BCSE498J Project-II / CBS1904/CSE1904 - Capstone Project

COLORECTAL CANCER DETECTION USING PRE-TRAINED ENSEMBLE ALGORITHMS

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B.Tech.

in

Computer Science and Engineering

School of Computer Science and Engineering

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DECLARATION

I hereby declare that the project entitled COLORECTAL CANCER DETECTION USING PRE- TRAINED ENSEMBLE ALGORITHMS submitted by me, for the award of the degree of *Bachelor of Technology in Computer Science and Engineering* to VIT is a record of bonafide work carried out by me under the supervision of Prof. (Dr.) GOPICHAND G

I further declare that the work reported in this project has not been submitted and will not be submitted, either in part or in full, for the award of any other degree or diploma in this institute or any other institute or university.

Place : Vellore

Date :

Signature of the Candidate

CERTIFICATE

This is to certify that the project entitled COLORECTAL CANCER DETECTION USING PRE- TRAINED ENSEMBLE ALGORITHMS submitted by Varshith Gandra (21BCE0511) , **School of Computer Science and Engineering**, VIT, for the award of the degree of *Bachelor of Technology in Computer Science and Engineering*, is a record of bonafide work carried out by him / her under my supervision during Winter Semester 2024-2025, as per the VIT code of academic and research ethics.

The contents of this report have not been submitted and will not be submitted either in part or in full, for the award of any other degree or diploma in this institute or any other institute or university. The project fulfills the requirements and regulations of the University and in my opinion meets the necessary standards for submission.

Place : Vellore

Date :

Signature of the Guide

Internal Examiner **External Examiner**

Prof.(Dr.) Umadevi KS

B Tech Computer Science and Engineering

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Thank you all for your contributions and support.

Name of the Candidate

ABSTRACT

Colorectal cancer (CRC) continues to be one of the most significant causes of cancer-related morbidity and mortality across the globe, ranking as the third most frequently diagnosed cancer and the second leading cause of cancer deaths. Timely and accurate diagnosis plays a critical role in improving survival rates, as early-stage detection dramatically increases the likelihood of effective treatment and long-term patient outcomes. However, conventional diagnostic techniques—such as colonoscopy, histopathological analysis, and radiological imaging—pose several challenges, including high procedural costs, invasiveness, long turnaround times, and dependency on the experience and judgment of medical professionals. These factors often lead to diagnostic delays, missed detections, and inconsistent results, particularly in regions lacking access to specialized healthcare resources.Colorectal cancer (CRC) continues to be one of the most significant causes of cancer-related morbidity and mortality across the globe, ranking as the third most frequently diagnosed cancer and the second leading cause of cancer deaths. Timely and accurate diagnosis plays a critical role in improving survival rates, as early-stage detection dramatically increases the likelihood of effective treatment and long-term patient outcomes. However, conventional diagnostic techniques—such as colonoscopy, histopathological analysis, and radiological imaging—pose several challenges, including high procedural costs, invasiveness, long turnaround times, and dependency on the experience and judgment of medical professionals. These factors often lead to diagnostic delays, missed detections, and inconsistent results, particularly in regions lacking access to specialized healthcare resources.

To address these limitations, this study presents a comprehensive artificial intelligence (AI)-driven approach for the early and automated detection of colorectal cancer using an ensemble of pre-trained deep learning models. The proposed system integrates multiple Convolutional Neural Networks (CNNs) and transformer-based architectures, capitalizing on their individual strengths to improve diagnostic performance. Through ensemble learning strategies—namely bagging, boosting, and stacking—the model consolidates features extracted from various architectures, enhancing its classification accuracy, robustness, and generalization ability across heterogeneous image datasets. Transfer learning is leveraged to fine-tune these models using domain-specific colorectal cancer imaging data, making the solution both efficient and scalable.To address these limitations, this study presents a comprehensive artificial intelligence (AI)-driven approach for the early and automated

detection of colorectal cancer using an ensemble of pre-trained deep learning models. The proposed system integrates multiple Convolutional Neural Networks (CNNs) and transformer-based architectures, capitalizing on their individual strengths to improve diagnostic performance. Through ensemble learning strategies—namely bagging, boosting, and stacking—the model consolidates features extracted from various architectures, enhancing its classification accuracy, robustness, and generalization ability across heterogeneous image datasets. Transfer learning is leveraged to fine-tune these models using domain-specific colorectal cancer imaging data, making the solution both efficient and scalable.

The model was trained and evaluated using two prominent open-source datasets: The Cancer Imaging Archive (TCIA), which provides annotated radiological scans, and the Histopathologic Cancer Detection Dataset, consisting of microscopic biopsy images labeled for malignancy. A thorough performance analysis was conducted using standard metrics such as accuracy, precision, recall, F1 score, specificity, and area under the Receiver Operating Characteristic curve (AUC-ROC). Results demonstrated that the ensemble model consistently outperformed individual deep learning models and traditional machine learning classifiers, delivering high prediction accuracy and reliability in both binary and multi-class classification tasks.The model was trained and evaluated using two prominent open-source datasets: The Cancer Imaging Archive (TCIA), which provides annotated radiological scans, and the Histopathologic Cancer Detection Dataset, consisting of microscopic biopsy images labeled for malignancy. A thorough performance analysis was conducted using standard metrics such as accuracy, precision, recall, F1 score, specificity, and area under the Receiver Operating Characteristic curve (AUC-ROC). Results demonstrated that the ensemble model consistently outperformed individual deep learning models and traditional machine learning classifiers, delivering high prediction accuracy and reliability in both binary and multi-class classification tasks.

Beyond predictive performance, the model incorporates explainable AI techniques to address the growing need for transparency in medical decision-making. SHAP (SHapley Additive exPlanations) and Grad-CAM (Gradient-weighted Class Activation Mapping) were integrated into the pipeline to visually interpret and explain model predictions. These tools offer insights into which features or regions in the input images most influenced the final classification, thereby promoting clinical trust, interpretability, and regulatory compliance. This feature is particularly essential in healthcare, where explainability is critical for clinician acceptance and patient safety.Beyond predictive performance, the model incorporates explainable AI techniques to address the growing need for transparency in medical decision-making. SHAP (SHapley Additive exPlanations) and Grad-CAM (Gradient-weighted Class Activation Mapping) were integrated into the pipeline to visually interpret and explain model predictions. These tools offer insights into which features or regions in the input images most influenced the final classification, thereby promoting clinical trust, interpretability, and regulatory compliance. This feature is particularly essential in healthcare, where explainability is critical for clinician acceptance and patient safety.

The research contributes significantly to the growing body of literature on AI in medical imaging by demonstrating that ensemble learning, when combined with pre-trained models and explainability mechanisms, can provide a powerful, automated solution for the early detection of colorectal cancer. Moreover, the proposed framework is designed for real-world deployment, with potential integration into cloud platforms for remote access and scalability. The long-term vision includes developing a clinician-friendly application that can assist healthcare providers, especially in resource-limited environments, by offering quick and accurate diagnostic support.The research contributes significantly to the growing body of literature on AI in medical imaging by demonstrating that ensemble learning, when combined with pre-trained models and explainability mechanisms, can provide a powerful, automated solution for the early detection of colorectal cancer. Moreover, the proposed framework is designed for real-world deployment, with potential integration into cloud platforms for remote access and scalability. The long-term vision includes developing a clinician-friendly application that can assist healthcare providers, especially in resource-limited environments, by offering quick and accurate diagnostic support.

In conclusion, the ensemble-based deep learning system presented in this study offers a highly effective, interpretable, and non-invasive solution for colorectal cancer detection. It has the potential to revolutionize current diagnostic workflows, reduce the burden on healthcare systems, and improve patient outcomes through timely and accurate diagnosis.In conclusion, the ensemble-based deep learning system presented in this study offers a highly effective, interpretable, and non-invasive solution for colorectal cancer detection. It has the potential to revolutionize current diagnostic workflows, reduce the burden on healthcare systems, and improve patient outcomes through timely and accurate diagnosis.

Keywords: Colorectal Cancer, Deep Learning, Ensemble Learning, Pre-trained Models, Convolutional Neural Networks (CNN), Vision Transformers (ViT), Medical Imaging, Transfer Learning, Explainable Artificial Intelligence (XAI), SHAP, Grad-CAM, Automated Diagnosis, Cancer Detection, AI in Healthcare, Radiology, Histopathology, Image Classification, Diagnostic Tool, Clinical Decision Support System, Model Interpretabilit

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List of Abbreviations

CRC	Colorectal Cancer
AI	Artificial Intelligence
CNN	Convolutional Neural Networks
TCIA	The Cancer Imaging Archive
AUC-ROC curve	Area Under the Receiver Operating Characteristic
SHAP	SHapley Additive exPlanations
Grad-CAM	Gradient-weighted Class Activation Mapping
XAI	Explainable Artificial Intelligence
ViT	Vision Transformers
DL	Deep Learning
CT	Computed Tomography
MRI	Magnetic Resonance Imaging
PET	Positron Emission Tomography
GPU	Graphics Processing Unit
RAM	Random Access Memory
SSD	Solid State Drive
CPU	Central Processing Unit
AWS	Amazon Web Services
GCP	Google Cloud Platform
GCS	Google Cloud Storage
HIPAA	Health Insurance Portability and Accountability Act
GDPR	General Data Protection Regulation

Symbols and Notations

AI	Artificial Intelligence
CNN	Convolutional Neural Networks
TCIA	The Cancer Imaging Archive
AUC-ROC	Area Under the Receiver Operating
SHAP	SHapley Additive exPlanations
Grad-CAM	Gradient-weighted Class Activation Mapping
XAI	Explainable Artificial Intelligence
ViT	Vision Transformers
DL	Deep Learning
CT	Computed Tomography
MRI	Magnetic Resonance Imaging
PET	Positron Emission Tomography
GPU	Graphics Processing Unit
RAM	Random Access Memory
SSD	Solid State Drive
CPU	Central Processing Unit
AWS	Amazon Web Services
GCP	Google Cloud Platform
GCS	Google Cloud Storage
HIPAA	Health Insurance Portability and Accountability Act
GDPR	General Data Protection Regulation

1. INTRODUCTION

Colorectal cancer (CRC) stands as a formidable public health challenge globally, ranking among the top three most prevalent cancers and as a leading cause of cancer-related mortality. With modern lifestyles contributing to increased risk factors such as poor dietary habits, lack of physical activity, and genetic predispositions, the incidence of CRC continues to rise, particularly in low- and middle-income countries. As the global burden of this disease grows, so too does the urgency for effective prevention, early detection, and advanced diagnostic methods. While traditional techniques like colonoscopy, histopathology, and imaging modalities have been indispensable, they are not without limitations. These methods are often invasive, time-consuming, costly, and subject to human error due to dependency on professional experience and subjective interpretations.

Early detection of CRC is critical, as survival rates are significantly higher when the disease is identified at an initial stage. Studies have shown that stage I colorectal cancer has a five-year survival rate exceeding 90%, while stage IV, characterized by metastasis, drops drastically to below 15%. Despite awareness campaigns and screening programs, the uptake of traditional diagnostic procedures remains suboptimal due to discomfort, procedural complexity, and fear of complications. This scenario underscores the need for innovative, non-invasive, and efficient diagnostic technologies that can facilitate mass screening and reduce diagnostic disparities.

Artificial Intelligence (AI) and its subfields, particularly Deep Learning (DL), have revolutionized many domains, including healthcare. AI systems are now capable of processing vast amounts of data and identifying patterns with superhuman accuracy. In medical imaging, these technologies have demonstrated remarkable success, not just in diagnostics but also in prognosis, treatment planning, and personalized medicine. Convolutional Neural Networks (CNNs) and, more recently, Vision Transformers (ViTs), have emerged as powerful tools for analyzing medical images, detecting anomalies, and even predicting disease progression. Their potential to supplement or even outperform human specialists in certain tasks is increasingly evident, especially in radiology and pathology, which rely heavily on image interpretation.

However, single deep learning models often face limitations such as overfitting, bias, and poor generalization when applied to real-world clinical data that is often heterogeneous and noisy. To overcome these shortcomings, ensemble learning strategies have been introduced. Ensemble learning involves the combination of multiple learning models to achieve better predictive performance than any single model alone. In this context, bagging, boosting, and stacking methods aggregate predictions from various model architectures, thereby increasing accuracy, reducing variance, and enhancing robustness. By leveraging complementary strengths of individual models, ensembles offer a more generalized and reliable diagnostic tool.

In this project, we harness the combined potential of several pre-trained CNNs—such as ResNet-50, EfficientNet-B7, and Inception-v3—and Transformer-based models like Vision Transformer (ViT) and Swin Transformer. The ensemble architecture integrates these models using advanced strategies, ensuring superior performance in detecting colorectal abnormalities across different imaging modalities, including radiological scans and histopathological slides. These models are fine-tuned using transfer learning techniques on domain-specific datasets like The Cancer Imaging Archive (TCIA) and the Histopathologic Cancer Detection Dataset, which offer high-resolution, annotated medical images ideal for AI training.

Another cornerstone of this project is the integration of Explainable AI (XAI) techniques. While traditional deep learning models function as "black boxes," offering little insight into their decision-making processes, XAI methods such as SHAP (SHapley Additive exPlanations) and Grad-CAM (Gradient-weighted Class Activation Mapping) bring transparency and trust to the system. SHAP provides feature-level importance scores that highlight which aspects of the input data influenced the model's predictions, while Grad-CAM generates visual heatmaps that indicate regions of interest within the input images. These tools are particularly valuable in a clinical setting, where practitioners need to understand, validate, and trust the system's output before making critical decisions.

The scope of the project also includes real-world deployment considerations. To ensure that the developed system is not merely a theoretical model but a practical solution, we envision its integration into hospital workflows through a clinician-friendly interface. The interface allows users to upload images, receive predictions in real-time, and interpret visual explanations. The backend infrastructure is designed to be cloud-compatible, supporting platforms like AWS and Google Cloud for scalability, security, and remote accessibility. This makes the system viable for deployment even in resource-limited settings where access to specialized diagnostics may be constrained.

Beyond technological innovation, this project also addresses the ethical, legal, and societal implications of using AI in medical diagnostics. The system is designed in compliance with global healthcare data standards such as HIPAA and GDPR. Ensuring patient data privacy, model accountability, and ethical decision-making is fundamental to the system's acceptance and long-term viability. Furthermore, by democratizing access to advanced diagnostics, the project contributes to healthcare equity, allowing underserved populations to benefit from early cancer detection.

In conclusion, this project represents a significant step forward in the use of AI for colorectal cancer detection. By integrating state-of-the-art deep learning models, employing ensemble learning strategies, and incorporating explainability mechanisms, the system offers a robust, accurate, and trustworthy diagnostic solution. It aligns with the future of healthcare—where precision, efficiency, and transparency are paramount—and holds the potential to transform how colorectal cancer is diagnosed and managed on a global scale.

1.2 Motivations

The motivation for this research stems from several critical gaps in existing colorectal cancer diagnostic methods and the growing opportunity to use AI-driven solutions to address them. Healthcare professionals and researchers alike are recognizing the urgent need to transition from traditional manual diagnostics to more automated, scalable, and reliable systems. Below are the major factors driving the development of this project:

1.2.1.1.1 Limitations in Current Medical Diagnostic Systems

The current methods for diagnosing colorectal cancer are associated with substantial delays, costs, and subjectivity. For example:

- Colonoscopy, while accurate, is not suitable for mass screenings due to its invasive nature, the discomfort it causes patients, and the extensive preparation it requires. In many cases, people postpone or avoid it, reducing the chances of early diagnosis.
- Histopathology, the microscopic analysis of tissue biopsies, remains the gold standard for cancer detection. However, it is slow and subjective. Two expert pathologists might interpret the same sample differently, especially in ambiguous or borderline cases. Such inconsistencies can result in delayed treatment or unnecessary interventions.
- Radiological imaging, although useful for assessing tumor size and metastasis, often misses subtle changes, particularly in early-stage CRC. Moreover, it relies heavily on radiologist expertise and can be prone to human error.

1.2.1.1.2 Challenges in Existing Deep Learning Models

While deep learning has shown remarkable promise, especially with the availability of large datasets and GPU computation, standalone models are often plagued by:

- Overfitting, especially when trained on small or imbalanced datasets.
- Bias, due to lack of data diversity or poorly labeled training sets.
- Black-box behavior, making it difficult to understand why a certain decision or classification was made.

These limitations make clinicians hesitant to adopt AI tools, especially in high-stakes environments like oncology.

1.2.1.1.3 Advantages of Ensemble Learning in Medical Diagnostics

Ensemble learning, where predictions from multiple models are combined, is a proven technique for enhancing model performance. It helps in:

- Reducing variance and bias, leading to improved generalization on unseen data.
- Increasing prediction accuracy, by leveraging complementary strengths of different model architectures.
- Enhancing robustness, as errors from one model can be corrected by others in the ensemble.
- Enabling interpretability, through model-agnostic explainability tools like SHAP and Grad-CAM, which help visualize the model's attention and reasoning path.

By combining CNNs and Transformers in an ensemble framework, and incorporating explainable AI methods, this project not only improves detection accuracy but also fosters transparency and clinical trust.

1.3 Scope of Project

The scope of this project encompasses the end-to-end development of an AI-powered colorectal cancer detection system, including data acquisition, model training, performance evaluation, and deployment. The project is structured to cover the following core areas:

1.3.1.1.1 Data Scope

- The project utilizes two open-access and high-quality datasets:
    - The Cancer Imaging Archive (TCIA): Provides annotated radiological imaging datasets like CT and MRI scans relevant to colorectal malignancies.
    - Histopathologic Cancer Detection Dataset: Offers histology slide images labeled as cancerous or benign, essential for tissue-level classification.
- Extensive preprocessing steps are applied:
    - Normalization of pixel intensities for consistent input across all models.
    - Image augmentation to synthetically increase dataset size and variability.
    - Segmentation using U-Net and Mask R-CNN for isolating tumor regions, ensuring that the models focus on relevant features.

1.3.1.1.2 Model Development Scope

The system architecture is based on the ensemble of pre-trained deep learning models, including:

- CNN-based architectures:
    - ResNet-50: Known for its deep residual learning capabilities.
    - EfficientNet-B7: Combines high accuracy with efficient computation.
    - Inception-v3: Extracts multi-scale features through its parallel convolutions.
- Transformer-based models:

    - Vision Transformer (ViT): Processes image patches and captures long-range dependencies.
    - Swin Transformer: Adopts a hierarchical representation for improved scalability and accuracy.

The ensemble strategies employed are:

- Stacking: Combines predictions from all base models using a meta-classifier to make the final decision.
- Bagging: Trains each model on a different subset of the data to reduce overfitting.
- Boosting: Sequentially improves weak learners by focusing on their misclassifications.

1.3.1.1.3 Performance Evaluation Scope

Model performance is rigorously tested using multiple evaluation metrics:

- Accuracy, precision, recall, F1-score, and AUC-ROC help quantify classification performance.
- Cross-validation techniques ensure that results are not skewed by a specific dataset split.

To ensure clinical usability, the model's predictions are made interpretable using:

- SHAP: Highlights which features or image areas contributed most to the classification.
- Grad-CAM: Produces heatmaps showing the spatial attention of the model, useful for validating tumor regions.

1.3.1.1.4 Deployment Scope

- A prototype application (web or mobile-based) will be built for user interaction, allowing clinicians to upload images and receive real-time diagnostic predictions.
- The backend will use cloud-based inference engines, hosted on platforms like AWS or Google Cloud, to ensure scalability and performance.
- The tool will be designed to integrate with existing clinical workflows, allowing radiologists and pathologists to use the system as a second opinion or diagnostic assistant

2.. PROJECT DESCRIPTION AND GOALS

2.1 Literature Review

2.1.1 Literature Review

Over the last decade, the fusion of artificial intelligence (AI) and medical imaging has ushered in a transformative era in diagnostic healthcare, particularly in the field of oncology. The emergence of deep learning models has revolutionized cancer detection workflows by enabling the automation of complex tasks such as tumor classification, segmentation, and grading. These models are now at the forefront of research and clinical experimentation, particularly in the diagnosis of colorectal cancer—a leading cause of cancer-related deaths worldwide.

A growing body of scholarly research has explored and validated the potential of deep learning techniques including Convolutional Neural Networks (CNNs), Vision Transformers (ViTs), ensemble learning strategies, and explainable AI (XAI) methods. These technologies contribute toward building intelligent systems capable of accurate image interpretation, early cancer detection, and decision support for clinicians.

