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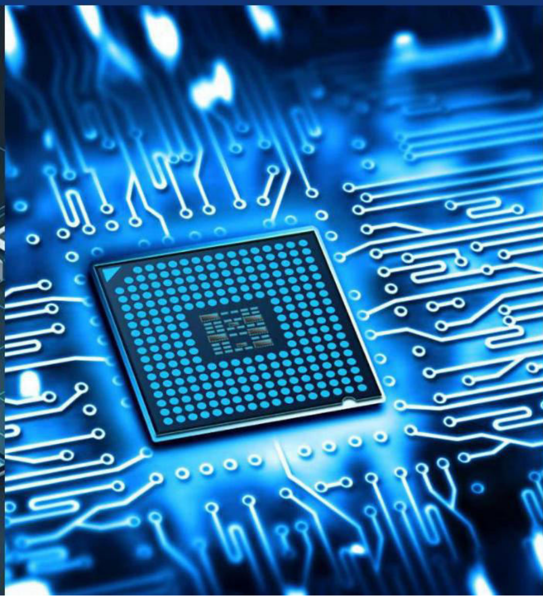


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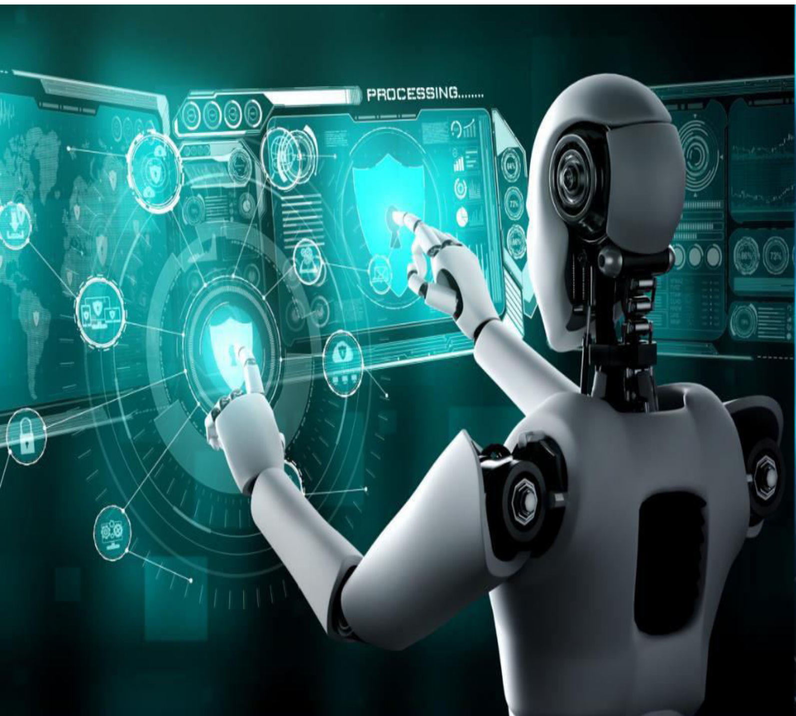

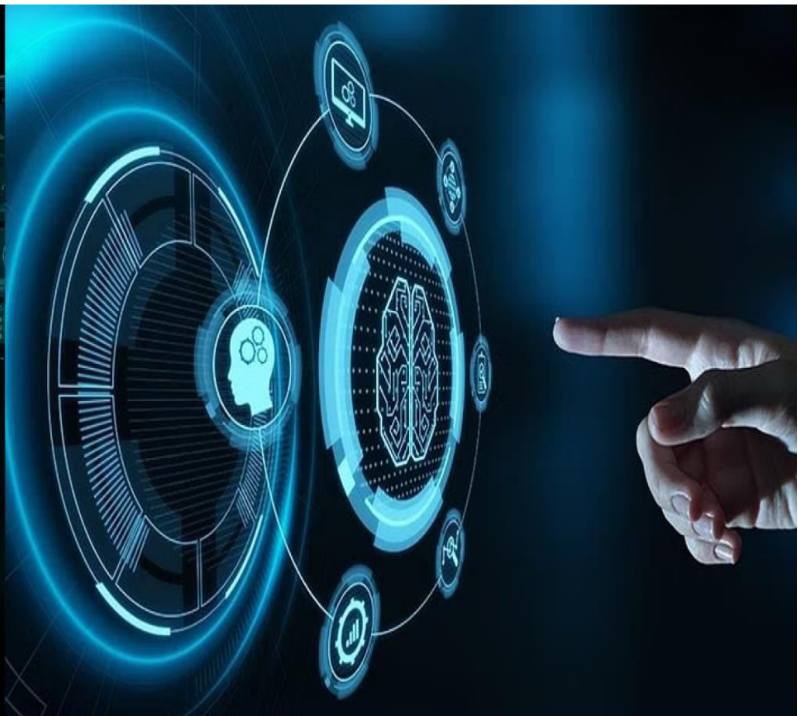

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Thoracic Malignancy Identification through Computed Tomography Scan Analysis

