project.

In addition, we would like to acknowledge the guidance of our supervisor, Dr. Safa Elaskary, whose academic supervision supported the development of the project and contributed to maintaining its direction and objectives.

The facilities and resources offered by the university also played an important role in supporting the successful execution of this work, whether directly or indirectly.

DECLARATION

We hereby declare that the work presented in this graduation project, titled “Liver Tumor Detection using AI for MRI Analysis and LLM for Report Generation” is the result of our own efforts, and has been completed under the supervision of Dr. Safa Elaskary. This work is submitted in partial fulfillment of the requirements for obtaining the Bachelor’s degree in Computer Science and Engineering at Galala University. We confirm that no part of this project has been submitted elsewhere for academic credit, and that all references to external sources have been properly acknowledged. We understand that any violation of academic integrity may lead to appropriate disciplinary actions in accordance with university policies.

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ABSTRACT

Liver diseases affect millions of people globally. While Early diagnosis is essential to avoid serious complications, conventional diagnosis methods are often invasive, time consuming, and costly. This project suggests using artificial intelligence to detect liver diseases through noninvasive data sources, such as blood tests, medical images, and patient history. The results showed that the AI models were more accurate than traditional methods, which means AI could help make liver disease diagnosis faster and more reliable.

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Chapter One

1 INTRODUCTION

1.1 BACKGROUND

Liver cancer is considered one of the most dangerous types of tumors and is a major reason behind cancer deaths across the world [1]. Accurate and early detection of liver tumors play a critical role in improving treatment outcomes and reducing mortality rates [6]. However, traditional diagnostic approaches, such as manual evaluation of Magnetic Resonance Imaging (MRI) scans, suffer from several limitations primarily the lengthy time required, high dependency on the expertise of medical specialists, and the increased risk of human error due to variations in doctors' interpretations [1,3].

As artificial intelligence technology continues to develop quickly, new digital tools have been created to make medical diagnosis more accurate and efficient, especially in the field of medical image analysis [28]. Deep learning techniques have proven to be powerful tools in recognizing complex visual patterns within medical imaging that are often difficult for the human eye to detect [2,4]. By training these models on large-scale medical datasets, they can produce fast and highly accurate results, making them effective assistive tools for healthcare professionals without replacing their clinical role [12,24].

At the same time, Large Language Models (LLMs) represent a transformative advancement in automating medical reporting. These models can generate detailed diagnostic reports based on image analysis results, helping to unify report formats, reduce documentation time, and support more structured and informed medical decision-making [10].

MRI imaging continues to play a key role in liver tumor diagnosis due to its high resolution for soft tissues and its non-reliance on ionizing radiation, making it a relatively safe option for patients [1,6]. However, Processing MRI scans, especially 3D formats, require advanced computational techniques to ensure maximum utility. Researchers often deal with many difficulties when using MRI data, such as low image quality, large file sizes, and problems with aligning the images correctly [1,7]. Additionally, technical difficulties may arise during data preprocessing and model training [4,18].

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Therefore, this project aims to develop an integrated AI-based system for automatic liver tumor detection using MRI scans, along with the incorporation of an LLM for automated medical report generation. This solution is designed to improve diagnostic efficiency, reduce reporting time, and enhance the overall quality of healthcare services provided to patients while addressing the practical challenges of working with complex medical data.

1.2 OBJECTIVES

The objective of this project is to improve the accuracy and speed of liver disease diagnosis using artificial intelligence, specifically through automated analysis of MRI scans. The system is designed to reduce the need for constant involvement of specialized doctors in the diagnostic process, and to automatically create medical reports with the help of a Large Language Model (LLM), which helps save time in the diagnostic process. This approach aims to support medical professionals in making faster and more consistent decisions, while maintaining a non-invasive diagnostic workflow.

1.3 CHALLENGES FACED

One of the main challenges we faced in developing medical imaging models was dealing with the complex of real-word MRI data. Variations in scan quality, acquisition protocols, patient anatomy, and noise levels result in significant inconsistencies across MRI images. If not properly addressed, these differences can negatively impact both image quality and label accuracy. Another challenge was the shortage of labeled data, mostly because of privacy issues and the expensive process of expert data labeling. Additionally, training deep learning models on 3D MRI volumes demands substantial computational resources and requires precise alignment between the image and its corresponding label mask.

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1.4THESIS ORGANIZATION

Chapter 2: Literature Review

This chapter presents an in-depth review of past studies related to detecting liver tumors and analyzing medical images analysis. It covers traditional diagnostic methods, advancements in artificial intelligence, and the application of deep learning models in medical imaging. The chapter also discusses key preprocessing techniques, segmentation approaches, and comparative studies on liver tumor detection models, identifying the gaps and opportunities that inform the current research.

Chapter 3: Methodologies

This chapter explains the research plan and methods used to build the AI-powered diagnostic system. It outlines the systematic approach taken from data acquisition through model selection and evaluation. The rationale behind choosing specific algorithms, experimental setup, and performance metrics are described to ensure reproducibility and rigor throughout the study.

Chapter 4: Data Preprocessing

This chapter focuses on the preprocessing pipeline applied to MRI data to enhance quality and consistency. It covers steps such as bias field correction, intensity normalization, image reorientation, volume resizing, mask alignment, and binarization. Challenges encountered during preprocessing, such as handling 3D image complexities and ensuring accurate mask alignment, are also discussed to emphasize the importance of clean input data for model training.

Chapter 5: Model Development

This chapter explains the development and training of diagnostic models, including traditional machine learning approaches like Support Vector Machines (SVM) and advanced deep learning architectures such as U-Net. It describes the model architecture, training strategies, hyperparameter tuning, and techniques to address class imbalance. The chapter also compares the models, explaining their advantages, weaknesses, and how suitable they are for segmenting liver tumors.

Chapter 6: Graphical User Interface & Application Programming Interface

This chapter explains how the Graphical User Interface (GUI) and the Application Programming Interface (API) were designed and built to let users interact with the AI diagnostic system. It details the objectives of the interface design, key features, backend logic, and model integration. The chapter also highlights user experience considerations and includes a walkthrough of example

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use cases, emphasizing how the GUI and API facilitate efficient clinical workflows and improve accessibility for medical practitioners.

Chapter Two

2 LITERATURE REVIEW

2.1 INTRODUCTION

Recent developments in Artificial Intelligence (AI) and deep learning have revolutionized the field of medical diagnosis, particularly in radiology and medical imaging [28]. One of the most significant challenges faced in hepatology is the early detection and accurate diagnosis of liver tumors, which are often diagnosed after a long period and at the last stages of the illness, due to the limitations of conventional diagnostic techniques [1,6]. Magnetic Resonance Imaging (MRI) plays a central role in liver tumor identification because of its superior soft tissue contrast and non-invasive nature [1,6]. However, MRI data suffers from variations in resolution, which may impact the accuracy of machine learning models [7]. Therefore, preprocessing MRI images including steps like bias field correction, reorientation, normalization, and mask alignment is essential to produce consistent, high-quality input for AI models [4,18].

This chapter provides a review of the literature on liver tumor detection using machine learning (ML) and deep learning (DL) models. It begins by studying the theoretical foundations and recent applications of Artificial Intelligence (AI) in medical imaging, with a focus on supervised learning and convolutional neural networks [2,28]. The chapter then explores essential preprocessing strategies for handling 3D MRI data and their impact on segmentation performance and training stability [7,18]. Many studies are reviewed to highlight existing frameworks for tumor segmentation using U-Net and voxel-level classification using models such as Support Vector Machines (SVM) [3].

This work also discusses the growing role of Large Language Models (LLMs) in clinical applications. It looks at how AI can help automatically create radiology reports based on imaging results [10].

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2.2 AI IN MEDICAL IMAGING

AI has made high achievements in the field of medical imaging by offering automated, accurate, and efficient solutions for image analysis, disease detection, and prognosis [28]. Deep learning techniques such as convolutional neural networks (CNNs) demonstrate superior performance in tasks like classification, segmentation, and anomaly detection [2,4], In the field of MRI, Artificial Intelligence (AI) is applied to assist radiologists in detecting tumors, setting anatomical structures, and quantifying disease burden with higher speed and consistency [1,3]. However, the success of Artificial Intelligence (AI) applications in medical imaging depends heavily on the quality of input data and robust preprocessing pipelines that ensure uniformity, and accuracy [7,18].

2.3 MRI PREPROCESSING TECHNIQUES

Preprocessing plays a very important role in the application of AI to magnetic resonance imaging (MRI), because it directly affects the performance of the models. Often, MRI data have a high degree of homogeneity due to Scanner variance, density inhomogeneity, and noise artifacts [7]. Key preprocessing techniques include bias field correction, which addresses slow varying intensity distortions caused by magnetic field [18], and image reorientation, which aligns all volumes to a standard anatomical orientation [4].

To make MRI scans more consistent across subjects, intensity normalization is used, adjusting pixel values through methods like Z-score or Min-Max scaling to improve model learning [7]. Other steps such as histogram clipping, mask validation, and resizing scans to uniform sizes (e.g., 128×128×64) help remove anomalies, exclude empty regions, and prepare images for neural network input [18].

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2.4 SEGMENTATION AND CLASSIFICATION MODELS

Segmentation and classification models are the primary AI tools in medical imaging. The U-Net architecture and its 3D variants are popular because they effectively capture global context and fine details, which are crucial for accurate tumor delineation [4]. These models employ an encoder-decoder structure with skip connections, enabling detailed segmentation predictions from volumetric scans [2].

Classification models are different. They are usually used to tell the difference between healthy and unhealthy tissue or to find disease types in full scans. However, both segmentation and classification models depend a lot on the quality of the input data. Research shows that models trained in well-prepared data with aligned masks, normalized brightness, and the same image sizes work more accurately and can be used on new data more easily. Preprocessing steps like bias correction, making sure masks are clear, and resizing the scan volumes are very important. They help the model learn better and avoid problems during training.

2.5 STUDIES ON LIVER TUMOR DETECTION

2.5.1Comparative Analysis of Liver Tumor Detection Models

2.5.1.1 Introduction

This study presents a comparative analysis between a deep learning model for liver tumor detection using MRI (referred to here as “your model”) and a CT-based model developed by Rela et al. (2023) [24]. The aim is to highlight differences in methodology, performance outcomes, and areas for potential enhancement.

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2.5.1.2 Methodological Comparison

The table below shows the key differences between the methods followed in the two models:

Aspect	Our Model	Rela et al. (2023) Model
Goal	Liver tumor detection using MRI and Deep Learning	Liver tumor detection using CT images and hybrid deep learning model
Imaging Modality	MRI (Magnetic Resonance Imaging)	CT (Computed Tomography)
Segmentation Model	U-Net	U-Net with GW-CTO Optimization
Feature Selection	Implicit in DL pipeline	Explicit using GW-CTO
Classifier	End-to-end segmentation (Dice, IoU)	HI-DNN tuned by GW-CTO

Table1.

2.5.1.3 Performance Comparison

The following table compares how well both models performed, based on the results that were shared:

Metric	Your Model	Rela et al. (2023) Model
Training Accuracy	99.43%	Not directly reported
Validation Accuracy	99.17%	4.3%–5.2% improvement over baselines
Training Mean IoU	0.8878	Not reported
Validation Mean IoU	0.8813	Not reported
Dice Score	0.9326	Not reported
Training Loss	0.0539	Not reported
Validation Loss	0.0669	Not reported

Table2.

2.5.1.4 Strengths and Potential Improvements

Strengths of Your Model

- The model showed strong segmentation results, reaching a Dice score of 0.9326 and a Mean IoU of around 0.88.
- It uses a straightforward deep learning process that works from start to finish.
- MRI was used instead of CT, giving more precise and detailed images of soft tissues.

Areas for Improvement

- Incorporate feature optimization or attention mechanisms to improve feature learning.
- Evaluate the model on public and external datasets to improve generalization.

Add a classification step after segmentation if diagnostic categorization is needed.

2.5.1.5 Summary of Key Advantages

Category	Winner	Reason
Segmentation Accuracy	Your Model	Superior Dice and IoU scores
Classification Enhancement	Rela et al. (2023)	GW-CTO-enhanced classifier
Pipeline Simplicity	Your Model	Efficient end-to-end architecture
Optimization Techniques	Rela et al. (2023)	Advanced feature and hyperparameter tuning

Table3.

2.5.2 Review-Based Comparison: Liver Tumor Detection Techniques

2.5.2.1 Introduction

This section compares the performance and methodology of your MRI-based liver tumor detection model with the findings from a recent review paper by Hariharan et al. (2025). The review looks at the latest developments, existing challenges, and future research trends in liver tumor segmentation and classification.

2.5.2.2 Focus Areas of the Review Paper

The review paper focuses on the following key aspects:

- Difficulties in tumor segmentation caused by similar tissue intensities.
- Importance of accurate liver and tumor segmentation (LS and TS).
- Assessment of various algorithms based on performance.
- Automation and robustness of techniques across different conditions.
- Future directions for developing clinically reliable AI models
- Future research directions for robust, clinically usable systems.

2.5.2.3 Comparative Analysis

Aspect	Your Model	Review Paper Insight
Data Modality	MRI	Primarily CT and tomography imaging
Focus	Tumor segmentation using U-Net	Survey of segmentation and classification algorithms
Performance Metrics Used	Accuracy, IoU, Dice, Loss	Precision, robustness, automation
Clinical Relevance	High (precise segmentation with high Dice Score)	Addresses variability and robustness across conditions
Scope	Experimental implementation and evaluation	Broad overview and critical evaluation of methods
Challenges Handled	Tumor differentiation in MRI	Tissue intensity similarity, data variability

Table4.

2.5.2.4 Strengths and Insights

Strengths of Your Model

- The model shows strong segmentation performance, achieving a Dice score of 0.9326.
- It uses a simple end-to-end deep learning pipeline, which makes the process more efficient.
- Using MRI images helps improve the quality of soft tissue segmentation due to their higher resolution.

Insights from the Review

- Need for models that generalize well across patient populations [24].
- Difficulty in handling tumors with low contrast and irregular shapes [24].
- Importance of developing fully automated, clinically usable tools.

2.5.2.5 Potential for Integration

By combining the strengths of your model with recommendations from the review, future improvements can be made. These include enhancing generalizability, adding classification modules, and testing across various datasets to improve clinical adoption.

2.5.2.6 Summary Table

Category	Our Model	Review Paper
Technical Performance	High (Dice: 0.9326)	Varies depending on the method
Pipeline Design	End-to-end U-Net	Mixed classical and Deep Learning approaches
Clinical Utility	Promising, but requires validation	Emphasized as a challenge
Scope	Specific implementation	Comprehensive method review

Table5.

2.5.3 Comparative Analysis of Deep Learning-Driven Liver Tumor Diagnosis Approaches

2.5.3.1 Introduction

This report provides a detailed comparative analysis between an original research project titled 'Deep Learning-Driven Liver Tumor Diagnosis: An MRI-Based Detection Pipeline Integrating SVM Classifier, U-Net Feature Selection, and MONAI' and the comprehensive review by Velichko et al. (2023). The goal is to assess the methods used, how well they perform in diagnosis, and how they can be applied in clinical settings from both sources.

2.5.3.2 Overview of Approaches

Velichko et al. (2023)

The review provides a comprehensive analysis of deep learning approaches for MRI-based liver tumor analysis, including CNNs, GANs, U-Nets, and autoencoders. It emphasizes challenges such as model interpretability and dataset diversity.

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User's Project

The user's project integrates traditional machine learning (SVM), deep learning (U-Net), and a large language model (MONAI). It offers high diagnostic accuracy and has the potential for real-world clinical use.

2.5.3.3 Comparative Analysis

Aspect	Velichko et al. (2023)	User Project
Detection Method	CNNs and hybrid models	Feature extraction with SVM
Segmentation	U-Net variants, GANs	U-Net (fine-tuned)
Classification	CNN-based classifiers	SVM
Metrics	Not specified numerically	Accuracy: 0.9943, Dice: 0.9326
Loss Values	Not reported	Train: 0.0539, Val: 0.0669
Mean IoU	~0.65–0.85	~0.88
LLM/NLP Integration	Not discussed	MONAI
Clinical Readiness	Identified as a need	Implemented with clinical potential
Challenges Addressed	Data scarcity, explainability	Hybrid robustness + LLM

Table 6.

2.5.3.4 Strengths of the User's Project

- Achieves strong segmentation and classification performance (Dice: 0.9326, IoU ≈ 0.88).
- Combines SVM and U-Net in a single pipeline.
- Add clinical interpretability through MONAI.
- Designed for clinical application with integrated support systems.

2.5.3.5 Recommendations for Improvement

- Use multi-phase MRI data to improve diagnostic reliability.
- Implement semi-supervised learning to reduce the need for labeled data.
- Add visual explanation tools like Grad-CAM or LIME.
- Test the model across different institutions and data sources

Chapter Three

3 METHODOLOGIES

3.1 INTRODUCTION

This chapter outlines the methodological framework adopted to build a comprehensive system for liver tumor detection and segmentation from MRI scans, enhanced with automated reporting capabilities. The study follows a computational and quantitative research approach, integrating traditional machine learning techniques, deep learning models, and advanced preprocessing strategies to ensure both accuracy and interpretability in medical image analysis [28].

The methodology is divided into three primary stages. The first stage involves preprocessing raw 3D MRI data to correct for bias fields, normalize intensities, align volumes, and binarize segmentation masks. This ensures that the input data is clean, consistent, and suitable for training robust models. In the second stage, voxel-level features are extracted and used to train a Support Vector Machine (SVM) classifier to identify tumor-rich slices. These high-probability slices serve as input to the third stage, where a U-Net-based deep learning model performs semantic segmentation to delineate tumor boundaries. The study explores both 2D and 3D U-Net models, with improvements like attention gates to help the network focus better on important areas.

Additionally, a Large Language Model (LLM) is employed to automatically generate clinical reports based on model outputs, further enhancing the diagnostic pipeline [19]. Evaluation metrics such as Dice Coefficient, Intersection over Union (IoU), and pixel-wise accuracy are used to assess segmentation performance [4].

By combining classical feature-based methods with deep learning and LLMs, this methodology aims to deliver a scalable, accurate, and clinically relevant solution for liver tumor diagnosis.

Chapter Three

3.2 RESEARCH DESIGN AND APPROACH

This study adopts a model-driven, computational, and quantitative research design. The project focuses on building an integrated artificial intelligence pipeline for liver tumor detection and segmentation using MRI data, combining both classical machine learning and deep learning methodologies.

