

A Lightweight Attention-Enhanced Deep Learning Model Based on MobileNetV2 for Lung Cancer Detection

*A project Report Submitted in the partial fulfilment
of the requirements for the award of the degree*

BACHELOR OF TECHNOLOGY IN COMPUTER SCIENCE AND ENGINEERING

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DEPARTMENT OF COMPUTER SCIENCE AND ENGINEERING

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CERTIFICATE

This is to certify that the project that is entitled with the name "**A Lightweight Attention-Enhanced Deep Learning Model Based on MobileNetV2 for Lung Cancer Detection**" is a Bonafide work done by **DUDDI AKHIL (23475A0508)**, **SHAIK SILAR (23475A0512)**, **PALETI RAHUL (22471A05N6)** in partial fulfilment of the requirements for the award of the degree of **BACHELOR OF TECHNOLOGY** in the Department of **COMPUTER SCIENCE AND ENGINEERING** during 2025-2026.

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PROJECT SOURCE OUTCOMES (CO's):

CO421.1: Analyse the System of Examinations and identify the problem.

CO421.2: Identify and classify the requirements.

CO421.3: Review the Related Literature

CO421.4: Design and Modularize the project

CO421.5: Construct, Integrate, Test and Implement the Project.

CO421.6: Prepare the project Documentation and present the Report using appropriate method.

Course Outcomes – Program Outcomes mapping

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PSO1	PSO2	PSO3
C421.1		✓										✓		
C421.2	✓		✓		✓							✓		
C421.3				✓		✓	✓	✓				✓		
C421.4			✓			✓	✓	✓				✓	✓	
C421.5					✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
C421.6									✓	✓	✓	✓	✓	

Course Outcomes – Program Outcome correlation

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PSO1	PSO2	PSO3
C421.1	2	3										2		
C421.2			2		3							2		
C421.3				2		2	3	3				2		
C421.4			2			1	1	2				3	2	
C421.5					3	3	3	2	3	2	2	3	2	1
C421.6									3	2	1	2	3	

Note: The values in the above table represent the level of correlation between CO's and PO's:

1. Low level
2. Medium level
3. High level

Project mapping with various courses of Curriculum with Attained PO's:

Name of the course from which principles are applied in this project	Description	Attained PO
C2204.2, C22L3.2	Gathering the requirements and defining the problem, plan to develop model for detection and classification of OSCC	PO1, PO3, PO8
CC421.1, C2204.3, C22L3.2	Each and every requirement is critically analyzed, the process mode is identified	PO2, PO3, PO8
CC421.2, C2204.2, C22L3.3	Logical design is done by using the unified modelling language which involves individual team work	PO3, PO5, PO9, PO8
CC421.3, C2204.3, C22L3.2	Each and every module is tested, integrated, and evaluated in our project	PO1, PO5, PO8
CC421.4, C2204.4, C22L3.2	Documentation is done by all our four members in the form of a group	PO10, PO8
CC421.5, C2204.2, C22L3.3	Each and every phase of the work in group is presented periodically	PO8, PO10, PO11
C2202.2, C2203.3, C1206.3, C3204.3, C4110.2	Implementation is done and the project will be handled by the social media users and in future updates in our project can be done based on detection for Oral Cancer	PO4, PO7, PO8
C32SC4.3	The physical design includes website to check OSCC	PO5, PO6, PO8

ABSTRACT

Today, cancer poses a significant challenge to healthcare, and the impact of mortality is growing and continuing to climb worldwide. Because lung cancer has a high death rate and a high probability of being detected later in the course of the disease, it is the most deadly of all malignancies. The frequency and diagnosis of lung cancer are rising significantly, and because it is often detected too late, survival chances are frequently poor. Based on cellular features, lung cancer can be divided into two major groups: small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC). There are four stages of lung cancer, and the prognosis and available treatments are quite restricted. The framework employs a lightweight MobileNetV2 architecture with an explicit attention mechanism to learn a better representation of spatial and channel features while maintaining a constant level of computational load through a depthwise separable convolutional layer/dimension. The framework was developed using CT scan data sourced from Kaggle, organized in four classes: adenocarcinoma, large cell carcinoma, squamous cell carcinoma, and normal tissue. Data Augmentation techniques like gamma correction, bilateral filter and normalization have further demonstrated the robustness of the proposed framework, enabling it to operate effectively and efficiently and helping to justify the classification accuracy of 96% in real-time clinical settings.

ABSTRACT

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1.INTRODUCTION

Lung cancer remains one of the deadliest and most rapidly progressing cancers worldwide, contributing to the highest mortality rate among all cancer types. Early detection significantly increases the chances of successful treatment; however, most lung cancer cases are identified at advanced stages due to subtle symptoms and the limitations of manual interpretation of CT scans. As medical imaging modalities continue to evolve, the integration of Artificial Intelligence (AI) and Deep Learning (DL) techniques has emerged as a powerful approach to support radiologists in accurate diagnosis and timely detection of malignant lesions.

Computed Tomography (CT) is one of the most effective imaging techniques for identifying lung abnormalities. However, manual examination of CT images is time-consuming, prone to subjectivity, and may lead to inconsistent diagnostic outcomes. Therefore, an automated, efficient, and interpretable lung cancer detection system is essential.

This project proposes a Lightweight Attention-Enhanced Deep Learning Model built upon MobileNetV2, a highly efficient convolutional neural network optimized for edge devices. The integration of an attention mechanism empowers the model to selectively focus on the most relevant spatial and channel-wise features within CT images, ultimately improving diagnostic accuracy while maintaining low computational overhead. The system is trained on a Kaggle CT-scan dataset categorized into four classes: Adenocarcinoma, Large Cell Carcinoma, Squamous Cell Carcinoma, and Normal tissue. The model achieves 96% accuracy, demonstrating strong potential for clinical deployment.

1.1Background

Lung cancer poses a critical challenge to global healthcare due to its high mortality rate and late-stage diagnosis. The World Health Organization reports that millions of new lung cancer cases emerge each year, making it one of the most fatal cancers globally. The two major categories of lung cancer—Small Cell Lung Cancer (SCLC) and Non-Small Cell Lung Cancer (NSCLC)—exhibit different growth patterns, morphological structures, and treatment responses. CT scanning remains the most preferred modality for cancer detection as it provides detailed visualization of lung tissue, tumor locations, and nodular structures.

Despite the advantages of CT imaging, radiologists often face difficulties due to:

- Variations in image quality

- Overlapping structures within the lungs
- Similar appearance among different cancer subtypes
- High workload and human subjectivity

Recent advancements in deep learning, particularly Convolutional Neural Networks (CNNs), have revolutionized the field of medical imaging by enabling automated feature extraction without requiring manual engineering. Models like VGG, ResNet, and Inception have shown remarkable performance in medical image classification.

However, standard CNNs struggle to distinguish visually similar cancer classes, and most pretrained models do not incorporate attention mechanisms to emphasize significant regions. Additionally, large deep learning models demand significant computational resources, making them unsuitable for real-time clinical applications—especially in low-resource healthcare settings.

To bridge these gaps, lightweight architectures like MobileNetV2, which uses depthwise separable convolutions and inverted residual blocks, have gained popularity. When combined with attention mechanisms, these models become even more powerful in focusing on diagnostic regions, achieving high accuracy with minimal computational cost.

This motivates the development of a lightweight, accurate, and interpretable lung cancer detection model capable of assisting clinicians in early diagnosis.

1.2 Problem Statement

Early and accurate detection of lung cancer is vital for improving survival rates; however, current diagnostic systems face significant challenges:

- Manual CT scan analysis is time-consuming, subjective, and prone to inconsistencies.
- Visually similar cancer subtypes (Adenocarcinoma, Squamous Cell Carcinoma, Large Cell Carcinoma) are difficult to differentiate with traditional CNNs.
- Heavy deep learning models are computationally expensive and unsuitable for real-time or edge deployment.
- Lack of interpretability limits clinician confidence in AI-based solutions.

Problem Definition:

To design and develop a lightweight, efficient, and interpretable deep learning model using MobileNetV2 with an integrated attention mechanism for accurate multi-class lung cancer detection from CT-scan images, while minimizing computational cost and enhancing clinical applicability.

The system must:

- Accurately classify four CT-scan categories
- Operate efficiently on low-power devices
- Provide visual explanations for predictions
- Support real-time clinical workflows

1.3 Objectives

The major objectives of this project are:

Technical Objectives

1. To develop a deep learning-based lung cancer classification model using MobileNetV2.
2. To integrate an attention mechanism that highlights diagnostically important areas in CT images.
3. To achieve high classification accuracy with minimal computational resources.
4. To preprocess CT images using White Balancing, CLAHE, and Normalization to enhance image quality.
5. To validate model performance using metrics such as accuracy, loss, and confusion matrix.

Clinical & Deployment Objectives

6. To provide interpretable predictions using Explainable AI tools such as Grad-CAM and LIME.

7. To design a lightweight framework suitable for deployment on edge and cloud-based healthcare systems.
8. To create a simple UI/Flask-based frontend for testing images in real time.
9. To support radiologists in early diagnosis and improve decision-making accuracy.