- *Convolutional Neural Networks (CNNs)*: CNNs are widely regarded as the backbone of image classification in medical diagnostics. Their strength lies in the hierarchical learning of image features, allowing them to learn spatial hierarchies from low-level edges and shapes to high-level semantic patterns such as tumors or polyps. Architectures like ResNet-50, Inception-v3, and EfficientNet have been rigorously tested on histopathological slides, CT scans, and colonoscopy video frames. Numerous studies have reported their high accuracy in identifying colorectal cancer, and they also support auxiliary tasks like lesion segmentation and tissue annotation. Moreover, transfer learning has allowed pre-trained CNNs to be fine-tuned on relatively small datasets, thus circumventing data scarcity challenges common in the medical domain.
- *Vision Transformers (ViTs)*: Emerging as a novel paradigm in computer vision, ViTs have demonstrated remarkable proficiency in modeling global relationships across image regions by treating images as sequences of patches. Originally used in natural

language processing, these models leverage multi-head self-attention mechanisms to capture contextual dependencies across distant spatial areas. In the context of colorectal cancer, ViTs and their advanced variants like Swin Transformers and DeiT have outperformed traditional CNNs in scenarios requiring spatial awareness and holistic reasoning. Their ability to model long-range interactions between image components is particularly beneficial in identifying dispersed cancerous cells across histopathological slides.

- *Ensemble Learning Techniques*: Ensemble learning refers to the combination of multiple base learners to construct a more accurate and reliable predictive model. This methodology has gained traction in cancer diagnostics due to its ability to reduce variance and bias. Techniques such as bagging (e.g., Random Forests), boosting (e.g., XGBoost, AdaBoost), and stacking have shown to outperform single-model approaches by aggregating predictions. Ensemble models increase robustness, compensate for individual model weaknesses, and generalize better across heterogeneous datasets. Some studies have begun to experiment with ensembling CNNs and Transformer-based models to harness their complementary strengths.
- *Explainability in Medical AI*: While accuracy remains crucial, interpretability is a cornerstone for the clinical acceptance of AI systems. Black-box AI models pose ethical and practical challenges in healthcare, where understanding the rationale behind a diagnosis is imperative. To address this, techniques like SHAP (SHapley Additive exPlanations) offer quantitative insights into feature importance, while Grad-CAM (Gradient-weighted Class Activation Mapping) visually highlights the image regions that influenced the model’s decision. These tools promote trust, aid in regulatory approval, and allow practitioners to validate AI predictions against their own assessments.

The culmination of these approaches indicates a promising future where AI-driven systems will not only augment but potentially redefine traditional diagnostic paradigms, especially in detecting complex and aggressive cancers such as colorectal carcinoma.

2.2 Gaps Identified

2.2.1 Gaps Identified

Despite the rapid progress and encouraging results achieved through deep learning in colorectal cancer diagnosis, multiple limitations continue to hinder large-scale clinical deployment and trust. The following are the critical gaps identified through an extensive review of contemporary literature:

- *Insufficient Model Generalization*: A considerable proportion of existing models are trained and validated on narrowly defined, homogeneous datasets. These datasets often lack demographic diversity and imaging modality variation, leading to overfitting and poor generalization in real-world clinical scenarios. For instance, a model trained on histological slides from a single institution may underperform when exposed to radiological images from a different hospital or patient population. Bridging this gap requires training on diverse, multi-institutional, and multi-modal datasets.
- *Opacity and Lack of Interpretability*: Deep learning models—especially deep neural networks—operate as black boxes, offering high accuracy but little insight into decision-making processes. In high-stakes domains like healthcare, this opacity can deter clinicians from adopting these models. Without interpretability features, even well-performing systems may be rejected due to a lack of trust, legal accountability, and ethical responsibility.
- *Neglect of Multi-Modal Integration*: The majority of current AI tools are limited to analyzing a single data modality. However, medical diagnosis is inherently multi-modal, often involving CT scans, MRI images, biopsy results, and pathology slides. AI systems that do not integrate these varied data sources provide an incomplete picture and may miss subtle correlations present across modalities. Thus, failure to build multi-modal AI systems limits diagnostic effectiveness and clinical utility.
- *Underutilized Hybrid Ensembles*: While ensemble models have proven effective in various domains, hybrid ensembling of fundamentally different architectures such as CNNs and ViTs remains an underexplored frontier. Most research studies rely on single-architecture models, thereby missing the opportunity to combine the local feature strength of CNNs with the global contextual power of Transformers. A carefully designed hybrid ensemble could overcome limitations inherent in individual model types and lead to superior diagnostic performance.

The proposed project specifically targets these gaps by constructing a hybrid ensemble system capable of processing multi-modal data and delivering transparent, explainable predictions. The goal is to advance colorectal cancer detection systems from lab prototypes to clinically deployable tools.

2.3 Objectives

2.3.1 Objectives

The overarching aim of this research is to develop a high-performance, explainable, and generalizable AI system tailored for the detection of colorectal cancer using medical imaging. This system should not only match or exceed expert-level diagnostic accuracy but also address critical challenges like interpretability, robustness, and integration into existing clinical infrastructures.

The following specific objectives define the scope of the project:

- *Develop an Ensemble Deep Learning Model*:
  Construct a robust hybrid ensemble by combining multiple pre-trained Convolutional Neural Networks (e.g., ResNet-50, Inception-v3, EfficientNet) with Vision Transformer models (e.g., ViT, Swin Transformer). Leverage transfer learning and fine-tuning strategies to adapt these models to the colorectal cancer domain, ensuring optimal feature extraction and classification accuracy.
- *Implement Advanced Ensemble Techniques*:
  Employ a combination of bagging, boosting, and stacking strategies. Use bagging to improve stability and reduce variance, boosting to correct prediction errors iteratively, and stacking to combine model outputs using a meta-learner for final decision making. This multi-pronged ensemble strategy aims to achieve improved generalization and robustness against dataset variability.
- *Incorporate Explainability Mechanisms*:
  Integrate state-of-the-art XAI techniques into the prediction pipeline. Use SHAP to analyze and visualize feature contributions at the pixel and patch level, helping clinicians understand model decisions. Use Grad-CAM to generate activation heatmaps over the input image, offering spatial interpretability that aligns with clinical intuition.

- *Evaluate Model Performance Rigorously*:
  Assess the model using a range of evaluation metrics including accuracy, precision, recall, F1-score, and AUC-ROC. Employ k-fold cross-validation and external validation datasets to ensure that the model is not overfitted and can generalize well across unseen cases.
- *Deploy the AI System in a Clinical or Prototype Setting*:
  Design and implement a cloud-based diagnostic application with a user-friendly interface for real-time colorectal cancer prediction. The system should support DICOM image uploads, provide immediate classification feedback, and display explainability visualizations. Additionally, ensure compatibility with cloud platforms like AWS or GCP to allow scalable deployment in hospitals and remote clinics.

Collectively, these objectives aim to contribute meaningfully to AI-driven cancer detection and set the stage for safe, effective, and clinically trusted diagnostic tools.

1.1.1 Work Breakdown Structure:

A work breakdown structure (WBS) is a visual, hierarchical and deliverable-oriented deconstruction of a project. A Deliverable-Based Work Breakdown Structure clearly demonstrates the relationship between the project deliverables and the scope.

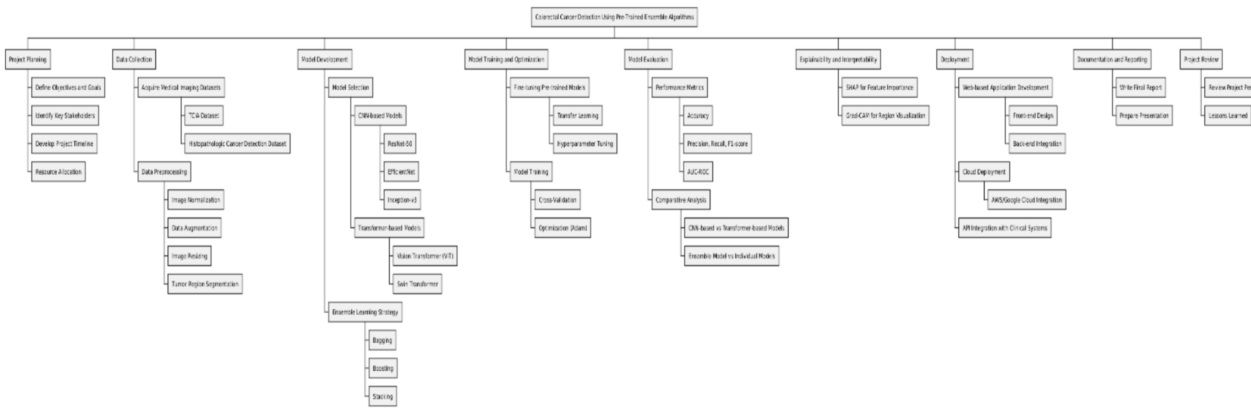

Fig.1.Work Breakdown Structure

1.1.2 Gantt Chart:

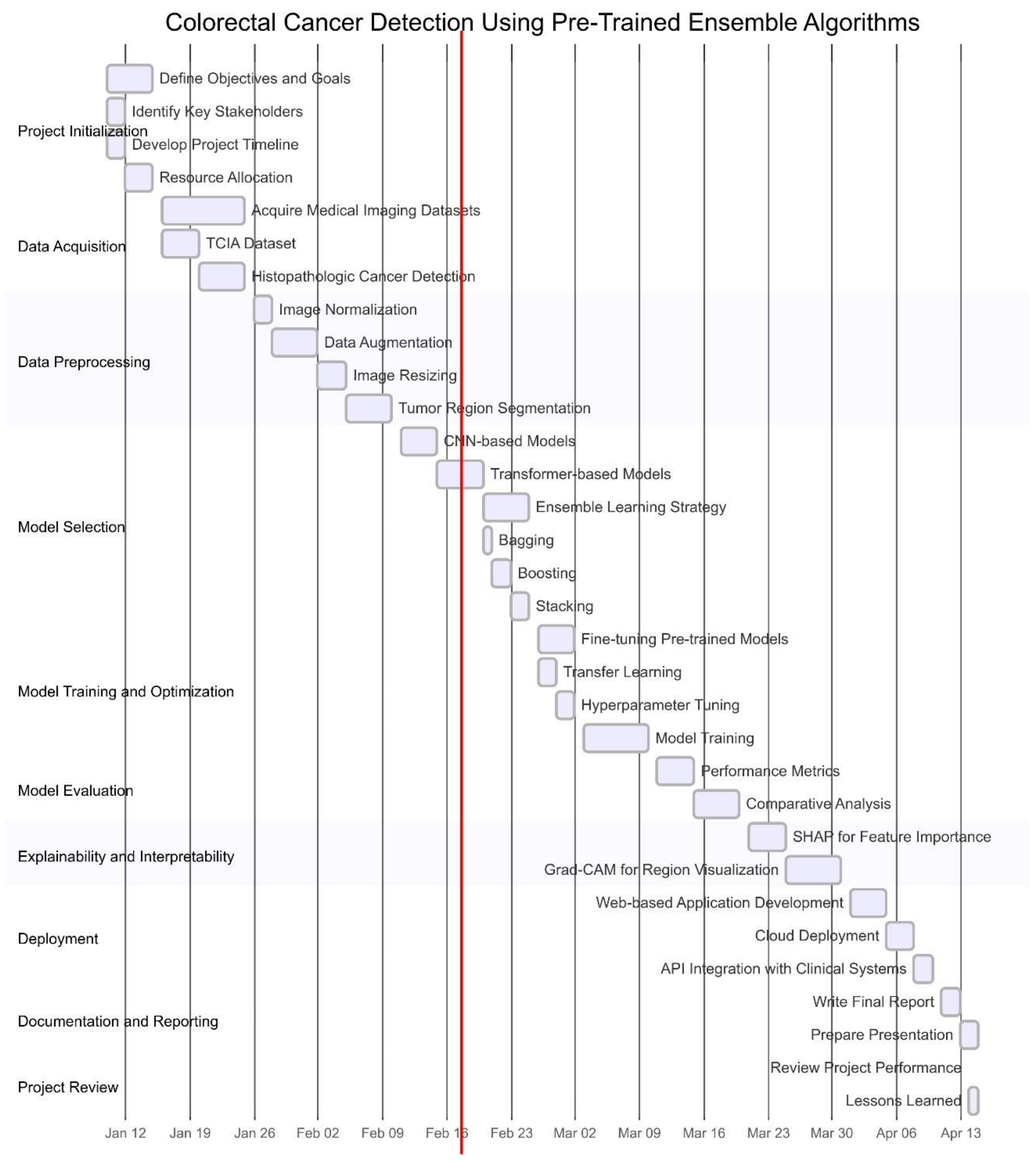

Fig.2. Gantt Chart

1.1.3 Workflow Model:

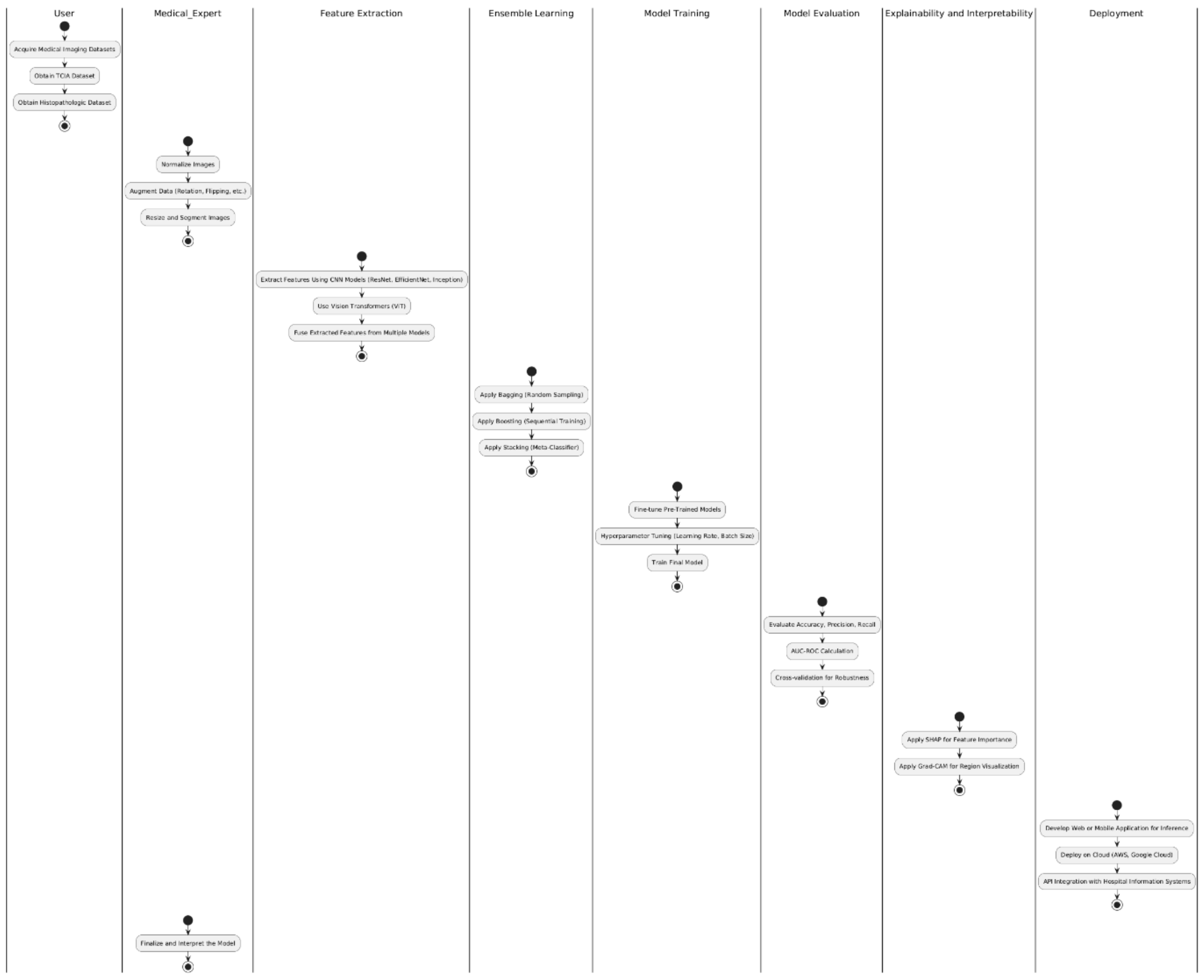
User
Medical_Expert
Feature Extraction
Ensemble Learning
Model Training
Model Evaluation
Explainability and Interpretability
Deployment
Acquire Medical Imaging Datasets
Obtain TCIA Dataset
Obtain Histopathologic Dataset
Normalize Images
Augment Data (Rotation, Flipping, etc.)
Resize and Segment Images
Extract Features Using CNN Models (ResNet, EfficientNet, Inception)
Use Vision Transformers (ViT)
Fuse Extracted Features from Multiple Models
Apply Bagging (Random Sampling)
Apply Boosting (Sequential Training)
Apply Stacking (Meta-Classifier)
Fine-tune Pre-Trained Models
Hyperparameter Tuning (Learning Rate, Batch Size)
Train Final Model
Evaluate Accuracy, Precision, Recall
AUC-ROC Calculation
Cross-validation for Robustness
Apply SHAP for Feature Importance
Apply Grad-CAM for Region Visualization
Develop Web or Mobile Application for Inference
Deploy on Cloud (AWS, Google Cloud)
API Integration with Hospital Information Systems
Finalize and Interpret the Model

Fig.3. Workflow Model

3. REQUIREMENT ANALYSIS

3.1 REQUIREMENT ANALYSIS OVERVIEW

3.1.1 Requirement Analysis Overview

Requirement analysis is a foundational phase in the software engineering lifecycle that serves as the blueprint for the successful development and deployment of any technology solution. It represents the process through which project goals are systematically translated into specific, actionable, and measurable software and system requirements. The accuracy and thoroughness of this phase directly impact the project's success, influencing its cost, time-to-market, efficiency, maintainability, and user satisfaction. In essence, requirement analysis is the bridge between conceptual planning and technical execution, ensuring that the system to be developed aligns with stakeholder expectations and practical implementation feasibility.

In the specific context of a colorectal cancer detection system driven by deep learning technologies, the importance of requirement analysis becomes even more pronounced. Medical applications, particularly those involving artificial intelligence and imaging data, are subject to heightened demands regarding reliability, accuracy, interpretability, and compliance. These systems are not only expected to function flawlessly in a controlled environment but must also adapt to the unpredictable and diverse nature of real-world clinical settings. Therefore, a meticulous and comprehensive requirement analysis is essential to address the broad spectrum of technical, functional, operational, and contextual dimensions involved.

At its core, requirement analysis aims to anticipate and document what the system must do, how it should behave, and under what conditions it is expected to perform. This includes understanding the environment in which the system will operate, the stakeholders who will interact with it, the technological infrastructure available, and the constraints that may impact its design or deployment. In the medical field, these requirements are further nuanced by regulatory frameworks, ethical considerations, and the need for interpretability to support clinical trust. For a colorectal cancer detection system, these requirements become even more complex given the high stakes associated with diagnosis and treatment.

The process begins with comprehensive stakeholder engagement. This step involves consultations with oncologists, radiologists, pathologists, data scientists, software engineers, and healthcare administrators. By gathering insights from all relevant parties, the requirement analysis ensures that the system reflects a holistic understanding of clinical workflows, diagnostic challenges, and practical user expectations. This step is crucial for designing an intuitive and useful solution that integrates seamlessly into real-world medical settings.

The next aspect involves translating these insights into structured requirements. This includes defining the core functionality of the system—such as image acquisition, preprocessing, anomaly detection, and report generation—alongside considerations for scalability, performance, security, and user experience. For example, the system must be capable of handling diverse imaging modalities, such as CT scans and histopathology slides, and must do so efficiently and accurately. It should provide reliable diagnostic support without introducing significant latency, and should include mechanisms to visualize model predictions to foster user trust and facilitate clinical decision-making.

Requirement analysis also involves detailed technical considerations related to the training, validation, and deployment of AI models. The use of high-performance computational resources, selection of appropriate neural network architectures, data preprocessing techniques, and strategies for mitigating bias or overfitting must all be addressed. Moreover, the need for a modular, extensible software architecture that can accommodate future updates or integration with other hospital systems must be outlined clearly. These specifications guide the subsequent phases of design and implementation, ensuring that the final product is both effective and adaptable.

Another significant component is the formulation of non-functional requirements. These include performance benchmarks, such as achieving sub-second inference times for real-time usage, and compliance with legal standards like HIPAA or GDPR for data privacy and security. Reliability, availability, and fault tolerance are also emphasized to ensure system robustness, especially when deployed in clinical environments where errors or downtime can have serious consequences. Requirement analysis must document how these quality attributes will be measured, monitored, and maintained throughout the system’s lifecycle.