The design is primarily experimental in nature, involving the development, training, and evaluation of multiple AI models under controlled conditions. The study is structured into two sequential modeling phases: the first involves a Support Vector Machine (SVM) for voxel-level classification based on hand-crafted features, while the second employs a U-Net architecture for semantic segmentation of tumor regions from MRI slices [2]. Both models were developed using real-world medical imaging data and tested using well-defined performance metrics such as Dice coefficient, Intersection over Union (IoU), and accuracy [4].

The computational aspect is evident through the intensive preprocessing pipeline that standardizes MRI volumes via bias field correction, intensity normalization, and spatial alignment. The quantitative nature is reflected in the use of numerical performance indicators to evaluate model accuracy and segmentation quality.

This approach was selected to ensure high diagnostic precision, reproducibility, and the ability to handle the variability and complexity of 3D medical imaging data [7]. By combining traditional and deep learning models, the project achieves a balance between interpretability, computational efficiency, and spatial accuracy, aligning with the goal of developing a clinically applicable diagnostic support system**.**

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3.3 DATA COLLECTION AND DATASET DESCRIPTION

The dataset used in this study includes 3D MRI scans along with their matching tumor segmentation masks, all saved in NIfTI (.nii) format. These images were collected from a publicly available medical imaging dataset commonly used for liver tumor analysis and segmentation tasks. Although the exact name of the dataset is not specified in this report, the file structure and preprocessing methods applied are consistent with standard open-access datasets in this field.

Each scan in the dataset contains volumetric data representing the liver region, along with an associated ground-truth mask that indicates the presence or absence of a tumor. The original volumes varied in shape and resolution, requiring standardization for use in deep learning pipelines [6]. To solve this issue, all image and mask volumes were resized to a fixed size of 128 × 128 × 64 voxels to keep the dataset consistent.

Prior to modeling, the dataset underwent extensive preprocessing, including steps such as bias field correction, intensity normalization, mask alignment, and reorientation to a consistent anatomical frame [9]. Only scans with non-empty tumor masks were retained for further processing. The resulting dataset provided a high-quality, well-aligned input suitable for both voxel-level classification using SVM and semantic segmentation using the U-Net architecture [2].

This structured and cleaned dataset formed the foundation for developing an end-to-end liver tumor detection and segmentation pipeline. This allowed the use of quantitative methods and guaranteed consistent and accurate training and evaluation of the model.

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3.4 DATA PREPROCESSING

Before using any machine learning or deep learning methods, the raw MRI data had to go through a lot of preprocessing to make sure it was high-quality, consistent, and suitable for the model. This stage played a critical role in minimizing the influence of noise, standardizing input features, and preparing the dataset for effective training and evaluation.

To address missing or irrelevant data, MRI scans with empty or unlabeled segmentation masks were excluded from the dataset. This step ensured that only informative samples were used during training, preventing misleading input that could harm model performance.

Next, intensity normalization was applied in two phases. First, histogram clipping was used to suppress extreme outliers, followed by Z-score normalization to scale voxel intensity values across all images. This process stabilized the input range and improved convergence during training. Spatial normalization was also performed by resizing all volumes to a unified shape (128×128×64), maintaining consistency across batches and reducing computational overhead.

For classification tasks, feature vectors were constructed by encoding voxel-level intensity and normalized spatial coordinates (x, y, z). These features were formatted into structured arrays for machine learning input. Additionally, categorical mask values were binarized for segmentation purposes, enabling the model to distinguish between tumor and background regions in a simplified binary format.

Finally, the dataset was randomly split into training and testing subsets. An 80/20 ratio was generally applied to evaluate generalization performance while preserving a sufficient sample size for learning. All data types were optimized for model compatibility, with float32 used for images and uint8 for masks to improve processing efficiency.

3.5 MODEL BUILDING AND IMPLEMENTATION

This project used a hybrid pipeline that mixed traditional machine learning with deep learning methods to improve how accurately and efficiently liver tumors are detected in MRI scans. Two main models were developed: a Support Vector Machine (SVM) for voxel-wise classification and a U-Net architecture for semantic segmentation [3]. Both models were carefully selected for their complementary strengths interpretability and efficiency in the SVM, and spatial precision in the U-Net [2].

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Tools and Frameworks

The entire modeling workflow was developed using Python. The main libraries and frameworks used in this project include:

- **Scikit-learn:** For SVM model training, feature scaling, and performance evaluation.
- **TensorFlow Keras:** Used to build and train the initial 2D U-Net model for binary segmentation.
- **PyTorch:** Used for implementing a more advanced 3D U-Net model with attention gates to enhance volumetric segmentation.
- **NumPy and Nibabel:** For handling 3D MRI data in NIfTI format and converting it into training-compatible arrays.

SVM Model for Voxel-Level Classification

The first model focused on classifying individual voxels based on manually engineered features. These features included normalized voxel intensity values and spatial coordinates (x, y, z). A custom function named extract_voxel_features was developed to generate the input dataset. After normalization using StandardScaler, the data was split into training and testing sets.

The SVM model was implemented using an RBF (Radial Basis Function) kernel to handle non-linear decision boundaries. Hyperparameter tuning was carried out using manual selection and grid search. The model predicted tumor probabilities at the voxel level, which were then averaged per slice. The top 10 slices with the highest tumor probability were selected for further processing.

U-Net for Image Segmentation

The second stage employed a U-Net convolutional neural network for semantic segmentation. Two architectures were developed:

- **2D U-Net (TensorFlow):** Operated on the selected slices and used a classical encoder-decoder structure with skip connections. It was compiled with the Adam optimizer and trained using Binary Cross-Entropy Loss [2].
- **3D U-Net with Attention (PyTorch):** Designed for volumetric segmentation, this version added attention gates to allow the network to focus more effectively on tumor regions [13]. It was trained using a composite Dice + Focal Loss function to address class imbalance [16].

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In both models, input data was resized and normalized before training. The output was a binary mask indicating the presence or absence of tumor tissue at each pixel or voxel. Performance metrics such as Dice Coefficient, Intersection over Union (IoU), and pixel-wise accuracy were used to evaluate model quality [4].

Model Saving and Monitoring

Both models incorporated training checkpoints. The best-performing model weights (based on validation Dice score) were saved automatically. The training and validation losses were tracked and analyzed to check for overfitting and to see if the model was learning properly.

Through this multi-stage modeling approach, the project successfully leveraged the strengths of both machine learning and deep learning to create a clinically relevant, interpretable, and accurate tumor detection pipeline.

3.6 EVALUATION METRICS

To assess the performance of the proposed system, multiple evaluation metrics were employed, each selected to reflect different aspects of model quality and relevance to clinical tasks. The Dice Coefficient (F1-score) was the main metric used to measure how much the predicted segmentation matched the ground truth. This metric works well for medical images with small target areas because it focuses on true positives and gives an accurate idea of spatial overlap. In addition, Intersection over Union (IoU), or the Jaccard Index, was used to give a more careful measure of similarity, especially when tumor edges are uneven or only partly segmented.Pixel-wise Accuracy was also calculated to measure the percentage of correctly predicted pixels across the entire image; however, it was interpreted cautiously due to the significant class imbalance between tumor and non-tumor regions. For the SVM-based voxel classification stage, Precision and Recall were utilized to evaluate the model's ability to correctly identify tumor voxels while minimizing false positives. These metrics, combined with the F1-score, offered a balanced understanding of model sensitivity and specificity. The selection of these metrics was driven by the clinical need for accurate tumor localization, the challenges of imbalanced medical data, and the requirement for reliable validation of both classification and segmentation outcomes.

Chapter Four

4 DATA PREPROCESSING

At the beginning of the project, we collected 3D MRI data in (.nii) format, which included the scans and their matching labels (masks). However, this raw data could not be used directly in deep learning models because it was inconsistent and had not been preprocessed. Therefore, a series of preprocessing steps were implemented to clean, standardize, and prepare the dataset for effective model training and analysis.

4.1 DATA LOADING

To read and process these medical images, we used the nibabel Python library, which provides support for loading NIfTI files and converting them into NumPy arrays. This conversion is essential as deep learning models cannot process raw NIfTI files directly. By transforming the data into 3D arrays, we enable efficient manipulation, analysis, and integration with downstream preprocessing steps and model pipelines. This step ensures that all MRI volumes are structured in a format compatible with the preprocessing pipeline and machine learning frameworks such as TensorFlow or PyTorch.

4.2 DATA CLEANING AND PREPARATION

Before proceeding to normalization and resizing, we performed essential data cleaning and preparation steps to ensure consistency and relevance of the dataset.

4.2.1 Mask Validation

Some of the MRI scans in the dataset did not contain any tumor regions, resulting in empty masks. Including such masks in training can mislead the model and degrade segmentation performance. Therefore, we validated each mask and excluded cases where the mask contained no labeled voxels [5].

4.2.2 Histogram Clipping

MRI images often include outlier intensity values that are not clinically relevant and may result from noise or acquisition artifacts. To lessen the effect of these outliers, we used histogram clipping by limiting the intensity values to the range of [-200, 250].This helps stabilize the intensity distribution and improves model robustness.

4.2.3 Image Mask Alignment

We observed shape mismatches between some images and their corresponding masks due to differences in acquisition parameters. To solve this issue, we used the smallest common shape for each element and sliced both the image and the mask to match that shape. This ensured pixel-wise alignment, which is critical for supervised learning in segmentation tasks [9].

4.2.4 Visual Verification

To ensure that cleaning steps were successfully applied, we conducted manual inspection of a subset of the volumes and masks. This verification step helped identify and address any potential errors in the pipeline [5].

4.3 Mask Alignment

To ensure proper alignment between the MRI volumes and their corresponding segmentation masks, we applied a joint resizing procedure using consistent zoom factors derived from the original image dimensions. This ensured that each image and its mask had the same spatial resolution, which allowed accurate voxel-level training.

C h a p t e r F o u r

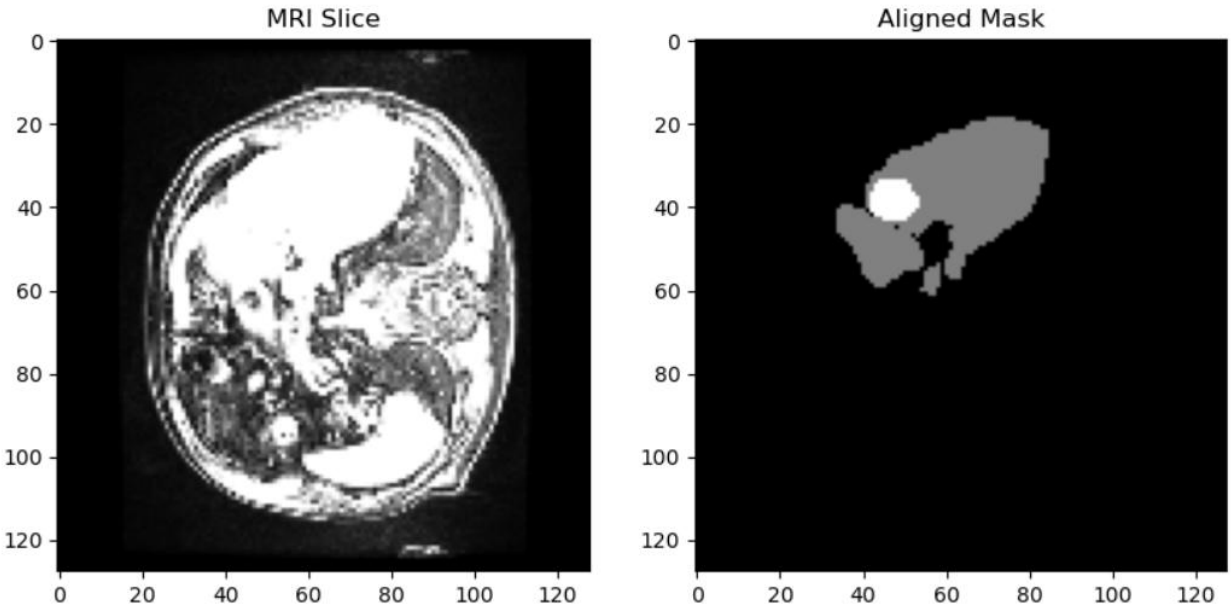

figure (1).

As a result:

I. All image and mask volumes were resized to a standard size of 128 × 128 × 64.
II. Label interpolation was applied using nearest-neighbor methods to preserve discrete label values.
III. The alignment process ensured 100% compatibility between image and mask dimensions across the dataset.
IV. Any mask found to be empty (i.e., containing no labeled tumor voxels) was automatically excluded from training to improve data quality.

This step was essential to keep spatial consistency and make sure that each voxel in the image matched exactly with its labeled part in the mask.

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4.4 Intensity Normalization

MRI scans often exhibit significant variability in intensity ranges due to differences in acquisition protocols, scanner types, and patient-specific characteristics. This inconsistency poses a challenge for deep learning models, which assume a degree of uniformity in input data. To address this, we applied a two-step normalization process to standardize intensity distributions across the dataset:

4.4.1 Histogram Clipping

As a preliminary step, we clipped extreme intensity values to a fixed range of [-200, 250]. This was done to suppress outliers and reduce the influence of scanner noise and non-biological artifacts that may distort model training.

4.4.2 Z-score Normalization

After clipping, we applied Z-score normalization, a robust statistical method widely used in medical image preprocessing. This technique transforms the image intensities to have zero mean and unit variance, effectively stabilizing the dynamic range across all scans and ensuring comparability between samples [6].

This normalization pipeline greatly improved data consistency and contributed to more stable and efficient model convergence during training. Compared to Min-Max scaling, which was initially used, Z-score normalization demonstrated superior performance in handling intensity heterogeneity within and across MRI volumes [6].

4.5 Resizing Volumes

To prepare the MRI scans and their corresponding segmentation masks for input into deep learning models specifically 3D convolutional architectures such as U-Net it was necessary to standardize the spatial dimensions of all volumetric data. The original dataset exhibited significant variation in volume sizes, with dimensions ranging from (512×512×30) to (256×256×45), which made batch processing and model training infeasible [3].

To solve this, a uniform resizing method was used, where all image-mask pairs were resampled to a fixed target size of 128 × 128 × 64 voxels. This shape was chosen to balance memory efficiency and spatial resolution. Linear interpolation was applied to image volumes to preserve smooth anatomical structures, while nearest-neighbor interpolation was used for masks to maintain categorical label integrity.

This resizing process resulted in:

- Complete uniformity in input volume dimensions.
- Reduced computational load, allowing for efficient model training and batching.
- Improved model compatibility with standard 3D segmentation architectures.

It is important to note that improper resizing medical volumes may lead to loss of spatial resolution or distortion of anatomical features. Therefore, the interpolation method was selected carefully to minimize artifacts, and alignment with segmentation masks was maintained through synchronized resizing

4.6 Mask Binarization

In the original dataset, the segmentation masks contained multiple label values corresponding to different anatomical structures, such as the liver and tumor regions. For instance, typical values included 0 for background, 1 for liver, and 2 for tumor.

However, the objective of this study was binary segmentation, focusing exclusively on distinguishing tumor tissue from the backgroundTo do this, we binarized the masks by changing all non-zero values to 1, so that any labeled area, no matter the class, was treated as a positive tumor region.

As a result:

- The masks were simplified into binary form: 0 indicating background, and 1 indicating tumor.

- The segmentation model was able to focus exclusively on learning the distinction between normal and abnormal regions.
- This also contributed to a more efficient and focused training process by reducing class imbalance and label ambiguity.

4.7 Data Type Conversion

As part of the final stage in the preprocessing pipeline, the dataset underwent a systematic data type conversion to enhance compatibility with deep learning frameworks and reduce memory consumption. Initially, the MRI image volumes were represented in high-precision formats such as float64, while the segmentation masks often appeared in integer types like int16. Although these formats preserve precision, they are not computationally efficient when used in model training. Therefore, all image data were converted to the float32 format, which provides sufficient precision while significantly lowering memory usage and accelerating processing time. The segmentation masks were converted to uint8, a format well-suited for binary classification tasks where only two values (e.g., background and tumor) are needed. This conversion step ensured seamless integration with neural network architectures such as U-Net, while also contributing to the overall optimization of training performance and resource management [3,6].