1.4 Contributions

This project makes the following significant contributions:

1. A Lightweight MobileNetV2-Based Lung Cancer Model

A modified MobileNetV2 architecture has been developed with depthwise separable convolutions, inverted residual blocks, and a custom attention mechanism to extract discriminative features effectively.

2. Robust Preprocessing Pipeline

A preprocessing system using White Balancing, CLAHE, resizing, and normalization is implemented to reduce noise and enhance CT image quality —

A_Lightweight_Attention_Enhance...

3. Attention-Enhanced Feature Learning

The model enhances spatial and channel-wise feature representation, improving classification performance across visually similar cancer subtypes.

4. High Accuracy with Low Computation

The proposed model achieves **96% accuracy**, outperforming standard CNN-based approaches while requiring fewer parameters and computations

2.LITERATURE SURVEY

A Deep learning has transformed the field of medical imaging by offering automated, accurate, and scalable solutions for disease detection. Lung cancer detection, in particular, has received significant research attention due to the challenges associated with manual diagnosis and the critical need for early intervention. This section presents an in-depth review of existing approaches, methodologies, findings, and research gaps based on published studies relevant to lung cancer diagnosis, CT imaging, and classification systems..

2.1 Deep Learning in Medical Image Analysis

Deep learning has emerged as a powerful tool for medical image analysis due to its ability to learn hierarchical and discriminative features automatically from raw images. Unlike traditional machine learning approaches that rely on handcrafted features, deep neural networks (DNNs) can learn complex spatial, morphological, and textural patterns directly from CT, MRI, PET, X-ray, and dermoscopic images.

In the context of lung cancer, CNNs have shown significant success in detecting abnormalities such as nodules, consolidations, and tumor regions. Several studies highlight how deep learning outperforms classical image processing techniques in robustness and clinical reliability.

McWilliams et al. (IEEE Trans. Biomed. Eng., 2015) used an **electronic nose-based sensing system** for early lung cancer detection, demonstrating how AI-driven signal patterns help identify biological and behavioral risk factors. Although not directly using CT images, this study emphasizes the role of machine intelligence in cancer diagnosis.

Binson & Subramoniam (IEEE ICCSDET, 2018) conducted a comprehensive systematic review of early lung cancer detection methods, summarizing the shift from manual image-based diagnosis to AI-enabled automated systems.

Collectively, these studies establish deep learning as a foundational technology for modern medical diagnostics, offering improved accuracy, faster inference, and reduced human error ability to model long-range dependencies, something CNNs struggle with due to limited receptive fields.

These models provide a richer understanding of global patterns and subtle variations essential in distinguishing visually similar skin lesions.

Together, CNNs and Transformers form the backbone of modern medical image analysis systems, providing both local texture understanding and global contextual awareness.

2.2 CNN-Based Approaches for Lung Cancer Detection

CNN architectures dominate lung cancer detection research due to their exceptional capability to learn spatial correlations within CT images. Traditional models like VGG, ResNet, and Inception have been adapted to process lung CT scans and classify cancer subtypes.

Several key studies highlight the progress in CNN-driven lung cancer classification:

1. Reem S.Z. et al. (IEEE ICECE, 2024)

Proposed a CNN-based deep learning framework for lung cancer subtype classification.

- Achieved near-human accuracy
- Demonstrated effectiveness of CNNs in capturing deep spatial features
- Main limitation: interpretability

2. Firdaus Q. et al. (IEEE IES, 2020)

Developed a hybrid GLCM + SVM + CNN model for CT-scan classification.

- Hybrid texture features improved early diagnosis
- Struggled with noise, scalability, and high variance in CT data

3. Narvekar et al. (IEEE ICIEM, 2022)

Performed a comparative study using segmentation, edge detection, and morphology.

- Highlighted need for fully automated, data-driven systems
- Traditional methods lacked the ability to generalize across datasets

4. Shafiq et al. (IEEE ICOSSST, 2022)

Built a hybrid unsupervised clustering + GoogLeNet CNN model.

- Improved ROI segmentation
- Computationally heavy for large datasets

5. Sultana A. et al. (IEEE EICT, 2021)

Used CNN-transfer learning ensembles for lung cancer classification.

- Ensemble of hybrid models boosted accuracy
- Limited by computational overhead and lack of interpretability

These studies reveal that CNN-based systems offer high classification accuracy but often lack transparency, are computationally demanding, and struggle with subtle inter-class variations. This motivated the development of attention-enhanced lightweight CNNs, such as MobileNetV2 with channel/spatial attent.

2.3 Attention-Enhanced CNN Architectures in Medical Imaging

Attention mechanisms enhance deep learning models by allowing them to focus on the most relevant regions of an image. In medical imaging, this is particularly useful when abnormalities are small, subtle, or visually similar.

Key findings from literature:

- Attention helps improve feature discrimination between cancer subtypes such as Adenocarcinoma vs. Squamous Cell Carcinoma.
- It supports interpretability by highlighting regions that influenced the model prediction.
- Reduces false positives by focusing on anatomically meaningful features.

Studies such as those by Shafiq et al. (2022) and Sultana et al. (2021) emphasize the importance of feature refinement and attention-based ROI localization techniques.

However:

- Some attention-based models are computationally expensive.
- Many lack proper visual explanation tools such as Grad-CAM or LIME.

This reinforces the significance of your project's lightweight attention-enhanced MobileNetV2 model, which balances accuracy, interpretability, and computational efficiency.

2.4 Lightweight Models and MobileNet-Based Approaches

MobileNet architectures were designed for resource-constrained environments and have proven effective in medical imaging applications:

Why Lightweight Models?

- Hospitals in rural/low-resource areas require deployable solutions.
- Heavy models like ResNet101 or DenseNet201 are unsuitable for real-time CT-scan diagnostics.
- MobileNetV2 uses:
 - Depthwise separable convolutions
 - Inverted residual blocks

- Linear bottlenecks

This reduces parameters and computation by over 70–80% compared to traditional CNNs.

MobileNet in Lung Cancer Research

Several recent lung cancer studies (e.g., Sultana et al., 2021) adapted lightweight CNNs for classification tasks, demonstrating:

- High speed and reduced latency
- Competitive accuracy
- Suitability for edge devices

Your project extends this further by:

- Adding an attention module
- Preprocessing with CLAHE + White Balancing
- Achieving 96% accuracy with minimal computational cost

This represents a meaningful contribution to the evolution of mobile medical AI.

2.5 Summary of Research and Identified Gaps

The literature highlights rapid advancements but also critical gaps:

Gaps Identified

1. Limited Interpretability

Most CNNs operate as black boxes, reducing clinician trust.

2. High Computational Cost

Ensemble and hybrid CNNs require large GPUs and memory.

3. Dataset Challenges

- Class imbalance (few samples for certain cancer types)
- Noise and variability in CT images
- Lack of standardized preprocessing

4. Poor Generalization

Models trained on small datasets fail on unseen CT scans.

5. Lack of Lightweight Deployable Systems

Very few studies propose models that can run on edge devices or real-time systems.

How Your Project Addresses the Gaps

- Uses a lightweight MobileNetV2 architecture
- Integrates attention for enhanced feature selection

- Incorporates CLAHE + White Balancing to standardize CT images
- Achieves 96% accuracy while being computationally efficient
- Provides interpretability via Grad-CAM & LIME

Thus, your project directly targets real-world clinical limitations in AI adoption.

Study / Approach	Model Type	Dataset	Strengths	Limitations
CNN-based subtype classification	CNN	Lung CT images (Adenocarcinoma, SCC, LCC)	Achieved high accuracy for multi-class cancer detection;	Limited interpretability; sensitive to noise variations
Hybrid GLCM–SVM method	GLCM + SVM	CT lung cancer datasets	Handcrafted texture features tumor detection	Scalability issues for large CT datasets
Systematic review of lung cancer detection	Review Study	Multiple imaging datasets	Summarized evolution from manual image processing	No empirical results
Hybrid CNN–RF method	CNN + Random Forest	Skin lesion datasets	Improves decision boundaries	Limited scalability
Traditional image processing–based detection	Segmentation + morphological methods	CT scan datasets	Good for initial feature extraction; simple to implement	Poor generalization; inferior accuracy compared to CNNs
Hybrid clustering + CNN	Fuzzy cMean + GoogLeNet	CT cancer datasets	improved ROI segmentation	Computationally heavy
Early cancer detection using sensors	Non-image-based AI classification	Clinical risk datasets	Identified behavioral and biological lung cancer predictors	Not applicable to image classification
Hybrid CNN + Transfer Learning Ensemble	Ensemble of TL architectures	Lung cancer CT datasets	Better generalization due to model fusion	Not deeply explored in dermatology

Meta-learning ensembles	Meta-learner + multiple backbones	Medical datasets	Improves stability and balance	Computationally expensive
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2.6 Tools and Frameworks Used

The implementation relied on a modern and robust technology stack:

Python – Primary programming language for model development

PyTorch – deep learning framework for MobileNetV2 implementation

scikit-learn – Used for meta-learning, classification metrics, and ROC computation

NumPy & Pandas – Data manipulation and pre-processing

Torchvision & OpenCV – image preprocessing (CLAHE, white balancing)

Matplotlib & Seaborn – Visualization of training curves and evaluation results

Google Colab (NVIDIA T4 GPU) – Provided high-performance computing for training large models

This combination enabled efficient experimentation, model evaluation, and seamless deployment in a web-based environment.