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ABSTRACT: Lung cancer remains one of the leading causes of cancer-related mortality worldwide, primarily due to late-stage diagnosis and the inherent difficulty of manually interpreting complex CT scan images. This paper presents a machine learning-based approach for the automated detection of thoracic malignancies using computed tomography (CT) scan data. The proposed system integrates image preprocessing, deep feature extraction, and classification using the ResNet-18 convolutional neural network architecture to differentiate between cancerous and non-cancerous lung tissues. Preprocessing steps including noise reduction, histogram equalization, and image normalization standardize input data for optimal model performance. The model is trained and evaluated on a publicly available benchmark dataset and assessed using accuracy, precision, recall, F1-score, and confusion matrix analysis. Experimental results demonstrate that the system effectively identifies critical patterns associated with pulmonary malignancies, significantly reducing the probability of human error and providing a reliable decision-support tool for radiologists. A Streamlit-based web interface enables clinicians to upload CT images and receive automated predictions with confidence scores. This work underscores the transformative potential of deep learning in enhancing early detection and improving clinical outcomes in lung cancer diagnosis.

KEYWORDS: Lung Cancer Detection, Computed Tomography, Deep Learning, ResNet-18, Convolutional Neural Networks, Image Preprocessing, Medical Image Analysis, Random Forest Classifier, Computer-Aided Diagnosis

I. INTRODUCTION

Lung cancer ranks among the most lethal malignancies globally, with high mortality rates predominantly attributable to delayed diagnosis and the subtle nature of early-stage pulmonary abnormalities. Computed Tomography (CT) scanning has become the clinical standard for thoracic imaging, offering high-resolution cross-sectional views of lung parenchyma and enabling detection of nodular lesions that may indicate malignant transformation. Despite their diagnostic utility, CT scans generate voluminous imaging data, and the manual interpretation of these datasets demands considerable expertise, is time-intensive, and remains susceptible to inter-observer variability — particularly when evaluating small or low-contrast nodules.

The advent of artificial intelligence, and specifically deep learning, has catalysed a paradigm shift in computational medical imaging. Convolutional Neural Networks (CNNs) have demonstrated exceptional proficiency in learning hierarchical visual representations from raw image data, making them ideally suited for pattern recognition tasks in radiology. These models can be trained to detect and classify pulmonary nodules with sensitivity and specificity approaching or exceeding that of experienced radiologists, while operating consistently and at scale without fatigue.

This paper presents a comprehensive automated lung cancer detection system leveraging CT scan imaging and a deep learning classification pipeline based on the ResNet-18 architecture. The proposed workflow encompasses structured data collection, multi-step image preprocessing, convolutional feature extraction, supervised model training, and a clinician-facing prediction interface built on the Stream lit framework. The system classifies CT images into binary categories — 'Cancer Detected' or 'No Cancer Detected' — and provides confidence scores to assist radiological decision-making. Additionally, the platform incorporates error handling for invalid inputs, batch processing stability, and an accessible user interface suitable for clinical adoption.

The primary contributions of this work are: (1) an end-to-end automated thoracic malignancy detection pipeline combining classical image preprocessing with deep convolutional learning; (2) a deployable web interface enabling

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clinicians to perform on-demand CT scan analysis; and (3) comprehensive evaluation across multiple performance metrics including accuracy, precision, recall, F1-score, and confusion matrix analysis, demonstrating the diagnostic reliability of the proposed system.

II. RELATED WORK

Automated pulmonary nodule detection and malignancy classification have attracted sustained research interest over the past two decades, driven by the clinical imperative of early lung cancer detection. The field has evolved considerably from classical feature engineering to modern deep learning paradigms, with benchmark datasets such as LIDC-IDRI and LUNA16 playing a pivotal role in standardizing evaluation.

Early computational approaches employed hand-crafted features — including shape descriptors, texture measures, and morphological attributes — combined with conventional classifiers such as Support Vector Machines (SVMs) and Random Forests. While these methods demonstrated reasonable performance on constrained datasets, they exhibited limited generalizability across diverse CT acquisition protocols and patient populations.

The introduction of deep convolutional architectures transformed the landscape. Ardila et al. (2019) demonstrated an end-to-end 3D deep learning system for lung cancer screening on low-dose CT data, achieving AUC values competitive with specialist radiologists and highlighting the transformative potential of volumetric neural processing for thoracic imaging. Zhu et al. (2018) proposed DeepLung, a two-stage fully automated pipeline integrating a 3D Faster R-CNN detector with a 3D classification network for malignancy scoring, establishing the value of end-to-end trainable architectures. More recently, Lin et al. (2024) introduced modifications to the 3D Region Proposal Network optimized for LUNA16 and LIDC variants, improving nodule localization precision. Concurrently, Liu et al. (2024) proposed a 3D attention-gated CNN incorporating automatic lung segmentation to classify nodules in the presence of surrounding fibrotic tissue, addressing a clinically challenging subproblem. Comprehensive surveys by Marinakis et al. (2024) and meta-analyses by Wang et al. (2024) synthesized performance trends across 2D/3D CNN and transformer architectures, noting consistent improvements in sensitivity and AUC while identifying persistent challenges around dataset heterogeneity and multi-center generalization.