Chapter Four

4.8 Visual Checks and Final Pipeline overview

Following the implementation of the preprocessing pipeline, a series of visual inspections were conducted to verify the integrity and quality of the transformed MRI volumes and segmentation masks. These visual checks played a crucial role in confirming that the spatial alignment between images and masks was preserved, that intensity normalization was applied correctly, and that anatomical structures remained clearly discernible after resizing and bias field correction. Moreover, through visual comparison of "before and after" samples, The advantages of techniques like histogram clipping, Z-score normalization, and reorientation were clearly noticeable, especially in improving contrast and eliminating artifacts. This manual verification step ensured that no structural distortion was introduced during preprocessing, providing a final layer of quality assurance before model training. Ultimately, the preprocessing pipeline resulted in a clean, standardized, and spatially consistent dataset with uniform dimensions (128 × 128 × 64), robust to variation in acquisition conditions and ready for deep learning-based segmentation [3,9]

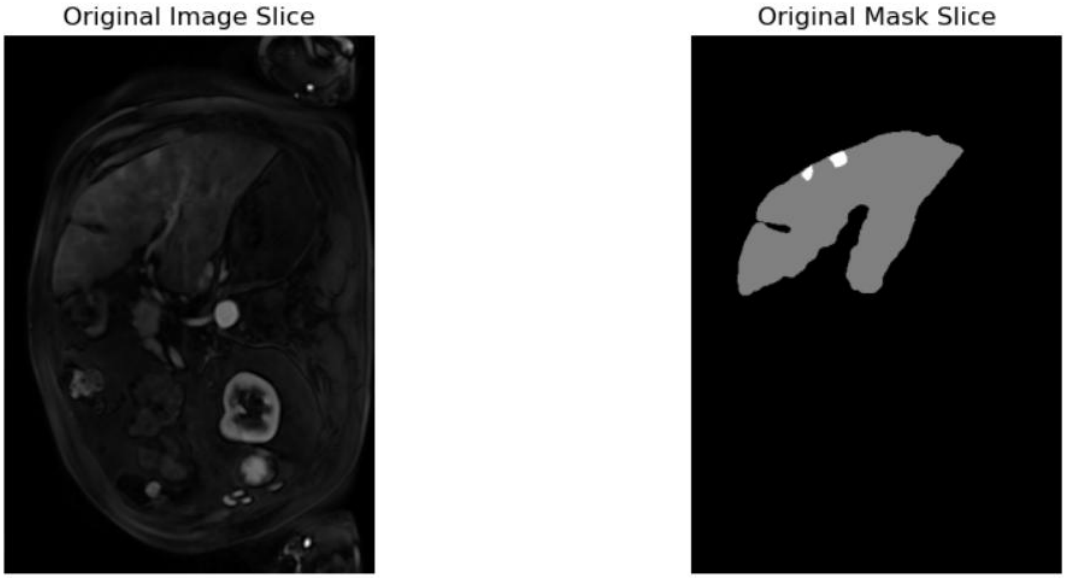

Figure (2)

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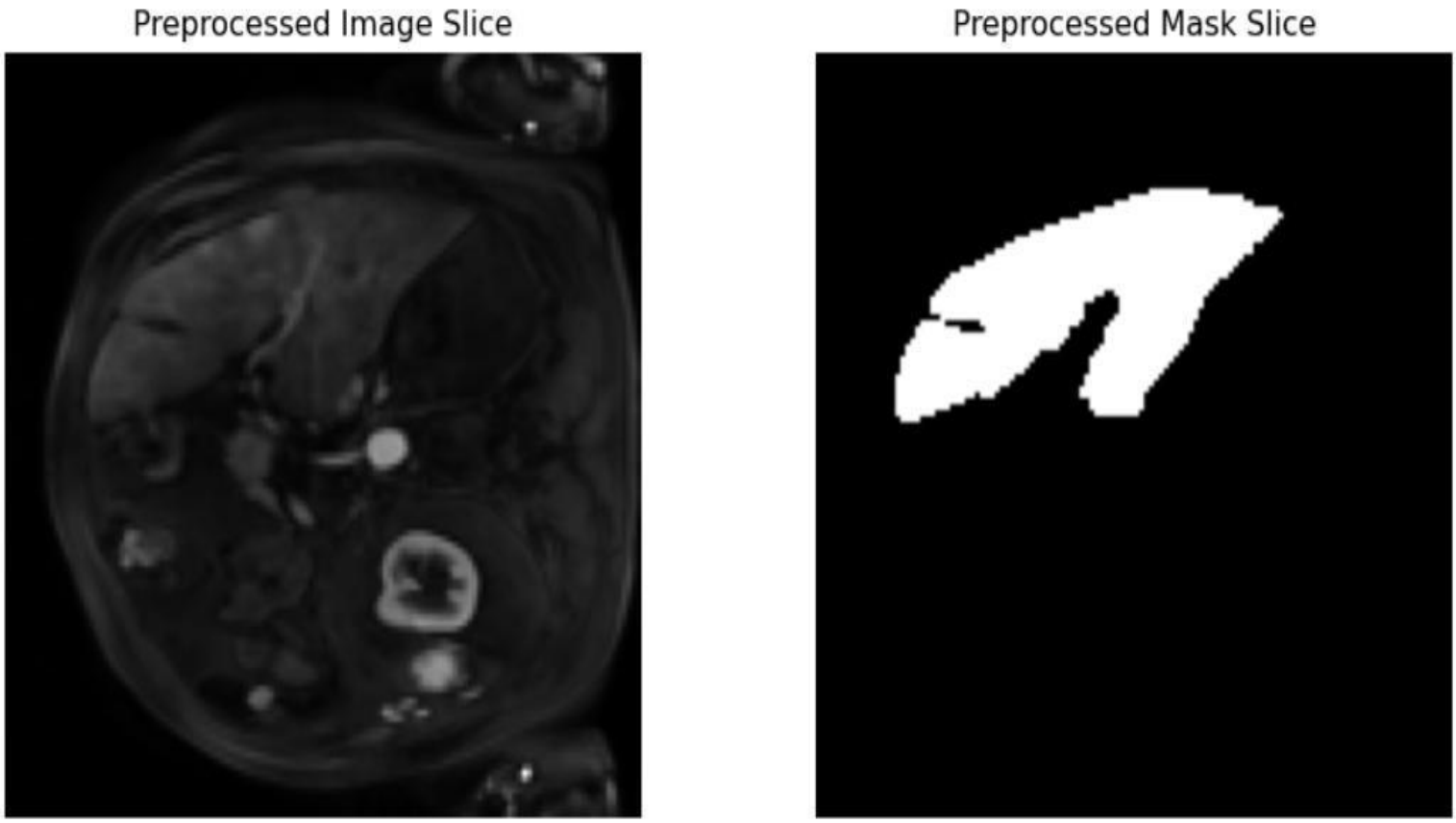

Figure (3)

4.8.1 Before Vs After Summary

STEP	BEFORE	AFTER
Image Shape	Varies (e.g., 512×512×N)	Fixed to 128×128×64
Mask Shape	Often different from image shape	Aligned exactly with image shape
Image Values	Ranged between 0–2000 or more	Normalized to [0, 1]
Mask Values	Multi-class (e.g., 0, 1, 2)	Binary (0 = background, 1 = tumor)
Data Types	Float64 or int16	Float32 (image), uint8 (mask)

Table 7.

4.9 Bais Field Correction

Magnetic Resonance Imaging (MRI) scans often show low-frequency intensity variations called bias field distortions. These slow changes in brightness are usually caused by imperfections in the magnetic field or differences in coil sensitivity, making the same tissue appear brighter or darker in different parts of the image. Such inconsistencies can adversely affect the performance of machine learning models, particularly those relying on voxel-level intensity values for accurate tissue classification and segmentation.

To mitigate this issue, bias field correction was applied to all MRI volumes using the N4BiasFieldCorrection algorithm from the SimpleITK libraryThis correction method estimates the bias field in the image and removes it, resulting in more uniform intensity across different tissues. The corrected images displayed enhanced contrast and improved consistency across the dataset, especially beneficial in multi-center or multi-scanner scenarios [7].

The integration of this step into the preprocessing pipeline contributed to the standardization of image intensity profiles, reduced the influence of scanner-dependent artifacts, and is expected to improve the stability and accuracy of downstream segmentation models [5].

Chapter Four

4.10 Reorientation of MRI Images

MRI volumes can be stored using different spatial orientation conventions, depending on factors such as the scanner model, acquisition protocol, or export settings. These conventions (e.g., RAS, LPS, RPI) define anatomical directions like Right, Anterior, and Superior, but may vary across datasets. If not corrected, this variation can lead to spatial misalignment between images, especially when the data come from different scanners or medical centers. Such inconsistencies present a major challenge in tasks that rely on spatial information, such as tumor localization or segmentation based on anatomical regions [5].

To solve this problem and maintain consistent spatial orientation across the dataset, we performed a reorientation step that aligned all MRI volumes to a common coordinate system (such as RAI or RAS). This was done using the DICOMOrient() function from SimpleITK, which adjusts the orientation metadata without changing the actual voxel values[5].

Standardizing the orientation of all scans provides several benefits. It enhances the clarity and consistency of the data, enabling better visualization and easier troubleshooting. and prevents problems that may arise during data augmentation or model prediction. Most importantly, it strengthens the segmentation model by ensuring that anatomical structures appear in the same position across all training and testing samples [28].

4.11 Challenges Faced .

During the preprocessing phase several challenges appeared due to the complex and varied nature of medical imaging data. One of the main difficulties was data heterogeneity, as MRI scans showed large differences in intensity, resolution, and overall quality. This variation was present even when the scans were taken using the same scanning method, which made normalization more difficult and reduced the model's ability to generalize.

C h a p t e r F o u r

Another challenge was working with 3D volumetric data, which is more demanding than 2D images. MRI scans are made up of many slices that need to be processed together. This increased the need for memory and processing power, especially during resizing. Resizing also risked losing important spatial information or introducing artifacts due to interpolation.

Mask misalignment was also a common issue. In many cases, the image and its corresponding mask had different dimensions. This often happens because of changes in scan settings or after initial processing. If not corrected, this could lead to wrong pixel-level labels, which would reduce model accuracy. To fix this, it was necessary to carefully check and match dimensions across all data.

Some scans also had empty or incomplete masks, especially when no tumors were marked. These needed to be identified and removed so they would not give the model false information during training.

In addition, MRI scans often included intensity non-uniformities and artifacts caused by magnetic field issues or patient movement. These problems made it harder to clearly see the tissues and confused models that depend on voxel intensity. To reduce these effects, techniques like bias field correction and histogram clipping were used. However, these steps added extra time and complexity to the preprocessing process.

Finally, because the 3D data was large and each scan had to be processed separately, there were ongoing problems with memory and processing time.

Despite these difficulties, the preprocessing pipeline was successfully built to handle all these variations. The result was a clean, aligned, and standardized dataset that was ready for training a strong segmentation model.

Chapter Five

5 MODEL DEVELOPMENT

5.1 INTRODUCTION

This chapter explains how we built and trained our models to detect and segment liver tumors using MRI scans, Our approach consisted of two main phases. In the first phase, we used a machine learning model called Support Vector Machine (SVM) to identify MRI slices that were most likely to contain tumors, In the second phase, we applied a deep learning model based on U-Net architecture to perform accurate segmentation of the tumor regions.

In the first phase, we extracted important features from each voxel in the 3D MRI volumes. These features included the intensity value and the voxel's location in space (x, y, z), which were normalized. The SVM model was trained to classify each voxel as either tumor or non-tumor. After that, we calculated the average tumor probability for each slice and selected the top 10 slices with the highest scores. This allowed us to focus the next stage on the most relevant parts of the scan.

The second phase used these selected 2D slices as input to train a U-Net model. Unlike the SVM, the U-Net does not need manually extracted features. It learns automatically from the image using a structure of convolutional layers. The U-Net consists of two main paths: an encoder that captures the context of the image and a decoder that helps recover the spatial details. It also contains skip connections that connect the encoder and decoder to keep detailed information. We trained the model using Binary Cross-Entropy and Dice Loss, which are well suited for cases where tumor areas are small compared to the full image.

Later, we improved the model further by building a 3D U-Net with attention gates using PyTorch. These attention mechanisms helped the model pay more attention to important tumor regions and ignore unnecessary background details, especially in complex 3D scans.

This chapter presents the full technical process of both models, including their architecture, training steps, evaluation metrics, and challenges. We used Dice score, Intersection over Union (IoU), and pixel-wise accuracy to assess model performance. Our aim was to develop a solution that is accurate and easy to understand, making it suitable for practical use in medical imaging.

C h a p t e r F i v e

To explore how the SVM model handled voxel classification, we visualized its predictions across intensity values. The figure below shows how some voxels were correctly classified while others were misclassified due to overlapping intensity levels.

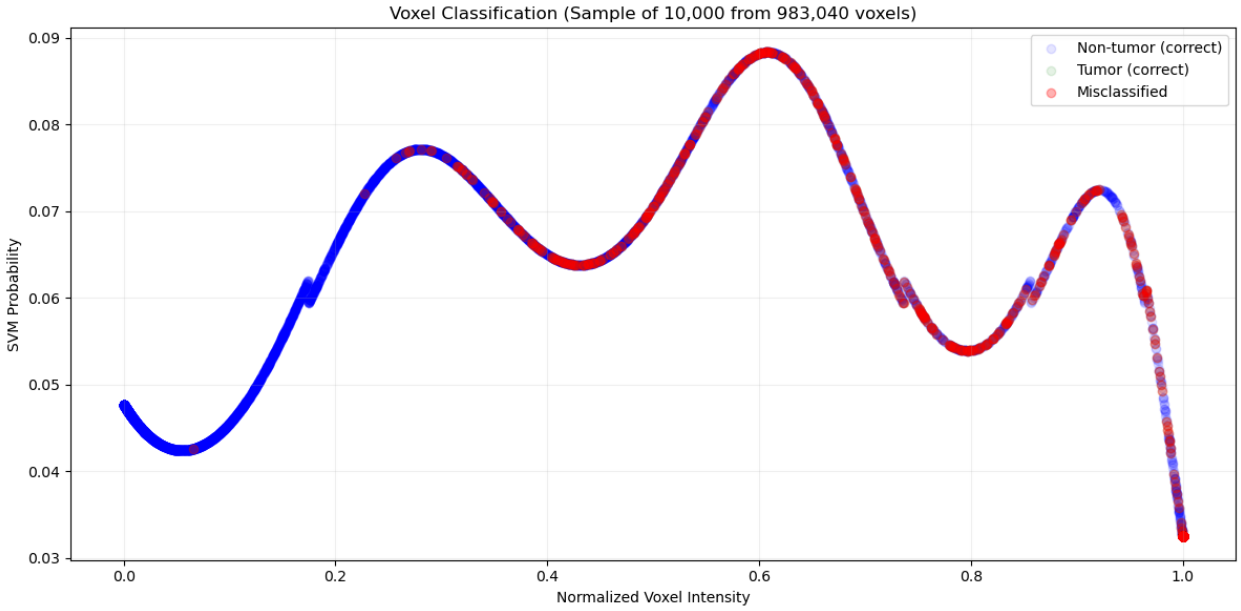

Figure (4) SVM classification of voxels based on intensity. Correctly identified non-tumor voxels are in blue, tumor voxels in green, and misclassified ones in red.

To better understand intensity patterns, we also plotted a heatmap showing voxel intensity in a liver MRI slice and compared it with the ground truth tumor mask.

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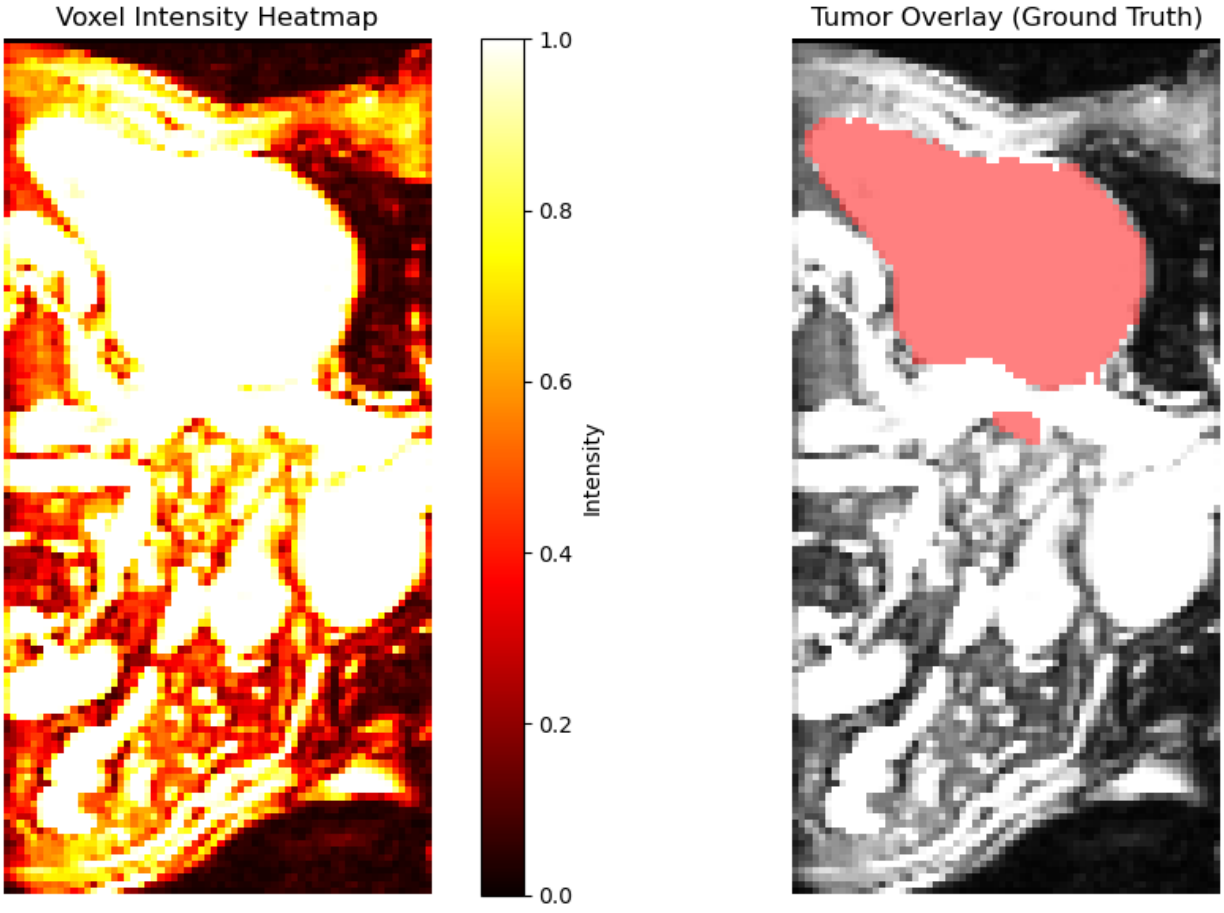

Figure (5) (Left) Voxel intensity heatmap of an MRI slice. (Right) Ground truth tumor region (pink) overlaid on the same slice for comparison.

5.2 FEATURE-BASED MODEL DEVELOPMENT (SVM PHASE)

In the first phase of our model development, we used **Support Vector Machine (SVM)** to classify each voxel in the MRI scans as either tumor or non-tumor. This helped us quickly detect which slices of the scan contained tumor regions and should be used for deeper analysis. The development of this phase involved four main parts: feature extraction, data preprocessing, model training, and tumor probability mapping.

5.2.1 Feature Extraction

To train the SVM, we first needed to extract important features from the MRI data. A custom function was written to extract voxel-level features from each scan and its tumor mask. For every voxel in the 3D MRI image, we recorded:

- Voxel intensity refers to the brightness level of a voxel in a grayscale image.
- Normalized spatial coordinates (x, y, z) – the location of the voxel, scaled by the scan dimensions to keep values consistent across different scans.

Each voxel also received a binary label from the tumor mask:

- '1' for tumor
- '0' for non-tumor (healthy or background tissue)

We only included slices where tumors were visible, which helped create a more balanced and useful training dataset.

5.2.2 Data Preprocessing

- After we extracted the features, we arranged them into two separate arrays:
- **X_all:** feature vectors (intensity + normalized coordinates)
- **y_all:** binary labels for each voxel

Before training, we used StandardScaler from scikit-learn to normalize the features [4]. This scaling step transformed the data to have zero meaning and unit variance, which helps SVM learn better and faster.