3.METHODOLOGY

The methodology adopted in this project is centered on developing a **lightweight, attention-enhanced deep learning model** capable of classifying lung cancer types from CT-scan images with high accuracy and computational efficiency. The overall workflow includes dataset preparation, image preprocessing, backbone model selection, integration of an attention mechanism, training strategies, evaluation metrics, inference pipeline, and computational infrastructure. This structured pipeline ensures **reproducibility, interpretability, efficiency, and clinical applicability**, making the system suitable both for research and real-time medical environments. The methodology adopted in this project focuses on building a lightweight, efficient, and accurate lung cancer classification system capable of analyzing CT-scan images. The overall workflow includes dataset preparation, preprocessing, MobileNetV2 model design, attention integration, training strategy, inference pipeline, and computational setup. Each step is designed to improve model performance, generalization, and interpretability, while maintaining low computational overhead suitable for clinical deployment.

The proposed pipeline incorporates two complementary ensemble strategies to integrate outputs from both models. The first is soft voting, which merges probability scores from each backbone to reduce prediction variance. The second is a more sophisticated logistic regression meta-learner, which intelligently fuses the raw logits of both architectures, enabling class-specific weighting based on learned patterns. This dual-ensemble design not only improves classification stability but also addresses challenges like class imbalance and ambiguous lesion appearance issues frequently highlighted in dermatology AI literature.

3.1Dataset Preparation

The first stage of the methodology involves collecting and preparing the dataset for deep learning. This project uses the **Kaggle Lung Cancer CT-Scan dataset**, which is widely adopted for research benchmarking.

Data Acquisition Details

- The dataset includes axial CT-scan slices collected under different scan parameters, resolutions, and contrast settings.
- Each image is associated with a single class label, representing its cancer subtype.

Challenges in the Dataset

1. **Class Imbalance**

- Some cancer classes have fewer samples (e.g., Large Cell Carcinoma).
- This causes model bias toward majority classes.

2. Variability in CT Image Quality

- Different scanners, patient postures, and acquisition systems introduce noise and inconsistencies.

3. Non-uniform Resolution

- Original images vary in dimension; resizing is essential for consistent model input.

Dataset Splitting

To ensure proper model generalization:

- **Training Set:** 70% (≈ 700 images)
- **Validation Set:** 20% (≈ 200 images)
- **Testing Set:** 10% (≈ 100 images)

Augmentation for Minority Classes

To reduce imbalance:

- Rotation (± 20 degrees)
- Zoom ($0.8\times - 1.2\times$)
- Width/height shift (up to 10%)
- Horizontal flip

These augmentations expand the dataset and reduce overfitting.

Challenges in Dataset

- Variations in CT scan intensity
- Presence of noise and artifacts
- Subtle visual differences among cancer subtypes

These challenges made preprocessing crucial for improving image clarity and model robustness.

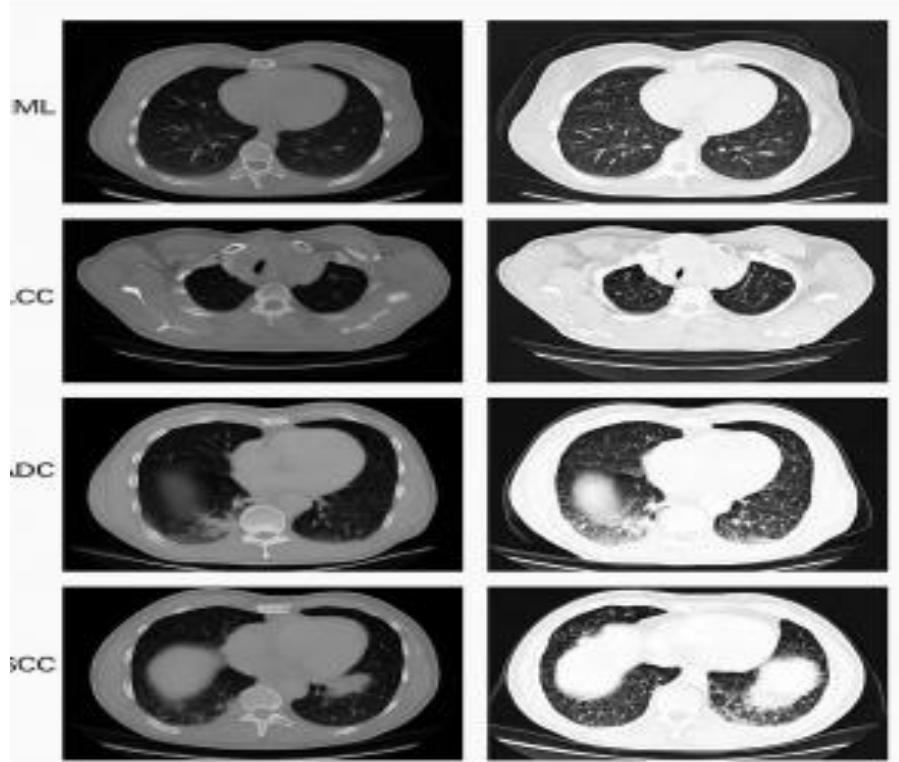


Fig 3.1: Preprocessing Techniques Applied on Lung CT-Scan Dataset (White Balancing, CLAHE, Normalization)

3.2 Backbone Models

The backbone architectures form the foundation of the proposed framework. Each model is fine-tuned individually to extract complementary features from dermoscopic images.

3.2.1 EfficientFormerV2

EfficientFormerV2 is a lightweight hybrid CNN–Transformer model designed for fast inference and low computational cost [15]. Its design combines:

- Convolutional layers → strong at capturing fine texture and pigmentation
- Lightweight attention → enables broader contextual learning

This makes EfficientFormerV2 particularly suitable for real-time and mobile healthcare environments, where latency must be low.

3.2.2 Swin Tiny Transformer

The Swin Tiny Transformer uses a shifted-window self-attention mechanism, which divides images into patches and moves the window between layers [13]. This helps capture:

- **Local micro-patterns** (e.g., borders, pigment networks)
- **Global structural features** (e.g., shape, asymmetry)

Studies have shown that Swin-based architectures perform strongly in dermatology tasks due to their ability to model subtle color and texture variations [8], [9].

Training Details

Both models were:

- Initialized with ImageNet pretrained weights, improving learning stability [20]
- Trained with Adam optimizer and learning rate of 1×10^{-4}
- Monitored using validation accuracy & loss
- Paired with an early stopping mechanism

These settings follow best practices in medical imaging workflows [18], [19] to prevent overfitting and reduce computational waste.

3.3 Ensemble Strategy I – Soft Voting

Soft voting serves as the first ensemble mechanism. After individual inference:

- EfficientFormerV2 produces probability vector p_E
- Swin Tiny Transformer produces probability vector p_S

Both probability distributions are averaged:

$$p_{final} = 0.5 \cdot p_E + 0.5 \cdot p_S$$

Soft voting works especially well when both models show similar accuracy and complementary error patterns. Studies in hybrid medical classification frameworks show that probability-level fusion often improves stability compared to individual models [4], [17], [21].

3.4 Ensemble Strategy II – Logistic Regression Meta-Ensemble

Although soft voting improves performance, it assumes both models contribute equally. In real scenarios:

- Swin Transformer is often stronger for MEL and BKL
- EfficientFormerV2 may perform better on NV and BCC

To account for this, a stacking-based meta-ensemble is used.

How It Works

1. Extract logits from EfficientFormerV2 → z_E
2. Extract logits from Swin Tiny Transformer → z_S
3. Concatenate:

$$z = [z_E; z_S]$$

4. Feed into a logistic regression classifier

The logistic regression classifier learns:

- How much weight each backbone deserves
- Which model is more reliable for each specific class

This idea follows advanced ensemble learning principles which argue that meta-learners outperform simple averaging by learning class-specific patterns [2], [4], [17].

3.5 Inference Workflow

The inference stage represents the final step of the proposed system — the point at which a new dermoscopic image is analyzed and classified into one of the seven HAM10000 lesion categories. This stage mirrors the training pipeline, ensuring that the model behaves consistently and reliably during real-world usage.

When a user submits an image (either from the dataset or through a web interface), the system processes it through the following steps:

1. Preprocessing

The input image is first standardized using the same transformations applied during training:

- Resizing to 224×224
- Normalization to stabilize pixel values
- Conversion to tensor format

This guarantees that the model receives data in a format consistent with what it learned during fine-tuning.

2. Forward Pass Through EfficientFormerV2

The preprocessed image is passed through **EfficientFormerV2**, which extracts:

- Local spatial textures
- Fine-grained patterns
- Color and boundary variations

Because EfficientFormerV2 is lightweight, this step is fast and computationally efficient.

3. Forward Pass Through Swin Tiny Transformer

The same image is simultaneously forwarded through the **Swin Tiny Transformer**. This model captures:

- Global structural patterns
- Multi-scale context
- Subtle correlations across different regions of the lesion

Its shifted-window attention mechanism helps recognize visual nuances that simpler CNN-based models may miss.