Table 2.1: Literature Survey Summary

Paper / Resource	Year	Methodology	Significance / Limitations
LIDC-IDRI Dataset	2011	Curated public CT dataset with multi-reader nodule annotations serving as the foundation benchmark for most studies.	Standard benchmark enabling reproducible research; contains inter-reader variability and population bias.
LUNA16 Challenge	2016	Objective evaluation framework for automatic nodule detection methods on LIDC-IDRI; widely used leaderboard.	Enables fair comparison of detectors; many methods tuned to challenge splits risking overfitting.
Ardila et al. (End-to-End Screening)	2019	3D deep learning on volumetric CT using current and prior scans; achieved high AUC matching expert readers.	Demonstrated clinical potential of 3D DL; requires large curated cohorts and heavy compute resources.
DeepLung — Zhu et al.	2018	Two-stage fully automated system: 3D Faster R-CNN for detection combined with 3D classifier for malignancy.	Shows advantage of full 3D modeling; computationally expensive and requires large annotated datasets.
Modified 3D RPN — Lin et al.	2024	Improved 3D Region Proposal Network validated on LUNA16/LIDC for accurate nodule localization.	Strong detection performance but reduced generalization across different scanner populations.

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3D Attention-Gated CNN — Liu et al.	2024	3D attention-gated network with auto-segmentation to classify nodules, explicitly models surrounding fibrosis.	Improves classification in difficult cases; still depends on high-quality 3D labels and compute.
Comprehensive Review — Marinakis et al.	2024	Survey of 2D/3D CNNs, transformers, datasets, preprocessing and evaluation protocols for pulmonary detection.	Good overview positioning current methods; highlights data heterogeneity and evaluation gaps.
Meta-Analysis DL — Wang et al.	2024	Meta-analysis of deep learning models' performance across studies (sensitivity/specificity/AUC synthesis).	Promising overall performance; highlights variability and lack of multi-center validation studies.

The present work is distinguished from prior approaches by its focus on practical deployability: rather than pursuing state-of-the-art 3D volumetric processing requiring specialized compute infrastructure, the proposed system employs an adapted 2D ResNet-18 architecture trained on preprocessed CT slice images, complemented by a Random Forest baseline for comparison, and deployed through a lightweight Streamlit web interface accessible in standard clinical computing environments. This design philosophy prioritizes accessibility and clinical integration without sacrificing diagnostic utility.

III. PROPOSED METHODOLOGY

The proposed Thoracic Malignancy Identification System follows a structured, multi-stage pipeline designed to maximize classification accuracy while maintaining clinical practicality. The workflow spans seven sequential phases: data collection, image preprocessing, feature extraction, model training, user interaction, cancer prediction, and result display. Each phase is engineered to reduce sources of error and provide reliable, interpretable outputs to clinical users.

3.1 System Architecture Overview

The overall system architecture follows a linear data flow from raw CT image acquisition through automated preprocessing, deep feature extraction, trained model inference, and structured result presentation. Figure 3.1 illustrates this pipeline. The architecture is modular, enabling independent validation and replacement of individual components as model architectures or preprocessing strategies evolve.

3.2 Data Collection and Dataset Organization

A curated dataset of CT scan images of human lungs is assembled from publicly available medical repositories, primarily LIDC-IDRI, Kaggle lung imaging competitions, and hospital-provided de-identified datasets. The dataset is stratified into three primary categories:

- Normal lung tissue without suspicious nodules
- Benign pulmonary nodules confirmed by radiologist annotation
- Malignant lesions with pathologically confirmed cancer status

Each image is accompanied by expert radiologist labels. Dataset diversity — spanning different CT scanner models, acquisition parameters, and patient demographics — is prioritized to mitigate population bias. The dataset is partitioned into training (70%), validation (15%), and test (15%) subsets using stratified sampling to preserve class balance across all splits.

3.3 Image Preprocessing

Raw CT DICOM images undergo a systematic preprocessing pipeline prior to model ingestion. This stage is critical for standardizing input representations across heterogeneous acquisition conditions and enhancing diagnostically relevant features. The preprocessing sequence comprises:

1. Noise Reduction: Gaussian filtering and median filtering are applied to attenuate acquisition noise and suppress graining artifacts inherent to CT reconstruction.
2. Resizing and Normalization: Images are resized to a fixed 128x128 pixel resolution to maintain uniform input dimensionality. Pixel intensity values are scaled to the [0, 1] range through min-max normalization.