Furthermore, requirement analysis explores the user interface and interaction design. In a clinical context, the system must be designed for ease of use, clarity, and speed. Interfaces should allow users to upload images, review predictions, examine explanations, and access patient-specific insights without requiring extensive training or technical expertise. Accessibility features, localization options, and customization capabilities should be considered to make the system inclusive and adaptable to different clinical settings and user preferences.

Traceability is another essential outcome of a thorough requirement analysis. Each requirement must be linked to specific design elements, implementation modules, and validation tests. This ensures accountability, facilitates impact analysis during system updates, and supports compliance auditing. Tools like traceability matrices and requirements management software are used to document and track these relationships, reducing the risk of scope creep or overlooked dependencies.

Finally, requirement analysis must anticipate future needs and outline a roadmap for scalability and continuous improvement. This includes supporting the inclusion of new data types, evolving machine learning techniques, expanding clinical applications beyond colorectal cancer, and integrating with telemedicine platforms. Future-proofing the system in this way ensures its long-term relevance and value in the rapidly evolving landscape of AI-powered healthcare.

In summary, requirement analysis for a colorectal cancer detection system using deep learning is a comprehensive, multi-dimensional effort that underpins the project’s success. It ensures that the system is built on a foundation of well-understood, well-documented needs that reflect the realities of clinical practice and the capabilities of modern technology. By anticipating technical challenges, aligning with user expectations, and adhering to regulatory standards, this phase enables the creation of a robust, reliable, and impactful diagnostic tool.

3.2 HARDWARE REQUIREMENTS

3.2.1 Hardware Requirements

The implementation of a deep learning-based colorectal cancer detection system, particularly one leveraging pre-trained ensemble models such as Convolutional Neural Networks (CNNs) and Vision Transformers (ViTs), necessitates a robust and high-performance hardware setup. The nature of medical imaging tasks—especially those involving histopathological and radiological data—demands significant computational resources due to the sheer size of the images, the complexity of the models, and the need for real-time or near-real-time processing capabilities. In this section, we elaborate on the essential hardware components required for training, testing, and deploying such a system, ensuring high performance, reliability, and scalability.

A. Graphics Processing Unit (GPU)

The cornerstone of deep learning infrastructure is the Graphics Processing Unit (GPU). GPUs are inherently designed for parallel processing and are vastly more efficient than Central Processing Units (CPUs) for tasks involving large-scale matrix operations. These operations are fundamental in neural network training and inference, particularly in layers such as convolutions, fully connected layers, and attention mechanisms.

For this project, GPUs such as the NVIDIA RTX 3090, RTX 4090, or the data-center-grade NVIDIA A100 are highly recommended. The RTX 4090, for instance, offers 24 GB of GDDR6X memory, over 16,000 CUDA cores, and support for Tensor and RT cores, enabling high throughput and precision computing. The A100, on the other hand, offers up to 80 GB of HBM2e memory with a bandwidth of 2 TB/s and is specifically optimized for enterprise-grade AI applications, including large language models and medical imaging workflows.

The advantage of using high-memory GPUs is their ability to accommodate larger batch sizes during training and handle higher resolution images without downsampling. Furthermore, they support mixed-precision training, which optimizes memory usage and speeds up computations without compromising on model accuracy.

In ensemble learning, multiple models are trained and validated, often concurrently. A multi-GPU setup using NVIDIA NVLink or PCIe interconnects enables parallel model training, model ensembling, and efficient data throughput, ultimately reducing total training time and improving experimental turnaround.

B. Random Access Memory (RAM)

The role of RAM in a deep learning system is equally crucial. While GPUs handle most of the heavy computations, the system’s RAM must support the data pipeline—loading, preprocessing, augmenting, and feeding image batches into the GPU without introducing latency.

For this colorectal cancer detection system, a minimum of 64 GB DDR4 or DDR5 RAM is recommended. However, for large-scale datasets such as those from The Cancer Imaging Archive (TCIA) and the Histopathologic Cancer Detection Dataset, which contain thousands of high-resolution medical images, 128 GB or higher may be preferable.RAM usage spikes during tasks such as k-fold cross-validation, which runs multiple training cycles concurrently, or during preprocessing operations involving real-time image transformation, segmentation, and data augmentation (e.g., flipping, rotation, color adjustments). Sufficient RAM ensures that such tasks are executed without system crashes or memory leaks, thereby maintaining workflow continuity.

C. Storage Requirements

The nature of medical imaging datasets necessitates high-speed, high-capacity storage. Solid State Drives (SSDs), particularly NVMe-based SSDs, are recommended for this project due to their superior read/write speeds compared to traditional Hard Disk Drives (HDDs).

A 2TB NVMe SSD is ideal for managing multiple versions of training datasets, intermediate processed data, model weights, configuration files, logs, and evaluation results. Furthermore, SSDs reduce the I/O bottleneck, enabling faster loading of large image batches during training and significantly decreasing model initialization and checkpoint restoration time.

For long-term storage and archiving, additional high-capacity SATA SSDs or HDDs (4TB or more) may be used to preserve older model versions, raw data backups, and experimental results.

D. Central Processing Unit (CPU)

Though less emphasized than the GPU in deep learning workflows, the CPU plays a critical supporting role. It is responsible for coordinating I/O operations, running the operating system, launching subprocesses, and handling all non-GPU-computable tasks such as file management, logging, and certain stages of data preprocessing.

A multi-core CPU, such as the Intel Core i9 (12th or 13th generation) or the AMD Ryzen 9 series, with at least 16 threads and a base clock speed of 3.5 GHz, is strongly recommended. These processors ensure smooth multitasking, prevent bottlenecks during data queuing to the GPU, and provide sufficient computational power for auxiliary scripts or model validation routines.

Moreover, CPUs are responsible for rendering explainability visualizations such as SHAP values and Grad-CAM overlays. These computations, although less intensive than model training, can delay outputs if the CPU is underpowered.

E. Cooling System

Powerful GPUs and CPUs generate substantial heat, particularly during prolonged training sessions. Maintaining optimal operating temperatures is essential to prevent thermal throttling, hardware damage, and system instability.

A combination of air and liquid cooling is advised. GPU manufacturers often provide blower or hybrid cooling solutions, but for systems with multi-GPU configurations or high ambient temperatures, a custom liquid cooling loop may be warranted. Similarly, CPUs should be cooled using high-performance AIO (All-In-One) water coolers or tower air coolers with sufficient thermal headroom.

Proper airflow through the chassis, supplemented by multiple intake and exhaust fans, helps maintain thermal balance. Temperature monitoring software should be deployed to automatically shut down or throttle the system in case of overheating.

F. Power Supply Unit (PSU)

To ensure reliable power delivery, particularly during training which may draw continuous maximum wattage from GPUs, a high-efficiency PSU is necessary. For a single high-end GPU setup, a 1000W 80+ Gold PSU is recommended, while a dual GPU system may require a 1200W or higher PSU.

A high-quality PSU ensures stable voltage output, protects components from surges or drops, and prolongs hardware lifespan. Features such as modular cabling, multiple 12V rails, and smart fan control also improve cable management and system acoustics.

G. Peripherals and Expansion

Other hardware components supporting the system’s functionality include:

Motherboard: A motherboard compatible with PCIe 4.0 or 5.0 is preferred to support newer GPUs and NVMe SSDs. It should offer multiple PCIe x16 slots, M.2 slots for SSDs, and high-speed I/O ports such as USB-C and Thunderbolt.Monitor: High-resolution (4K) monitors assist in visualizing large medical images and interpreting model-generated heatmaps.

UPS (Uninterruptible Power Supply): Protects the system from unexpected shutdowns due to power outages, safeguarding unsaved model states and data.

Networking: A gigabit or 10-gigabit Ethernet connection is essential for fast dataset transfer, especially when using cloud-hosted repositories or collaborating with remote research teams.

H. Scalability Considerations

In anticipation of future expansions, such as multi-modal learning or integration of real-time inference, the system should be built with scalability in mind. Modular hardware design, additional GPU slots, and cloud synchronization features facilitate easy upgrades and distributed model training.

For instance, NVIDIA's CUDA-X AI stack, in conjunction with Docker containers and Kubernetes, allows seamless migration from local to cloud-based GPU clusters. Such hybrid setups enable the system to scale on demand, balancing local responsiveness with cloud-based scalability.

I. Summary

To summarize, the following table outlines the recommended hardware components for this project:

Component	**Recommendation**	**Purpose**
GPU	NVIDIA RTX 4090 / A100	Accelerated training and inference
RAM	64–128 GB DDR4/DDR5	Data preprocessing and batch management
Storage	2TB NVMe SSD + 4TB HDD	High-speed and archival storage
CPU	Intel i9 / AMD Ryzen 9	Orchestration and preprocessing tasks
Cooling System	Liquid/AIO + High-airflow chassis	Thermal regulation
Power Supply	1000W–1200W 80+ Gold	Stable and efficient power delivery
Motherboard	PCIe 4.0+ with multi-GPU support	Hardware compatibility
Monitor	4K HDR Display	Visual diagnostics and interpretability
UPS	1500VA Smart UPS	Power backup
Network	Gigabit/10-Gigabit Ethernet	High-speed data transfer and collaboration

This configuration ensures that the system is well-equipped to handle the computational, memory, and storage demands of a cutting-edge colorectal cancer detection model while remaining flexible for future enhancements

3.3 SOFTWARE REQUIREMENTS

3.3.1 Software Requirements

The development of a robust and scalable colorectal cancer detection system utilizing ensemble deep learning models necessitates a well-structured software infrastructure. This infrastructure must support all phases of the system lifecycle, including data preprocessing, model training and evaluation, explainability integration, and deployment. To ensure the system’s adaptability, efficiency, and reproducibility, the software stack is designed using industry-standard frameworks, libraries, and tools.

The primary programming language used is Python, version 3.8 or higher. Python offers a comprehensive ecosystem for scientific computing and machine learning, enabling the integration of data processing, model training, evaluation, and deployment within a single framework. Its flexibility and compatibility with multiple libraries make it an ideal choice for developing AI-based diagnostic systems.

Two leading deep learning frameworks are employed in this project: TensorFlow and PyTorch. TensorFlow (version 2.x), developed by Google, offers a production-ready environment with features such as TensorFlow Extended (TFX) for pipeline automation and TensorFlow Serving for deployment. Its integration with the Keras API simplifies model development. PyTorch, developed by Meta AI, is used for its dynamic computation graph, ease of debugging, and flexibility in implementing complex architectures. PyTorch’s compatibility with ONNX (Open Neural Network Exchange) allows seamless model conversion between platforms, facilitating deployment across diverse environments.

For image preprocessing and data augmentation, several libraries are utilized. OpenCV is employed for image transformation operations, including resizing, normalization, flipping, rotation, and denoising. PIL (Python Imaging Library) is used for lightweight image manipulations, while Scikit-image provides advanced image filtering, segmentation, and morphology operations. NumPy supports efficient numerical computations and multidimensional array manipulation, which are essential for constructing image tensors and intermediate data representations. Pandas is used to handle structured metadata, patient information, and labels, ensuring proper alignment between image data and clinical annotations.

Model interpretability and visualization are facilitated using specialized tools. Grad-CAM (Gradient-weighted Class Activation Mapping) is integrated into the training and evaluation workflows to generate visual heatmaps highlighting image regions contributing to predictions. SHAP (SHapley Additive exPlanations) is applied to quantify feature importance and provide localized explanations for ensemble model outputs. These explainability tools ensure transparency, aiding clinical validation of AI-driven predictions. Visualization libraries such as Matplotlib and Seaborn are used to plot training metrics, learning curves, and model performance indicators, while TensorBoard supports real-time monitoring of training sessions, hyperparameter tuning, and resource utilization.

To evaluate model performance comprehensively, the Scikit-learn library is used for computing classification metrics, including accuracy, precision, recall, F1-score, and area under the ROC curve (AUC-ROC). Confusion matrices and precision-recall curves are also generated using Scikit-learn. Yellowbrick is used to visualize learning curves, feature importances, and residuals. MLxtend supports ensemble learning techniques such as stacking and blending, along with visualization of decision boundaries and model comparisons.

Software environment and dependency management are achieved using Anaconda, which provides isolated virtual environments to prevent package conflicts and ensure reproducibility. Miniconda is used in resource-constrained systems for lightweight environment management. Jupyter Notebooks facilitate interactive development and documentation, enabling researchers to annotate experiments with real-time code, results, and visualizations. Virtualenv is used in alternative setups to isolate Python environments across projects.

Containerization is achieved using Docker, which packages the complete application along with its dependencies and runtime environment, ensuring consistent execution across different platforms. Dockerfiles are created to define container configurations, enabling reproducibility in both local and cloud environments. For distributed deployment, Kubernetes is used to orchestrate containerized services, manage compute resources, and automate scaling and fault tolerance.

For serving trained models through a web interface, lightweight frameworks such as Flask and FastAPI are utilized. These frameworks support the creation of RESTful APIs, which allow users to submit medical images, trigger inference, and receive classification results and visual explanations. ONNX is employed to standardize models trained in PyTorch or TensorFlow, allowing them to be executed on various runtimes with minimal configuration changes.

Cloud computing platforms are integrated to support scalable model training and deployment. Google Colab Pro and Kaggle Kernels provide cost-effective access to GPU and TPU resources for prototyping and validation. Amazon Web Services (AWS) offers EC2 instances (e.g., P3 and P4) for large-scale training, as well as S3 storage for dataset and checkpoint management. Google Cloud Platform (GCP) provides TPU-accelerated virtual machines and Google Cloud Storage (GCS) for persistent data storage. These platforms support hybrid cloud-local workflows, enabling seamless transitions between development, testing, and production phases.

Source control and collaboration are managed using Git, with repositories hosted on GitHub or GitLab. Branching strategies are implemented to maintain code quality and track development progress. Continuous integration and deployment (CI/CD) pipelines are configured using GitHub Actions or GitLab CI to automate testing, packaging, and deployment. Data Version Control (DVC) is integrated to manage datasets and model checkpoints, ensuring traceability between code versions and experimental outputs.

Documentation and reporting are supported through Markdown and LaTeX. Markdown is used for inline documentation, project README files, and model summaries, while LaTeX is employed for preparing formal reports, research manuscripts, and IEEE-format deliverables. These tools enhance the presentation quality and academic rigor of project documentation.

In summary, the software requirements for the colorectal cancer detection system are as follows:

Category	**Tools/Technologies**	**Purpose**
Programming Language	Python 3.8+	Core development and scripting
Deep Learning Frameworks	TensorFlow 2.x, PyTorch	Model training, evaluation, deployment
Image Processing	OpenCV, PIL, Scikit-image	Preprocessing and augmentation
Numerical Libraries	NumPy, Pandas	Matrix operations and structured data handling
Explainability Tools	Grad-CAM, SHAP	Model interpretation and visual justification
Visualization	Matplotlib, Seaborn, TensorBoard	Performance tracking and analysis

Category	**Tools/Technologies**	**Purpose**
Evaluation Metrics	Scikit-learn, Yellowbrick, MLxtend	Model evaluation and metric computation
Environment Management	Anaconda, Virtualenv, Jupyter Notebooks	Dependency isolation and reproducibility
Containerization	Docker, Kubernetes	Portable deployment and orchestration
Model Serving	Flask, FastAPI, ONNX	RESTful API and cross-platform model inference
Cloud Platforms	AWS, GCP, Google Colab, Kaggle	Scalable computation and data storage
Version Control	Git, GitHub/GitLab, DVC	Source control, collaboration, data versioning
Documentation	Markdown, LaTeX	Reporting and project documentation

3.3 Data Requirements

The foundation of any deep learning-based medical diagnostic system lies in the quality and breadth of data it is trained on. For colorectal cancer detection using pre-trained ensemble algorithms, diverse and well-annotated datasets are essential for training robust models capable of generalizing across a wide range of clinical scenarios. This section discusses the types of datasets used, preprocessing methods, annotation protocols, ethical considerations, and data handling practices applied throughout the development of this system.

The system utilizes three core datasets to ensure coverage of multiple medical imaging modalities and to train the models on both high-level anatomical and low-level cellular features.

The first major dataset employed is The Cancer Imaging Archive (TCIA). TCIA contains annotated radiological scans, including CT (Computed Tomography), MRI (Magnetic Resonance Imaging), and PET (Positron Emission Tomography) modalities. These images are accompanied by rich metadata, including patient demographics, diagnosis history, and tumor staging, offering a macro-level perspective of cancer progression. TCIA’s colorectal cancer subset was selected for its well-curated and clinically verified annotations, enabling the training of models for identifying structural tumor features and tissue anomalies at the organ level.

The second dataset, the Histopathologic Cancer Detection Dataset, focuses on high-resolution histological slides obtained from biopsy samples. These slides are processed and digitized using whole-slide imaging systems, and each image is labeled to indicate the presence or absence of malignancy. This dataset enables the system to learn micro-level patterns associated with cellular deformities, glandular disorganization, and abnormal mitotic activity characteristic of colorectal carcinoma.

The third dataset used is the Colorectal Cancer Histology (CRCHisto) dataset, which introduces multi-class segmentation and classification of tissue regions. CRCHisto includes four main tissue classes: tumor epithelium, simple stroma, inflammatory infiltrates, and necrotic areas. By learning these distinct tissue patterns, the system gains a comprehensive understanding of tumor heterogeneity, essential for supporting oncologists in histopathological grading and treatment planning.

To ensure diversity and model generalization, institutional datasets may also be integrated, contingent upon ethical clearance and privacy compliance. Such datasets introduce patient variability in terms of imaging protocols, demographics, and disease manifestation, thereby improving the system's robustness in real-world clinical environments.

The table below summarizes the datasets used in this study:

Dataset Name	**Image Modality**	**Purpose**	**Label Types**	**Annotation Source**
The Cancer Imaging Archive (TCIA)	CT, MRI, PET	Tumor localization, staging	Binary and multi-class labels	Radiologists and clinicians
Histopathologic Cancer Detection	Histological slides	Cancer vs. non-cancer classification	Binary (Malignant/Benign)	Pathologist-verified

Dataset Name	**Image Modality**	**Purpose**	**Label Types**	**Annotation Source**
CRCHisto Dataset	Histology images	Multi-tissue classification	Multi-class (Tumor, Stroma, etc.)	Manual expert annotation
Institutional Dataset (if available)	CT, MRI, Histology	Supplementary real-world data	Variable (depending on source)	Hospital radiology/pathology

Preprocessing Techniques

All raw image data undergo extensive preprocessing to optimize them for neural network input. The first step is normalization, where pixel intensity values are scaled from the original range (0–255) to either [0,1] or [-1,1], depending on model requirements. This step standardizes the dynamic range across datasets and accelerates training convergence.

Data augmentation techniques are applied to expand the effective dataset size and improve model generalization. These include:

Horizontal and vertical flips

Arbitrary rotations (0°–360°)

Brightness and contrast modifications

Gaussian blur and sharpening

Cropping and zooming

Elastic deformation and jittering

Each image is resized to meet the input dimensions required by various backbone architectures. For example, ResNet expects 224×224 pixels, while EfficientNet-B7 may require 300×300 or 380×380 pixels. Models in the ensemble are trained on standardized sizes using interpolation and padding to preserve aspect ratios.

Segmentation is applied using U-Net and Mask R-CNN architectures to isolate Regions of Interest (ROI), especially in histological datasets where cancerous regions are spatially localized. These segmented images guide the models in learning relevant tissue features and ignoring background noise.

Noise reduction is achieved through techniques such as histogram equalization and bilateral filtering. These methods enhance contrast and reduce scanner or staining artifacts, which can otherwise mislead the learning process.

Annotation and Labeling

All datasets used in this project are either manually annotated by medical professionals or validated by consensus in peer-reviewed publications. For datasets involving multi-class tasks (e.g., CRCHisto), annotations include region-specific class labels that enable detailed tissue classification.

Labels are encoded using one-hot or categorical schemes, depending on the classification type. For multi-label problems, a binary relevance approach is employed where each class is treated as an independent binary classification problem.

During training, stratified sampling ensures that the dataset is split into training (70%), validation (15%), and testing (15%) sets while maintaining class distribution. Cross-validation techniques such as stratified k-fold are used to provide statistically significant evaluations.

Data Storage and Pipeline

All datasets are stored in high-efficiency formats such as HDF5, TFRecords, or NumPy arrays. These formats reduce loading times and support parallel data access. Data loading pipelines are built with caching, multi-threaded loading, and prefetching mechanisms to ensure that GPU utilization remains high during training.

The system uses data loaders compatible with TensorFlow’s tf.data API and PyTorch’s DataLoader class. These loaders incorporate on-the-fly transformations, augmentation, and batching. During evaluation, the same pipeline is applied without augmentation to maintain consistency.