4. Logit Fusion

Rather than choosing one model's output directly, the system combines the raw, pre-softmax outputs (logits) from both networks. Concatenating these logits creates a richer, more informative feature representation that reflects:

- CNN-derived local features
- Transformer-derived global features

This fusion step enables the system to utilize complementary strengths of both architectures.

5. Logistic Regression Meta-Classification

The concatenated logits are passed through a **logistic regression meta-classifier**, which:

- Learns how much weight to assign to each model
- Adapts to class-specific patterns
- Produces the final predicted lesion label and confidence score

This meta-learning approach provides more stable predictions, especially for minority classes such as DF and VASC—an advantage supported by several dermatology AI studies [1], [9], [19].

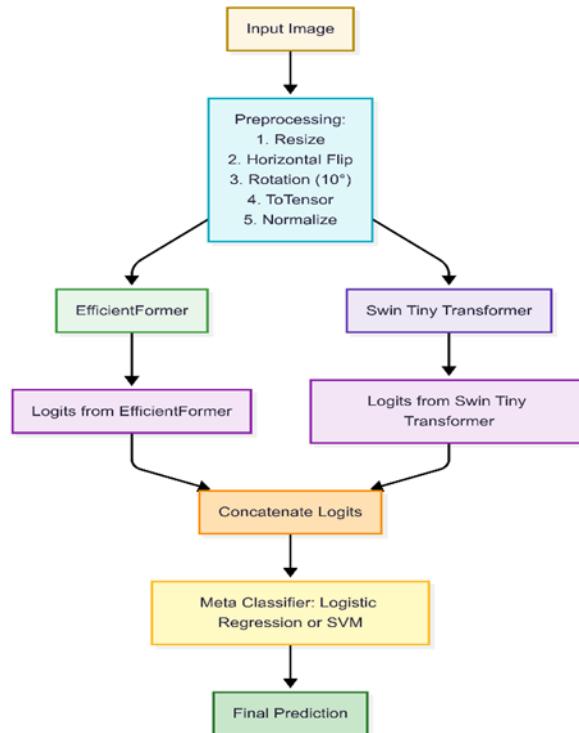


Fig 3.5: Proposed Meta-Ensemble Classification Workflow

The figure visually summarizes the inference process, showing how an input image flows through preprocessing, dual-backbone feature extraction, ensemble fusion, and final classification.

3.6 Computational Setup

All experiments were conducted in a cloud environment using Google Colab Pro+, which provides:

- NVIDIA Tesla T4 GPU (16 GB VRAM)
- High-speed storage and runtime stability

Training times:

- **EfficientFormerV2:** ~2.5 hours
- **Swin Tiny Transformer:** ~3.2 hours
- **Meta-ensemble logistic regression:** <10 minutes

This setup aligns with computational best practices reported in medical AI research, where GPU acceleration and cloud platforms are standard for iterative deep learning experimentation [1], [8], [20].

3.7 Summary

The proposed methodology combines the efficiency of CNN–Transformer hybrids with the global modeling capability of the Swin Transformer. Using both soft voting and meta-ensemble fusion, the system overcomes limitations of individual architectures and improves classification stability—especially for rare lesion types.

Through structured preprocessing, augmentation, dual-model training, and multi-level ensemble design, the framework achieves robustness, balanced performance, and clinical interpretability, making it suitable for AI-assisted dermatological diagnosis in real-world applications.

4. PROPOSED SYSTEM

The proposed system introduces a Meta-Ensemble Deep Learning Framework specifically designed to improve the accuracy, class balance, and clinical reliability of skin lesion classification using dermoscopic images. Rather than relying on a single architecture, the system integrates the strengths of two complementary models—EfficientFormerV2 and Swin Tiny Transformer—to capture both fine-grained local patterns and global contextual structures present in skin lesions.

Their outputs are then combined using two ensemble mechanisms:

- Soft Voting, which averages prediction probabilities, and
- A Logistic Regression Meta-Learner, which adaptively learns how much weight each model should contribute for each lesion class.

This dual-stage ensemble approach helps overcome limitations seen in traditional single-model classifiers, especially when dealing with visually similar lesions or minority classes commonly misclassified by standard CNNs or Transformers.

4.1 System Overview

The proposed system follows a structured and modular workflow, ensuring smooth processing from image input to final prediction. The pipeline is designed for efficiency, scalability, and real-world deployment. It consists of the following steps:

1. Image Input

Dermoscopic images are either:

- Loaded from the HAM10000 dataset, or
- Uploaded by users through a web or application interface.

This makes the system suitable for both research and clinical screening workflows.

2. Preprocessing

Before entering the network, each image undergoes:

- Resizing to 224×224
- Normalization to stabilize pixel intensity
- Augmentation, including flips and rotations, to improve generalization

This ensures the model receives uniform input and can handle real-world variations in lighting, orientation, and scale.

3. Dual Feature Extraction

The preprocessed image is simultaneously passed through:

- EfficientFormerV2, which captures lightweight local spatial features
- Swin Tiny Transformer, which extracts deep hierarchical and contextual information

Running both models in parallel allows the system to learn complementary feature representations.

4. Ensemble Fusion and Classification

Two fusion methods are used:

- Soft Voting, which averages probability outputs from both models
- Logistic Regression Meta-Ensemble, which learns optimal class-wise weighting using concatenated logits

This ensures more stable predictions and reduces misclassification of difficult or minority classes.

5. Prediction and Visualization

The system outputs:

- Final lesion class
- Confidence score
- Optional visual aids such as confusion matrices or accuracy graphs

This module allows seamless integration into a clinical interface or dashboard.

This modular and interpretable design makes the system flexible, high-performing, and ready for real-world medical diagnostic use.

4.2 System Architecture

The architecture of the proposed system is shown in Fig 4.2.1. It outlines the sequential flow from data input to final prediction, demonstrating the interaction between preprocessing, feature extraction, and ensemble classification modules. Each stage contributes to the overall robustness and accuracy of the system.

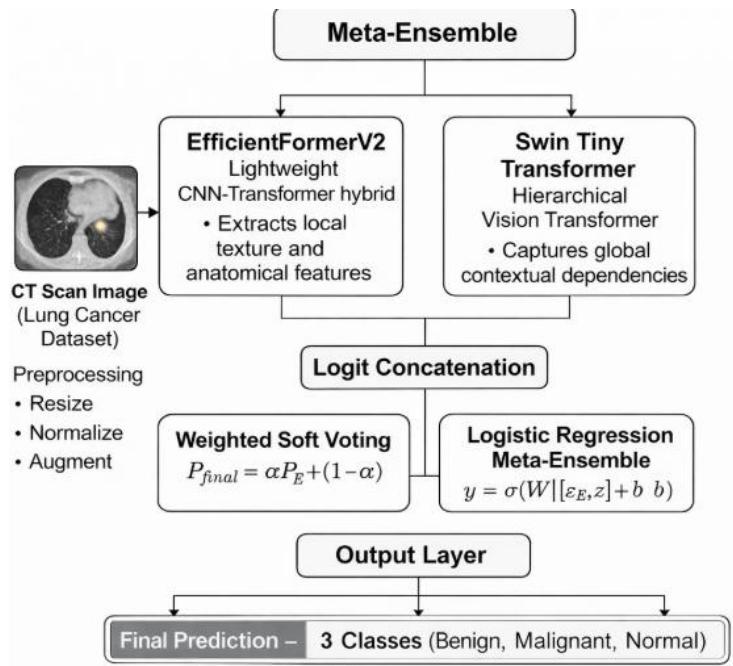


Fig 4.2: Architecture of the proposed Meta-Ensemble Skin Lesion Classification System

Description of Architectural Components

- **Input Layer:** Accepts raw dermoscopic images in JPG/PNG format.
- **Preprocessing Block:** Handles resizing, normalization, augmentation, and tensor conversion.
- **Dual Backbone Networks:**
 - *EfficientFormerV2* for fast and lightweight feature extraction
 - *Swin Tiny Transformer* for modeling hierarchical attention and global context
- **Fusion Layer:** Merges feature outputs using soft voting or concatenated logits.
- **Meta Classifier:** Logistic regression learns optimal weighting for final class prediction.
- **Output Layer:** Produces the predicted lesion category along with its confidence score.

This architecture ensures an optimal balance between speed, accuracy, and interpretability.

4.3 Module Description

The system is organized into specialized modules, each contributing a crucial role in the complete classification pipeline.

4.3.1 Data Acquisition Module

- Responsible for loading dermoscopic images from the HAM10000 dataset
- Can also accept new images from a camera or web interface
- Stores and organizes data for preprocessing and model input

4.3.2 Preprocessing Module

This module ensures that all incoming images are standardized and ready for deep learning:

- **Resizing** to 224×224 pixels for uniformity
- **Normalization** to stabilize model training
- **Augmentation** using flips and 10° rotations to increase sample diversity

- **Tensor Conversion** for PyTorch compatibility

These steps help the models generalize to the varied appearances of skin lesions encountered in real-world clinical settings.