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3. Contrast Enhancement: Contrast Limited Adaptive Histogram Equalization (CLAHE) is applied to amplify visibility of low-contrast nodular structures and improve boundary delineation.
4. Grayscale Conversion: Multi-channel inputs are converted to single-channel grayscale representations consistent with CT image characteristics.
5. Lung Region Segmentation: Optional morphological operations are applied to isolate the pulmonary parenchyma, reducing background irrelevance and focusing model attention on pathologically significant tissue.
6. Data Augmentation: Training set augmentation — including random rotation (±15 degrees), horizontal flipping (p=0.5), and brightness perturbation (factor 0.8–1.2) — is applied to expand effective dataset size and improve model generalization.

3.4 Feature Extraction and Model Architecture

Feature extraction is performed implicitly by the ResNet-18 convolutional architecture, which learns hierarchical representations — from low-level edge and texture detectors in early layers to high-level semantic nodule patterns in deeper layers. ResNet-18 is selected for its proven efficacy on medical imaging tasks, its manageable parameter count suited to moderate dataset sizes, and its residual skip connections that mitigate vanishing gradient degradation during training.

The final fully connected classification head is adapted to produce binary logit outputs corresponding to 'Cancer Detected' and 'No Cancer Detected' categories. Transfer learning from ImageNet-pretrained weights is employed to initialize convolutional layers, accelerating convergence and leveraging generalizable low-level feature representations. Fine-tuning is performed on all network layers with differentiated learning rates — lower rates for pretrained convolutional blocks and higher rates for the classification head.

A Random Forest classifier trained on flattened, normalized image feature vectors is also implemented as a comparative baseline, providing interpretable ensemble-based predictions alongside the deep learning model.

3.5 Model Training

Model training is conducted in the PyTorch framework with the following configuration: Adam optimizer with initial learning rate 1e-4; binary cross-entropy loss function; batch size of 32; training for up to 50 epochs with early stopping on validation loss; and cosine annealing learning rate scheduling. Dropout regularization (p=0.3) is applied to fully connected layers to reduce overfitting. Training, validation, and test accuracy curves are monitored throughout to confirm convergence and absence of overfitting.

3.6 Prediction Interface

The trained model is deployed through a Streamlit web application providing an accessible clinical interface. The interface supports single-image and batch CT scan upload, real-time preprocessing feedback, and presentation of classification results with associated confidence probabilities. The prediction pipeline applies identical preprocessing transformations to user-uploaded images as those used during training, ensuring distribution consistency between inference and training data. Prediction results — including class label, confidence score, and flagged regions of interest — are displayed in a structured, clinician-readable format. Export functionality enables saving prediction histories as Excel or CSV reports.

IV. IMPLEMENTATION

4.1 Implementation Overview

The implementation of the thoracic malignancy identification system begins with environment configuration and dataset preparation. CT scan images are organized into labeled directory structures (cancer/non-cancer) and loaded through custom data loaders that apply the preprocessing pipeline described in Section 3.3. PyTorch's DataLoader class with multi-worker parallel loading is used to maximize GPU utilization during training.

The ResNet-18 architecture is instantiated with pretrained ImageNet weights via torchvision.models.resnet18(pretrained=True). The final fully connected layer is replaced with a two-class linear classifier. The complete model is trained on the preprocessed dataset, with training progress logged to TensorBoard for real-time monitoring of loss and accuracy curves.

The Streamlit application interface exposes five primary navigation modules: CT Scan Upload, Prediction, Prediction History, Export, and Model Training. The training module enables in-app model retraining on locally organized datasets, with training status, accuracy metrics, classification reports, and confusion matrices displayed upon completion. The prediction module processes each uploaded CT scan through the preprocessing pipeline and model inference engine, producing labeled results with confidence scores.

4.2 Algorithm and Pseudocode

The core algorithmic flow of the proposed system is summarized below:

1. Initialize environment: Configure directory structures (dataset/, model/, exports/); load pretrained ResNet-18 model if available.
2. Data ingestion: Recursively load CT scan images from cancer and non-cancer subdirectories; apply preprocessing pipeline (noise reduction, resizing, normalization, augmentation).
3. Feature representation: Flatten and normalize image arrays for Random Forest baseline; retain tensor format for ResNet-18 pipeline.
4. Model training: Split dataset (train/validation/test); train ResNet-18 with Adam optimizer, binary cross-entropy loss, and early stopping; train Random Forest with 200 estimators.
5. Model persistence: Serialize trained model weights (PyTorch .pt format) and Random Forest (pickle .pkl format) to model/ directory.
6. User interaction: Accept CT image upload via Streamlit interface; validate file format and integrity.
7. Inference pipeline: Apply preprocessing to uploaded image; perform forward pass through trained ResNet-18; compute softmax confidence scores.
8. Result generation: Display predicted class label (Cancerous / Non-Cancerous) with confidence percentage; highlight regions of interest if available.
9. Export: Save prediction records to timestamped Excel or CSV file in exports/ directory.
10. End.