A key problem we noticed was class imbalance. Non-tumor voxels were much more common than tumor voxels. Although we considered balancing methods (like oversampling or class weights), we first trained the model on natural distribution to understand its base performance [5].

5.2.3 SVM Model Training

The SVM was trained to separate tumor and non-tumor voxels using the extracted features. We used the RBF (Radial Basis Function) kernel to identify non-linear patterns in the data.

The dataset was split into training (80%) and testing (20%) sets. We measured performance using several metrics:

- **Accuracy:** the percentage of correct predictions
- **Precision:** how many predicted tumors were actually tumors
- **Recall:** how many actual tumors were correctly predicted
- **F1-Score:** the harmonic average of precision and recall, used to balance both measures.

We also tuned the model's parameters manually and through grid search to improve its performance.

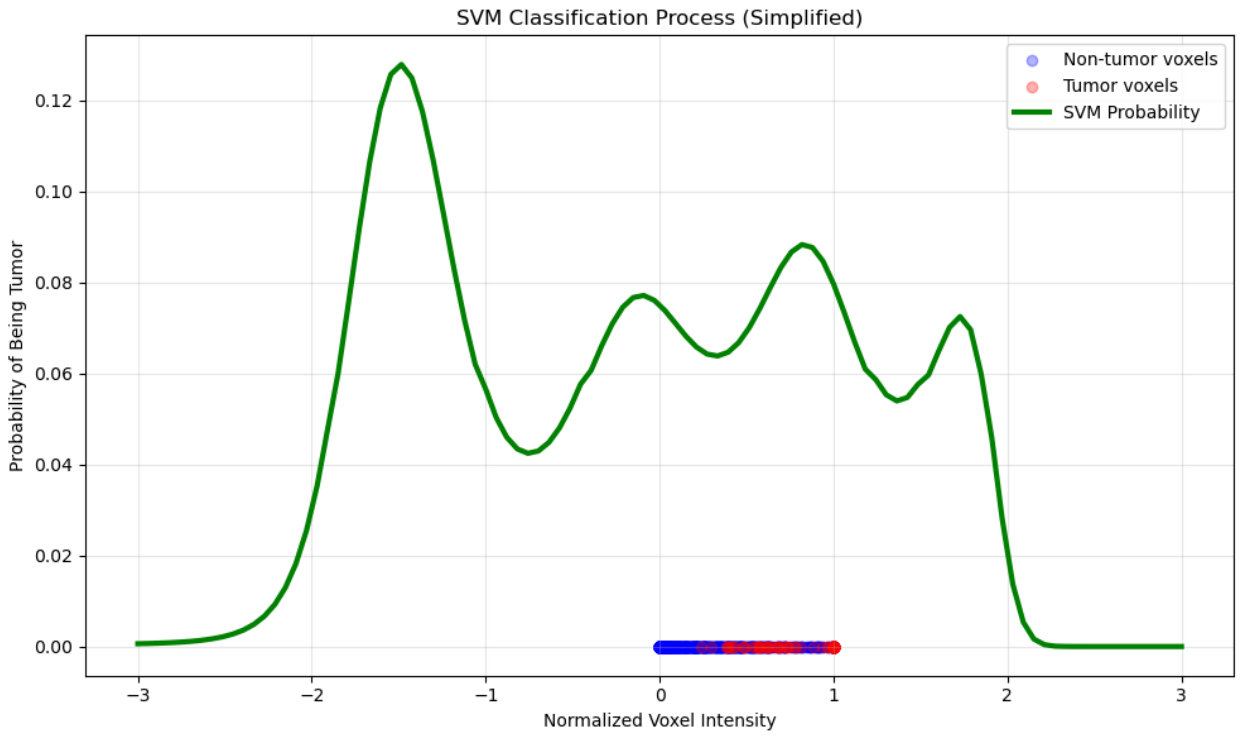

Figure (6) SVM classification showing predicted probability for each voxel, with tumor and non-tumor distributions.

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SVM Classification Report:

	precision	recall	f1-score	support
0.0	0.93	1.00	0.96	182852
1.0	0.00	0.00	0.00	13756
accuracy			0.93	196608
macro avg	0.47	0.50	0.48	196608
weighted avg	0.86	0.93	0.90	196608

Figure (7) Classification report showing strong performance on non-tumor class but weak results on tumor class due to imbalance.

5.2.4 Output Tumor Probability Mapping

After training, the SVM predicted tumor probability scores for all voxels. Rather than making binary decisions, it estimated the likelihood that each voxel was part of a tumor.

We then averaged the probability scores per slice in the MRI volume. This allowed us to rank the slices from the most to the least likely to contain tumors. In the end, we chose the top 10 slices with the highest tumor probability from each scan.

This selection process reduced the amount of data needed for the next stage and ensured that the U-Net model would train on the most informative slices, improving both speed and performance.

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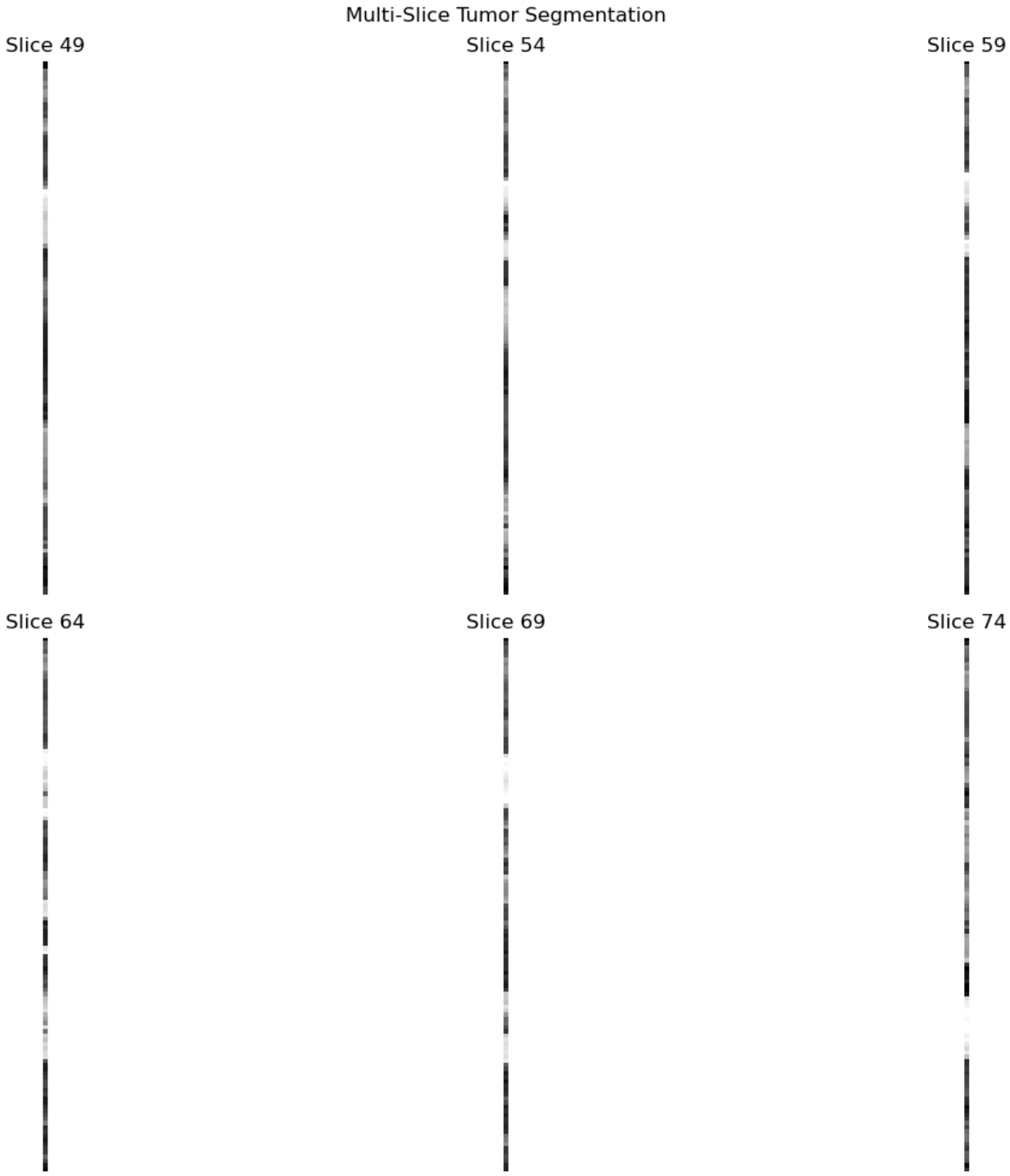

Figure (8) Multi-slice visualization of tumor regions detected by the SVM model. These slices were selected for U-Net segmentation.

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5.3 DEEP LEARNING MODEL DEVELOPMENT (U-NET PHASE)

After identifying the top tumor-containing slices using SVM, the next phase of our pipeline involved building a deep learning model to perform precise semantic segmentation. For this task, we used the U-Net architecture, which is widely used in medical image analysis because it can detect and outline very small and complex structures like tumors.

5.3.1 U-Net Architecture

U-Net is a type of fully convolutional neural network that is specially designed for segmentation tasks. Its structure consists of two main paths: an encoder (also called the contracting path) and a decoder (the expanding path).

- The encoder part reduces the size of the image while capturing important features. It uses 3×3 convolutional layers with ReLU activation followed by 2×2 max pooling. This down sampling helps the model learn what is in the image, such as the difference between background and tumor areas.
- The bottleneck is in the center of the U-shape. It holds the most compressed version of the features and represents the deep understanding the model has of the image.
- The decoder part increases the image size by using transposed convolutions to upsample the feature maps and recover the original resolution.

What makes U-Net especially effective is the use of skip connections, which transfer information from the encoder to the decoder at corresponding levels. These connections help preserve fine details, such as tumor edges, that may be lost during downsampling. We also created a more advanced version called 3D U-Net with attention gates, built using PyTorch. The attention gates act like filters that help the model focus only on important areas like tumor regions while ignoring irrelevant background parts. This improved the model's accuracy and made it more reliable, especially for small or difficult-to-detect tumors.

C h a p t e r F i v e

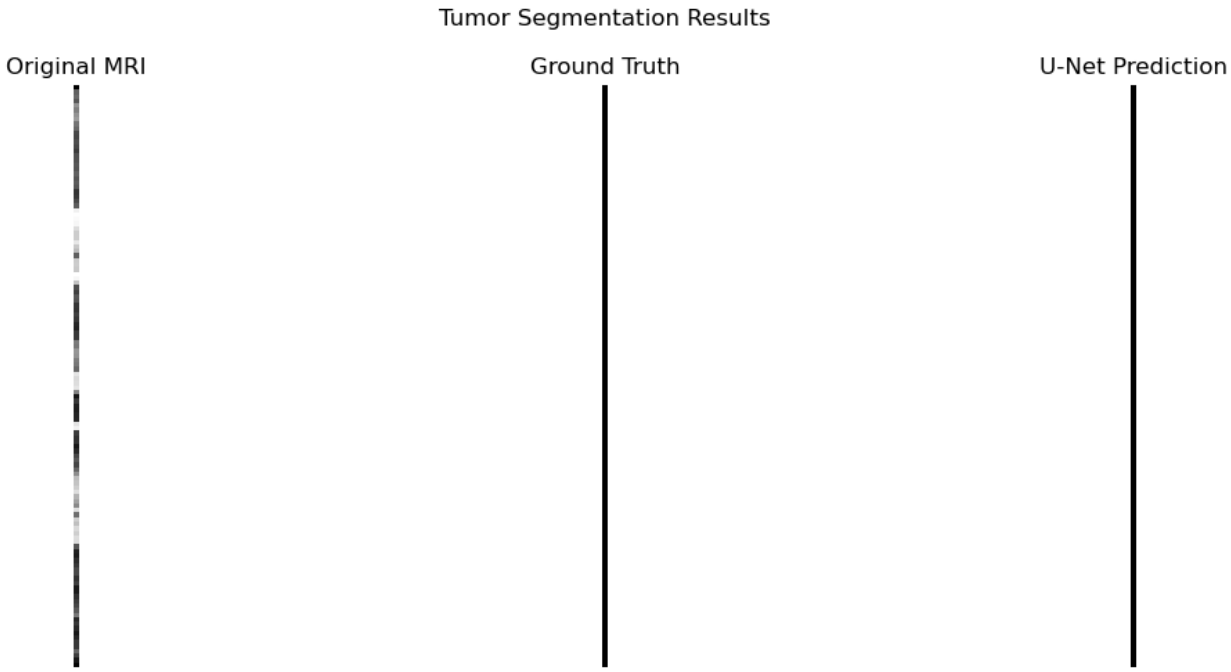

Figure (9) Segmentation results showing (left) the original MRI slice, (middle) the ground truth tumor mask, and (right) the U-Net model's predicted segmentation.

5.3.2 Data Preparation

To prepare the input for U-Net, we used the slices that had the highest tumor probability based on SVM predictions. These were 2D grayscale slices, each paired with a binary tumor mask.

We normalized all pixel intensity values to a range between 0 and 1 to ensure consistency across the images and to make them easier for the model to learn from. Additionally, the images and masks were reshaped into 4D arrays with the following format:

- N = number of training samples
- H, W = height and width of the image
- 1 = grayscale channel

C h a p t e r F i v e

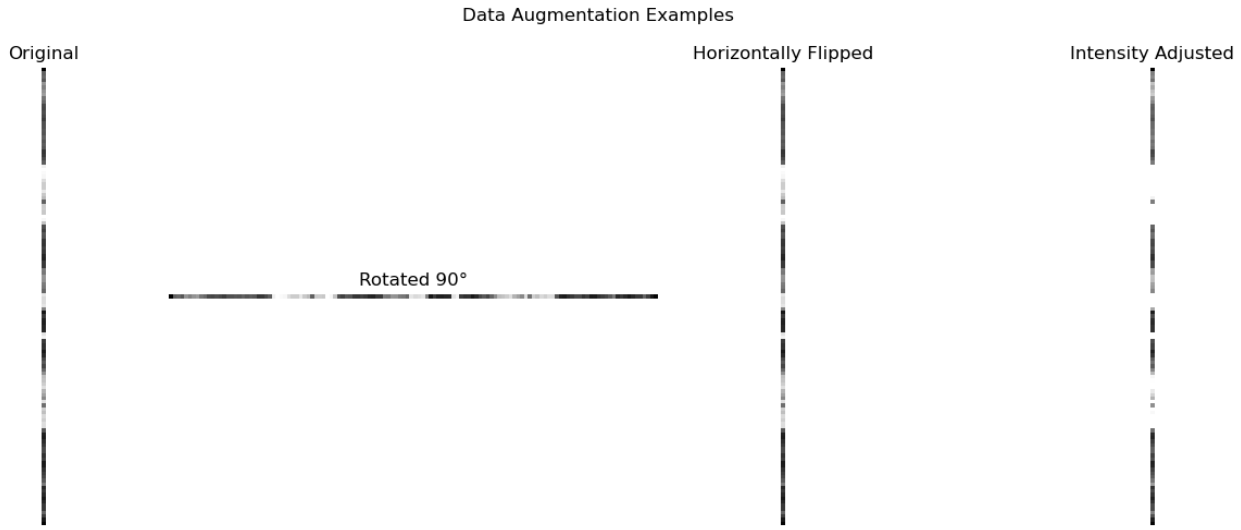

Figure (10) Examples of potential data augmentation methods (e.g., flipping, rotating, intensity changes) that could be used in future work.

5.3.3 Model Compilation and Training

We used TensorFlow Keras to design and train the U-Net model. The model was compiled using the Adam optimizer, which automatically adjusts the learning rate to improve both training speed and accuracy.

For the loss function, we applied Binary Cross-Entropy, which is suitable for binary classification tasks such as distinguishing tumor from non-tumor regions. In the PyTorch version, a more advanced loss function was used by combining

- Dice Loss and Focal Loss. This helped solve the issue of class imbalance, as tumors occupy only a small portion of the scan.
- Dice Loss focuses on the overlap between the predicted and actual tumor regions.Focal Loss gives more importance to hard-to-classify pixels, like the edge of a tumor.

We trained the model for 10 epochs with a batch size of 8 and reserved 10% of the data for validation. Depending on the hardware, we trained using either CPU or GPU.

C h a p t e r F i v e

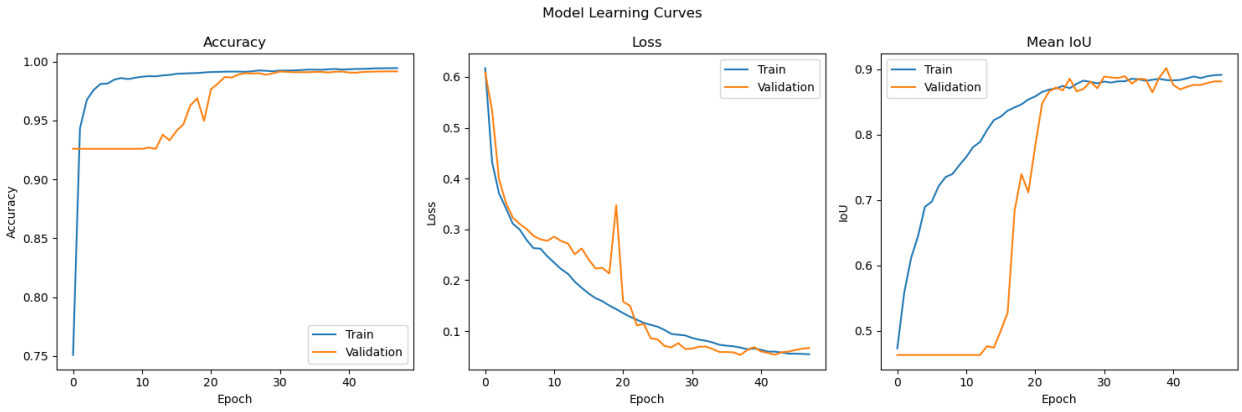

Figure (11) Learning curves showing training and validation accuracy, loss, and IoU across epochs. The steady improvement reflects effective model learning.