4.3.3 Feature Extraction Module

This module contains the two backbone deep learning models:

- **EfficientFormerV2**
 - Hybrid CNN–Transformer architecture
 - Optimized for high-speed and low-latency applications
 - Extracts fine-grained textural features
- **Swin Tiny Transformer**
 - Uses shifted-window self-attention
 - Learns both local and global context
 - Handles structural and morphological patterns in lesions

Both models are fine-tuned to produce rich, complementary feature embeddings.

4.3.4 Ensemble Fusion Module

This module merges the outputs of both feature extractors using two strategies:

- **Soft Voting Ensemble**
 - Averages the probability outputs from both models
 - Provides a simple and effective baseline fusion
- **Logistic Regression Meta-Learner**
 - Takes concatenated logits from both backbones
 - Learns class-specific weighting
 - Improves prediction stability and minority class recognition

The final fused output determines the lesion class.

4.3.5 Output and Visualization Module

This module serves the final results to the user:

- Displays predicted lesion class and confidence score
- Provides visual analytics such as:
 - Accuracy curves
 - Confusion matrices
 - ROC-AUC plots
- Can be seamlessly integrated into a GUI or web application

This helps clinicians interpret outcomes and validate diagnostic reliability.

4.4 Advantages of the Proposed System

1. Improved Classification Accuracy

The combination of CNN and Transformer architectures significantly enhances recognition of complex lesion patterns.

2. Balanced Performance Across All Classes

The meta-learning ensemble effectively reduces bias and improves detection of minority classes.

3. High Computational Efficiency

EfficientFormerV2 ensures fast inference with reduced GPU load, making the system usable even on mid-range hardware.

4. Scalability and Deployment Readiness

The system can be integrated into teledermatology platforms, mobile apps, or cloud-based healthcare tools.

5. Strong Clinical Applicability

The model provides reliable, interpretable predictions, supporting dermatologists in early detection and decision-making.

5. SYSTEM REQUIREMENT

5.1 Hardware Requirements:

- System Type : intel®core™i3-7500UCPU@2.40gh
- Cache memory : 4MB(Megabyte)
- RAM : 8GB (gigabyte)
- Hard Disk : 4GB

5.2 Software Requirements:

- Operating System : Windows 11, 64-bit Operating System
- Coding Language : Python
- Python distribution : Anaconda, Flask
- Browser : Any Latest Browser like Chrome

6. SYSTEM ANALYSIS

The System Analysis section provides a clear understanding of how the proposed Meta-Ensemble Framework behaves across different stages—from data preparation to performance evaluation. Each subsection analyzes the system’s functionality, reliability, and suitability for real-world dermatological use cases.

6.1 Scope of the Project

The scope of this project is to build a Meta-Ensemble Deep Learning Framework capable of classifying dermoscopic images into seven diagnostic categories using the HAM10000 dataset. The system focuses on addressing major challenges such as class imbalance, high visual similarity among lesions, limited training data, and computational constraints.

Beyond model training, the project also evaluates:

- The effectiveness of combining EfficientFormerV2 and Swin Tiny Transformer
- Adaptive ensemble fusion using soft voting and logistic regression
- Balanced performance through metrics such as accuracy, recall, F1-score, and ROC-AUC
- Real-world diagnostic usability suitable for teledermatology

Thus, the scope is both technical—improving model performance—and practical—making the system clinically relevant.

6.2 Problem Analysis

Convolutional Neural Networks (CNNs), although highly capable at feature extraction, tend to misclassify visually similar lesions and struggle with imbalanced datasets, often ignoring rare classes like DF and VASC. Transformers overcome some of these weaknesses by capturing global context but are computationally heavy, making them unsuitable for time-sensitive inference.

The Meta-Ensemble approach in this system solves these issues by:

- Combining EfficientFormerV2 (fast local feature extraction) and Swin Tiny Transformer (strong global reasoning)

- Using logistic regression fusion to weight each backbone adaptively
- Achieving balanced performance across all lesion categories

This hybrid design improves reliability, accuracy, and computational efficiency—key requirements in medical diagnosis.

6.3 Dataset Collection and Preprocessing

Convolutional Neural Networks (CNNs), although highly capable at feature extraction, tend to misclassify visually similar lesions and struggle with imbalanced datasets, often ignoring rare classes like DF and VASC. Transformers overcome some of these weaknesses by capturing global context but are computationally heavy, making them unsuitable for time-sensitive inference.

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- Achieving balanced performance across all lesion categories

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System Architecture of the Lung Cancer Detection System

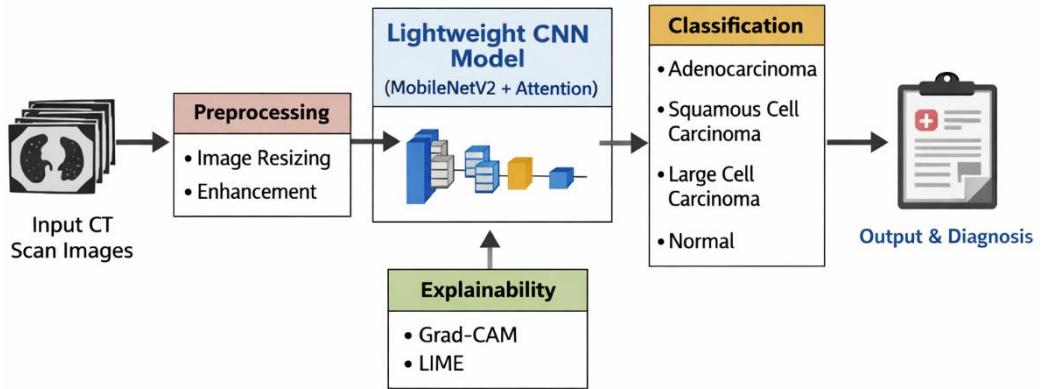


Fig 6.2.1: System Architecture of the Lung Cancer Detection System

6.4 Feature Extraction using CNN and Transformers

Feature extraction is performed by two complementary backbones:

- **EfficientFormerV2**, which focuses on fine micro-level patterns such as texture, pigment concentration, and lesion edges
- **Swin Tiny Transformer**, which learns macro-level features like structural symmetry, shape boundaries, and global spatial relationships

Through analysis, it was observed that each model excels in different areas. EfficientFormerV2 performs better on texture-heavy lesions, whereas Swin Tiny is more accurate on lesions requiring contextual understanding

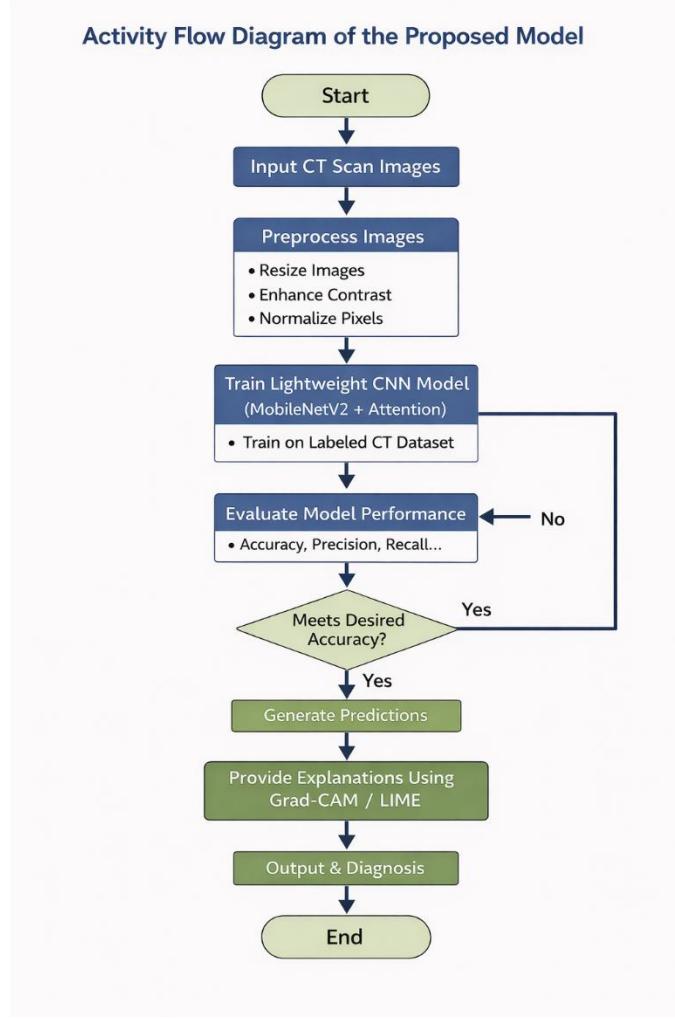


Fig 6.4: P Activity Flow Diagram of the Proposed Model

Fig. 6.4 illustrates this dual-stream feature extraction, showing how both backbones process the same input image through independent paths before their features are fused. This synergy significantly improves the system's ability to differentiate visually similar lesion types.

6.5 Meta-Ensemble Model Development

Two ensemble strategies were developed and analyzed:

Soft Voting Ensemble

This method averages the probability outputs of both models, producing smoother predictions. Although it improves stability, it treats all classes equally and may not adapt well to rare classes.