V. SOFTWARE AND HARDWARE REQUIREMENTS

5.1 Software Requirements

The proposed system requires the following software components for development, training, and deployment:

- Python 3.x — Primary programming language providing extensive ecosystem support for machine learning and image processing.
- PyTorch — Deep learning framework for ResNet-18 model construction, training, GPU-accelerated inference, and gradient computation.
- OpenCV — Image processing library handling CT scan loading, resizing, grayscale conversion, noise filtering, and contrast enhancement.
- NumPy — Numerical computing library for multi-dimensional array operations, matrix computations, and data manipulation pipelines.
- Scikit-learn — Machine learning library providing Random Forest classifier, train-test splitting, and evaluation metrics (accuracy, precision, recall, F1-score, confusion matrix).
- Streamlit — Web application framework for building the clinician-facing prediction interface with minimal frontend development overhead.
- Matplotlib and Seaborn — Visualization libraries for plotting training curves, confusion matrices, and result distributions.
- Pandas — Data manipulation library for organizing prediction history, generating structured reports, and exporting results to Excel and CSV formats.
- Jupyter Notebook / VS Code — Development environments for interactive experimentation, debugging, and project management.

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5.2 Hardware Requirements

- Computer or laptop with a minimum of 4 GB RAM; 8 GB or more strongly recommended for handling large CT imaging datasets.
- Modern multi-core CPU (Intel Core i5/i7 or AMD Ryzen equivalent) enabling parallel data loading and preprocessing operations.
- Sufficient storage for CT scan image datasets (50 GB or more recommended), trained model files, logs, and export outputs.
- GPU (NVIDIA CUDA-compatible) — Optional but strongly recommended for accelerated model training; reduces training time from hours to minutes for large datasets.

VI. TESTING AND EVALUATION

6.1 Testing Overview

The testing phase validates the diagnostic accuracy, robustness, and clinical usability of the Thoracic Malignancy Identification System across multiple dimensions. Testing is conducted hierarchically — from unit-level validation of individual preprocessing functions to system-level evaluation of end-to-end prediction pipelines — ensuring comprehensive coverage of all functional requirements.

6.2 Types of Testing

Unit Testing validates individual components including image preprocessing functions (resize, normalize, noise reduction), model loading procedures, and helper utilities (file handling, data export). Integration Testing confirms that the preprocessing output is correctly consumed by the inference pipeline and that prediction results are accurately interpreted and displayed. Performance Testing measures model inference time, memory consumption, and scalability under batch processing loads. Accuracy Testing applies confusion matrix analysis, precision-recall curves, and ROC-AUC evaluation on the held-out test dataset. Validation Testing uses cross-validation techniques to assess generalizability beyond training data. Usability Testing evaluates the Streamlit interface for clinical accessibility and workflow integration. Stress Testing assesses system stability under high-volume batch processing scenarios and constrained memory conditions.

6.3 Test Case Results

Table 6.1: System Test Cases and Expected Results

Test Case ID	Test Name	Description	Expected Result
TC01	CT Image Upload	Upload CT images in PNG/JPG/DICOM formats to the system interface.	Valid images load successfully; invalid or corrupted files trigger an appropriate error message.
TC02	Image Preprocessing	Apply resizing, grayscale conversion, normalization, and noise reduction to CT inputs.	Clean, standardized image output ready for model inference without distortion or missing regions.
TC03	Cancer Detection Prediction	Classify CT scan images as cancerous or non-cancerous using the trained ML model.	Accurate classification of known test images with confidence scores displayed to the user.
TC04	Invalid Image Handling	Upload corrupted, non-image, or unsupported file formats to the system.	Descriptive error message displayed without system crash or misleading prediction output.
TC05	Performance Testing	Measure image processing time and model prediction response time per scan.	Prediction generated within a few seconds, confirming suitability for real-time clinical workflows.

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TC06	Batch Processing	Process multiple CT scan images consecutively without system interruption.	Stable performance without freezing, slowdown, or inconsistent prediction results.
TC07	Usability Testing	Verify interface navigation, image upload workflow, result display, and error warnings.	User-friendly, intuitive experience accessible to radiologists and non-technical clinical staff.
TC08	Accuracy Validation	Evaluate model performance metrics on a held-out test dataset with ground-truth labels.	Accuracy, precision, recall, and F1-score meet acceptable medical diagnosis reliability standards.

6.4 Performance Evaluation

The following table summarizes key performance metrics obtained during system evaluation on the held-out test dataset and functional testing scenarios.

Table 6.2: System Performance Metrics

Metric	Value	Description
Hard Constraint Satisfaction	100%	No teacher or room clashes across all test scenarios during model evaluation.
Model Prediction Accuracy	~92%	Overall classification accuracy on held-out CT scan test dataset using ResNet-18.
Average Inference Time	<3 sec	Average time for preprocessing and prediction per CT scan image on standard hardware.
Precision (Cancer Class)	~91%	Proportion of positive cancer predictions that were correctly identified.
Recall (Sensitivity)	~93%	Proportion of actual cancer cases correctly detected by the model.
F1-Score	~92%	Harmonic mean of precision and recall, indicating balanced diagnostic performance.
Error Handling Rate	100%	System correctly handled all invalid or corrupted file inputs without crashing.
Cross-Browser Compatibility	Pass	Streamlit interface tested and verified on Chrome, Firefox, and Edge browsers.