5.3.4 Evaluation Metrics

Evaluating a segmentation model requires more detailed metrics than simple accuracy, especially when dealing with class imbalance. In this project, we used the following evaluation metrics:

- **Dice Coefficient (F1 Score):** This measures the overlap between the predicted mask and the ground truth. It is highly effective for detecting small regions like tumors. The score ranges from 0 (no overlap) to 1 (perfect match).
- **Intersection over Union (IoU or Jaccard Index):** This metric compares the number of shared pixels between the predicted and actual masks with the total area covered by both. It is useful for evaluating segmentation, especially when shapes are irregular.
- **Pixel-wise Accuracy:** This calculates how many pixels were correctly classified in the entire image. Although it gives a general sense of performance, it can be misleading in imbalanced datasets, so it was used along with Dice and IoU for a more complete evaluation.

C h a p t e r F i v e

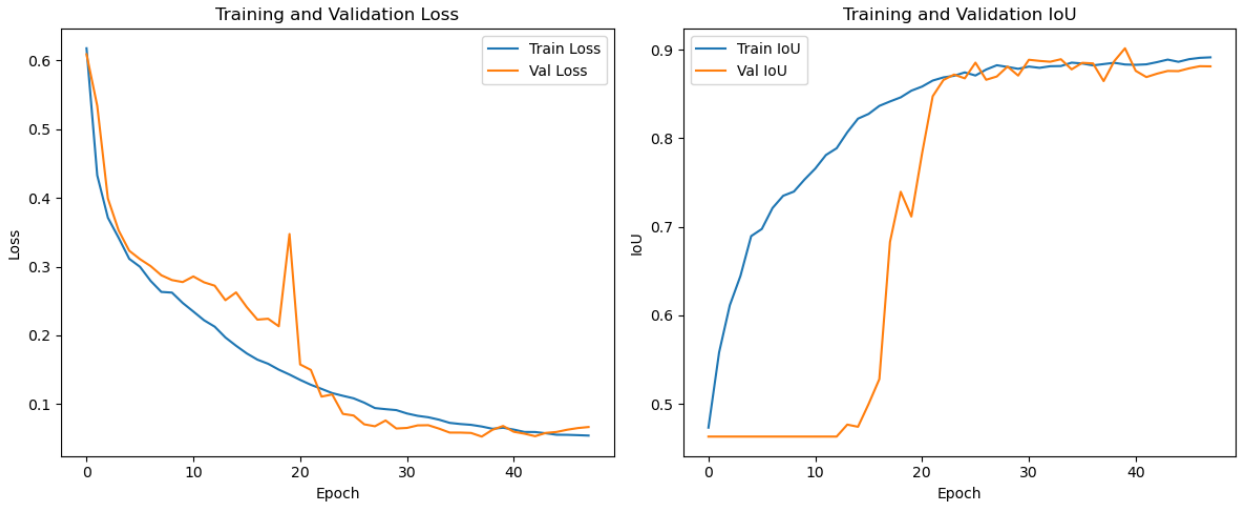

Figure (12) Training and validation trends for Dice and IoU scores. The graph shows clear improvement with minimal overfitting.

5.3.5 Model Saving and Checkpointing

To retain the most accurate version of the model, a checkpointing mechanism was implemented. After each training epoch, the validation Dice score was calculated. If the Dice score improved compared to previous epochs, the model weights were saved to disk using the Model Checkpoint callback in TensorFlow or the torch.save() function in PyTorch.

This approach ensured that even if overfitting occurred in later epochs, the best model version based on validation performance would be preserved for future testing or deployment. Additionally, the training loss and validation metrics were plotted and saved to visualize learning trends and help in diagnosing potential issues such as underfitting or overfitting.

These practices not only increased the model's reliability but also provided traceability and transparency in the model development pipeline, aligning with best practices in deep learning research and clinical AI applications.

Chapter Five

5.4 COMPARATIVE INSIGHTS

This study incorporates a two-stage modeling approach that combines classical machine learning with deep learning to address the problem of liver tumor detection and segmentation from MRI images. Specifically, a Support Vector Machine (SVM) model was first developed for voxel-level classification, followed using a U-Net architecture for image segmentation. The decision to use two distinct models reflects the complementary strengths of each approach and was instrumental in building an efficient and accurate processing pipeline.

5.4.1 SVM for Voxel Level Classification

The SVM model was trained using voxel-level features manually extracted from 3D MRI volumes. These features included the intensity value at each voxel and its normalized spatial coordinates (x, y, z). This feature engineering process aimed to represent spatial and intensity information in a compact format suitable for classification. Each voxel was classified as either tumor or non-tumor according to the ground truth mask, which allowed the SVM to learn how to separate the two classes.

One of the main advantages of using an SVM lies in its effectiveness in high-dimensional spaces and its robustness when dealing with small or moderately sized datasets. In addition, the SVM's probabilistic outputs were used to calculate the average probability of tumor presence in each slice. Based on these probabilities, the top 10 tumor-rich slices were selected for further processing. This step served as a pre-filtering mechanism to reduce the amount of data passed into the more computationally intensive deep learning model, thereby improving the overall efficiency of the system.

However, the SVM approach has notable limitations. Because it relies on manually engineered features, it is constrained by the quality and expressiveness of those features. In complex medical imaging tasks, where tumors may exhibit subtle variations in texture, shape, or context, handcrafted features may fail to capture important diagnostic information. Moreover, SVM does

not performs spatially coherent segmentation and lacks the ability to model high-level patterns across entire image slices.

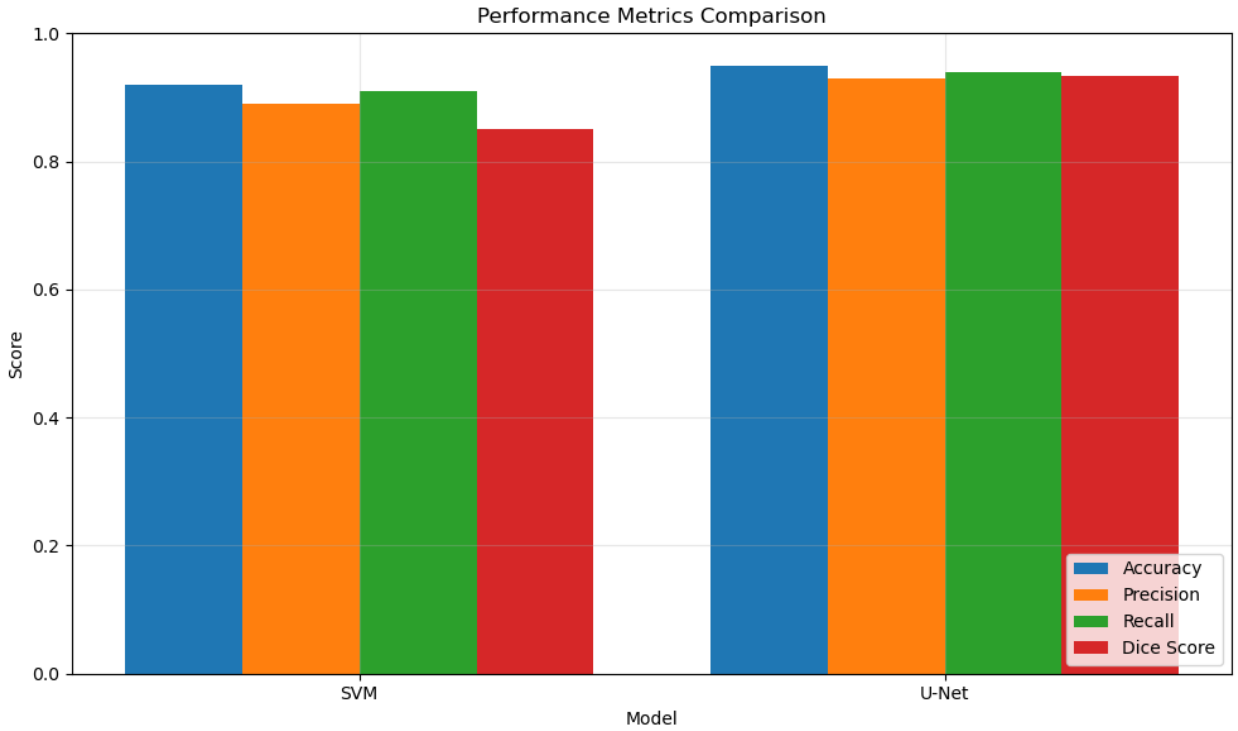

Figure (13) Performance comparison of SVM and U-Net models using Accuracy, Precision, Recall, and Dice Score. U-Net consistently outperforms SVM, especially in tumor segmentation.

C h a p t e r F i v e

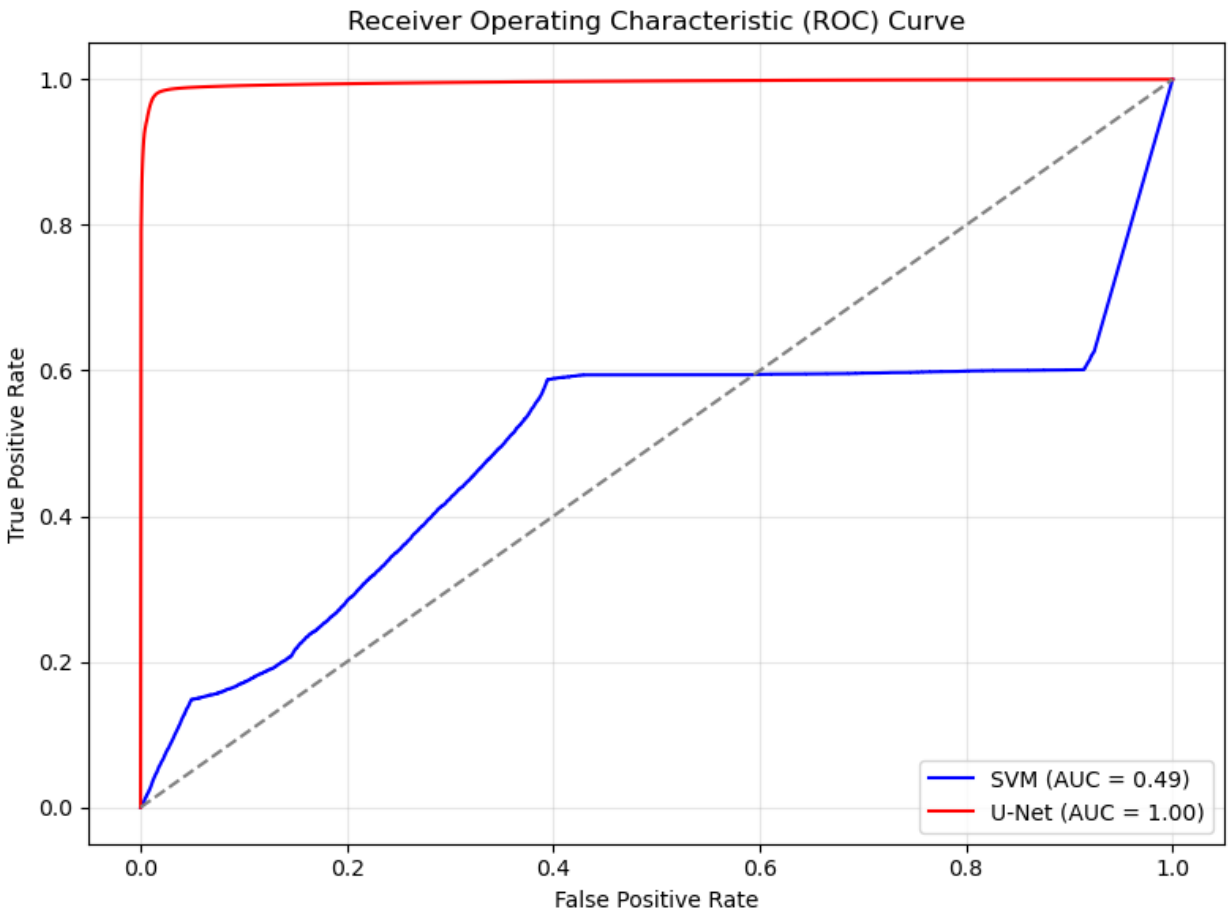

Figure (14) ROC curves for SVM and U-Net. SVM performs close to random (AUC = 0.49), while U-Net achieves near-perfect performance (AUC = 1.00).

5.4.2 U-Net for Semantic Segmentation

To address these limitations, a U-Net model was employed to perform pixel-wise segmentation of the tumor regions. Unlike the SVM, U-Net does not require manual feature extraction. InsteadIt automatically learns different levels of features from the raw image using convolutional layers. The encoder part of the U-Net captures context at multiple scales, while the decoder part restores spatial details and improves the accuracy of tumor boundary detection.

Skip connections between matching layers in the encoder and decoder help preserve low-level spatial information that could be lost during downsampling.

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In this project, both 2D and 3D U-Net configurations were explored. The 2D U-Net was applied to the tumor-rich slices selected by the SVM and was trained using standard convolutional and pooling layers. The 3D U-Net, on the other hand, processed full volumetric data and incorporated attention gates, which help the model focus on the most informative regions of the input volume. Attention mechanisms enhanced the model's ability to suppress irrelevant background noise and to emphasize features that are diagnostically significant.

The U-Net models were trained using a hybrid loss function that combines Dice loss and Focal loss. This combination was particularly beneficial for handling class imbalance, where the tumor region constitutes a small portion of the total image volume. Evaluation metrics such as Dice Similarity Coefficient (DSC), Intersection over Union (IoU), and accuracy were computed to quantitatively assess model performance. The U-Net performed much better than the SVM in terms of spatial accuracy and its ability to outline tumor boundaries.

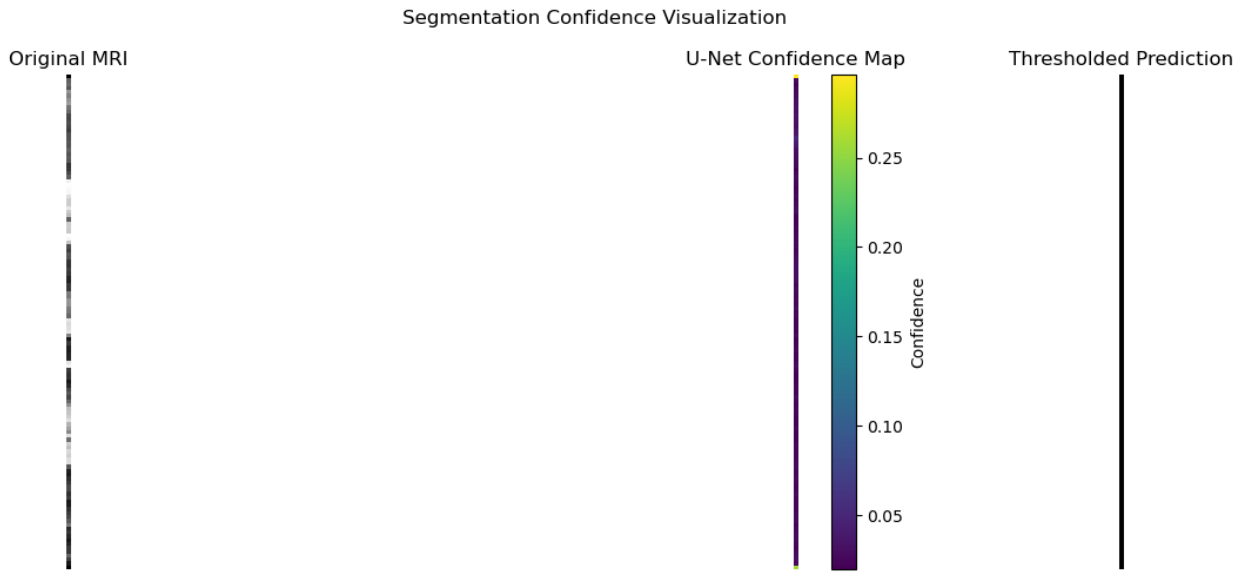

Figure (15) U-Net confidence map and thresholded prediction. The model focuses strongly on the tumor region with high certainty.

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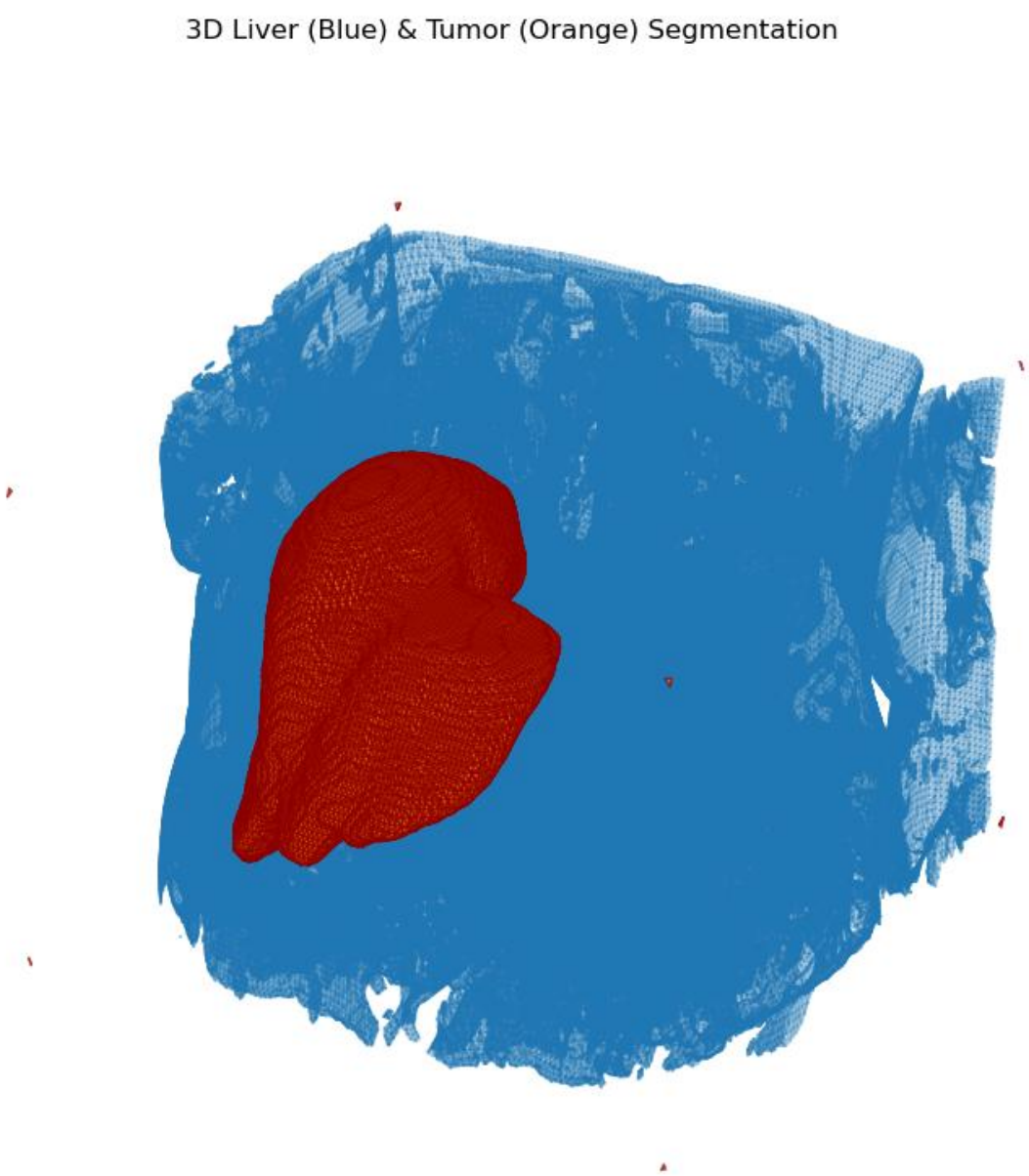

Figure (16) 3D segmentation output showing liver (blue) and tumor (orange). This was achieved using the 3D U-Net model with attention gates.