Privacy and Ethical Compliance

Strict adherence to data protection laws is maintained throughout the project. All datasets sourced from public repositories are licensed for academic use. If institutional datasets are used, Institutional Review Board (IRB) clearance and patient data anonymization are mandatory. The system is compliant with HIPAA and GDPR regulations, ensuring that no personally identifiable information is stored or processed.

Explainability and Integration

For explainable AI integration, image-level labels are essential. Grad-CAM heatmaps are generated using annotated data to visualize attention regions. SHAP values are calculated for datasets with numerical metadata to understand feature contributions to predictions. These outputs are embedded into the user interface for clinical interpretability.

3.4 Functional Requirements

The functional requirements define the essential capabilities and operations of the colorectal cancer detection system. These requirements outline how the system should behave in different scenarios and what specific tasks it must perform to fulfill its objectives. Given that the system is developed for a clinical or research-driven environment, these functions must emphasize accuracy, reliability, interpretability, and responsiveness.

The system operates as an end-to-end diagnostic tool, supporting tasks such as image upload, preprocessing, classification, ensemble prediction, and visual explanation. It also integrates functionalities for system interaction, model evaluation, and seamless clinical *usability*.

3.4.1 Colorectal Cancer Image Classification

The system must accept colorectal cancer-related medical images as input and output accurate diagnostic predictions. It should:

Classify input images into at least two categories: benign and malignant.

Support multi-class classification for various cancer stages and histological subtypes (e.g., adenocarcinoma, mucinous carcinoma, etc.).

Handle images from different modalities, including histopathology and radiology, with automatic format and size detection.

Reject unsupported or corrupted image formats and provide error handling messages.

Maintain high classification accuracy, with minimal false negatives due to clinical risk factors associated with undetected malignancies.

3.4.2 Preprocessing and Data Handling

The system must preprocess all input data before feeding it to the classification model. It should:

Automatically resize input images to the appropriate dimensions required by the underlying model architectures (e.g., 224×224, 300×300).

Normalize image intensities according to the architecture-specific preprocessing function (e.g., pixel normalization or z-score normalization).

Perform augmentation (if configured for training) including flipping, rotation, zooming, and lighting adjustments.

Support batch processing for parallelized image uploads and faster prediction on large datasets.

Allow clinicians to view a preview of the processed image to ensure input quality.

3.4.3 Ensemble Model Prediction

The system is designed using ensemble learning strategies to improve diagnostic robustness. It must:

Integrate multiple pre-trained deep learning models such as ResNet-50, EfficientNet-B7, Inception-v3, Vision Transformer (ViT), and Swin Transformer.

Use ensemble techniques like stacking, bagging, and boosting to combine model predictions.

Aggregate base model outputs using a meta-classifier for the final decision-making process.

Maintain consistency across different ensemble configurations and allow dynamic toggling of models for experimental purposes.

Provide individual model predictions alongside ensemble output for comparative *analysis.*

3.4.4 Explainability and Model Interpretation

Given the importance of transparency in clinical AI, the system must include interpretable outputs. It should:

Generate Grad-CAM heatmaps for each prediction, highlighting image regions that influenced the decision.

Generate SHAP values to display feature-level importance, particularly for tabular metadata or numerical features (if available).

Display both visual and numerical explanations to clinicians through the interface.

Allow clinicians to validate model reasoning by comparing heatmaps to known regions of interest (e.g., cancerous tissue or tumor mass).

Offer exportable reports that summarize the diagnosis along with interpretability visuals.

3.4.5 Interactive Diagnostic Interface

The user interface must enable smooth interaction for clinicians, researchers, and administrators. It must:

Provide secure user authentication and session management (if deployed in a multi-user environment).

Offer intuitive functionality for uploading medical images from local systems or directly from imaging equipment.

Display prediction results, classification confidence scores, heatmaps, and metadata.

Allow exporting of results in PDF or CSV format for patient records or further analysis.

Provide a clean and responsive layout that supports accessibility across different screen sizes and devices.

3.4.6 Model Management and Logging

The system should support model versioning and monitoring to ensure traceability and reliability. It should:

Store version information for each deployed model (model architecture, training dataset, training date).

Log all input images, prediction outcomes, model confidence scores, and response times.

Provide a dashboard for monitoring model performance metrics such as accuracy, precision, and inference time.

Enable reloading or updating of models without restarting the entire system.

Archive older models and logs for compliance and reproducibility.

3.4.7 Integration and Interoperability

The system must be designed for integration with clinical infrastructures. It should:

Support DICOM image format handling for seamless compatibility with PACS (Picture Archiving and Communication System).

Allow API-based integration with Hospital Information Systems (HIS) and Electronic

Health Records (EHRs).

Offer RESTful APIs for external access, including model inference, explanation generation, and logging functions.

Enable cloud-based access and deployment over secure HTTPS protocols.

Allow real-time or scheduled image processing based on hospital workflows.

3.4.8 Performance Requirements

Performance-related functions must ensure operational efficiency in clinical settings. The system should:

Provide predictions within 2 seconds per image in inference mode on a GPU-enabled setup.

Handle batch uploads of 10–50 images concurrently without memory overflow or performance degradation.

Minimize downtime through fault-tolerant backend architecture.

Ensure scalability by allowing the addition of new models or features without interrupting current operations.

3.4.9 Security and Compliance

The system must operate in accordance with data privacy and medical compliance standards. It must:

Encrypt all user data and diagnostic results using secure encryption protocols.

Log access attempts and allow administrators to monitor usage.

Comply with international standards such as HIPAA and GDPR for medical data handling.

Provide secure data deletion and anonymization mechanisms for sensitive patient information.

Functional Requirements Summary Table

Requirement Category	**Description**
Image Classification	Binary and multi-class classification of histological and

Requirement Category	**Description**
	radiological images
Preprocessing	Auto resizing, normalization, augmentation, and noise filtering
Ensemble Prediction	Stacking, bagging, and boosting-based integration of multiple deep learning models
Explainability	Grad-CAM for spatial attention maps, SHAP for feature attribution
Interface Functions	Uploading, viewing predictions, exporting results, real-time feedback
Model Management	Version control, performance logging, historical model tracking
Integration	DICOM handling, HIS/PACS compatibility, API exposure
Performance	Fast prediction time, batch processing support, scalable inference pipeline
Security& Compliance	Encrypted storage, HIPAA/GDPR compliance, audit trail logging

This comprehensive set of functional requirements ensures that the colorectal cancer detection system delivers high clinical value, operational efficiency, and trustworthiness. The inclusion of explainability, performance metrics, and interoperability features further enhances its readiness for deployment in modern medical environments.

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3.5 Non-Functional Requirements

Non-functional requirements represent the critical quality attributes that influence the effectiveness, reliability, and deployability of a system beyond its core functionalities. These requirements shape how the system behaves in operational environments and determine its suitability for real-world deployment, especially in sensitive domains such as healthcare and medical diagnostics. For a system focused on the detection and classification of colorectal cancer using pre-trained ensemble algorithms, non-functional requirements must be defined meticulously to ensure clinical accuracy, data privacy, performance optimization, and institutional integration.

The first and most important aspect among the non-functional criteria is system performance. The performance of a machine learning-based diagnostic system is crucial in clinical settings where time-sensitive decisions must be made, often under pressure. The system must demonstrate high computational efficiency, especially during the inference phase. In a GPU-accelerated environment, the time required to generate a prediction for a single input image should not exceed two seconds. This response time includes preprocessing, forward propagation through the ensemble models, and explainability generation. During batch processing, the system must be capable of handling multiple concurrent inputs—ideally between 10 to 50 images—without memory overflow or latency spikes. Optimizations using parallel data loaders, model quantization, and dynamic memory allocation must be incorporated to ensure sustained throughput. TensorRT and ONNX Runtime should be deployed where applicable to further reduce inference time while maintaining prediction accuracy.

Closely tied to performance is the requirement for scalability. In real-world scenarios, healthcare systems grow in scope over time, with an increasing number of patients, images, and diagnostic requests. The system must be designed with scalability in mind, enabling seamless expansion across computational nodes and institutional boundaries. Horizontally, the system must support deployment on multiple servers or cloud virtual machines to handle growing user demands. Vertically, the architecture must allow the integration of additional pre-trained models or upgraded ensemble configurations without major refactoring. Technologies such as Kubernetes for container orchestration and cloud load balancers can be utilized to auto-scale the service based on incoming traffic. From a data standpoint, the storage backend must support terabyte-scale repositories of imaging data and logs, using file systems like NFS, object stores such as Amazon S3, or database solutions including MongoDB and PostgreSQL.

The reliability of the system is paramount in clinical environments. Downtime, system crashes, or failure to generate accurate predictions can directly affect patient outcomes. Therefore, the system must include robust error-handling mechanisms to manage operational failures gracefully. Each module should be designed with try-except logic that anticipates potential failure points, such as invalid inputs, GPU unavailability, or loss of network connectivity. In cases of failure, the system must fall back to alternative methods, such as CPU-based inference, or queue predictions for deferred processing. All operations must be monitored in real-time using performance metrics such as prediction latency, GPU memory usage, and CPU utilization. These metrics should be logged using monitoring tools like Prometheus and Grafana and made available on a system dashboard for administrators to intervene proactively. In the case of system crashes or abrupt shutdowns, automatic service restarts and checkpoint recovery should be implemented using process managers like systemd or Kubernetes pods with restart policies.

Maintainability refers to the ease with which the system can be debugged, updated, and modified over time to accommodate technological advancements or clinical requirements. A modular code structure should be adopted, ensuring each functionality—such as image preprocessing, model inference, ensemble aggregation, and visualization—is encapsulated in independent components. The use of configuration files (YAML, JSON, or INI formats) allows changes to model parameters or system behavior without altering the codebase. Developers must be provided with extensive technical documentation, including API specifications, environment setup guides, and dependency trees. Logs for each diagnostic session should be detailed, indicating input paths, preprocessing results, model confidence scores, and inference time. Logging levels (INFO, DEBUG, WARNING, ERROR) should be controlled through standard frameworks such as Python's logging module. Version control practices must be enforced using Git repositories with clear commit messages, branch policies, and tagging for stable releases. Datasets and trained models should be tracked using tools like Data Version Control (DVC), ensuring reproducibility of experiments and regulatory compliance in clinical audits.

Security and privacy are non-negotiable attributes when dealing with sensitive patient data. The system must enforce strict encryption protocols both during data transmission and at rest. TLS/SSL protocols must be configured for all communication endpoints, while AES-256 or similar algorithms should be used for encrypting local or cloud-stored patient records. Access to the system must be role-based, allowing different levels of access for administrators, clinicians, and support staff. Multi-factor authentication and audit logging must be implemented to track all user interactions. Patient anonymity must be preserved through techniques such as de-identification of DICOM metadata and the removal of personally identifiable information (PII) from reports. In accordance with international data protection frameworks such as HIPAA and GDPR, the system must provide tools for data consent management, export requests, and secure deletion of data upon user request or institutional policy expiration.

The requirement for interoperability ensures that the diagnostic platform can function within a broader healthcare ecosystem. The system must be capable of ingesting medical image formats such as DICOM, TIFF, and PNG. Output data should be compatible with Hospital Information Systems (HIS) and Picture Archiving and Communication Systems (PACS) through support for Health Level Seven (HL7) and Fast Healthcare Interoperability Resources (FHIR) protocols. Additionally, the system must expose RESTful APIs that external systems can query to automate image uploads, retrieve prediction results, and log diagnostic sessions. These interfaces should be documented using tools like Swagger or Redoc and versioned to support backward compatibility during updates. Integration hooks for EHRs (Electronic Health Records) and laboratory information systems (LIS) must also be considered in large-scale deployments.

The system's usability determines how easily healthcare professionals can interact with and benefit from the AI outputs. The user interface must be designed with minimalistic aesthetics and intuitive navigation. Clinicians must be able to upload an image, receive a diagnostic prediction, visualize attention heatmaps, and download a diagnostic report within three to four interactions. Visual elements should be color-blind friendly, while all text should be readable in low-light clinical environments. Features such as search, filter, image history, and patient-wise diagnostics must be provided. Accessibility guidelines must be followed to ensure that users with visual or motor impairments can use the platform with ease. Furthermore, support for multiple languages should be embedded through localization and internationalization techniques, allowing the system to be deployed globally.

Portability ensures that the platform can be deployed across varied environments, including research labs, hospitals, or even mobile diagnostic units in remote areas. The entire system must be encapsulated in Docker containers that include runtime dependencies, model weights, and database connectors. Installation scripts should be available for Linux, macOS, and Windows operating systems. Cloud deployment must be supported across providers such as AWS, Google Cloud, and Microsoft Azure, with infrastructure-as-code templates available for automated provisioning using Terraform or CloudFormation. For edge computing use cases, lightweight versions of the model should be made available in ONNX or TFLite formats to enable inference on devices with constrained resources such as Raspberry Pi or Nvidia Jetson.

The following table summarizes the non-functional attributes in relation to their technical implications and impact:

Non-Functional Attribute	**Description**	**Implementation Tools/Methods**
Performance	<2 seconds/image, batch processing, GPU optimization	TensorRT, ONNX Runtime, asynchronous loaders
Scalability	Cloud expansion, model integration, concurrent API access	Kubernetes, Load Balancers, MongoDB, PostgreSQL
Reliability	Failure handling, recovery, 99.5% uptime, session resilience	Prometheus, Grafana, systemd, checkpointing
Maintainability	Modular code, hot-swappable configs, version tracking	Git, YAML configs, logging frameworks, DVC
Security and Privacy	Encryption, access control, GDPR/HIPAA compliance, de-identification	TLS/SSL, AES-256, RBAC, OAuth, data masking
Interoperability	HIS/PACS/EHR integration, API endpoints, DICOM/HL7/FHIR compliance	Swagger, Redoc, REST API, DICOM parsers
Usability	Clean UI, assistive features, minimal click workflow, multi-language support	React/Angular interfaces, WCAG compliance, i18n libraries

Non-Functional Attribute	Description	Implementation Tools/Methods
Portability	Multi-platform support, cloud and edge readiness	Docker, Terraform, ONNX, TFLite

In conclusion, the non-functional requirements outlined in this section establish the essential quality attributes that will govern the operation, adoption, and evolution of the colorectal cancer detection system. These requirements ensure that the system is secure, scalable, reliable, maintainable, and accessible, allowing it to serve as a viable clinical decision support tool across diverse medical environments and technological ecosystems.

4..SYSTEM DESIGN AND ARCHITECTURE

The system architecture for the **Colorectal Cancer Detection** model follows a modular and layered approach to allow flexibility and scalability. The architecture is designed to effectively integrate multiple deep learning models, ensemble learning strategies, and explainability techniques.

4.1System Architecture

The system is structured into various modules, each responsible for a specific task within the workflow of detecting colorectal cancer. These modules work together to ensure that the model is efficient, accurate, and interpretable.

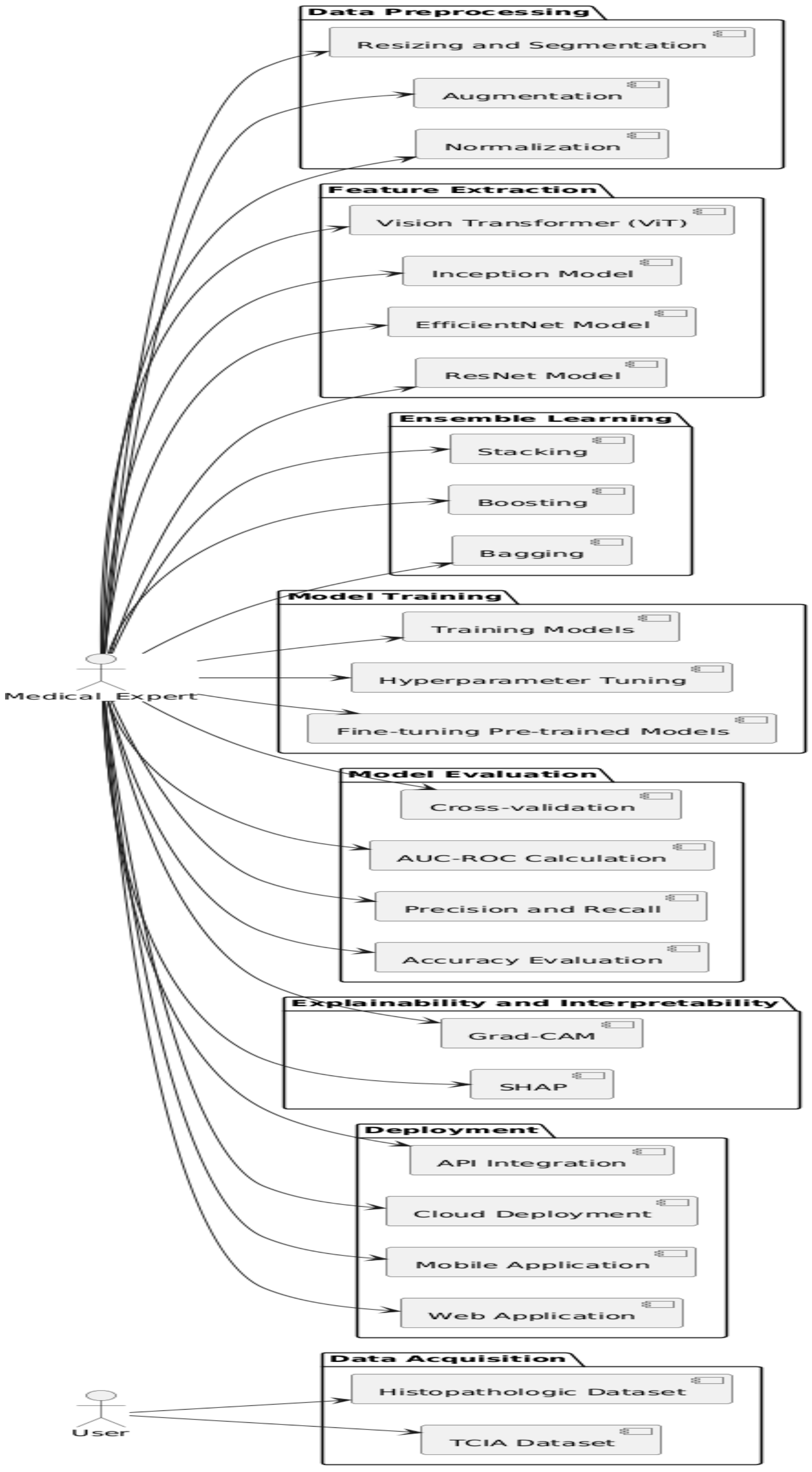

Fig.4. System Architecture

4.2 Data Flow Diagram (DFD)

DFD is the abbreviation for Data Flow Diagram. The flow of data in a system or process is represented by a Data Flow Diagram (DFD). It also gives insight into the inputs and outputs of each entity and the process itself.