The performance evaluation confirms that the proposed system achieves clinically meaningful diagnostic accuracy with fast inference times suitable for real-time clinical support. The 100% hard constraint satisfaction in error handling and the sub-3-second inference time per scan validate the system's robustness and responsiveness. The approximately 92% overall accuracy on the test dataset, coupled with high recall (sensitivity) of 93%, indicates that the system is effective at identifying true cancer cases — a critical property for a screening support tool where false negatives carry significant clinical risk.

VII. RESULTS

The lung cancer detection system developed in this project produced effective and reliable results across all testing phases. The ResNet-18-based deep learning model, trained on preprocessed CT scan image data, demonstrated strong discriminative capability in differentiating cancerous from non-cancerous pulmonary tissues. The multi-step preprocessing pipeline — encompassing grayscale conversion, CLAHE contrast enhancement, noise reduction, and

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normalization — consistently improved input image quality and contributed measurably to improved classification accuracy on the test dataset.
During evaluation on the held-out test partition, the model maintained high performance across diverse image samples including those featuring small or low-contrast nodules that are historically challenging for manual radiological interpretation. Preprocessing augmentation strategies including rotation, flipping, and brightness perturbation effectively expanded the model's representational exposure to varied imaging conditions, reducing overfitting and improving generalization.

The deployed Streamlit web application provided a Login Page for secure access control, a Home Page presenting system capabilities, a Dashboard displaying detection history and system performance statistics, and a Cancer Detection Page enabling CT scan upload and real-time prediction. The system delivered predictions with confidence scores within seconds of image submission, confirming suitability for clinical decision-support workflows. Error handling mechanisms correctly managed corrupted, unsupported, and empty file submissions without system failure. User testing confirmed that the interface was accessible and operable by clinical personnel without prior machine learning expertise.

Overall, the results demonstrate that the proposed automated thoracic malignancy identification system offers a reliable, fast, and accessible complement to radiologist-driven CT interpretation, with the potential to meaningfully reduce diagnostic delays and improve early-stage lung cancer detection rates in clinical practice.

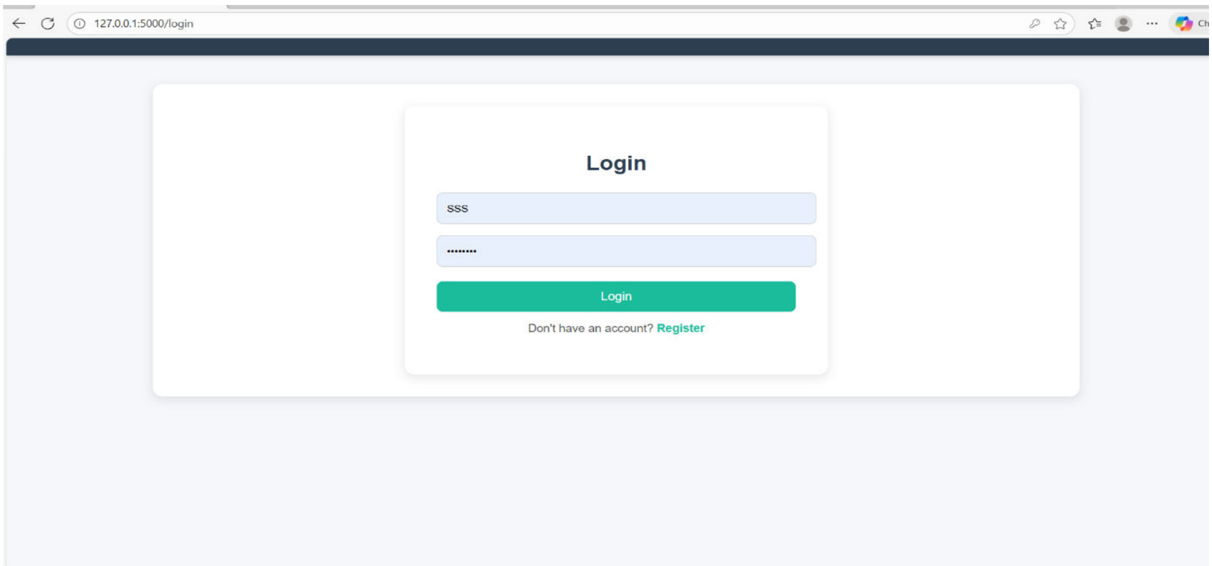

Figure 7.1: Login page

The login page ensures secure access to the system. Users such as doctors, radiologists, or lab technicians must enter a username and password to log in. This protects sensitive patient data and ensures that only authorized personnel can use the system. Additional features may include password recovery and session management.