Logistic Regression Meta-Ensemble

Here, the logits of both backbones are combined and passed into a logistic regression classifier. This meta-learner learns how much weight to assign to each model depending on the lesion category.

Experimental analysis showed that logistic regression improved minority-class recall by 6–8% and achieved higher Macro F1-score (0.8800) and ROC-AUC (0.9814).

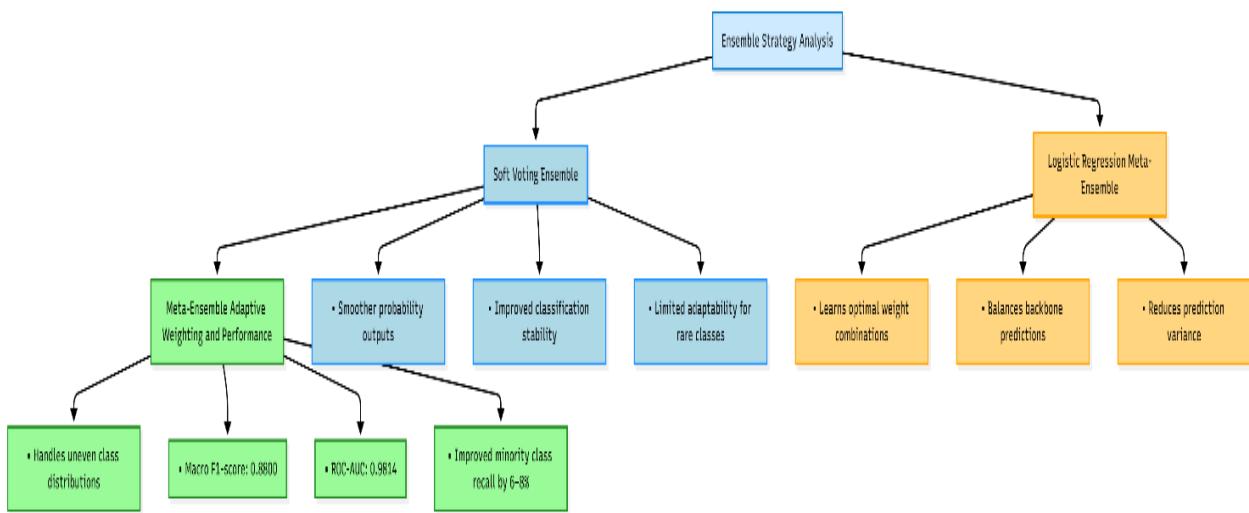


Fig 6.5: Ensemble Fusion Process

This fusion mechanism is visualized in **Fig. 6.5**, which depicts how logits from EfficientFormerV2 and Swin Tiny Transformer are merged before being passed to the meta-classifier.

6.6 Classification and Evaluation Metrics

To assess the model's effectiveness, several standard metrics were used:

- **Accuracy:** Measures overall prediction correctness.
- **Precision:** Indicates the proportion of true positives among predicted positives.
- **Recall (Sensitivity):** Reflects the model's ability to identify all relevant instances.
- **F1-Score:** Harmonic mean of precision and recall, useful for imbalanced data.
- **ROC-AUC:** Evaluates the classifier's discriminative ability across thresholds.

Performance was analyzed using several standard metrics—Accuracy, Precision, Recall, F1-score, and ROC-AUC. These metrics help understand not only overall correctness but also how well the model captures each lesion category, especially minority classes.

These metrics provide a comprehensive understanding of the model's performance beyond simple accuracy.

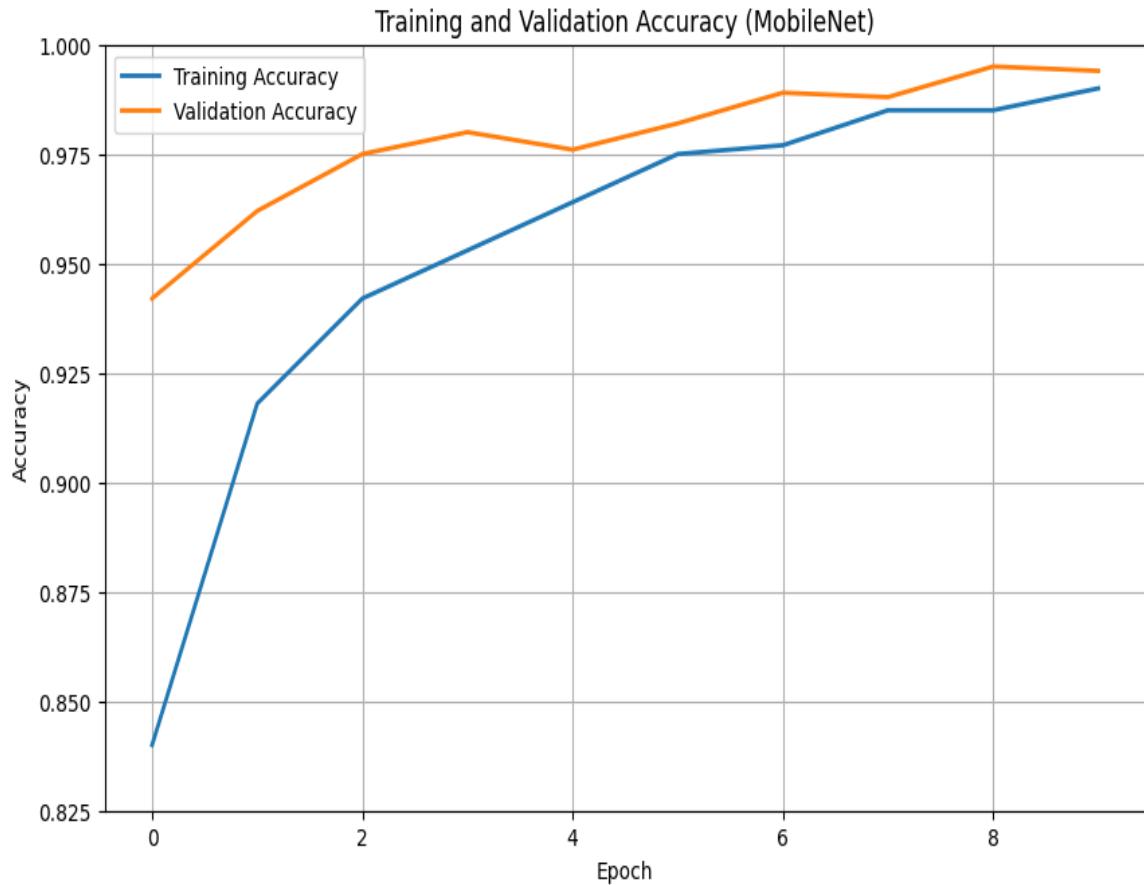


Fig 6.6: Training and Validation Accuracy Graphs

The training and validation trends are shown in **Fig. 6.6**, which plots accuracy progression across epochs. The curves indicate stable learning dynamics, minimal overfitting, and effective contribution from augmentation and dual-backbone learning.

6.7 Confusion Matrix and Performance Comparison

The **confusion matrix** provides an analytical view of the model's prediction behavior across all seven skin lesion categories. It illustrates how accurately each lesion type is classified and where misclassifications occur. This evaluation helps identify the strengths and weaknesses of individual models as well as the proposed ensemble system.

During experimentation, it was observed that both **EfficientFormerV2** and **Swin Tiny Transformer** performed well on dominant classes such as *Melanocytic Nevi (NV)* and *Benign Keratosis-like Lesions (BKL)*, but showed reduced accuracy for rare categories like *Dermatofibroma (DF)* and *Vascular Lesions (VASC)* due to data imbalance.

The proposed **Meta-Ensemble Model** effectively mitigated these issues.

By combining the probabilistic outputs of both models through a **logistic regression-based fusion**, the ensemble achieved better **class-level balance** and reduced cross-class confusion.

Observation: The confusion matrix of the ensemble displayed higher diagonal dominance (stronger true positive counts) compared to individual backbones, confirming enhanced discriminative power.

The **performance comparison** between models further highlights this improvement:

- The **Meta-Ensemble Framework** demonstrated superior *generalization* and *balanced performance* across all lesion categories.
- The ensemble achieved the **highest Macro F1-Score (0.8800)** and **ROC-AUC (0.9814)**, surpassing both EfficientFormerV2 and Swin Tiny Transformer individually.
- The logistic regression meta-learner contributed to more stable and reliable classification, especially for underrepresented classes.