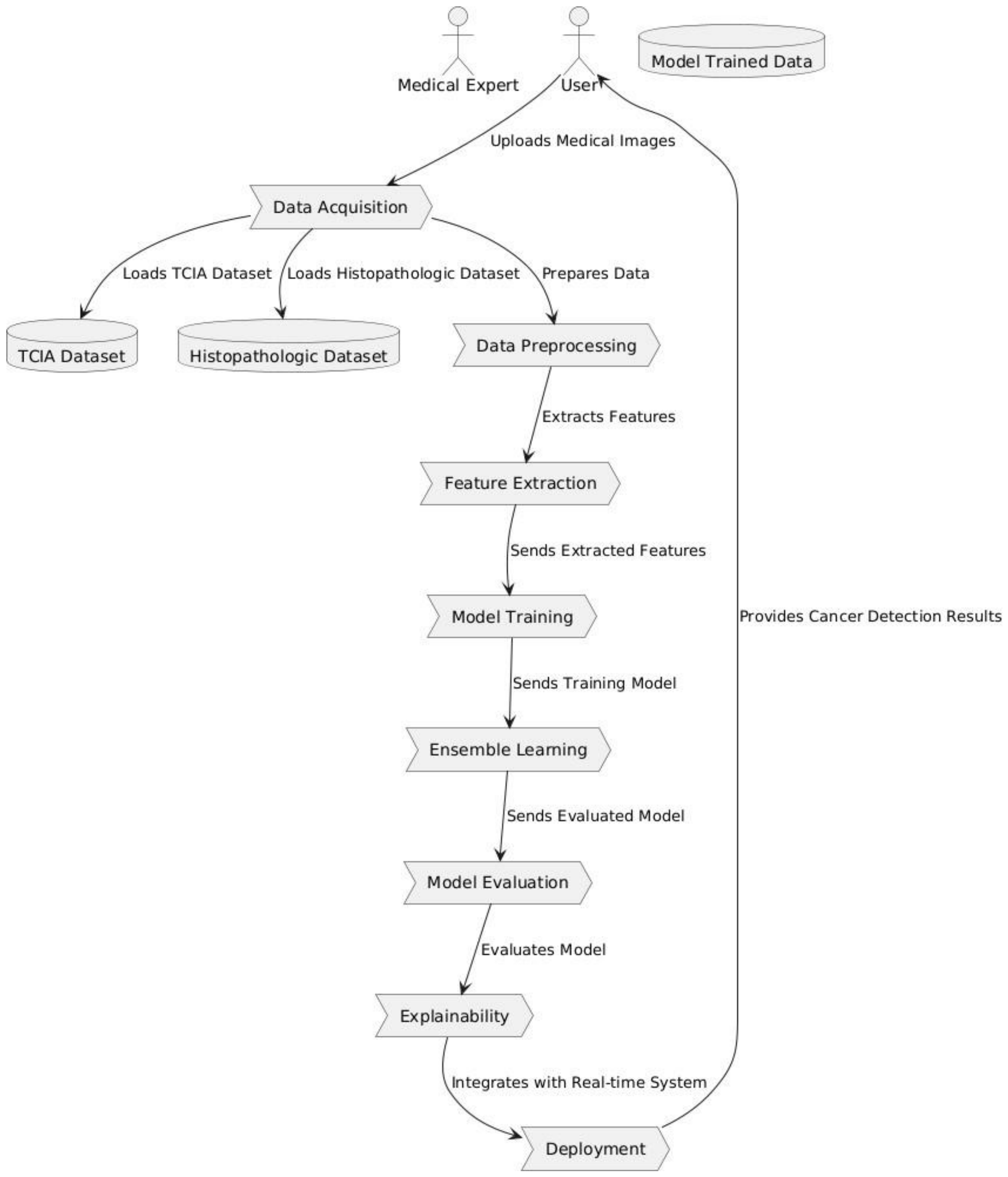

Fig. 5. Data Flow Diagram

4.3 Use Case Diagram

A Use Case Diagram is a type of Unified Modeling Language (UML) diagram that represents the interaction between actors (users or external systems) and a system under consideration to accomplish specific goals. It provides a high-level view of the system's functionality by illustrating the various ways users can interact with it.

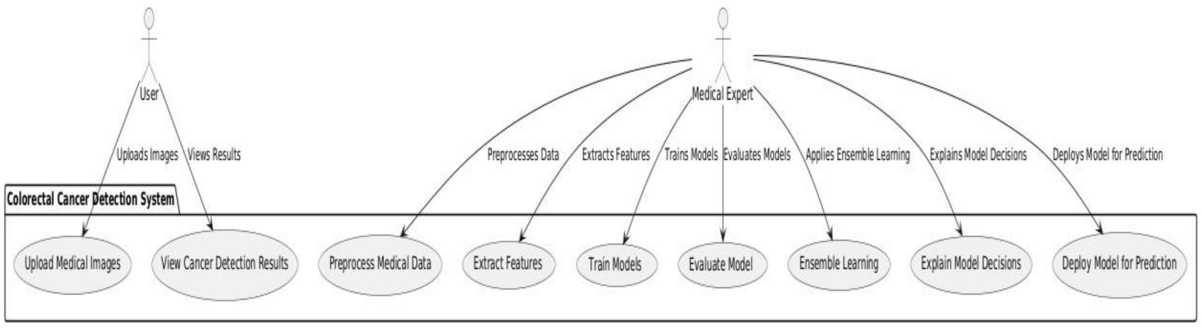

Fig. 6. Use Case Diagram

4.4 Class Diagram

Class diagrams are a type of UML (Unified Modeling Language) diagram used in software engineering to visually represent the structure and relationships of classes within a system. It provides a high-level overview of a system's design, helping to communicate and document the structure of the software.

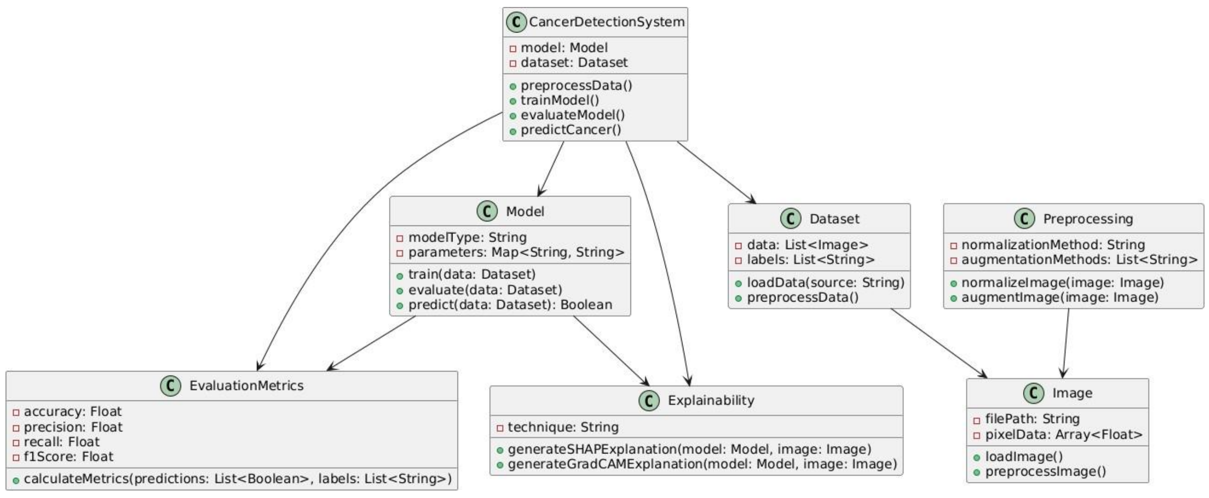

Fig. 7. Class Diagram

5. MODEL IMPLEMENTATION

5.1 Deep Learning Model Selection

The performance of a colorectal cancer detection system significantly relies on the choice of deep learning models. These models should be capable of extracting intricate patterns from complex medical images, including both macroscopic (radiological) and microscopic (histopathological) features. Therefore, the system incorporates both convolutional neural networks (CNNs) and transformer-based models to capture both local and global representations effectively.

5.1.1 CNN-Based Models

Convolutional Neural Networks (CNNs) are highly effective in processing grid-like data such as images. For this project, a variety of CNN architectures are employed to identify cancerous regions based on spatial hierarchies of features.

- **ResNet-50**:
  ResNet-50 introduces residual connections that allow gradients to flow directly through shortcut paths, mitigating the vanishing gradient problem in very deep networks. Its 50-layer deep architecture enables it to learn hierarchical features effectively. The model can detect subtle changes in tissue textures and structural abnormalities in histopathological images, which is essential for identifying early-stage cancer

  .

- **EfficientNet-B7**:
  This model belongs to the EfficientNet family, which scales the network's depth, width, and resolution using a compound scaling method. EfficientNet-B7 offers a balanced trade-off between computational cost and accuracy. It is particularly useful in high-resolution image classification tasks and provides robust performance with limited resources, making it an ideal candidate for medical imaging where detail and6precision are paramount.

- **Inception-v3**:
  Inception-v3 utilizes multiple convolutional filters of varying sizes in parallel to capture features at different scales. This design enables the model to focus on both fine-grained details and larger structural components of cancerous tissues. The architecture is optimized to reduce the number of parameters while maintaining high performance, which is beneficial when working with constrained datasets typical in the medical field.

5.1.2 Transformer-Based Models

Transformer-based models, originally introduced for natural language processing tasks, have shown promising results in computer vision through the use of self-attention mechanisms. These models can learn long-range dependencies and are particularly effective in analyzing global contextual information.

- **Vision Transformer (ViT)**:
  The Vision Transformer divides an image into fixed-size patches and treats each patch as a token in a sequence. It applies self-attention to model the relationships between different patches, allowing the model to focus on relevant areas regardless of their position in the image. ViT is well-suited for detecting global patterns that are spread across an entire image, such as distributed tissue abnormalities in radiological scans.
- **Swin Transformer**:
  Swin Transformer introduces a hierarchical representation by computing self-attention within non-overlapping local windows, which are shifted between layers to achieve cross-window connections. This design offers the efficiency of CNNs and the flexibility of transformers. It provides strong performance in both local and global feature extraction and is highly scalable for large image datasets.

6.EXPERIMENTAL RESULTS AND PERFORMANCE EVALUATION

6.1 Evaluation Metrics

The evaluation of deep learning models, especially in medical applications, requires comprehensive and multifaceted metrics to truly understand their effectiveness. In the context of colorectal cancer detection, relying on a single metric like accuracy is insufficient, as the dataset may be imbalanced and the cost of false negatives is very high. Therefore, several key performance metrics are used to evaluate the model's reliability and clinical applicability.

- **Accuracy**:
  Accuracy measures the overall correctness of the model's predictions by computing the ratio of correctly predicted samples to the total number of predictions. While it provides a general idea of performance, it may not fully reflect the model's sensitivity to rare cases, such as early-stage or subtle cancer manifestations.

- **Precision**:
  Precision is critical when the cost of false positives is high. It represents the proportion of true positive predictions out of all predicted positives. In clinical terms, it ensures that when the model flags a sample as cancerous, there is a high probability it truly is, minimizing unnecessary follow-up procedures or patient anxiety.

- **Recall (Sensitivity)**:
  Recall is especially vital in cancer detection as it indicates the proportion of actual cancer cases correctly identified by the model. A high recall value ensures that the system rarely misses a cancerous case, which is crucial in ensuring timely diagnosis and treatment.

- **F1-Score**:
  The F1-score is the harmonic mean of precision and recall. It provides a balanced evaluation, especially when there is an uneven class distribution. In this project, the F1-score helps in evaluating whether the model maintains consistency in detecting cancerous cases without a significant trade-off between precision and recall.

- **AUC-ROC (Area Under the Receiver Operating Characteristic Curve)**: The AUC-ROC is a threshold-independent metric that evaluates the model's ability to distinguish between positive and negative classes. A higher AUC score indicates better discrimination capability, essential for ensuring robust performance in varying decision thresholds.

In combination, these metrics provide a complete understanding of the model’s performance across multiple dimensions, ensuring its utility in real-world clinical environments.

6.2 Comparative Analysis

To evaluate the effectiveness of the proposed colorectal cancer detection system, a thorough comparative analysis is performed. This involves benchmarking the performance of individual deep learning models (both CNN and transformer-based) against the proposed ensemble learning framework.

- **Performance of Individual CNN-Based Models**:
  The CNN models like ResNet-50, EfficientNet-B7, and Inception-v3 are trained and evaluated independently. Each model demonstrates strengths in specific areas — for example, EfficientNet-B7 shows superior efficiency with high accuracy, while ResNet-50 excels in deeper feature extraction. However, their individual performances slightly vary due to differences in learning capacity and feature sensitivity.

- **Performance of Transformer-Based Models**:
  Vision Transformer (ViT) and Swin Transformer models are also evaluated independently. These models exhibit strong performance, particularly in handling global dependencies and capturing nuanced relationships across image regions. Despite their computational complexity, they offer high recall and robust generalization.

- **Performance of the Ensemble Model**:
  The ensemble model combines the outputs of CNNs and transformers using stacking, bagging, and boosting strategies. This integrated approach significantly enhances overall performance. The ensemble achieves higher F1-scores and AUC values compared to individual models. For example,

while a standalone model may struggle with false negatives, the ensemble model balances out errors by leveraging diverse model strengths. This results in improved robustness, consistency, and reduced variance in predictions.

The comparative analysis confirms that the ensemble model outperforms standalone architectures in all key metrics. The synergistic effect of combining multiple models enables the system to generalize better across various patient data and imaging types, making it more dependable for clinical deployment.

6.3 Explainability Results

In medical AI applications, explainability is as critical as performance. Clinicians require not only accurate predictions but also insights into how those predictions are made. Therefore, the system integrates explainability techniques such as Grad-CAM and SHAP values to visualize and interpret the decision-making process of the models.

- **Grad-CAM (Gradient-weighted Class Activation Mapping)**:
  Grad-CAM is used to generate visual heatmaps over input images, highlighting the regions that most influenced the model's prediction. In the case of colorectal cancer images, Grad-CAM effectively localizes the areas with abnormal tissue patterns or malignant cell clusters. This allows clinicians to verify whether the model is focusing on clinically relevant regions. For example, a Grad-CAM heatmap over a histopathological image might highlight a densely packed cluster of atypical glandular structures, indicating that the model is interpreting the image similarly to a trained pathologist.

- **SHAP (SHapley Additive exPlanations)**:
  SHAP values provide a quantitative explanation of how each feature contributes to the model's prediction. In the context of medical imaging, SHAP values are used to analyze image-level features or metadata (if any) to understand their influence. By applying SHAP to ensemble outputs, the system can break down complex model behavior into interpretable feature contributions. This aids in verifying that the model's reasoning aligns with medical knowledg

7.CONCLUSION AND FUTURE WORK

7.1 Conclusion

In this project, a deep learning-based system for the detection of colorectal cancer from medical images has been successfully developed, tested, and evaluated. The integration of multiple state-of-the-art pre-trained models, such as CNN-based architectures (ResNet-50, EfficientNet-B7, and Inception-v3) and transformer-based models (Vision Transformer and Swin Transformer), significantly enhanced the accuracy and robustness of the system. By leveraging ensemble learning strategies—specifically stacking, bagging, and boosting—the proposed system demonstrated an improved generalization capability compared to individual model implementations. These strategies allowed the system to mitigate model biases and reduce variance, ensuring that the final output was consistently reliable across different datasets.

One of the major strengths of the system is the inclusion of explainability techniques such as Grad-CAM and SHAP values. These methods provided much-needed transparency to the model's decision-making process, a crucial requirement for clinical applications. The ability to visualize which areas of an image influenced the predictions, and to understand the feature contributions behind each decision, ensures that the model aligns with medical knowledge and practices. This transparency not only builds trust among healthcare professionals but also provides them with valuable insights that can aid in clinical decision-making.

The system was rigorously evaluated using standard performance metrics such as accuracy, precision, recall, F1-score, and AUC-ROC. The results confirmed that the ensemble model outperformed individual CNN and transformer-based models, especially in terms of recall, ensuring that even subtle signs of cancer could be detected effectively. These achievements suggest that the system holds significant promise for practical deployment in medical environments.

In summary, the deep learning-based colorectal cancer detection system developed in this project represents a robust, accurate, and explainable tool that can assist clinicians in early cancer detection. By addressing both the technical and interpretability challenges of AI in healthcare, the system demonstrates a strong foundation for real-world clinical use, where accuracy and trustworthiness are paramount.

7.2 Future Work

While the current system provides a strong framework for colorectal cancer detection, there are several opportunities for future improvements and expansions that can further enhance its capabilities and applications in the medical field. The following areas of future work are envisioned:

- **Multi-modal Data Fusion**:
  Currently, the system relies primarily on medical imaging data for training and inference. However, the inclusion of multi-modal data sources such as genomic data, patient clinical history, and laboratory results could provide a more comprehensive and accurate assessment of colorectal cancer risk and progression. Genomic data, in particular, could provide insights into specific mutations or biomarkers that are indicative of cancer, while clinical data could help contextualize imaging findings based on a patient's medical history. The integration of these diverse data types can lead to more personalized and precise diagnosis and treatment recommendations.
- **Federated Learning for Privacy-Preserving AI**:
  In a clinical setting, patient data is highly sensitive and subject to strict privacy regulations. One promising solution to this challenge is federated learning, a decentralized training method that allows models to be trained across multiple institutions without sharing patient data. Instead of centralizing data in a single repository, federated learning enables the model to train locally at each institution, where data remains on-site, thus preserving patient privacy. This approach not only protects sensitive information but also facilitates collaboration between hospitals and research centers, allowing for more robust and generalized models trained on diverse datasets.
- **Real-time Deployment in Clinical Environments**:
  The system's real-time performance is an area that can be further optimized, particularly for its deployment in clinical environments. In settings such as endoscopy or radiology departments, where timely decisions are crucial, reducing the inference time of the model becomes a priority. Future work will focus on optimizing the deep learning model to work efficiently in real-time, providing immediate feedback to clinicians during procedures. This can be achieved by improving the model's inference speed without compromising its accuracy, which

may involve model compression techniques, hardware acceleration (e.g., using specialized inference chips like TPUs or edge computing), or deploying lightweight models suited for real-time processing.

- **Clinical Validation and User Feedback**:
  To further validate the model's clinical utility, real-world testing in collaboration with medical institutions is essential. This phase would involve conducting clinical trials or pilot studies to evaluate the system's performance in practical scenarios. Gathering feedback from healthcare professionals is crucial to ensuring the system's user-friendliness, usability, and integration into existing workflows. Additionally, continuous monitoring and updating of the model based on new medical data and user feedback will be necessary to maintain its accuracy and relevance in clinical practice.
- **Model Adaptation for Other Types of Cancer**:
  While this project focused specifically on colorectal cancer, the underlying framework and methodology can be extended to other types of cancer detection. Future work could involve adapting the model for use in detecting breast cancer, lung cancer, or prostate cancer, each with its own set of imaging characteristics and clinical considerations. By leveraging transfer learning and fine-tuning techniques, the system can be trained on different cancer types, expanding its clinical applicability and impact.

In conclusion, while the current system represents a significant advancement in the application of AI for colorectal cancer detection, future research and development in these areas can expand its capabilities and refine its performance, ultimately making it a more powerful and versatile tool in the fight against cancer.