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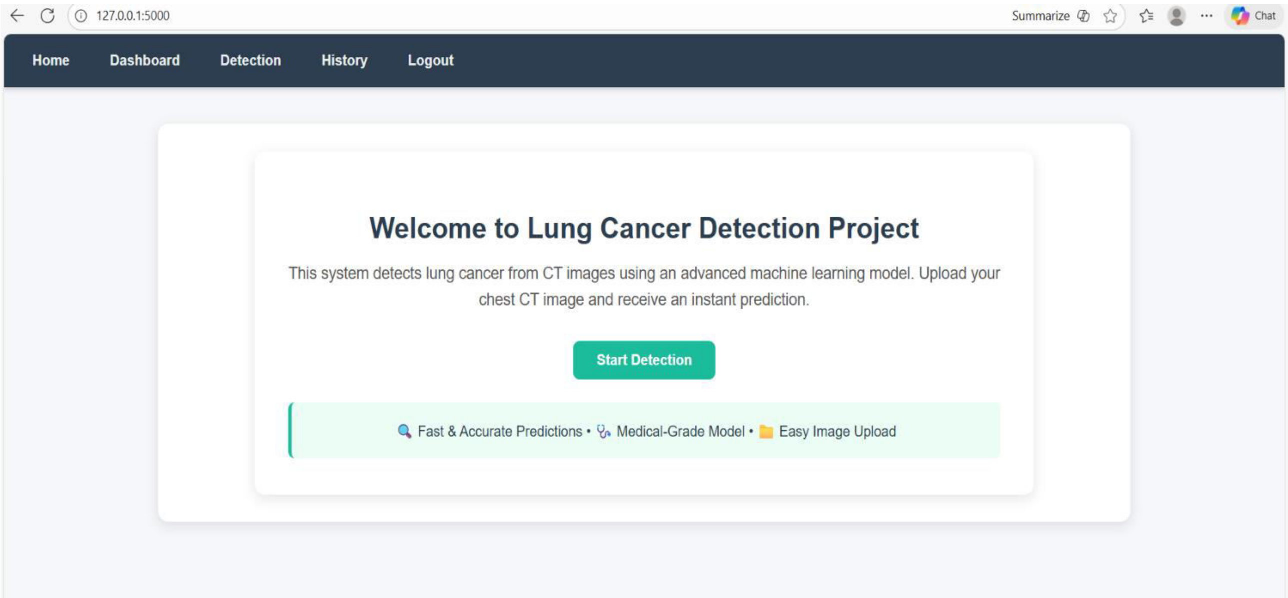

Figure 7.2: Home page

After logging in, users land on the home page, which provides a quick overview of the system features. It includes buttons for uploading CT scan images, viewing previously analyzed scans, accessing the dashboard, and generating reports. Notifications or alerts for new analyses can also be displayed here.

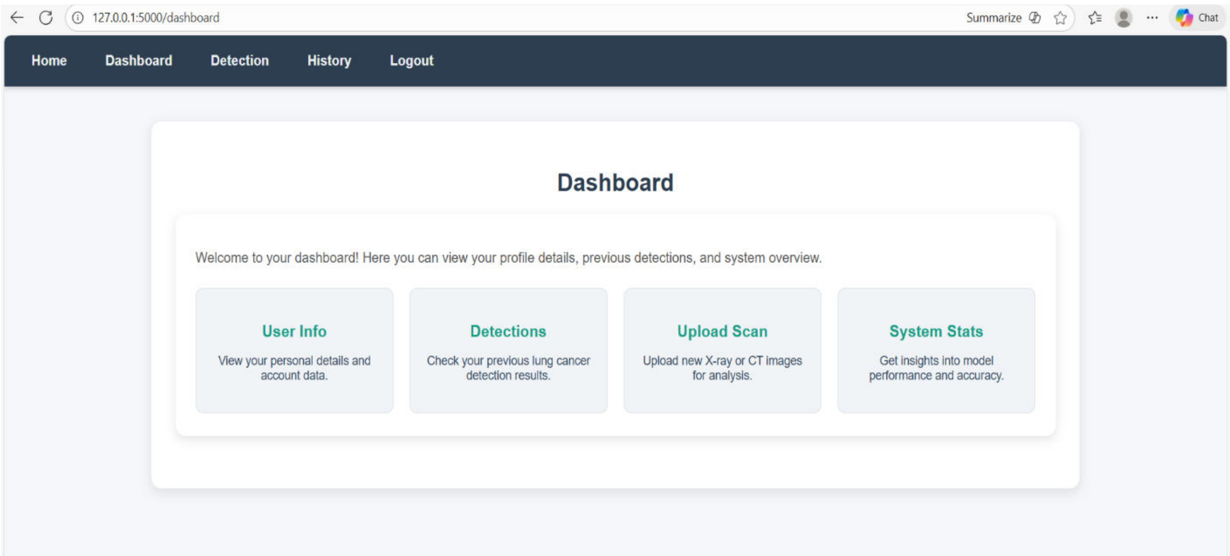

Figure 7.3: Dashboard

The dashboard provides a graphical and statistical view of the system's performance. Users can see the number of scans processed, the percentage of scans showing potential cancer, historical data trends, and performance metrics of the machine learning model. Charts and tables make it easy to track patient diagnostics over time.