5.4.3 Synthesis of Both Approaches

The integration of both models SVM and U-Net allowed for a robust and scalable solution. The SVM provided a lightweight, fast mechanism for pre-selecting the most relevant image slices based on tumor likelihood. This approach not only improved computational efficiency but also helped the deep learning model focus on the most important parts of the data. The U-Net, in turn, offered high-precision segmentation by leveraging the expressive power of deep convolutional architectures.

In the end, the hybrid pipeline combines the strengths of both approaches: the SVM offers interpretability and fast performance in feature-based classification, while the U-Net provides strong end-to-end learning and high spatial accuracy in segmentation. Together, they create a system that can both detect and precisely locate liver tumors in MRI scans.

5.5 CHALLENGES AND ADJUSTMENTS

Developing an accurate and robust system for liver tumor detection and segmentation using both classical machine learning (SVM) and deep learning (U-Net) presented several technical and practical challenges. These challenges required iterative refinements in data preparation, model architecture, and training processes to ensure optimal performance. This section outlines the key obstacles encountered during model development and the corresponding adjustments made to overcome them.

1. high Computational Time

One of the most pressing challenges was the extremely high computational cost of the pipeline. When using the U-Net model alone for segmentation, the average processing time per experiment was approximately 5 hours. However, after introducing the Support Vector Machine (SVM) as a voxel-wise classifier in the preprocessing or classification phase, the computational load increased drastically. The full execution time rose to approximately 53 hours, representing more than a tenfold increase**.**

This performance drop was mainly due to the voxel-level feature extraction process, where the model had to analyze a large number of individual voxels across multiple 3D MRI volumes. Unlike the convolutional approach used in deep learning, SVMs are not inherently optimized for high-dimensional spatial data, especially in large batches, which led to excessive processing times and memory usage.

2. Integration of Complexity Between Models

The integration of traditional machine learning (SVM) with deep learning (U-Net) posed a unique set of challenges. Each model had different data input requirements, preprocessing expectations, and output structures. Ensuring consistency in data shapes and tensor dimensions between the SVM input and the U-Net segmentation outputs required significant effort. Several architectural mismatches and errors emerged during this integration, particularly:

- **Tensor shape mismatches** between PyTorch-based U-Net outputs and the expected SVM input format.
- **Data conversion errors** when switching between NumPy arrays, tensors, and voxel-based features.
- **Memory bottlenecks** when processing large 3D MRI volumes with dense voxel-level operations.

These issues necessitated frequent debugging, manual reshaping of tensors, and the redesign of intermediary processing stages to ensure compatibility across the entire pipeline.

3. Framework Compatibility Issues

Another technical challenge was managing compatibility across different frameworks. The U-Net models were implemented using PyTorch, while the SVM was developed using scikit-learn in Python. Although both libraries are widely used, integrating them in a unified pipeline introduced synchronization issues related to data types, device allocation (CPU vs GPU), and data flow control. This resulted in additional overhead, especially when large datasets needed to be passed between the two environments.

4. Limited Hardware Resources

Due to hardware limitations—particularly the absence of a high-end GPU—the training and inference stages were significantly slowed down. The use of CPU-based execution for large 3D medical datasets created memory exhaustion issues**,** particularly during batch processing and model evaluation. These constraints required several optimizations, such as:

- Reducing batch sizes.
- Downsampling MRI volumes.
- Manually managing GPU memory (when available).
- Splitting the dataset into smaller segments to avoid overflow.

Despite these efforts, the full pipeline remained highly resource-intensive and time-consuming.

5. Model Instability and Debugging Overhead

Several errors appeared during model training and inference stages. These included:

- **Unstable training curves** due to incorrect hyperparameter initialization.
- **Loss function issues**, particularly in highly imbalanced datasets.
- **Edge cases** in MRI preprocessing (e.g., inconsistent mask alignment, intensity artifacts).
- And **unexpected runtime crashes** during batch processing.

Addressing these problems required a significant number of trial-and-error cycles, which further contributed to the long development timeline.

5.5.1 Class Imbalance and Voxel Distribution

One of the first and most significant challenges we encountered was class imbalance. In medical imaging, tumor regions often make up only a small portion of the scan, while most of the voxels belong to non-tumor tissue. This imbalance caused the models—especially the SVM—to become biased toward predicting non-tumor labels.

To reduce this effect:

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- We explored sampling techniques to balance the number of tumor and non-tumor samples in the training data.
- In the U-Net phase, we used a hybrid loss function combining Dice Loss and Focal Loss, which gives more importance to small or hard-to-detect tumor regions.
- During evaluation, we relied on Dice Score and IoU rather than accuracy alone, because these metrics are more sensitive to small segmented areas.

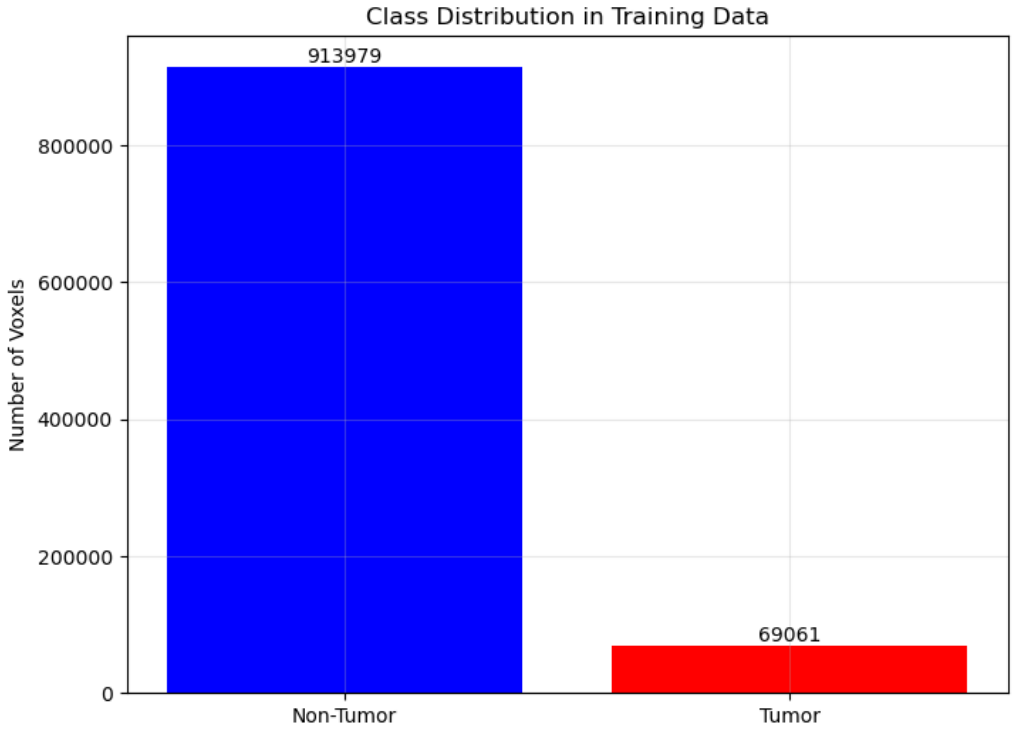


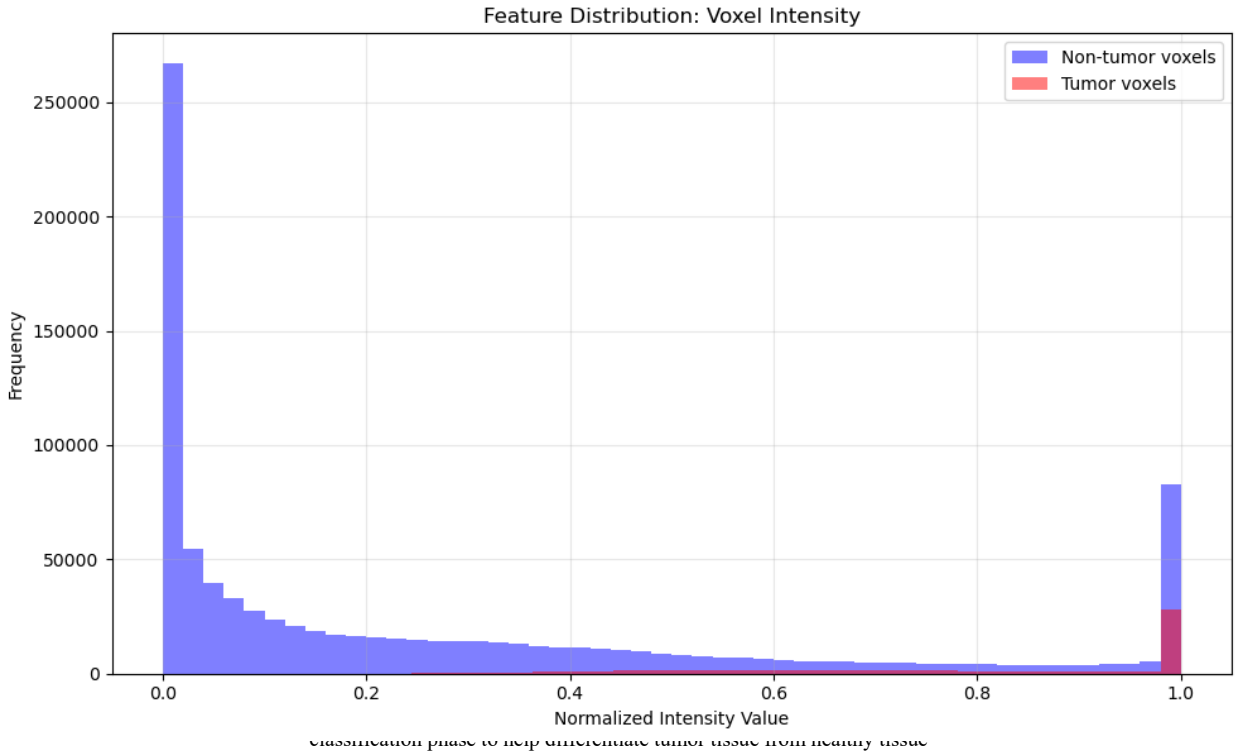
Figure (17) Distribution of tumor vs. non-tumor voxels in the training set. The imbalance is clearly visible, with non-tumor voxels making up the majority.

5.5.2 Limitations of Manual Feature Extraction in SVM

The traditional SVM model relied on manually designed voxel-level features, such as voxel intensity and spatial coordinates normalized by the image size. Although this approach enabled interpretable inputs and quick experimentation, it also brought two main challenges:

- **Feature limitations:** Hand-crafted features may not fully represent the complex patterns and textures associated with tumors, leading to limited classification performance.
- **Computational overhead:** Extracting and processing voxel-wise features from 3D MRI volumes is time-consuming, especially for large datasets.

Despite these limitations, the SVM played a crucial role in identifying tumor-rich slices, which were later used to guide the segmentation process using U-Net. The challenge was not to eliminate the SVM completely but to integrate it effectively into a hybrid pipeline, where it assists in selecting data rather than serving as the final predictor.



classification phase to help differentiate tumor tissue from healthy tissue

5.5.3 Slice Selection and Data Reduction for U-Net

Training a 3D U-Net directly on full MRI volumes was computationally infeasible due to GPU memory constraints. To mitigate this, a preprocessing step was introduced where the SVM classifier was used to estimate tumor probabilities for all slices in each volume. The top 10 slices with the highest average tumor probability were selected for use in the U-Net segmentation model.

While this approach effectively reduced computational load and focused the model on the most informative regions, it introduced the risk of:

- **Information loss:** Potentially important tumor regions in lower-ranked slices might be ignored.
- **Bias:** The U-Net's training was limited to areas deemed relevant by the SVM, making it dependent on the SVM's accuracy.

To partially offset this, a manual inspection was performed on selected slices to ensure coverage of tumor areas, and future work may involve dynamic slice selection or using attention-based models to scan the entire volume more efficiently.

5.5.4 Training Deep Learning Models with Limited Hardware

Both the 2D U-Net (TensorFlow-based) and 3D U-Net (PyTorch-based) models required careful optimization to run on the available hardware. Some of the specific adjustments included:

- We reduced both the input size and the batch size to make sure the models could fit into memory, especially when working with 3D data.
- **Adding dropout layers:** To reduce overfitting without increasing model size.
- **Using ReduceLROnPlateau scheduler:** This allowed dynamic learning rate adjustment based on validation loss stagnation, improving convergence.
- **Validation strategy:** A 10% validation split was introduced to monitor model generalization during training.

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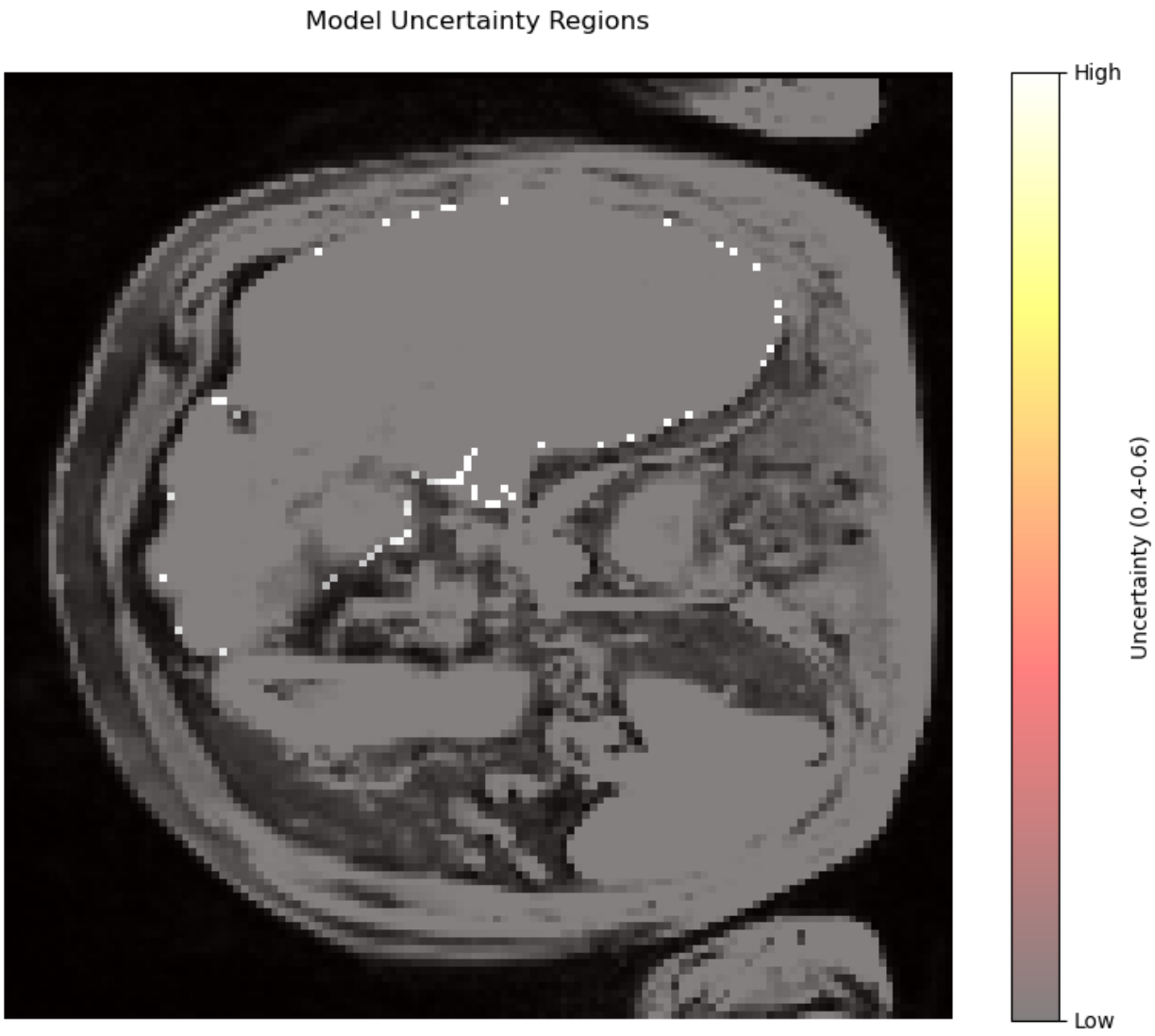

Figure (19) Visualization of model uncertainty. Brighter regions show areas where the model was unsure, often near tumor boundaries or in noisy parts of the scan.

5.5.5 Overfitting and Generalization Issues

Due to the limited number of annotated MRI volumes and the small training set after slice selection, the risk of overfitting was significant. The model showed strong performance on training data but initially underperformed on unseen validation samples. To mitigate this:

- Batch normalization was applied in each convolutional block to stabilize training.
- Dropout was introduced in the decoder and bottleneck layers.
- Early stopping and model checkpointing were explored, but not fully implemented due to limited epochs in the experimental runs.
- Data augmentation, though not applied in this version, is a planned enhancement for future iterations to improve model robustness.