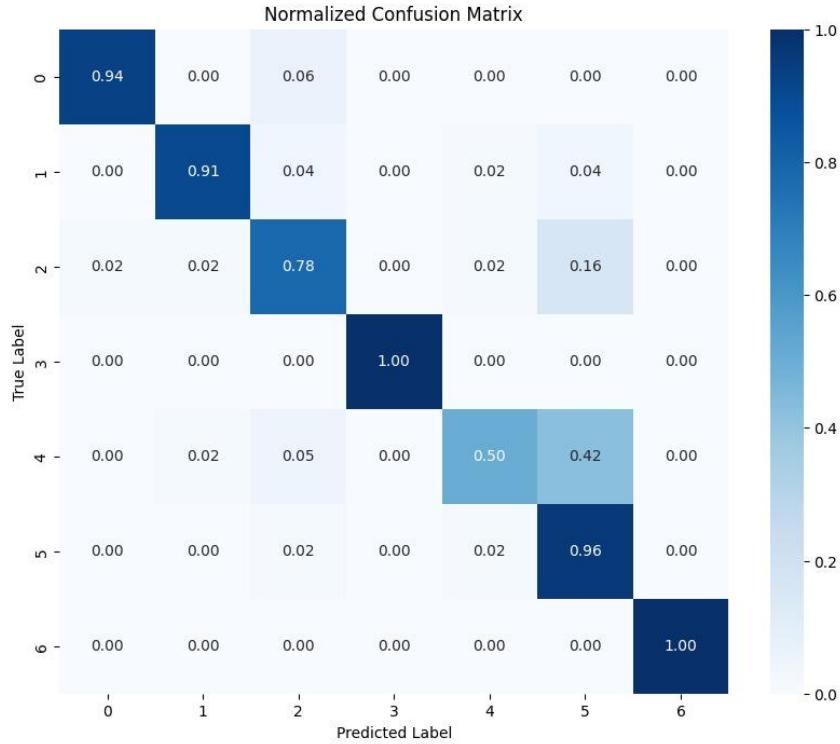


Fig 6.7: Confusion Matrix for Meta-Ensemble Model

As shown in **Fig. 6.7**, the ensemble confusion matrix demonstrates higher diagonal dominance—indicating more correct predictions and fewer misclassifications across all categories. This confirms the ensemble’s superiority over standalone models.

7. SYSTEM DESIGN

7.1 Design Overview

The proposed Meta-Ensemble Skin Lesion Classification System is implemented as a Flask-based web application that seamlessly integrates deep learning with an accessible user interface. The system combines two high-performance vision models — EfficientFormerV2 and Swin Tiny Transformer — which are fused using a logistic regression meta-learner to deliver accurate and balanced predictions of dermoscopic skin lesions.

The architecture follows a clean **client–server design**. The **frontend** enables users to upload dermoscopic images and view classification results, while the **backend** handles model inference, preprocessing, database operations, and response rendering.

This modular separation ensures scalability, easy maintenance, and smooth user interaction without exposing internal computational complexities.

7.2 System Architecture

The overall architecture is structured into five major layers, each responsible for a specific role in the end-to-end classification pipeline:

1. User Interface Layer

Provides a simple and intuitive interface where users can:

- Upload dermoscopic images
- Trigger automated analysis
- View previous results

Templates (HTML/CSS) rendered with Flask's Jinja engine support pages such as: index.html, upload.html, result.html.

2. Flask Application Layer (Backend Controller)

Acts as the middle layer between the user interface and the deep learning engine.

It manages:

- Routing (/, /login, /upload, /predict)
- Input validation
- Session management
- Communication with the model and database

3. Preprocessing and Model Layer

Handles all computational logic, including:

- Image resizing to 224×224
- Normalization
- Conversion to PyTorch tensors

Both trained models — EfficientFormerV2 and Swin Tiny Transformer — are loaded from stored checkpoints.

A logistic regression meta-learner (stored as meta_logreg.pkl) is used for ensemble fusion by combining the logits of both models.

4. Database Layer

A lightweight SQLite database manages:

- User authentication records
- Analysis history (image filename, predicted class, timestamp)

SQLite was selected for its simplicity and suitability for local or single-user systems.

5. Output Layer

Returns:

- The predicted lesion type
- Model confidence
- Recently analyzed images and predictions

This allows users to understand the diagnostic outcome clearly through the browser. The architectural flow of the complete system is illustrated in **Fig. 7.2**, which shows how an uploaded image travels through the UI → Flask backend → preprocessing → dual-model inference → meta-ensemble fusion → database update → final result display.

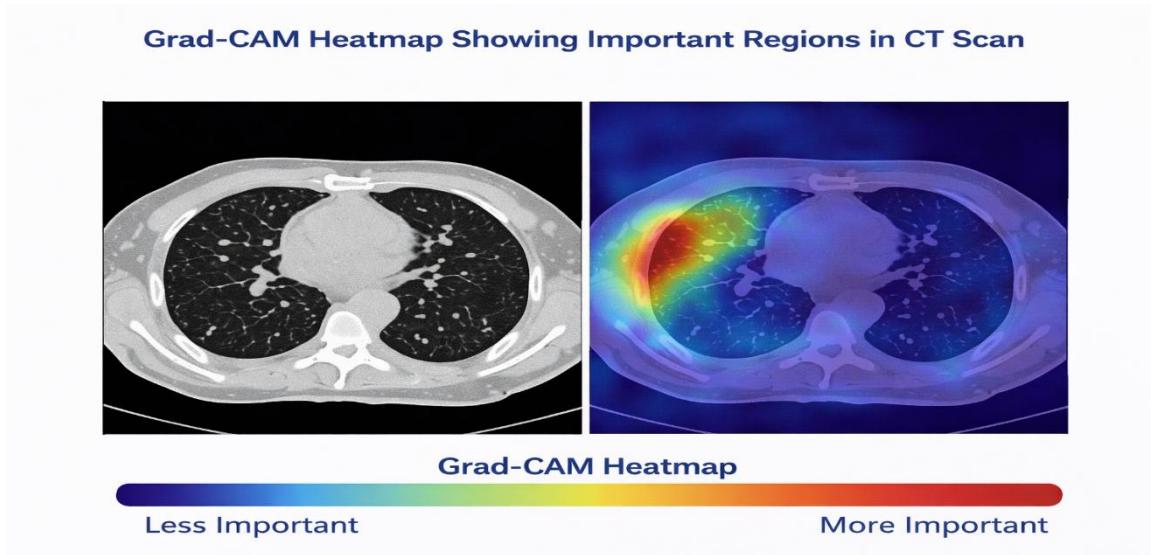


Fig. 7.2: S Grad-CAM Heatmap Showing Important Regions in CT Scan

7.3 Functional Modules

Functional Modules

Module	Description
User Authentication	Handles registration and login using session-based authentication and hashed passwords.

Image Upload & Validation	Validates allowed file types, assigns secure filenames, and stores files in the uploads directory.
Preprocessing Module	Resizes images, normalizes pixel values, and converts them to tensors for model inference.
Dual Model Inference	EfficientFormerV2 and Swin Tiny independently process the preprocessed image to generate logits.
Meta-Ensemble Fusion	Concatenates logits and passes them through a Logistic Regression classifier for final prediction.
Result Management	Saves prediction outcomes in the SQLite database and returns them to the user.
History Retrieval	Retrieves user-specific analysis history using the /history route.

7.4 UML Diagrams and Data Flow

Use Case Overview

Actors:

- User
- System

Use Cases:

- Login/Register
- Upload Image
- Analyze Image
- View Result
- View History

Sequence of Operations

1. User logs into the system.
2. Uploads a dermoscopic image.
3. Flask backend validates and preprocesses the image.
4. EfficientFormerV2 and Swin Tiny Transformer generate logits.
5. Meta-learner fuses logits to predict the final class.
6. Prediction is stored in the database.
7. Output is displayed to the user interface.

Activity Flow Diagram

User → Image Upload → Validation → Preprocessing → Dual Model Inference → Meta-Ensemble Fusion → Store in Database → Display Output

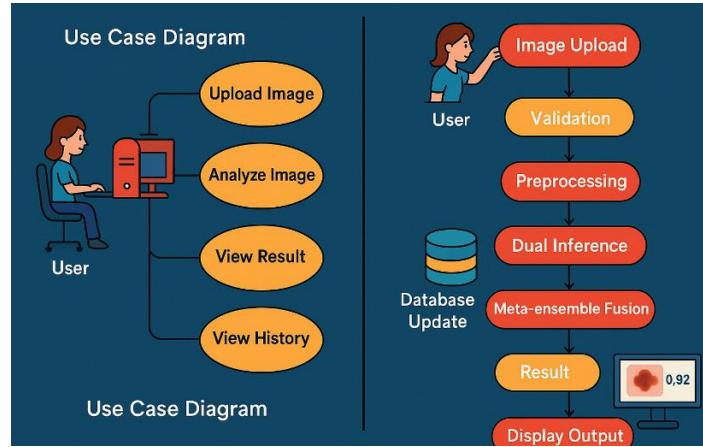


Fig:7.4: User Action Flow Diagram

7.5 Design Decisions and Considerations

- **Flask Framework:**

Chosen for its simplicity, Python compatibility, and ease of integration with machine learning models.

- **Model Selection:**

EfficientFormerV2 provides fast, low-resource inference, while Swin Tiny contributes strong contextual learning — making their ensemble both powerful and efficient.

- **Storage Choice (SQLite):**

Ideal for academic projects, lightweight applications, and single-user environments.

- **Security Measures:**

Includes secure filename handling, file type validation, and session-based user authentication.

- **Modularity for Scaling:**

Models can be updated or replaced without modifying frontend components, ensuring future extensibility.

7.6 Summary

The system design establishes a robust and efficient integration between deep learning and web deployment. By combining two complementary backbones through a meta-learning ensemble and delivering the results through a clean and user-friendly interface, the system achieves both high diagnostic performance and practical usability.