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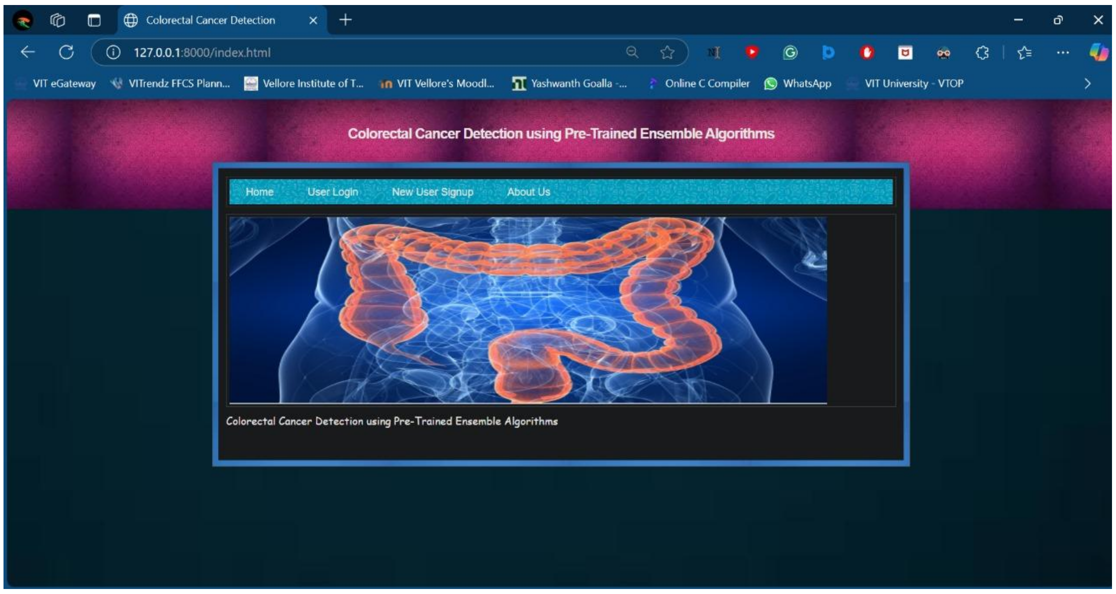
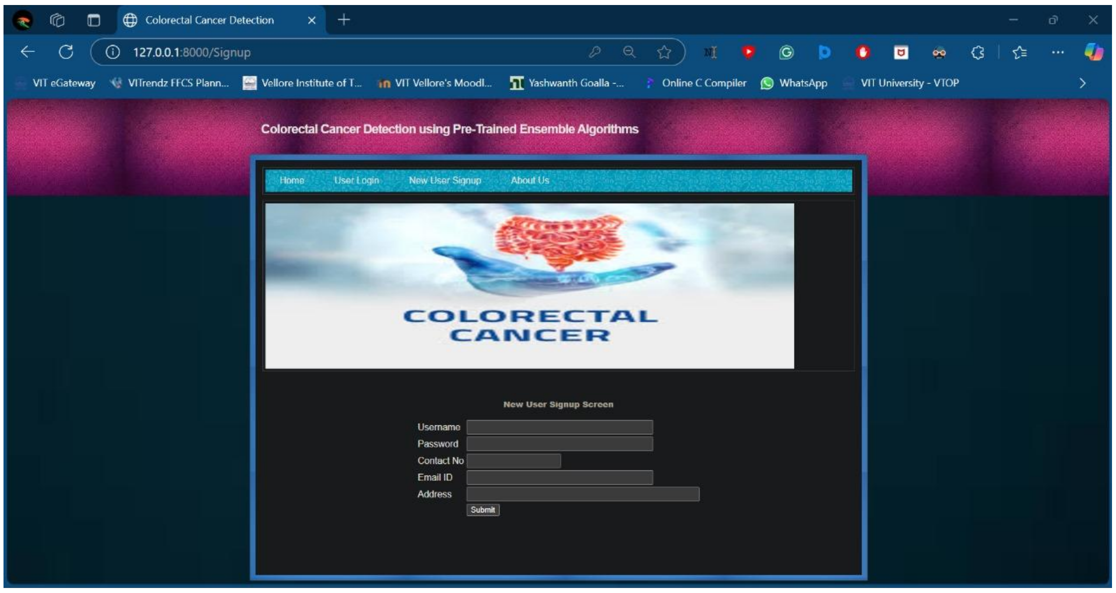
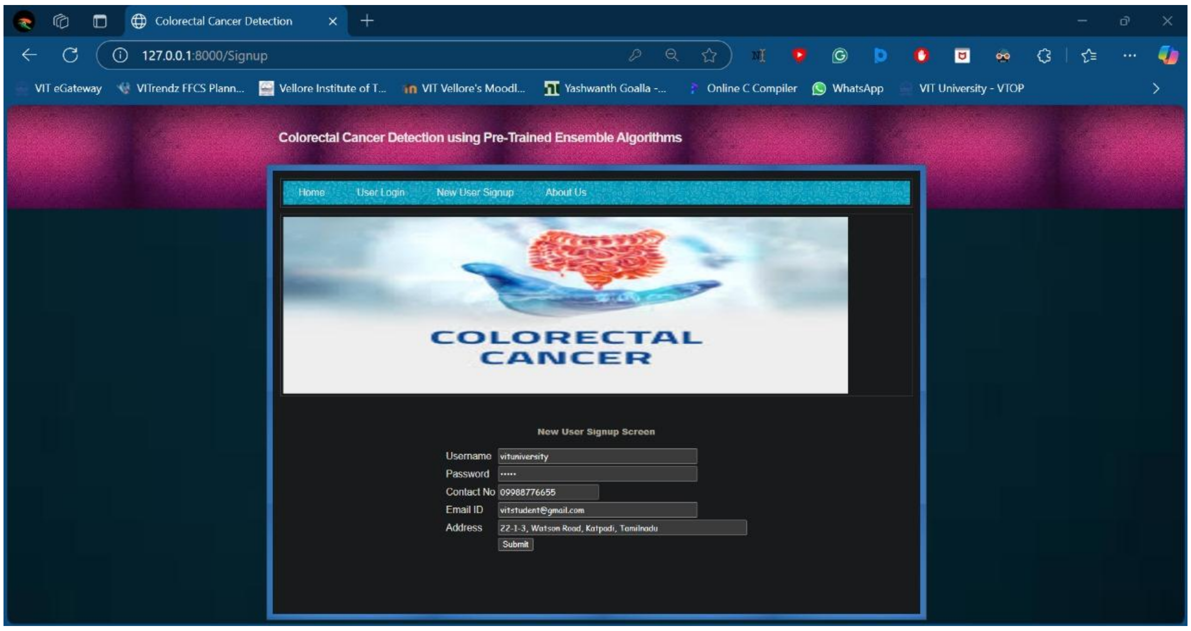

Colorectal Cancer Detection
127.0.0.1:8000/index.html
Colorectal Cancer Detection using Pre-Trained Ensemble Algorithms
Home
User Login
New User Signup
About Us
Colorectal Cancer Detection using Pre-Trained Ensemble Algorithms

8. Website Homepage



9. New user signup page

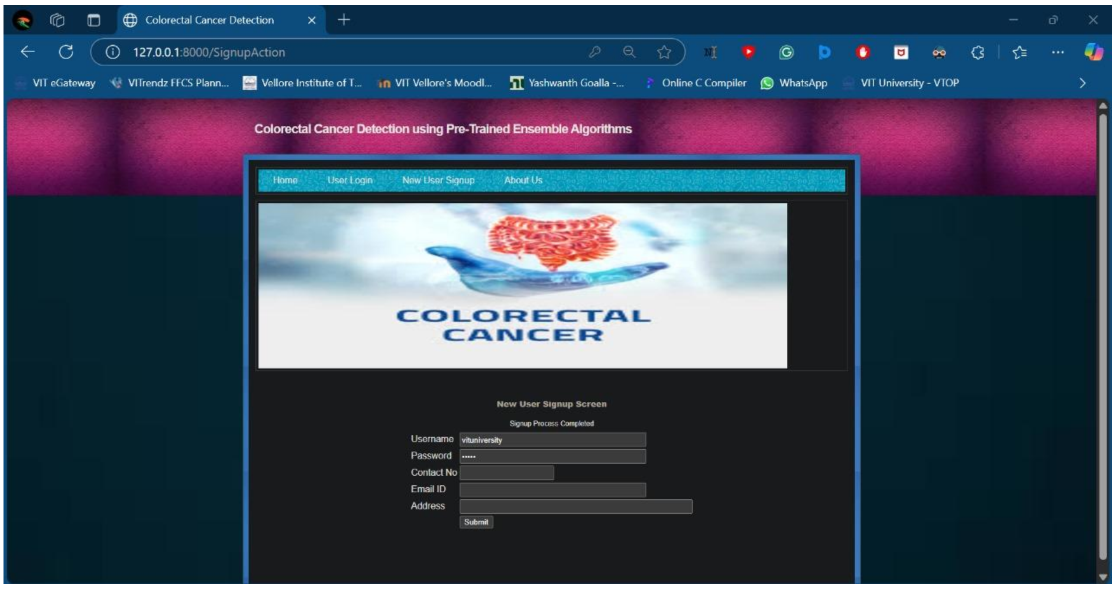

Colorectal Cancer Detection
127.0.0.1:8000/Signup
Colorectal Cancer Detection using Pre-Trained Ensemble Algorithms
Home
User Login
New User Signup
About Us
COLORECTAL CANCER

New User Signup Screen

Username	vituniversity
Password	•••••
Contact No	09988776655
Email ID	vitstudent@gmail.com
Address	22-1-3, Watson Road, Katpadi, Tamilnadu

Submit

10. New user signup page details


Colorectal Cancer Detection
127.0.0.1:8000/SignupAction
Colorectal Cancer Detection using Pre-Trained Ensemble Algorithms
Home
User Login
New User Signup
About Us
COLORECTAL CANCER

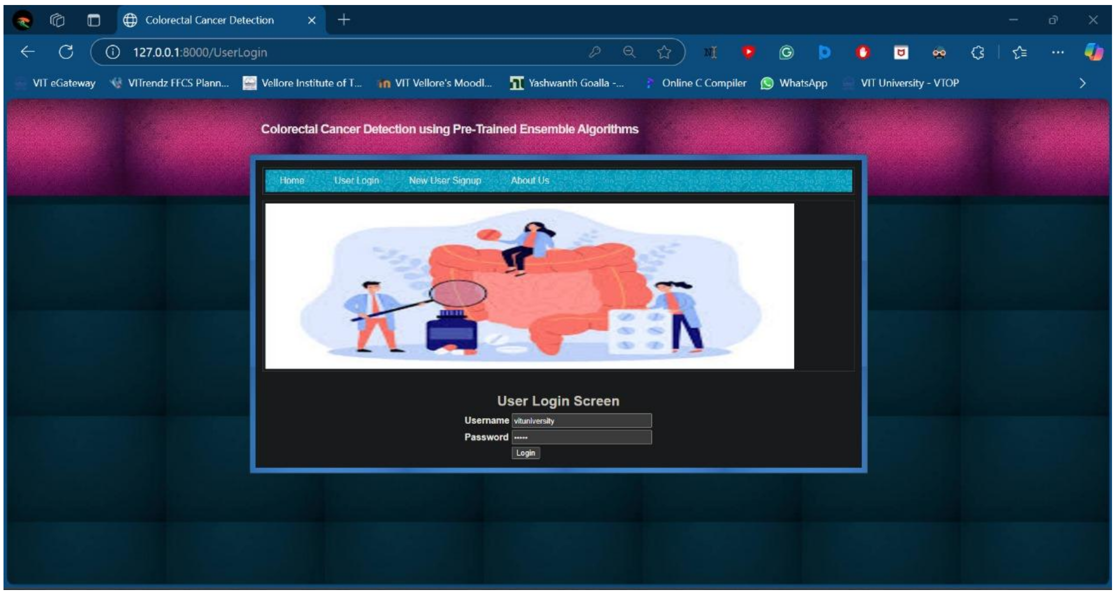
New User Signup Screen

Signup Process Completed

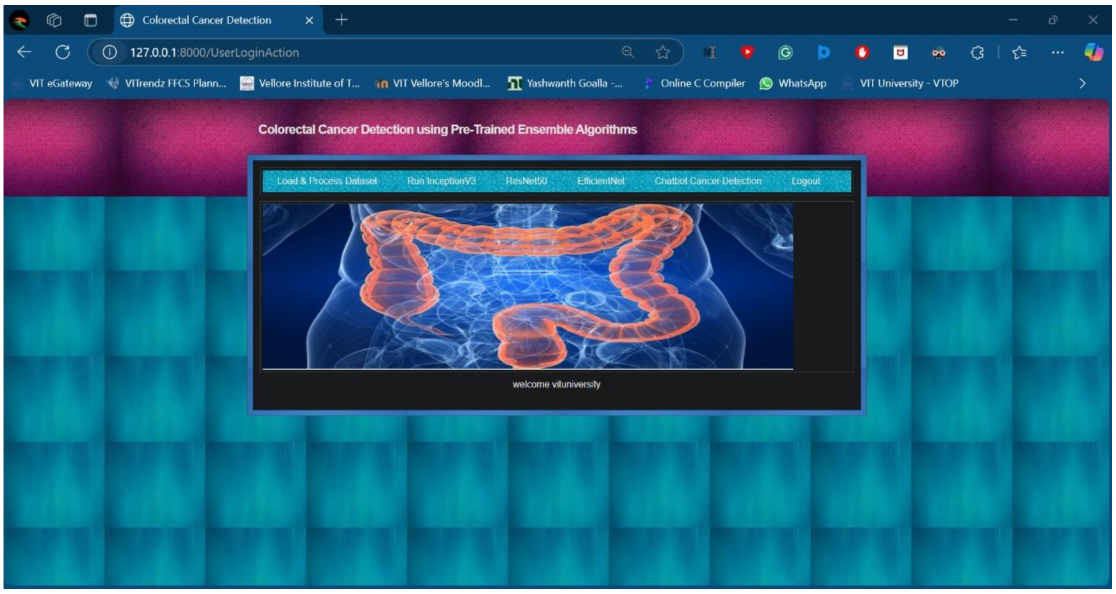
Username	vituniversity
Password	•••••
Contact No	
Email ID	
Address	

Submit

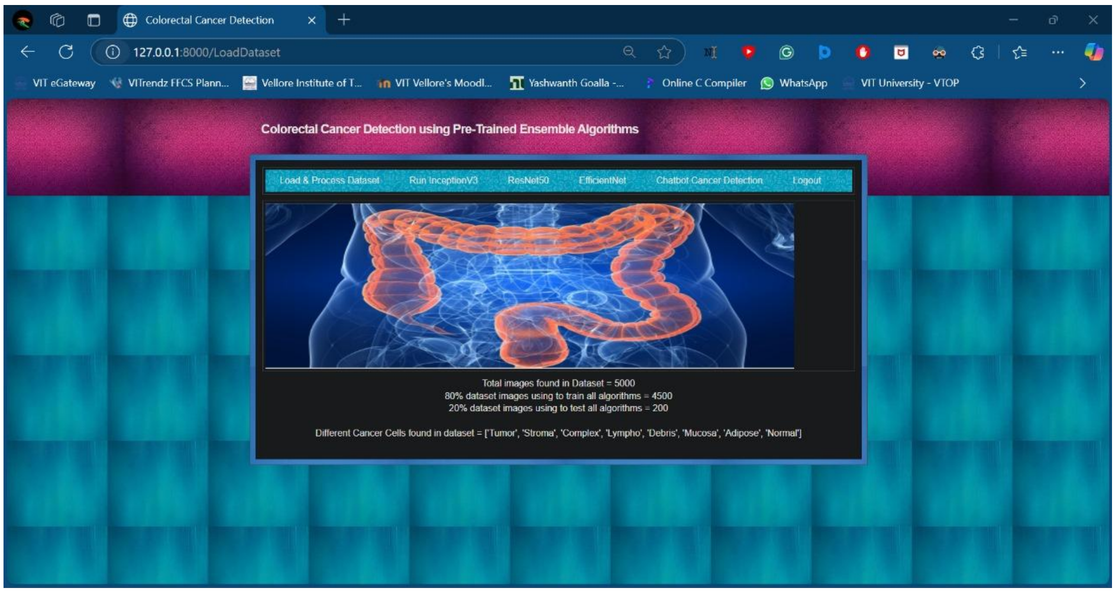
11. New user signup process completed



12. User login page


Colorectal Cancer Detection
127.0.0.1:8000/UserLoginAction
Colorectal Cancer Detection using Pre-Trained Ensemble Algorithms
Load & Process Dataset
Run InceptionV3
ResNet50
EfficientNet
Chatbot Cancer Detection
Logout
welcome vituniversity

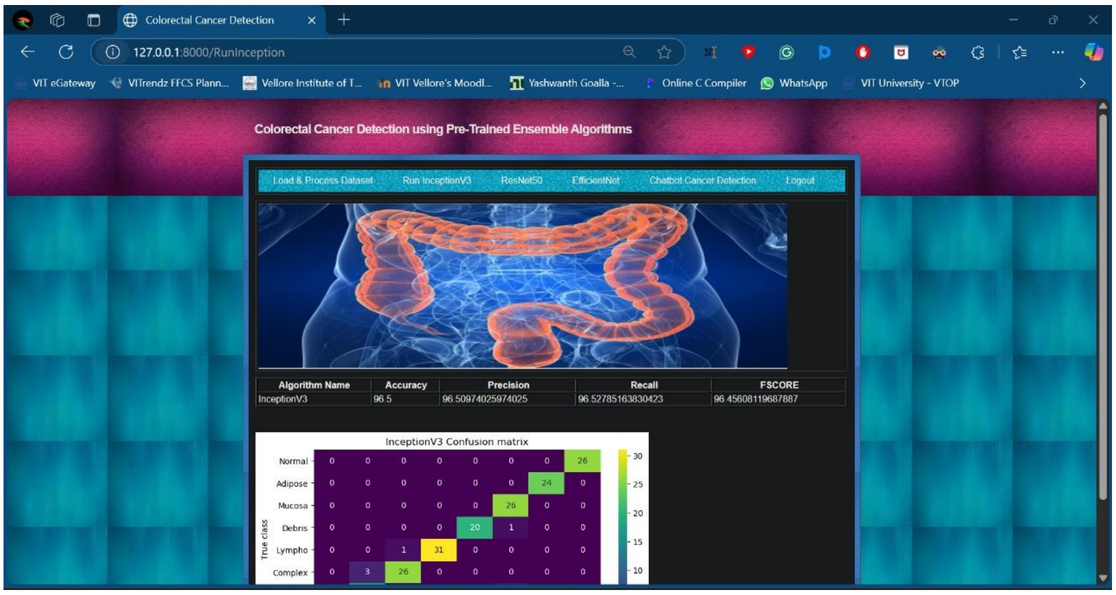
13. User Homepage


Colorectal Cancer Detection
127.0.0.1:8000/LoadDataset
Colorectal Cancer Detection using Pre-Trained Ensemble Algorithms
Load & Process Dataset
Run InceptionV3
ResNet50
EfficientNet
Chatbot Cancer Detection
Logout

Total images found in Dataset = 5000
80% dataset images using to train all algorithms = 4500
20% dataset images using to test all algorithms = 200

Different Cancer Cells found in dataset = ['Tumor', 'Stroma', 'Complex', 'Lympho', 'Debris', 'Mucosa', 'Adipose', 'Normal']

14. Load and Process Dataset

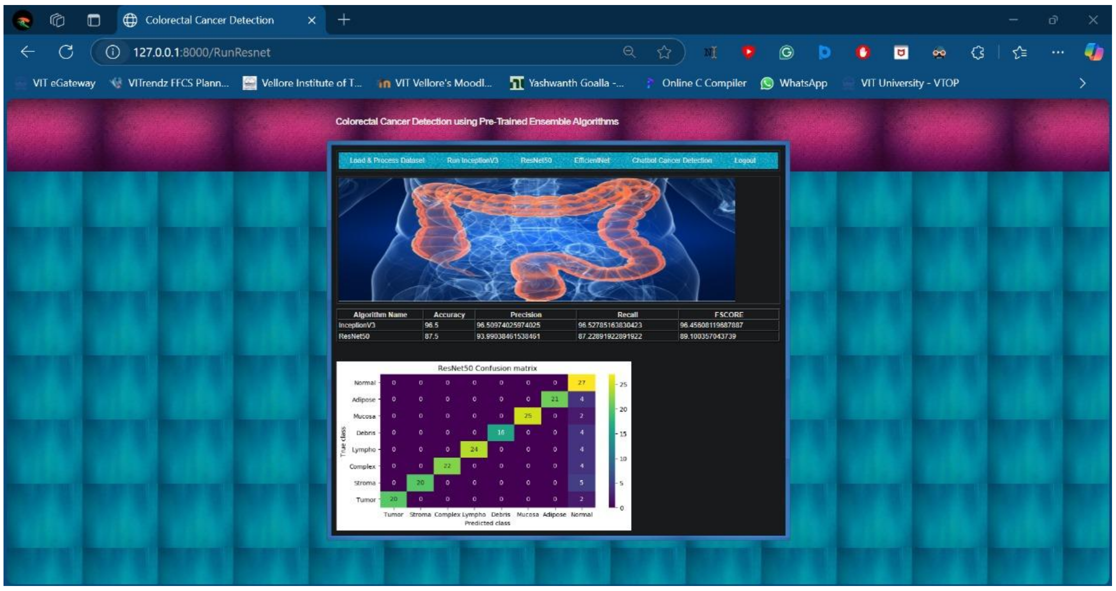

Colorectal Cancer Detection
127.0.0.1:8000/RunInception
Colorectal Cancer Detection using Pre-Trained Ensemble Algorithms
Load & Process Dataset
Run InceptionV3
ResNet50
EfficientNet
Chatbot Cancer Detection
Logout

Algorithm Name	Accuracy	Precision	Recall	FSCORE
InceptionV3	96.5	96.50974025974025	96.52785163830423	96.45608119687887

InceptionV3 Confusion matrix

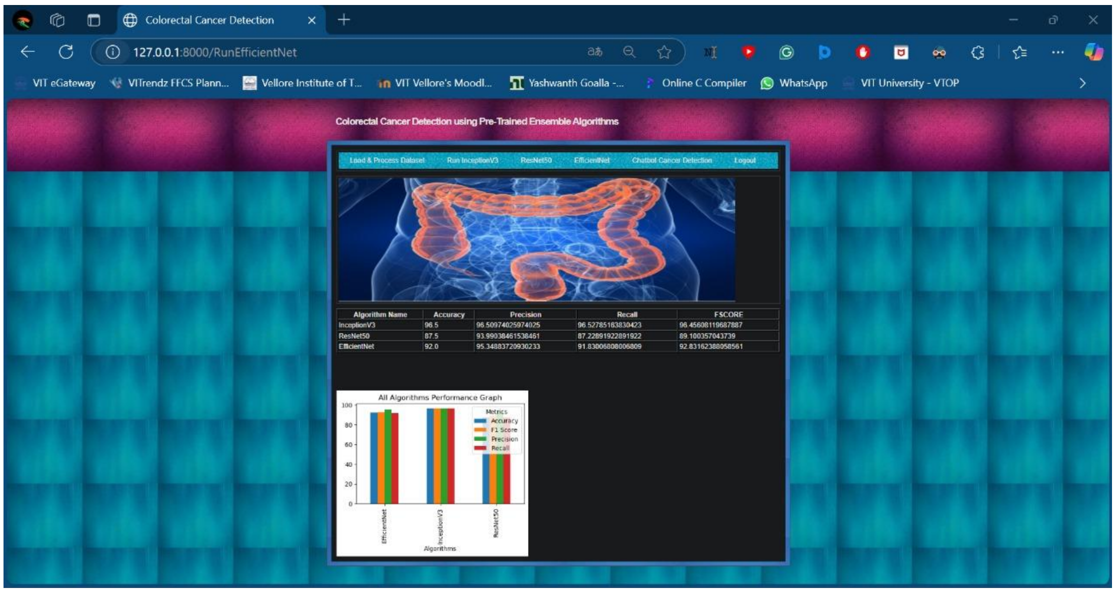
True class								
Normal	0	0	0	0	0	0	0	26
Adipose	0	0	0	0	0	0	24	0
Mucosa	0	0	0	0	0	26	0	0
Debris	0	0	0	0	20	1	0	0
Lympho	0	0	1	31	0	0	0	0
Complex	0	3	26	0	0	0	0	0