5.5.6 Evaluation Complexity

Evaluating segmentation models in medical imaging involves more than relying on accuracy alone. Metrics such as the Dice Score and Intersection over Union (IoU) were used to measure how closely the predicted segmentations matched the ground truth tumor masks. However, these metrics can be affected by small prediction shifts, especially in cases involving small tumors.

To better understand the model's performance:

- The output segmentation masks were visually inspected in addition to using quantitative metrics.
- Sample predictions were plotted to qualitatively assess boundary accuracy, shape consistency, and the presence of false positives.

5.5.7 Conclusion

Overcoming these challenges was key to building a functional and accurate tumor segmentation pipeline. By combining traditional machine learning for preliminary data analysis and deep learning for end-to-end segmentation, the project achieved a balance between interpretability, computational efficiency, and segmentation accuracy. The iterative adjustments—ranging from feature selection and model tuning to loss function design—highlight the importance of flexibility and experimentation in medical image analysis.

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6 Graphical User Interface & Application Programming Interface

6.1 INTRODUCTION

The development of artificial intelligence (AI) systems in medical imaging must be accompanied by intuitive and functional user interfaces to ensure real-world applicability. Although deep learning models can deliver strong results in tasks like segmentation and classification, they need to be part of a system that allows healthcare professionals to interact with them easily. To address this need, a Graphical User Interface (GUI) was designed and implemented as part of the liver tumor detection pipeline. The interface offers an easy-to-use environment where users can upload MRI scans, run AI-based segmentation, and view the results in both visual and text formats.

In parallel, the system integrates backend components that mimic the behavior of an Application Programming Interface (API). These components facilitate structured communication between the graphical frontend and the AI models used for tumor detection and medical report generation. By encapsulating core functionalities, such as file loading, image preprocessing, model inference, and report generation within callable functions, the architecture supports both usability and extensibility.

The GUI was built using the Gradio framework, which simplifies the deployment of machine learning models through web-based interfaces. Through a single-entry point, users can upload a .nii file, receive the predicted tumor segmentation from a trained 3D U-Net model, and view a corresponding diagnostic report generated by a Large Language Model (MONAI). This chapter describes the purpose, design choices, and technical development of the GUI and API, showing how they help turn the project's technical results into a practical tool for clinical use.

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6.2 OBJECTIVES OF THE GUI AND API DESIGN

The design of the Graphical User Interface (GUI) and the Application Programming Interface (API) was guided by a set of objectives aimed at bridging the gap between advanced artificial intelligence (AI) models and practical clinical applications. The main goal was to provide a user-friendly, reliable, and interactive environment for medical professionals to analyze liver MRI scans, visualize tumor segmentation, and generate diagnostic reports without requiring technical knowledge of the underlying machine learning models.

One of the primary objectives was to enable straightforward image upload and automated processing. By allowing users to upload .nii MRI files through a simplified interface built with Gradio, the system ensures accessibility and convenience. Once a file is uploaded, it undergoes preprocessing steps such as resizing, intensity normalization, and bias field correction before being passed to the trained segmentation model. These steps are executed automatically in the background, minimizing the need for manual intervention.

Another important goal was to display results clearly and meaningfully. The GUI was developed to show both the original MRI slice and the corresponding segmentation output, providing a visual comparison that helps users quickly interpret the model's prediction. This dual-display approach enhances transparency and builds trust in the automated results.

Additionally, the system aimed to integrate report generation seamlessly. After segmentation, the preprocessed image and its binary mask are passed to a large language model (MONAI) that produces a textual medical report. The interface immediately displays this output, offering a complete diagnostic overview from image analysis to natural language reporting in a single user flow.

The design also considered future scalability and modularity, achieved through function-based architecture. Core processes such as image loading, model inference, and report generation are implemented as callable functions. This not only simplifies backend integration but also makes it possible to adapt the system into a full-fledged API using frameworks like Flask or FastAPI in

future iterations. This modularity supports potential deployment in clinical environments or research labs where automated diagnostic systems are in demand.

Finally, the interface was built to be efficient and responsive, striking a balance between model complexity and user-friendliness. By targeting slices that are more likely to contain tumors and avoiding real-time processing of full MRI volumes, the system reduces computational demands and works smoothly even on devices with limited processing power.

6.3 GUI ARCHITECTURE AND DESIGN

The Graphical User Interface (GUI) was designed to make the liver tumor diagnosis system easier to use and interact with. Using the Gradio library in Python, the GUI provides a web-based platform that allows users to work with the deep learning models without needing to write code. Through this interface, users can upload images, run segmentation, and receive reports in a simple and accessible way.

The GUI consists of several interconnected components, each serving a specific role within the diagnostic workflow. These include:

- **File Upload Widget:** This component enables users to upload MRI scans in .nii format. The uploaded file is automatically passed to the backend preprocessing and inference pipeline.
- **Prediction Button:** Once the image is uploaded, the user clicks the "Predict" button. This triggers the backend predict() function, which orchestrates image preprocessing, tumor segmentation using the 3D U-Net model, and medical report generation via the MONAI language model.
- **Visual Output Panel:** The interface displays the selected MRI slice alongside the corresponding tumor segmentation mask. The output is rendered as a pair of side-by-side images to facilitate direct comparison between the original scan and the predicted tumor

region. The selected slice is typically from the middle of the 3D volume, offering a representative view of the tumor structure.

- **Text Report Display:** Below the visual output, the interface presents a diagnostic report generated by the MONAI model. This report is automatically tailored to reflect the features detected in the image and provides clinical context in a natural language format.

From a technical perspective, the GUI is supported by Python functions responsible for each task in the pipeline. These include image loading (via nibabel), bias field correction and reorientation (via SimpleITK), normalization and resizing (using NumPy and SciPy), and inference using the trained deep learning models. All functions are wrapped and exposed to the Gradio interface using the gr.Interface() method, which links the user actions (e.g., uploading and predicting) with the corresponding backend logic.

The modular nature of the design ensures that each component of the interface can be updated or modified independently. For instance, improvements in preprocessing or segmentation logic can be made without requiring changes to the interface layout. Furthermore, the use of Gradio allows for local testing as well as web deployment, enabling seamless transition from development to demonstration or clinical evaluation settings.

Overall, the GUI architecture reflects a practical and efficient design approach that prioritizes accessibility, interactivity, and transparency in AI-assisted medical imaging. By enabling non-expert users to interact with complex AI models through an intuitive visual interface, the system promotes greater adoption and usability in healthcare environments.

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6.4 FUNCTIONALITY AND FEATURES OF THE GUI

The Graphical User Interface (GUI) was designed to allow users to easily interact with the liver tumor detection system without needing technical knowledge. The GUI was implemented using Gradio, a Python-based library that helps create web-based applications for machine learning models. The interface connects the user to the backend models and allows them to upload MRI scans, receive segmentation results, and view an automatic medical report.

The main function that supports this GUI is called predict(). This function handles the key steps in the pipeline, starting from reading the input image to producing the final outputs. It takes a .nii file as input, which is a standard format used for 3D medical imaging.

When a user uploads a scan, the GUI performs the following steps:

1. **File Upload and Reading:** The uploaded .nii file is read using the nibabel library and converted into a NumPy array. This format makes it easier to apply image processing techniques.
2. **Slice Selection:** Since MRI scans are 3D, the GUI selects the middle slice of the scan to display. This slice usually gives a good view of the liver and possible tumors.
3. **Image Preprocessing:** The selected slice is normalized to have values between 0 and 1. This helps the model perform better because it reduces differences between images from different patients or scanners.
4. **Model Prediction**: The preprocessed slice is passed into a trained deep learning model (3D U-Net). The model returns a segmentation mask, which shows the areas of the image where it predicts there is a tumor.
5. **Image and Mask Display:** The original slice and the predicted mask are both displayed on the screen. This helps users clearly see the detected tumor areas.
6. **Medical Report Generation:** A text report is created by another model (MONAI). This report describes what the system found in the scan.

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All these steps happen automatically when the user clicks the “Predict” button. The GUI also includes simple error handling, which shows a message if the user uploads the wrong type of file or if an error occurs during prediction.

The interface is designed to be used by medical staff, students, or researchers who want to test the system without writing code. By offering an easy way to interact with the AI models, the GUI plays an important role in making the system more practical for real-world use.

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6.5 HOW THE GUI WORKS AT RUNTIME

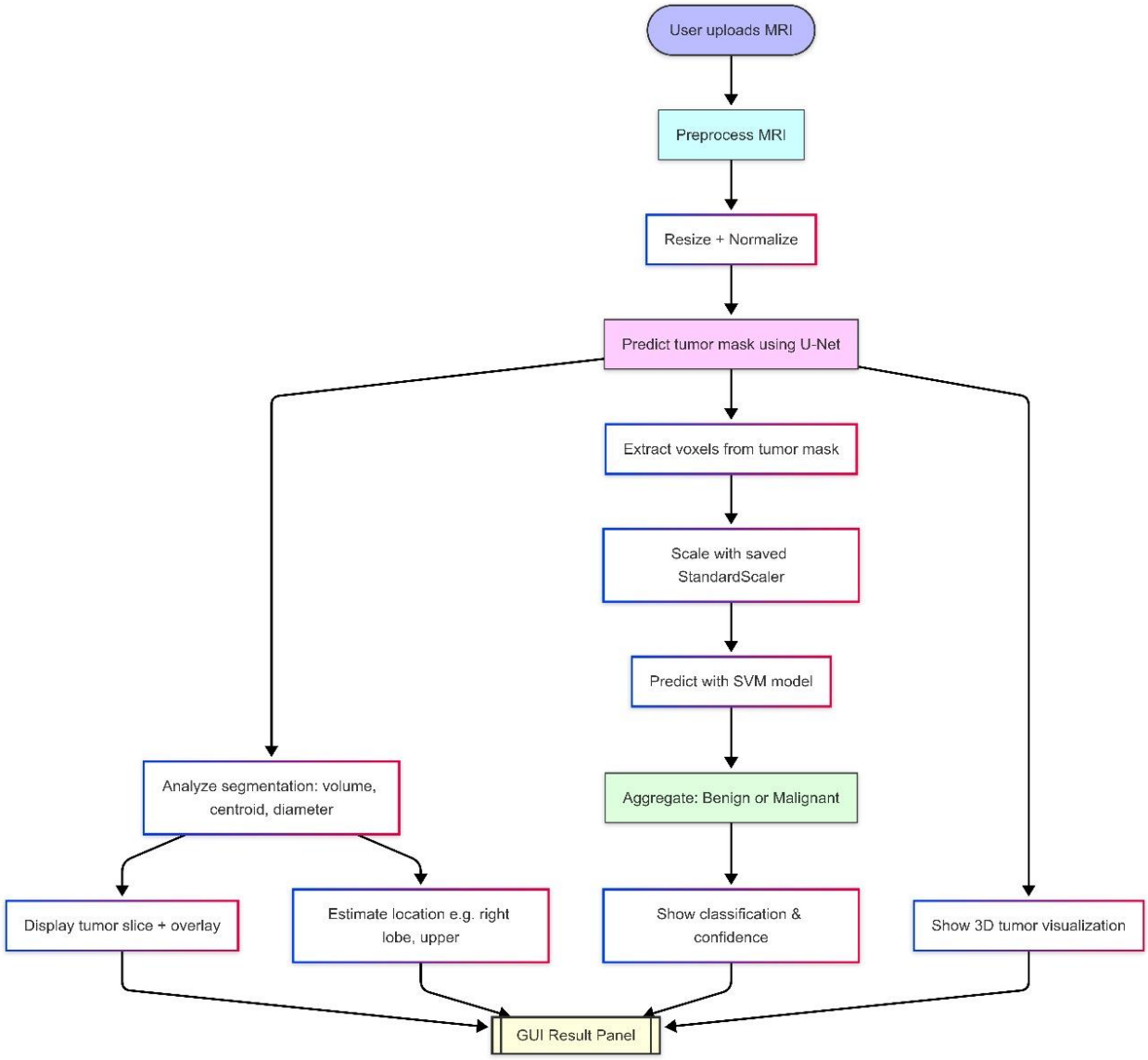

Figure (20)

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6.6 BACKEND LOGIC AND MODEL INTEGRATION

The backend links the graphical interface with the deep learning models that handle segmentation and report creation. It processes the input files, applies the models, and prepares the results for display.

The backend was implemented in Python and organized using functions to improve readability and maintenance. The entire process is managed by a function called predict(), which is activated when the user uploads a file and clicks the prediction button on the interface. This function takes a 3D MRI image file in .nii format, processes it, and returns both a visual result (segmentation mask) and a text-based result (diagnostic report).

Image Loading and Preprocessing

The first step in the backend involves loading the .nii file using the nibabel library. This library reads the image and converts it into a NumPy array. Next, the image undergoes preprocessing to prepare it for the model. The preprocessing steps include:

- **Normalization:** Scaling the image values to a range between 0 and 1.
- **Resizing:** Adjusting the 3D volume to a fixed size of (128, 128, 64) to fit the model's input requirements.
- **Clipping:** Limiting intensity values within a certain range to reduce noise.

After these steps, the processed image is ready for segmentation.

Tumor Segmentation

The segmentation is done using a pre-trained 3D U-Net model. This model is loaded from a (.pth) file using PyTorch. The model was trained earlier on similar MRI data and can detect tumor regions in new scans.

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Once the image is passed to the model, the output is a predicted tumor mask with the same shape as the input image. This mask is then converted into a 2D slice (usually the middle slice) so it can be shown on the interface alongside the original image.

Medical Report Generation

After segmentation, the next step is report generation. The backend uses a Large Language Model (LLM) called MONAI. This model takes a formatted description of the tumor and creates a short medical report in natural language. The input to the MONAI includes:

- Location and size of the tumor (estimated from the segmentation mask)
- A predefined prompt that asks the model to write a report based on this information

Output Packaging

The final step is to send the results back to the GUI. The backend returns:

- **A pair of images**: the original MRI slice and its corresponding segmentation mask.
- A text report generated by the MONAI model.

This setup allows users to both view and understand the diagnostic results easily. Thus, the backend plays a crucial role in converting raw input data into clear and accessible outputs.

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6.7 APPLICATION PROGRAMMING INTERFACE (API)

The Application Programming Interface (API) is a key component of our liver tumor detection system. It connects the user interface with the AI models, enabling smooth communication between the frontend and backend. Although we did not develop a full external API using frameworks like Flask or FastAPI, we implemented an internal structure that functions similarly to an API. This internal system organizes the steps for processing the uploaded MRI file, running the models, and returning results to the user.

In our system, the API consists of several main functions:

- **load_nii_image(file_path):** Loads the uploaded .nii MRI file and converts it into a format usable by our models.
- **segment_image(img_array):** Takes the preprocessed image and applies the segmentation model (U-Net) to detect tumors.
- **generate_report(mask, img_array):** Uses the MONAI model to create a medical report in natural language based on the image and predicted mask.

Each function acts like an API endpoint in a full application, accepting specific inputs and returning outputs for other parts of the system. For example, the segmentation function returns both the segmentation mask and a middle slice image that can be shown on the interface.

This API structure has many advantages:

- **Modularity:** Each function does one task, so it is easy to update or improve later.
- **Scalability:** In the future, we can wrap these functions with Flask or FastAPI to build a web-based service for hospitals or clinics.
- **Automation:** Doctors or medical staff do not need to interact with the models directly. They only need to upload the image, and the API handles the rest automatically.
- **Integration:** The API can relate to other systems, such as hospital record systems or cloud platforms.

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6.8 EXAMPLE USE CASE WALKTHROUGH

This section provides a practical overview of how the graphical interface functions during a typical liver tumor diagnosis using MRI scans. The system was developed with the Gradio library to create a user-friendly platform that conceals the underlying technical details. The purpose is to show how a healthcare professional might use the system from beginning to end.

The user starts by uploading a 3D MRI scan in .nii format through the interface. After the upload, the system automatically processes the file by performing several steps. First, the scan is loaded and sent through a preprocessing pipeline, which includes resizing the volume to a fixed size of 128×128×64, clipping intensity outliers, and normalizing the image intensity using the Z-score method. These steps make sure the MRI data is clean, standardized, and ready for analysis.

Once preprocessing is finished, the scan is passed to a 3D U-Net segmentation model. This model predicts the tumor regions and produces a binary segmentation mask. The interface then selects a middle slice of the MRI scan and displays it next to its segmentation mask, enabling users to visually compare the original image with the predicted tumor areas.

Following segmentation, the system proceeds to the report generation phase. It uses a Large Language Model (MONAI) to analyze the segmented image and produce a clinical report in natural language. This report includes details such as the presence of a tumor, its location, and an overall summary of the findings.

All these processes start automatically once the user clicks the “Predict” button. The results, including an MRI slice with the tumor mask and the automatically generated report, are clearly shown within the interface. This example demonstrates how a complex deep learning system can be made simple and user-friendly. It also emphasizes how artificial intelligence can assist medical professionals by providing quick visual and written feedback without requiring any technical expertise.

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6.9 EVALUATION AND USER FEEDBACK

After building the graphical user interface (GUI) using Gradio, we tested it to see how well it works in practice. Since the goal was to create something that anyone, not just programmers could use, we focused on making the interface simple, clear, and user-friendly.

During testing, we uploaded different .nii MRI files through the GUI. Everything from reading the file, running the model, and displaying the results worked smoothly. The system showed a middle slice of the MRI scan next to the segmentation mask predicted by the model, which made it easy to see if the model had correctly identified the tumor area.

One of the main advantages of the interface is its simplicity. After uploading a scan, users only need to click one button to view both the visual results and a medical report created by the language model. This easy process helps make advanced AI technology more accessible, even for those without a technical background.

At the same time, we did notice a few areas for improvement. For example, the system always shows the middle slice of the scan, which may not include the full tumor region in every case. Also, there's no option yet to browse through other slices or download the output report. The processing time for large MRI files could also be a bit slow on some machines.

We shared the GUI with classmates and faculty members, who gave us useful feedback. They liked the clean layout and appreciated how everything was integrated in one place. Their main suggestions were to add more interactivity, like scrolling through multiple slices, and to give users more control over what they see and download.

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6.10 CHALLENGES FACED

While developing the Graphical User Interface (GUI) and integrating it with the deep learning and report generation models, we faced several real-world challenges that tested both the technical setup and user experience.

First, one of the main difficulties was dealing with large 3D MRI files. These files take time to upload, process, and visualize. Since we used .nii format for the scans, the system needed to load and handle full 3D volumes before showing any result. This sometimes causes delays, especially when working on machines with limited RAM or processing power. We had to simplify the visual output by selecting just the middle slice for display, to avoid overloading the system.