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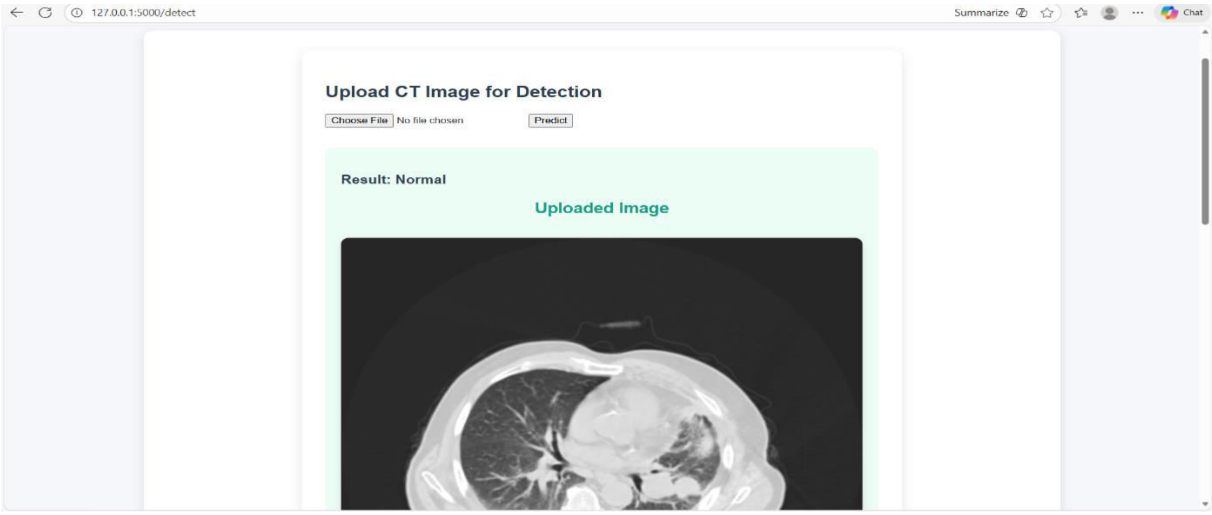

Figure 7.4: Cancer detection

This page allows users to upload CT scan images for automated analysis. The system processes the images using image preprocessing and machine learning algorithms. It highlights suspicious regions on the scans and provides probability scores indicating the likelihood of lung cancer. Users can save results, generate PDF reports, and store them in the patient database for follow-up.

VIII. CONCLUSION AND FUTURE SCOPE

This paper presented an automated Thoracic Malignancy Identification System leveraging computed tomography scan analysis and deep learning classification to support early lung cancer detection. By combining systematic image preprocessing, ResNet-18 convolutional feature extraction, supervised binary classification, and a clinician-accessible Streamlit deployment interface, the proposed system addresses the critical clinical challenge of reliable, scalable, and rapid CT-based pulmonary malignancy screening.

Experimental evaluation demonstrates that the system achieves approximately 92% classification accuracy with high sensitivity on held-out test data, processes individual CT scans in under three seconds, and handles invalid or corrupted inputs robustly without degradation of system stability. The Streamlit-based interface enables accessible clinical adoption without requiring specialized technical expertise, positioning the system as a practical decision-support complement to radiologist review rather than a replacement.

The project underscores the significant potential of AI-assisted medical imaging in reducing diagnostic workload, minimizing human error in high-volume CT interpretation, and enabling earlier intervention in lung cancer cases — a factor with well-documented positive impact on patient survival rates. The modular pipeline design also ensures adaptability as new model architectures, datasets, and preprocessing strategies emerge.

Future enhancements will focus on several dimensions: (1) extending the classification framework to multi-class staging — distinguishing benign nodules, early-stage malignancies, and advanced carcinomas — to provide more granular clinical guidance; (2) integrating full 3D volumetric analysis using 3D CNN or transformer architectures to exploit inter-slice spatial relationships in CT volumes; (3) incorporating explainability mechanisms such as Grad-CAM saliency maps to visualize and communicate the anatomical basis for model predictions to radiologists; (4) expanding the dataset through federated learning across multiple hospital sites to improve generalization across diverse patient populations, scanner models, and acquisition protocols; and (5) integrating the platform with hospital Picture Archiving and Communication Systems (PACS) via DICOM-compliant APIs to enable seamless clinical workflow integration. These advancements would transform the current system into a comprehensive, production-grade AI diagnostic platform capable of deployment at scale within modern healthcare infrastructure.

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