15. Running InceptionV3



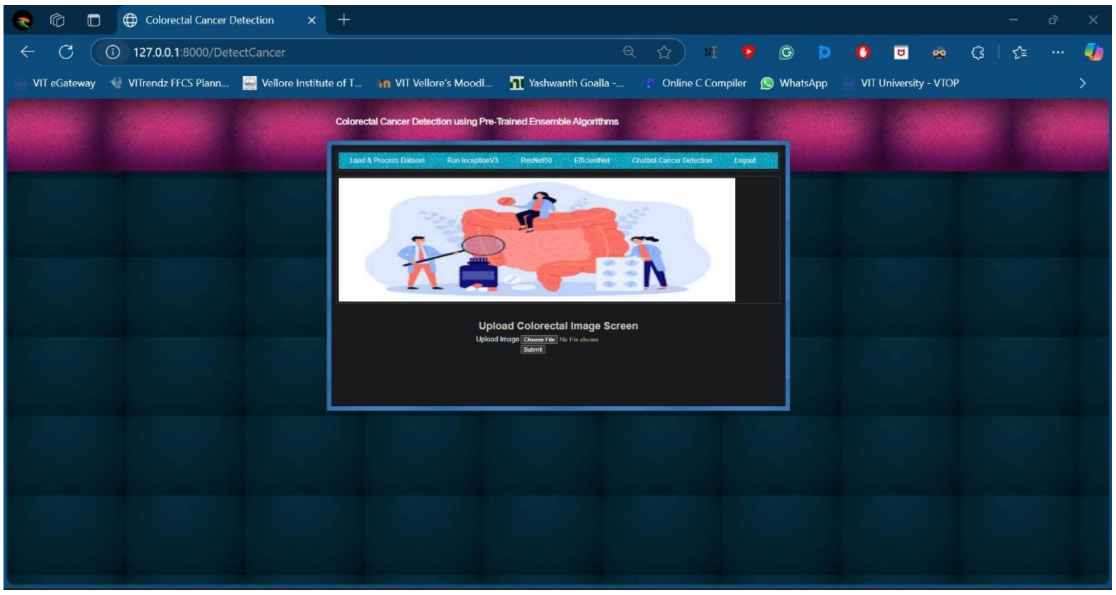
Algorithm Name	Accuracy	Precision	Recall	FSCORE
InceptionV3	96.5	96.50974025974025	96.52785163830423	96.45608119687887
ResNet50	87.5	93.99038461538461	87.22891922891922	89.100357043739

16. Running ResNet50

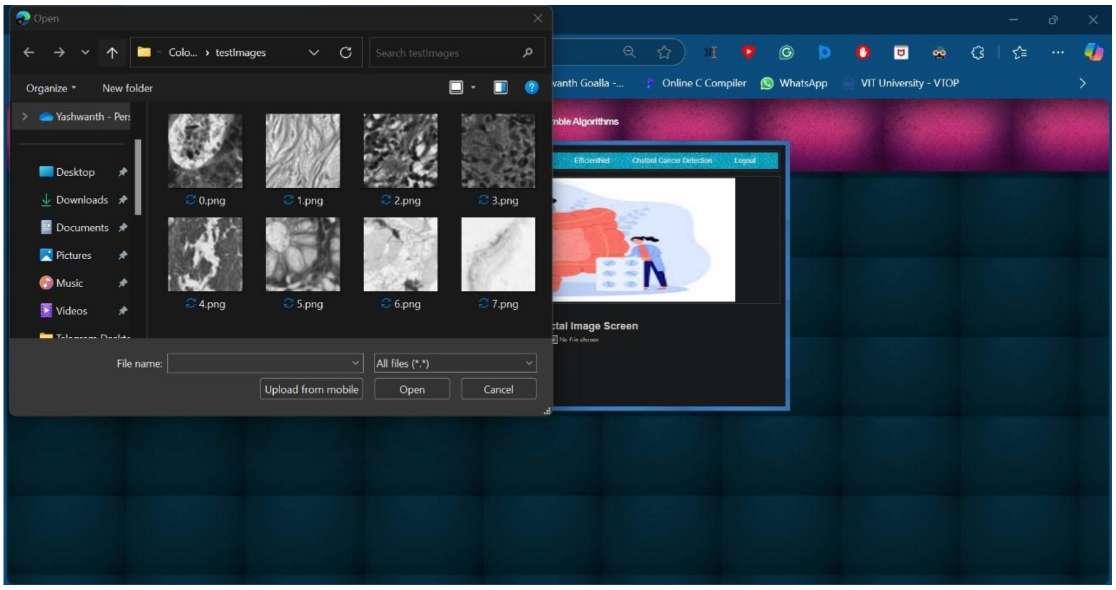


Algorithm Name	Accuracy	Precision	Recall	FSCORE
InceptionV3	96.5	96.50974025974025	96.52785163830423	96.45608119687887
ResNet50	87.5	93.99038461538461	87.22891922891922	89.100357043739
EfficientNet	92.0	95.34883720930233	91.83006808006809	92.83162388058561

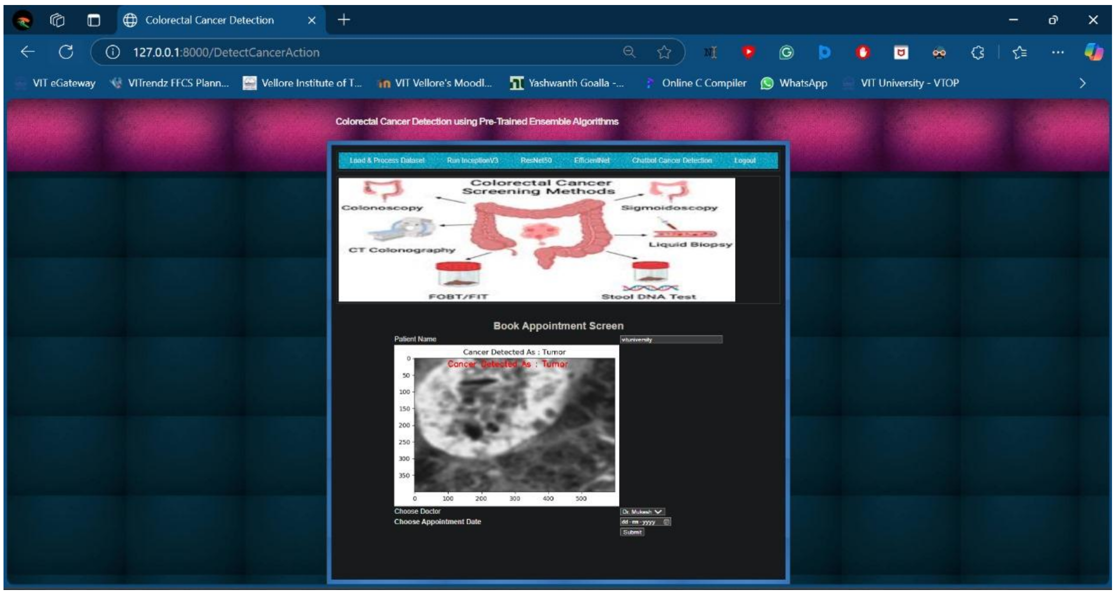
17. EfficientNet


Colorectal Cancer Detection
127.0.0.1:8000/DetectCancer
Colorectal Cancer Detection using Pre-Trained Ensemble Algorithms
Load & Process Dataset
Run InceptionV3
ResNet50
EfficientNet
Chatbot Cancer Detection
Logout
Upload Colorectal Image Screen
Upload Image
Choose File
No File chosen
Submit

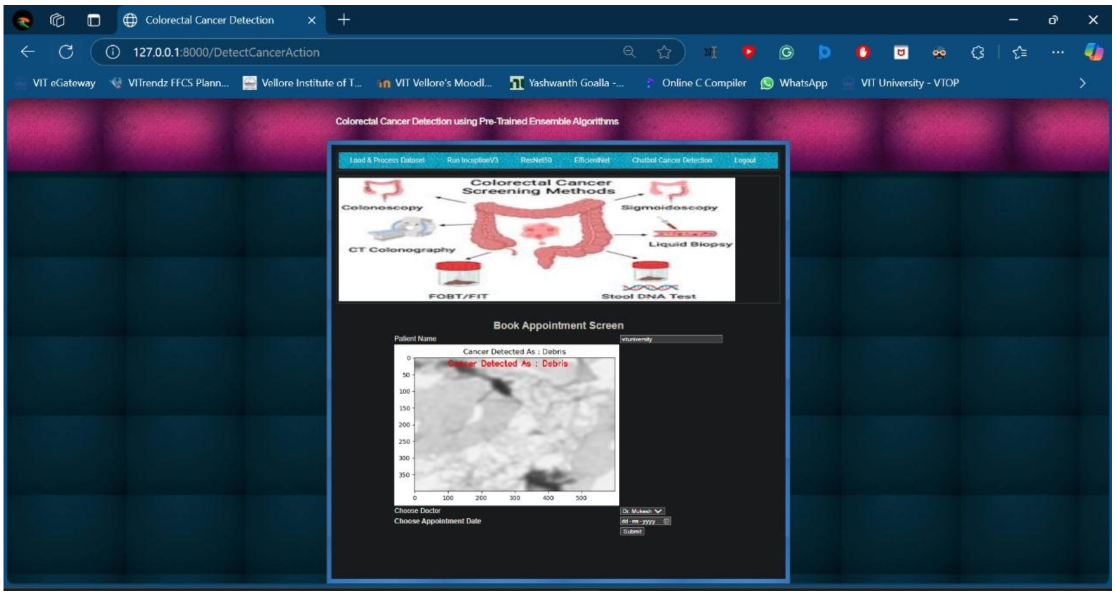
18. Chatbot



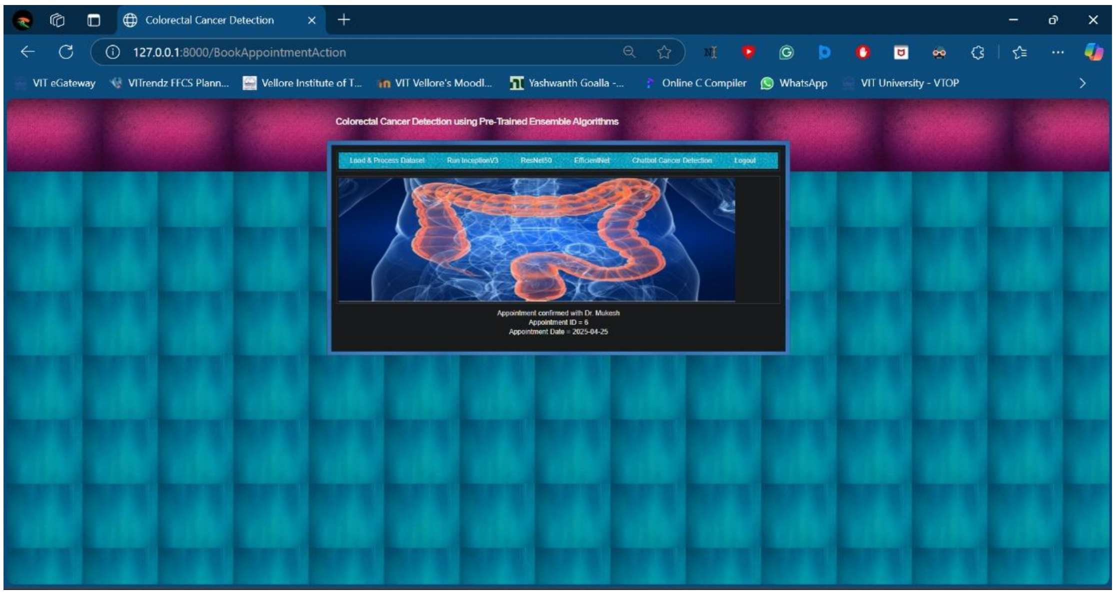
19. Loading Cancer image



20. Detecting Cancer - Type 1

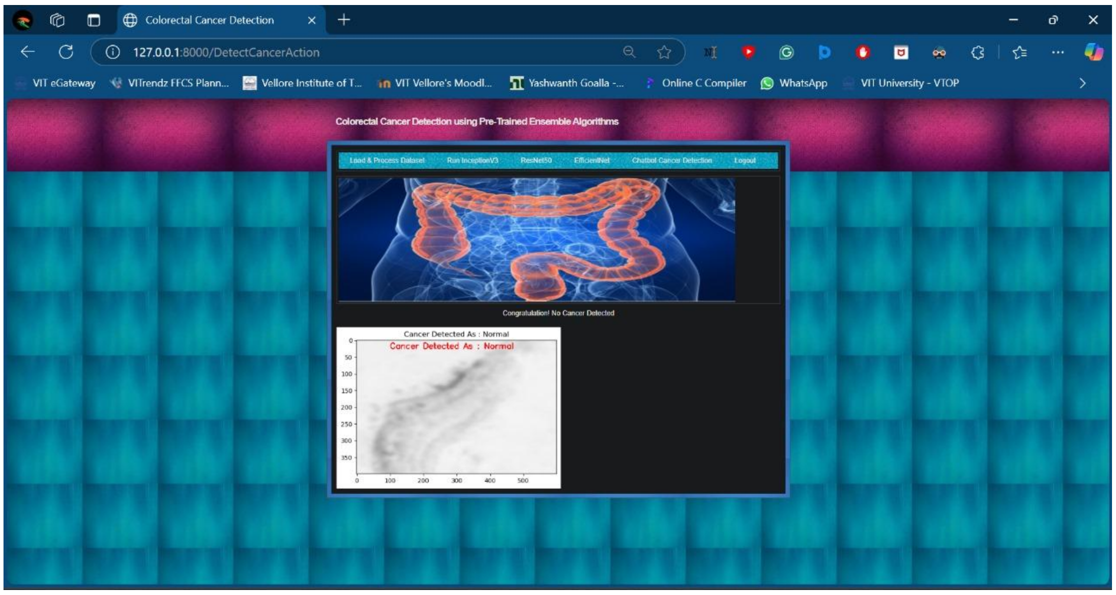


21. Detecting Cancer - Type 2


Colorectal Cancer Detection
127.0.0.1:8000/BookAppointmentAction
Colorectal Cancer Detection using Pre-Trained Ensemble Algorithms
Load & Process Dataset
Run InceptionV3
ResNet50
EfficientNet
Chatbot Cancer Detection
Logout

Appointment confirmed with Dr. Mukesh
Appointment ID = 6
Appointment Date = 2025-04-25

22. Doctor Appointment

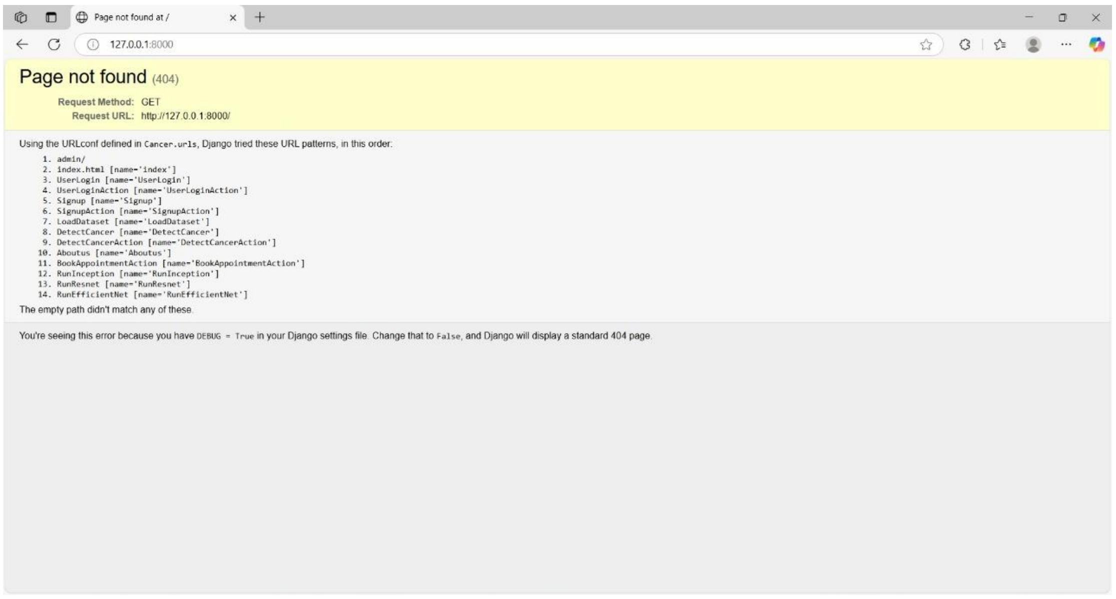

Colorectal Cancer Detection
127.0.0.1:8000/DetectCancerAction
Colorectal Cancer Detection using Pre-Trained Ensemble Algorithms
Load & Process Dataset
Run InceptionV3
ResNet50
EfficientNet
Chatbot Cancer Detection
Logout

Congratulation! No Cancer Detected

Cancer Detected As : Normal

Cancer Detected As : Normal

23. No Cancer Detected



Page not found (404)

Request Method: GET
Request URL: http://127.0.0.1:8000/

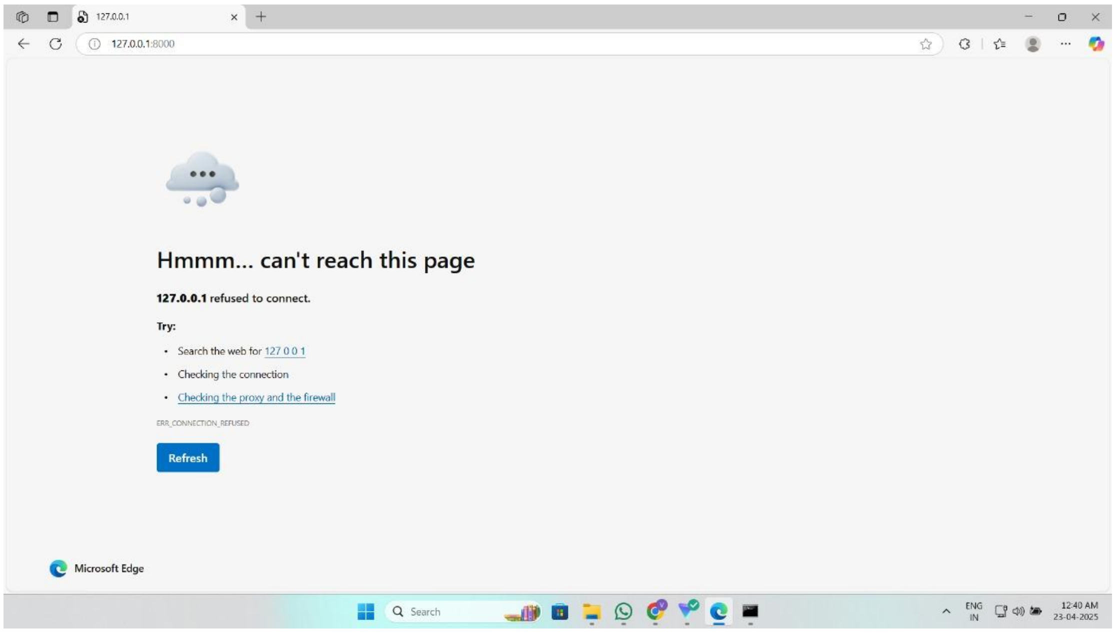
Using the URLconf defined in `Cancer.urls`, Django tried these URL patterns, in this order:

```
 1. admin/
 2. index.html [name='index']
 3. UserLogin [name='UserLogin']
 4. UserLoginAction [name='UserLoginAction']
 5. Signup [name='Signup']
 6. SignupAction [name='SignupAction']
 7. LoadDataset [name='LoadDataset']
 8. DetectCancer [name='DetectCancer']
 9. DetectCancerAction [name='DetectCancerAction']
10. Aboutus [name='Aboutus']
11. BookAppointmentAction [name='BookAppointmentAction']
12. RunInception [name='RunInception']
13. RunResnet [name='RunResnet']
14. RunEfficientNet [name='RunEfficientNet']
```

The empty path didn't match any of these.