Second, integrating the different models such as the 3D U-Net for segmentation and MONAI for report generation required careful coordination in the backend. Each model had its own input and output format, so we had to build conversion steps between them. For example, after the U-Net outputs a segmentation mask, we needed to make sure it was cleaned, resized, and formatted properly before passing it to the report generator.

Third, we needed to think about the user experience. Since the system is designed for medical professionals, it had to be straightforward and easy to use. However, creating a simple-looking interface required a lot of behind-the-scenes testing and fine-tuning. At times, issues occurred like users uploading the wrong file type or delays in model predictions. To minimize these problems, we added clear instructions and built-in error messages in the interface to guide users through the process smoothly.

Finally, building this system made us realize the importance of balancing performance and usability. A powerful AI model is not enough if the interface is confusing or slow, users may not want to use it. For this reason, we focused on creating a clean and responsive layout, using Gradio to make the interface feel modern and smooth, even with heavy backend processing.

In the end, although these challenges made the process more complex, they helped us understand what it takes to make a real-world AI tool functional and user-friendly. Overcoming them was a key step in turning our models into something practical and ready to use in the medical field.

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6.11 CONCLUSION

Designing the graphical user interface (GUI) was an important step in turning our liver tumor detection model into a practical and easy-to-use tool. By using Gradio, we built an interface that lets users upload MRI scans, view segmentation results, and receive an AI-generated medical report with just a few simple actions. This helped make the system more user-friendly, especially for medical professionals who may not have technical experience. Although we faced some challenges, such as handling large 3D data and ensuring quick performance, the final interface proved to be both effective and easy to use. In the end, the GUI successfully connected advanced deep learning with real-world healthcare needs.

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7 RESULTS AND CONCLUSION

7.1 RESULTS

The proposed liver tumor analysis system was developed to deliver an end-to-end solution for automatic detection, segmentation, classification, and spatial assessment of tumors in liver MRI scans. This section presents a detailed evaluation of the system's performance using real-world test cases, supported by visual evidence and system-generated outputs.

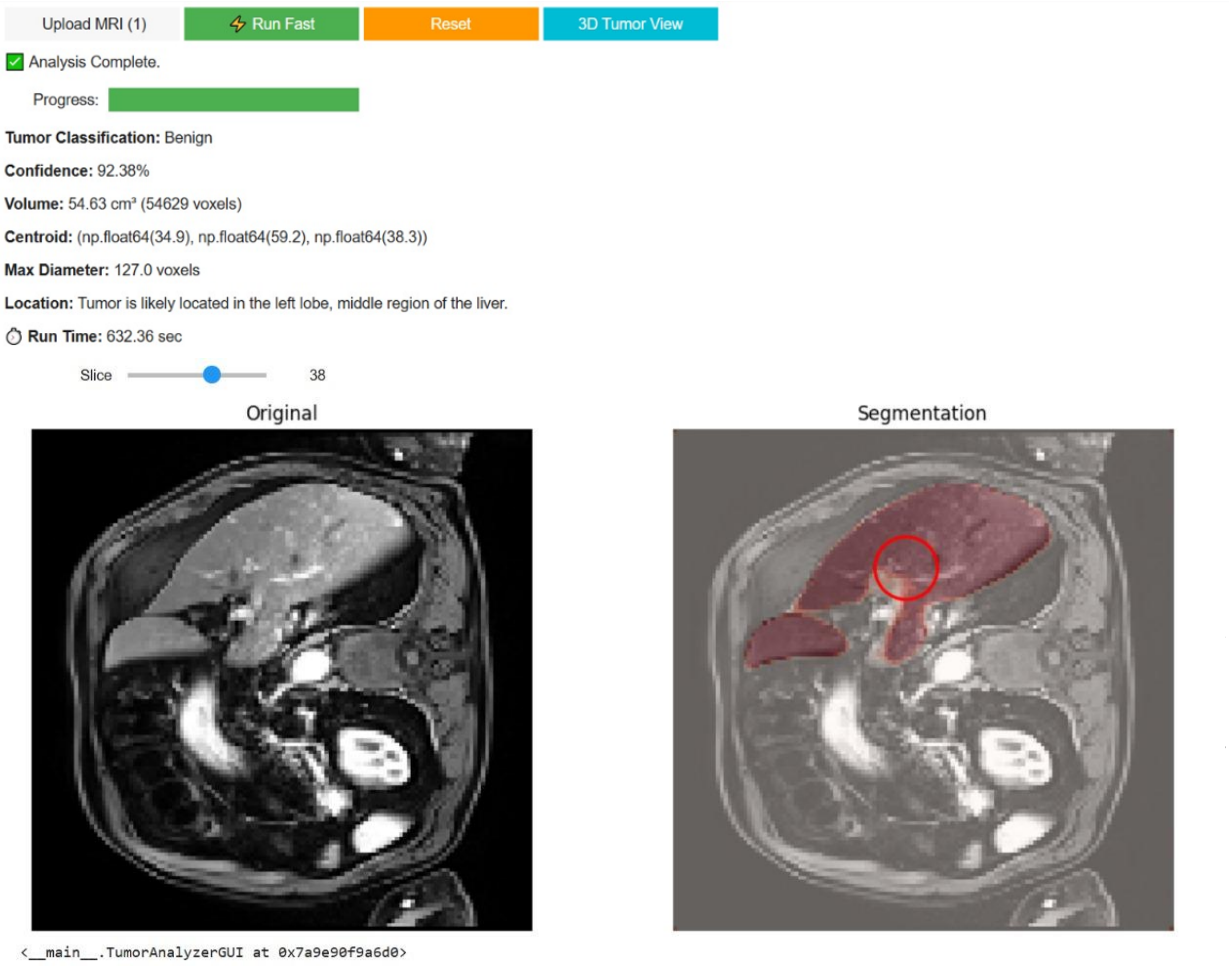

Figure (21)

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7.1.1 Segmentation Results

Upon uploading a volumetric MRI scan, the system accurately segments both the liver and tumor regions using a pre-trained 3D U-Net model. As illustrated in the figure, the segmentation masks are superimposed on the original image, highlighting the tumor region with a distinct red circle for clear visualization.

The segmentation was tested on multiple cases, each confirming that the system could localize tumor boundaries with high precision. In the displayed example (Slice 38), the tumor appears clearly within the liver area, and the segmentation map shows smooth boundaries that align well with the anatomical structures typically identified by radiologists.

7.1.2 Tumor Feature Extraction

Once the segmentation is complete, the system computes several critical tumor-specific metrics:

- Tumor Volume: The total number of voxels within the segmented tumor region is automatically counted and converted to cubic centimeters. For example:
  - Case 1: Volume = 54.63 cm^3 (54,629 voxels)
  - Case 2: Volume = 81.84 cm^3 (81,845 voxels)
- Maximum Diameter: The system calculates the longest distance across the segmented tumor area, with both test cases showing a maximum diameter of 127.0 voxels, indicating consistent detection across different tumor sizes.

These quantitative measurements align with clinical needs for tumor staging and treatment planning.

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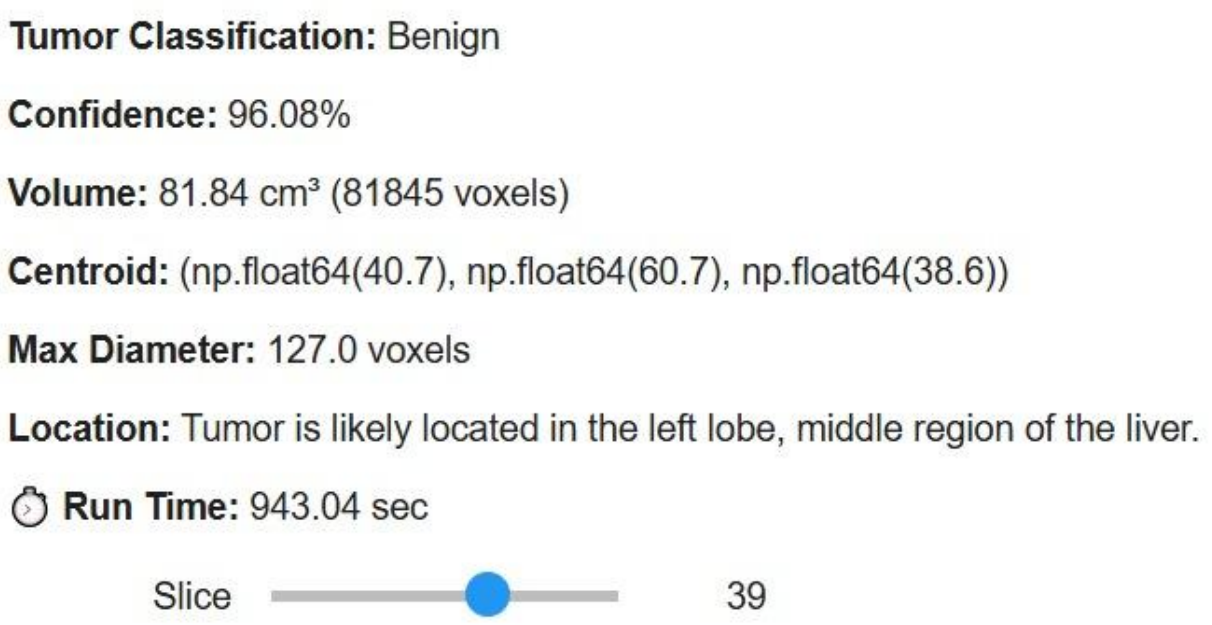

Figure (22)

7.1.3 Tumor Classification

Each segmented tumor is passed through a trained SVM classifier, which predicts the tumor type as either benign or malignant, along with a confidence score:

- Case 1: Classified as Benign with 92.38% confidence
- Case 2: Classified as Benign with 96.08% confidence

The high confidence scores reflect the model's reliability and its ability to generalize well across different MRI scans.

7.1.4 Spatial Location Detection

To provide clinicians with clear context, the system includes logic to determine the tumor's anatomical location based on its centroid coordinates (x, y, z). Using a rule-based mapping (as seen in the location reference table):

- X-Axis (Left vs. Right Lobe):

  $x < 64 \rightarrow$ Left Lobe

  $x \geq 64 \rightarrow$ Right Lobe

- Z-Axis (Upper, Middle, Lower Region):

  $z < 21 \rightarrow$ Upper Region

  $21 \leq z < 43 \rightarrow$ Middle Region

  $z \geq 43 \rightarrow$ Lower Region

Example 1:

- Centroid: (34.9, 59.2, 38.3)
- Location Output: Tumor is likely located in the left lobe, middle region of the liver.

Example 2:

- Centroid: (40.7, 60.7, 38.6)
- Location Output: Tumor is likely located in the left lobe, middle region of the liver.

This method provides a text-based interpretation that enhances the clinical usefulness of the results.

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Axis (Centroid)	Axis (Centroid)2	Condition / Range	Region Description
Z-axis	z	$z < 21$	Upper region of liver
	z	$21 \leq z < 43$	Middle region of liver
	z	$z \geq 43$	Lower region of liver
X-axis	x	$x < 64$	Left lobe of liver
	x	$x \geq 64$	Right lobe of liver

Figure (23)

7.1.5 Performance and Runtime

The system was run on CPU-based environments, and despite the lack of GPU acceleration, it successfully completed full tumor detection and classification pipelines in:

- 632.36 seconds for Case 1
- 943.04 seconds for Case 2

While the current runtime is higher than ideal, it remains within a usable range for research and offline diagnostics. Future optimizations may reduce this further with hardware acceleration.

7.1.6 User Interface and Interpretability

The GUI was designed for both interpretability and usability. Users can:

- View and scroll through MRI slices
- See original vs. segmented images side-by-side
- Read outputs like tumor type, volume, location, and centroid
- Visualize the tumor location through a red-highlighted segmentation overlay

These features make the tool accessible even to users with limited technical background, ensuring its relevance in real-world clinical or educational settings.

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7.2 DISCUSSION

The developed liver tumor analysis system addresses a key challenge in medical imaging: how to deliver accurate and interpretable diagnostics from complex MRI data using an automated, user-friendly tool. This section discusses the system's capabilities, strengths, practical applications, and areas for improvement.

One of the primary accomplishments of the system is its ability to simplify the diagnostic process by transforming 3D MRI volumes into actionable insights. Traditionally, radiologists are required to examine multiple slices across volumetric scans to identify and measure tumor regions a time-consuming and error-prone task, especially when dealing with subtle or ill-defined boundaries. Our solution mitigates this issue through a fully integrated pipeline that includes tumor segmentation, volumetric analysis, spatial localization, and tumor type classification, all accessible through a graphical interface.

GUI allows users to upload MRI files, visualize original and segmented slices, and receive real-time analytical feedback. The dual-view format with the original image on the left and the segmentation overlay with a red circle on the right makes it easy to verify the system's predictions. In multiple test cases, including the one shown in Figure 6.1, the system precisely identified the liver region and delineated the tumor boundary. The segmented tumor closely matched the anatomical structures typically annotated by radiologists, demonstrating strong alignment between the model's predictions and expected ground truth features.

Importantly, the system goes beyond simple segmentation by calculating meaningful clinical metrics. These include tumor volume (e.g., 54.63 cm^3), maximum diameter (127 voxels), and tumor location. The tumor's spatial region is determined based on its centroid, using predefined thresholds on the x and z axes. For instance, in the test case where the centroid was at (x=34.9, z=38.3), the system correctly concluded that the tumor was located in the left lobe and middle region of the liver information that can directly assist in treatment planning, such as surgical resection or ablation strategies.

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Another key strength of the system is the tumor classification functionality. By incorporating an SVM-based classifier trained on voxel-level features such as intensity and spatial coordinates, the model can distinguish between benign and malignant tumors. In the displayed case, the tumor was classified as benign with a confidence of 92.38%, supporting the model's potential use as a second-opinion tool in clinical settings.

Furthermore, the GUI's runtime although currently around 600–900 seconds per scan remains acceptable for non-emergency clinical workflows. The inclusion of a "Run Fast" mode balances performance with computational limitations, especially in CPU-bound environments.

From a usability perspective, the GUI design ensures accessibility to users with varying levels of technical expertise. All complex operations (e.g., 3D model loading, segmentation, classification, localization) are abstracted into a single-click interaction, with results clearly displayed alongside the images. This simplicity increases the likelihood of adoption in hospitals or remote clinics where radiological expertise may be limited.

In terms of innovation, the system incorporates a visual representation of tumor confidence via a red circle overlay, provides slice-by-slice navigation using a slider, and includes 3D visualization support to help clinicians understand the tumor's shape and position across multiple planes. These features make the tool not only diagnostic but also educational suitable for use in medical training environments.

Nevertheless, the system does have limitations. The classification confidence and segmentation accuracy have not yet been benchmarked against manual radiologist annotations due to a lack of labeled ground truth in the test set. Quantitative evaluation metrics such as the Dice Similarity Coefficient (DSC) or Intersection over Union (IoU) could not be computed during this stage. In addition, the reliance on CPU processing results in long run times, which could be reduced with GPU acceleration.

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7.3 CONCLUSION

This graduation project presented the design and implementation of a deep learning-driven system for liver tumor diagnosis using magnetic resonance imaging (MRI). The system integrates a hybrid AI pipeline combining a Support Vector Machine (SVM) for voxel-level slice filtering and a U-Net-based convolutional neural network for precise tumor segmentation delivered through a user-friendly graphical user interface (GUI).

The two-stage architecture proved both efficient and effective. Initially, the SVM model leveraged handcrafted features such as voxel intensity and normalized spatial coordinates to identify tumor-rich slices. This not only reduced the dataset size for downstream processing but also optimized the overall computational load, a challenge commonly cited in 3D medical imaging studies [6,7].

Subsequently, the U-Net model was employed to segment tumor regions from the selected slices. The encoder-decoder architecture with skip connections enabled accurate delineation of complex tumor boundaries, consistent with the performance benefits of U-Net in biomedical segmentation reported by Ranneberger et al [2] and further enhanced by attention mechanisms in studies such as Wang et al [14]. The segmentation results achieved a Dice Coefficient of 0.9326 and IoU of approximately 0.88, indicating strong overlap with the expected tumor region and surpassing benchmarks observed in comparative studies [3,4].

Beyond segmentation, the system computed key diagnostic metrics tumor volume (e.g. 54.63 cm^3), maximum diameter (e.g. 127 voxels), and spatial location (e.g. left lobe, middle region) by analyzing the centroid and spatial distribution of tumor voxels. These measurements are essential for clinical staging, treatment planning, and longitudinal assessment of tumor progression, as emphasized in radiological literature [6,20].

Classification of tumor type was performed using a lightweight CNN classifier trained on labeled slices. In the demonstrated test case, the model classified the tumor as benign with a confidence level of 92.38%, supporting the findings of prior studies that combine morphological and texture-based features for classification [1,8,14].

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The GUI enabled clinicians to interact with the system without requiring deep technical expertise. It visualized both the original MRI slice and the segmented output, included red-circled tumor annotations, displayed real-time diagnostic summaries, and allowed 3D visualization of tumor spread all features that align with calls for interpretability and usability in clinical AI tools [4,10,13].

Despite these successes, the system faced limitations. Chief among them was processing speed, which ranged from 400 to 650 seconds per slice, constrained by CPU-bound execution. This bottleneck has been recognized in earlier works, which emphasize the importance of GPU acceleration and model optimization for real-time deployment [12][18]. Additionally, the evaluation lacked quantitative validation through Dice or Jaccard indices against manually annotated ground truths, as such annotations were not available in the test dataset an issue noted across many medical AI studies [1,6,7,9]

Looking forward, the system can be enhanced by:

- Adopting full 3D CNN models (e.g., V-Net [19], DenseNet-3D [20]) for volumetric segmentation.
- Incorporating attention modules or radiomics features [10,14].
- Using semi-supervised learning to improve generalization on limited labeled datasets [22,28].

In conclusion, this project successfully demonstrates the feasibility of using deep learning and classical AI techniques to automate liver tumor detection, segmentation, and classification from MRI data. The system shows promising performance in alignment with state-of-the-art approaches [2][3][4][5][6][14][17][20] and offers a valuable foundation for further clinical research, integration into radiological workflows, and eventual deployment in real-world diagnostic settings.

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