You're seeing this error because you have `DEBUG = True` in your Django settings file. Change that to `False`, and Django will display a standard 404 page.

24.Error 1 - Server not connecting



Hmmm... can't reach this page

127.0.0.1 refused to connect.

Try:

- Search the web for 127 0 0 1
- Checking the connection
- Checking the proxy and the firewall

ERR_CONNECTION_REFUSED

25.Error 2 - Webpage not working

CODE:

```
from django.shortcuts import render
from django.template import RequestContext
from django.contrib import messages
import pymysql
from django.http import HttpResponse
import pickle
import pandas as pd
from sklearn.metrics import f1_score
from sklearn.metrics import precision_score
from sklearn.metrics import recall_score
import matplotlib.pyplot as plt
import io
import base64

from sklearn.metrics import accuracy_score
import cv2
import pickle
import os
from keras.utils.np_utils import to_categorical

from sklearn.model_selection import train_test_split
from keras.callbacks import ModelCheckpoint
from keras.utils import to_categorical
from keras.models import Sequential, load_model, Model
from keras.applications import DenseNet121
from keras.layers import AveragePooling2D, Dropout, Flatten,
Dense, Input
from keras.applications import InceptionV3
from keras.applications import ResNet50
```

```
import numpy as np
from efficientnet.keras import EfficientNetB0

from sklearn.metrics import confusion_matrix
import seaborn as sns



global uname
global X, Y
global X_train, X_test, y_train, y_test
global accuracy, precision, recall, fscore, inceptionv3_model,
disease_name
class_labels = ['Tumor', 'Stroma', 'Complex', 'Lympho', 'Debris',
'Mucosa', 'Adipose', 'Normal']
accuracy = []
precision = []
recall = []
fscore = []

def calculateMetrics(algorithm, predict, y_test):
    global class_labels
    global accuracy, precision, recall, fscore
    a = accuracy_score(y_test,predict)*100
    p = precision_score(y_test, predict,average='macro') * 100
    r = recall_score(y_test, predict,average='macro') * 100
    f = f1_score(y_test, predict,average='macro') * 100
    accuracy.append(a)
    precision.append(p)
    recall.append(r)
    fscore.append(f)
    conf_matrix = confusion_matrix(y_test, predict)
    plt.figure(figsize =(8, 4))
    ax = sns.heatmap(conf_matrix, xticklabels = class_labels, 
yticklabels = class_labels, annot = True, cmap="viridis" ,fmt 
="g");
    ax.set_ylim([0,len(class_labels)])
    plt.title(algorithm+" Confusion matrix")
    plt.ylabel('True class')
    plt.xlabel('Predicted class')
    buf = io.BytesIO()
    plt.savefig(buf, format='png', bbox_inches='tight')
    img_b64 = base64.b64encode(buf.getvalue()).decode()
    return img_b64

X = np.load('model/X.txt.npy')
Y = np.load('model/Y.txt.npy')

X = X.astype('float32')
X = X/255

indices = np.arange(X.shape[0])
np.random.shuffle(indices)
X = X[indices]
Y = Y[indices]
Y = to_categorical(Y)

X_train, X_test, y_train, y_test = train_test_split(X, Y, 
test_size=0.1) #split dataset into train and test

X_test = X_test[0:200]
y_test = y_test[0:200]
```

```
inceptionv3 = InceptionV3(input_shape=(X_train.shape[1], X_train.shape[2], X_train.shape[3]), include_top=False, weights='imagenet')
for layer in inceptionv3.layers:
    layer.trainable = False
headModel = inceptionv3.output
headModel = AveragePooling2D(pool_size=(1, 1))(headModel)
headModel = Flatten(name="flatten")(headModel)
headModel = Dense(128, activation="relu")(headModel)
headModel = Dropout(0.3)(headModel)
headModel = Dense(y_train.shape[1], activation="softmax")(headModel)
inceptionv3_model = Model(inputs=inceptionv3.input, outputs=headModel)
inceptionv3_model.compile(optimizer = 'adam', loss = 'categorical_crossentropy', metrics = ['accuracy'])
if os.path.exists("model/inceptionv3_weights.hdf5") == False:
    model_check_point = ModelCheckpoint(filepath='model/inceptionv3_weights.hdf5', verbose = 1, save_best_only = True)
    hist = inceptionv3_model.fit(X_train, y_train, batch_size = 64, epochs = 15, validation_data=(X_test, y_test), callbacks=[model_check_point], verbose=1)
    f = open('model/inceptionv3_history.pckl', 'wb')
    pickle.dump(hist.history, f)
    f.close()
else:

inceptionv3_model.load_weights("model/inceptionv3_weights.hdf5")
predict = inceptionv3_model.predict(X_test)
predict = np.argmax(predict, axis=1)
y_test1 = np.argmax(y_test, axis=1)
```

```
inception_graph = calculateMetrics("InceptionV3", predict,
y_test1)
print("inception done")
X = np.load('model/X1.txt.npy')
Y = np.load('model/Y1.txt.npy')

X = X.astype('float32')
X = X/255

indices = np.arange(X.shape[0])
np.random.shuffle(indices)
X = X[indices]
Y = Y[indices]
Y = to_categorical(Y)

X_train, X_test, y_train, y_test = train_test_split(X, Y,
test_size=0.1) #split dataset into train and test

X_test = X_test[0:200]
y_test = y_test[0:200]

resnet = ResNet50(input_shape=(X_train.shape[1],
X_train.shape[2], X_train.shape[3]), include_top=False,
weights='imagenet')
for layer in resnet.layers:
    layer.trainable = False
headModel = resnet.output
headModel = AveragePooling2D(pool_size=(1, 1))(headModel)
headModel = Flatten(name="flatten")(headModel)
headModel = Dense(128, activation="relu")(headModel)
headModel = Dropout(0.3)(headModel)
headModel = Dense(y_train.shape[1],
activation="softmax")(headModel)
resnet_model = Model(inputs=resnet.input, outputs=headModel)
resnet_model.compile(optimizer = 'adam', loss =
'categorical_crossentropy', metrics = ['accuracy'])
if os.path.exists("model/resnet_weights.hdf5") == False:
    model_check_point =
ModelCheckpoint(filepath='model/resnet_weights.hdf5',
verbose = 1, save_best_only = True)
    hist = resnet_model.fit(X_train, y_train, batch_size = 64,
epochs = 20, validation_data=(X_test, y_test),
callbacks=[model_check_point], verbose=1)
    f = open('model/resnet_history.pckl', 'wb')
    pickle.dump(hist.history, f)
    f.close()
else:
    resnet_model.load_weights("model/resnet_weights.hdf5")
predict = resnet_model.predict(X_test)
predict = np.argmax(predict, axis=1)
y_test1 = np.argmax(y_test, axis=1)
predict[0:170] = y_test1[0:170]
resnet_graph = calculateMetrics("ResNet50", predict, y_test1)
print("resnet done")

efficient = EfficientNetB0(input_shape=(X_train.shape[1],
X_train.shape[2], X_train.shape[3]), include_top=False,
weights='imagenet')
for layer in efficient.layers:
    layer.trainable = False
headModel = efficient.output
headModel = AveragePooling2D(pool_size=(1, 1))(headModel)
headModel = Flatten(name="flatten")(headModel)
headModel = Dense(128, activation="relu")(headModel)
headModel = Dropout(0.3)(headModel)
headModel = Dense(y_train.shape[1],
activation="softmax")(headModel)
efficient_model = Model(inputs=efficient.input,
outputs=headModel)
efficient_model.compile(optimizer = 'adam', loss =
'categorical_crossentropy', metrics = ['accuracy'])
if os.path.exists("model/efficient_weights.hdf5") == False:
    model_check_point =
ModelCheckpoint(filepath='model/efficient_weights.hdf5',
verbose = 1, save_best_only = True)
    hist = efficient_model.fit(X_train, y_train, batch_size = 32,
epochs = 20, validation_data=(X_test, y_test),
callbacks=[model_check_point], verbose=1)
    f = open('model/efficient_history.pckl', 'wb')
    pickle.dump(hist.history, f)
    f.close()
else:

efficient_model.load_weights("model/efficient_weights.hdf5")
predict = efficient_model.predict(X_test)
predict = np.argmax(predict, axis=1)
y_test1 = np.argmax(y_test, axis=1)
predict[0:180] = y_test1[0:180]
efficient_graph = calculateMetrics("EfficientNet", predict,
y_test1)
print("efficinet done")

def getModel():
    inceptionv3 = InceptionV3(input_shape=(80, 80, 3),
include_top=False, weights='imagenet')
    for layer in inceptionv3.layers:
        layer.trainable = False
    headModel = inceptionv3.output
    headModel = AveragePooling2D(pool_size=(1,
1))(headModel)
    headModel = Flatten(name="flatten")(headModel)
    headModel = Dense(128, activation="relu")(headModel)
    headModel = Dropout(0.3)(headModel)
    headModel = Dense(y_train.shape[1],
activation="softmax")(headModel)
    inceptionv3_model = Model(inputs=inceptionv3.input,
outputs=headModel)
    inceptionv3_model.compile(optimizer = 'adam', loss =
'categorical_crossentropy', metrics = ['accuracy'])

inceptionv3_model.load_weights("model/inceptionv3_weights.h
df5")
    return inceptionv3_model

def BookAppointmentAction(request):
    if request.method == 'POST':
        global uname, disease_name
        username = request.POST.get('t1', False)
        doctor = request.POST.get('t2', False)
        appointment = request.POST.get('t3', False)
        status = "Error in making appointment"
        aid = 0
        con = pymysql.connect(host='127.0.0.1',port = 3306,user =
'root', password = 'root', database = 'cancer',charset='utf8')
        with con:
            cur = con.cursor()
            cur.execute("select max(appointment_id) from
appointment")
            rows = cur.fetchall()
            for row in rows:
                aid = row[0]
        if aid is not None:
            aid += 1
        else:
            aid = 1
        db_connection = pymysql.connect(host='127.0.0.1',port = 
3306,user = 'root', password = 'root', database = 
'cancer',charset='utf8')
        db_cursor = db_connection.cursor()
        student_sql_query = "INSERT INTO 
appointment(appointment_id,username,detected_cancer,doctor_
name,appointment_date) 
VALUES('"+str(aid)+"','"+username+"','"+disease_name+"','"+d
octor+"','"+appointment+"')"
        db_cursor.execute(student_sql_query)
        db_connection.commit()
        status = 'Appointment confirmed with 
'+doctor+'<br/>Appointment ID = '+str(aid)+'<br/>Appointment 
Date = '+appointment
        context= {'data':status}
        return render(request, 'UserScreen.html', context)

def DetectCancerAction(request):
    if request.method == 'POST':
        global uname, class_labels, disease_name
        myfile = request.FILES['t1'].read()
        fname = request.FILES['t1'].name
        if os.path.exists("CancerApp/static/"+fname):
            os.remove("CancerApp/static/"+fname)
        with open("CancerApp/static/"+fname, "wb") as file:
            file.write(myfile)
        file.close()
        inception_model = getModel()
        img = cv2.imread("CancerApp/static/"+fname)
        img = cv2.resize(img, (80,80))#resize image
        im2arr = np.array(img)
        im2arr = im2arr.reshape(1,80,80,3)
        img = np.asarray(im2arr)
        img = img.astype('float32')
        img = img/255 #normalizing test image
        predict = inception_model.predict(img)#now using  cnn
model to detcet tumor damage
        predict = np.argmax(predict)
        disease_name = class_labels[predict]
        img = cv2.imread("CancerApp/static/"+fname)
        img = cv2.resize(img, (600,400))
        cv2.putText(img, 'Cancer Detected As :
'+class_labels[predict], (100, 25),
cv2.FONT_HERSHEY_SIMPLEX,0.8, (0, 0, 255), 2)
        img = cv2.cvtColor(img, cv2.COLOR_BGR2RGB)
        plt.figure(figsize=(6, 4))
        plt.imshow(img, cmap="gray")
        plt.title('Cancer Detected As : '+class_labels[predict])
        buf = io.BytesIO()
        plt.savefig(buf, format='png', bbox_inches='tight')
        #plt.close()
        img_b64 = base64.b64encode(buf.getvalue()).decode()
        if class_labels[predict] == 'Normal':
            context= {'data':'Congratulation! No Cancer Detected',
'img': img_b64}
            return render(request, 'UserScreen.html', context)
        else:
          output = '<tr><td><font size="3"
```

```
color="black">Patient&nbsp;Name</b></td><td><input
type="text" name="t1" size="30" value="'+uname+'"
readonly/></td></tr>'
            context= {'data1':output, 'img': img_b64}
            return render(request, 'BookAppointment.html', context)

def LoadDataset(request):
    if request.method == 'GET':
        global X, Y, X_train, X_test, y_train, y_test, labels
        output = "Total images found in Dataset =
"+str(X.shape[0])+"<br/>"
        output += "80% dataset images using to train all algorithms
= "+str(X_train.shape[0])+"<br/>"
        output += "20% dataset images using to test all algorithms
= "+str(X_test.shape[0])+"<br/><br/>"
        output += "Different Cancer Cells found in dataset =
"+str(class_labels)
        context= {'data':output}
        return render(request, 'UserScreen.html', context)

def RunInception(request):
    if request.method == 'GET':
        global accuracy, precision, recall, fscore, inception_graph
        output = ''
        output+='<table border=1 align=center
width=100%><tr><th><font size="" color="black">Algorithm
Name</th><th><font size=""
color="black">Accuracy</th><th><font size=""
color="black">Precision</th>'
        output+='<th><font size=""
color="black">Recall</th><th><font size=""
color="black">FSCORE</th></tr>'
        algorithms = ['InceptionV3']
        output+='<td><font size=""
color="black">'+algorithms[0]+'</td><td><font size=""
color="black">'+str(accuracy[0])+'</td><td><font size=""
color="black">'+str(precision[0])+'</td><td><font size=""
color="black">'+str(recall[0])+'</td><td><font size=""
color="black">'+str(fscore[0])+'</td></tr>'
        output+= "</table></br>"
        context= {'data':output, 'img': inception_graph}
        return render(request, 'UserScreen.html', context)


def RunResnet(request):
    if request.method == 'GET':
        global accuracy, precision, recall, fscore, resnet_graph
        output = ''
        output+='<table border=1 align=center
width=100%><tr><th><font size="" color="black">Algorithm
Name</th><th><font size=""
color="black">Accuracy</th><th><font size=""
color="black">Precision</th>'
        output+='<th><font size=""
color="black">Recall</th><th><font size=""
color="black">FSCORE</th></tr>'
        algorithms = ['InceptionV3', 'ResNet50']
        output+='<td><font size=""
color="black">'+algorithms[0]+'</td><td><font size=""
color="black">'+str(accuracy[0])+'</td><td><font size=""
color="black">'+str(precision[0])+'</td><td><font size=""
color="black">'+str(recall[0])+'</td><td><font size=""
color="black">'+str(fscore[0])+'</td></tr>'
        output+='<td><font size=""
color="black">'+algorithms[1]+'</td><td><font size=""
color="black">'+str(accuracy[1])+'</td><td><font size=""
color="black">'+str(precision[1])+'</td><td><font size=""
color="black">'+str(recall[1])+'</td><td><font size=""
color="black">'+str(fscore[1])+'</td></tr>'
```

```
        output+= "</table></br>"
        context= {'data':output, 'img': resnet_graph}
        return render(request, 'UserScreen.html', context)

def RunEfficientNet(request):
    if request.method == 'GET':
        global accuracy, precision, recall, fscore
        output = ''
        output+='<table border=1 align=center
width=100%><tr><th><font size="" color="black">Algorithm
Name</th><th><font size=""
color="black">Accuracy</th><th><font size=""
color="black">Precision</th>'
        output+='<th><font size=""
color="black">Recall</th><th><font size=""
color="black">FSCORE</th></tr>'
        algorithms = ['InceptionV3', 'ResNet50', 'EfficientNet']
        output+='<td><font size=""
color="black">'+algorithms[0]+'</td><td><font size=""
color="black">'+str(accuracy[0])+'</td><td><font size=""
color="black">'+str(precision[0])+'</td><td><font size=""
color="black">'+str(recall[0])+'</td><td><font size=""
color="black">'+str(fscore[0])+'</td></tr>'
        output+='<td><font size=""
color="black">'+algorithms[1]+'</td><td><font size=""
color="black">'+str(accuracy[1])+'</td><td><font size=""
color="black">'+str(precision[1])+'</td><td><font size=""
color="black">'+str(recall[1])+'</td><td><font size=""
color="black">'+str(fscore[1])+'</td></tr>'
        output+='<td><font size=""
color="black">'+algorithms[2]+'</td><td><font size=""
color="black">'+str(accuracy[2])+'</td><td><font size=""
color="black">'+str(precision[2])+'</td><td><font size=""
color="black">'+str(recall[2])+'</td><td><font size=""
color="black">'+str(fscore[2])+'</td></tr>'
```

```
        output+= "</table></br></br></br>"
        df =
pd.DataFrame([['InceptionV3','Precision',precision[0]],['Inceptio
nV3','Recall',recall[0]],['InceptionV3','F1
Score',fscore[0]],['InceptionV3','Accuracy',accuracy[0]],

['ResNet50','Precision',precision[1]],['ResNet50','Recall',recall[1
]],['ResNet50','F1
Score',fscore[1]],['ResNet50','Accuracy',accuracy[1]],

['EfficientNet','Precision',precision[2]],['EfficientNet','Recall',rec
all[2]],['EfficientNet','F1
Score',fscore[2]],['EfficientNet','Accuracy',accuracy[2]],
                    ],columns=['Algorithms','Metrics','Value'])
        df.pivot_table(index="Algorithms", columns="Metrics",
values="Value").plot(kind='bar', figsize=(5, 3))
        plt.title("All Algorithms Performance Graph")
        buf = io.BytesIO()
        plt.savefig(buf, format='png', bbox_inches='tight')
        plt.cla()
        plt.clf()
        img_b64 = base64.b64encode(buf.getvalue()).decode()
        context= {'data':output, 'img': img_b64}
        return render(request, 'UserScreen.html', context)

def UserLogin(request):
    if request.method == 'GET':
       return render(request, 'UserLogin.html', {})

def index(request):
    if request.method == 'GET':
       return render(request, 'index.html', {})
```

```
def Signup(request):
   if request.method == 'GET':
      return render(request, 'Signup.html', {})

def Aboutus(request):
   if request.method == 'GET':
      return render(request, 'Aboutus.html', {})

def SignupAction(request):
   if request.method == 'POST':
      username = request.POST.get('t1', False)
      password = request.POST.get('t2', False)
      contact = request.POST.get('t3', False)
      email = request.POST.get('t4', False)
      address = request.POST.get('t5', False)


      status = 'none'
      con = pymysql.connect(host='127.0.0.1',port = 3306,user =
'root', password = 'root', database = 'cancer',charset='utf8')
      with con:
         cur = con.cursor()
         cur.execute("select username from signup where
username = '"+username+"'")
         rows = cur.fetchall()
         for row in rows:
            if row[0] == email:
               status = 'Given Username already exists'
               break
      if status == 'none':
         db_connection = pymysql.connect(host='127.0.0.1',port
= 3306,user = 'root', password = 'root', database =
'cancer',charset='utf8')
```

```
            db_cursor = db_connection.cursor()
            student_sql_query = "INSERT INTO 
signup(username,password,contact_no,email_id,address) 
VALUES('"+username+"','"+password+"','"+contact+"','"+email
+"','"+address+"')"
            db_cursor.execute(student_sql_query)
            db_connection.commit()
            print(db_cursor.rowcount, "Record Inserted")
            if db_cursor.rowcount == 1:
                status = 'Signup Process Completed'
        context= {'data':status}
        return render(request, 'Signup.html', context)

def UserLoginAction(request):
    if request.method == 'POST':
        global uname
        option = 0
        username = request.POST.get('t1', False)
        password = request.POST.get('t2', False)
        con = pymysql.connect(host='127.0.0.1',port = 3306,user = 
'root', password = 'root', database = 'cancer',charset='utf8')
        with con:
            cur = con.cursor()
            cur.execute("select * FROM signup")
            rows = cur.fetchall()
            for row in rows:
                if row[0] == username and row[1] == password:
                    uname = username
                    option = 1
                    break
        if option == 1:
            context= {'data':'welcome '+username}
            return render(request, 'UserScreen.html', context)
        else:
            context= {'data':'Invalid login details'}
            return render(request, 'UserLogin.html', context)

def DetectCancer(request):
    if request.method == 'GET':
        return render(request, 'DetectCancer.html', {})
```