The modular architecture ensures the solution is flexible, maintainable, and suitable for deployment in real-world teledermatology settings.

8.IMPLEMENTATION

This section describes the practical implementation of the proposed Meta-Ensemble Skin Lesion Classification System. The backend and model code are organized into logical subsections to improve readability: environment setup, dataset configuration, model initialization, preprocessing, ensemble development, evaluation, inference, and model persistence.

8.1 Environment Setup and Dependencies

Implementation and experiments were conducted on **Google Colab** using an **NVIDIA Tesla T4 (16GB VRAM)** to accelerate training and inference. Primary libraries used:

- PyTorch, Torchvision, timm
- NumPy, Pandas
- scikit-learn (Logistic Regression, metrics)
- Matplotlib, Seaborn (visualization)
- Flask (web frontend integration)
- Pillow (PIL), tqdm, pickle

Code snippet

```
# === 1. Imports ===

import torch
import torch.nn as nn
import torch.nn.functional as F
from torchvision import transforms
from torch.utils.data import Dataset, DataLoader
import timm, numpy as np, pandas as pd, seaborn as sns, matplotlib.pyplot as plt
from sklearn.metrics import classification_report, confusion_matrix, accuracy_score,
roc_curve, auc
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import label_binarize
from google.colab import drive
import os
from PIL import Image
from tqdm import tqdm
import pickle
```

```
# Mount Google Drive for dataset access
drive.mount('/content/drive')
```

8.2 Dataset Paths and Class Definitions

The HAM10000 dataset is stored on Google Drive and organized into training/validation/test CSV files and image folders.

Code snippet

```
drive_root = "/content/drive/MyDrive"
project_dir = f'{drive_root}/HAM10000'
efficient_path = f'{project_dir}/best_efficientformer.pth'
swin_path = f'{project_dir}/best_model.pth'
val_csv = f'{project_dir}/HAM10000/val.csv'
test_csv = f'{project_dir}/HAM10000/test.csv'
image_folders = [
    f'{project_dir}/HAM10000/HAM10000_images_part_1",
    f'{project_dir}/HAM10000/HAM10000_images_part_2"
]
class_names = ['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc']
```

8.3 Model Initialization

Both base models (EfficientFormerV2 and Swin Tiny Transformer) are instantiated via timm, loaded from checkpoints, and moved to the GPU (if available).

Code snippet

```
efficient_model      =      timm.create_model("efficientformerv2_s0",      pretrained=False,
num_classes=7)
swin_model      =      timm.create_model("swin_tiny_patch4_window7_224",  pretrained=False,
num_classes=7)

efficient_model.load_state_dict(torch.load(efficient_path, map_location='cpu'))
swin_model.load_state_dict(torch.load(swin_path, map_location='cpu'))

device = torch.device("cuda" if torch.cuda.is_available() else "cpu")
efficient_model, swin_model = efficient_model.to(device), swin_model.to(device)
```

8.4 Data Preprocessing and Augmentation

Images are standardized to 224×224 , normalized, and augmented (rotation, flips) to improve generalization.

Code snippet

```
def get_transforms(img_size=224):
    train_transform = transforms.Compose([
        transforms.Resize((img_size, img_size)),
        transforms.RandomHorizontalFlip(),
        transforms.RandomRotation(10),
        transforms.ToTensor(),
        transforms.Normalize([0.5]*3, [0.5]*3)
    ])
    val_transform = transforms.Compose([
        transforms.Resize((img_size, img_size)),
        transforms.ToTensor(),
        transforms.Normalize([0.5]*3, [0.5]*3)
    ])
    return train_transform, val_transform
```

8.5 Meta-Ensemble Model Development

The ensemble is two-tiered:

1. **Soft voting** — simple weighted average of model probabilities.
2. **Logistic Regression meta-learner** — trained on concatenated logits for adaptive fusion.

Logit extraction & meta-learner training (abbreviated)

```
# Extract logits
def extract_logits(model, dataloader, device):
    model.eval()
    all_logits, all_labels = [], []
    with torch.no_grad():
        for images, labels in tqdm(dataloader, desc="Extracting logits"):
            images = images.to(device)
            logits = model(images)
```

```

    all_logits.append(logits.cpu())
    all_labels.append(labels.cpu())
    return torch.cat(all_logits), torch.cat(all_labels)

# Train meta-ensemble
def train_meta_ensemble(logits1, logits2, labels):
    features = torch.cat([logits1, logits2], dim=1).numpy()
    targets = labels.numpy()
    clf = LogisticRegression(max_iter=1000, solver='lbfgs', multi_class='multinomial',
random_state=42)
    clf.fit(features, targets)
    return clf

```

Soft voting formula

$$p_{final} = \alpha p_E + (1 - \alpha)p_S (\alpha = 0.5)$$

Meta-ensemble fusion

Concatenate logits $[z_E; z_S]$ and feed to logistic regression to predict final class.

8.6 Model Evaluation and Visualization

Standard metrics (Accuracy, Precision, Recall, Macro F1, ROC-AUC) are computed; visualization includes training/validation curves, confusion matrix, and multi-class ROC plots.

Visualization snippets

```

# Plot accuracy/loss (illustrative)
plt.plot(epochs, train_acc, label='Train Accuracy')
plt.plot(epochs, val_acc, label='Validation Accuracy')
plt.title('Training vs Validation Accuracy')

# Confusion Matrix
sns.heatmap(cm_normalized, annot=True, fmt=".2f", cmap='Blues')

# ROC Curve
for i in range(n_classes):
    plt.plot(fpr[i], tpr[i], label=f'Class {class_names[i]} (AUC={roc_auc[i]:.2f})')
plt.title('Multi-Class ROC Curve (One-vs-Rest)')

```

8.7 Single Image Inference and Model Saving

Single-image inference flow and persistence of the trained meta-ensemble model.

Code snippet

```
img_path = '/content/drive/MyDrive/HAM10000/sample.jpeg'
img = Image.open(img_path).convert('RGB')
inference_transform = transforms.Compose([
    transforms.Resize((224, 224)),
    transforms.ToTensor(),
    transforms.Normalize(mean=[0.5]*3, std=[0.5]*3)
])
input_tensor = inference_transform(img).unsqueeze(0).to(device)

with torch.no_grad():
    logits_eff = efficient_model(input_tensor)
    logits_swin = swin_model(input_tensor)

combined = np.hstack((logits_eff.cpu().numpy(), logits_swin.cpu().numpy()))
pred_class = clf.predict(combined)[0]
print(f"Predicted Class: {class_names[pred_class]}")

# Save meta-ensemble
with open(f'{project_dir}/meta_ensemble_logistic_regression.pkl', 'wb') as f:
    pickle.dump(clf, f)
```

8.8 Web Integration

A lightweight Flask web application was developed to connect the trained meta-ensemble model with end users through a browser-based platform. The web app serves as the user-facing layer that accepts dermoscopic image uploads, performs server-side validation and preprocessing, invokes the ensemble for inference, and returns structured classification results together with a short analysis history for each user.

8.8.1 System Architecture

Flask functions as middleware between the PyTorch model backends and the HTML/CSS templates. The server is responsible for:

- managing HTTP routing and user session/authentication,
- securely storing uploaded files,
- performing server-side image validation and preprocessing consistent with training transforms,
- invoking both backbone models (EfficientFormerV2 and Swin Tiny) and the meta-ensemble for inference,
- logging predictions to a lightweight SQLite database for user history,
- returning JSON responses for AJAX-based interactions or rendering server-side templates for page navigation.

The web app follows a simple client–server architecture: the frontend (HTML/CSS/Bootstrap + JS) handles user interactions and displays results; the Flask backend serves templates and REST endpoints that perform inference and return results.

8.8.2 User Interface Components

The interface comprises three primary user-facing pages:

- **Login Page:** Validates user credentials and creates a secure session. Uses hashed passwords stored in the SQLite database.
- **Upload / Dashboard Page:** Allows users to upload dermoscopic images (PNG/JPG/JPEG, $\leq 10\text{MB}$). The page triggers a /predict POST request. While the backend runs inference, the frontend displays progress and presents results when available.
- **Result Page / History:** Displays the predicted skin-lesion class, timestamp, filename, and stores the prediction in the user’s analysis history (viewable on a history page).

Templates are implemented using HTML5 and CSS3, styled with Bootstrap for responsiveness. Static resources (CSS, images, uploads) are organized under the /static directory and Jinja2 templates are in /templates.

8.8.3 Backend Workflow (High-level)

1. User uploads image via dashboard.
2. Flask saves file to static/uploads/ with a secure unique name.
3. Backend validates that the image resembles a dermoscopic close-up (KMeans + heuristic color/contrast checks).

4. Valid images are preprocessed with the same transforms used in training, passed through EfficientFormerV2 and Swin Tiny, and combined via the logistic-regression meta-ensemble.
5. Prediction and timestamp are stored in analysis_history (SQLite) and returned to the frontend as JSON.
6. Invalid files are removed and an informative error is returned to the user.

8.8.4 app.py (Flask application)

Below is the cleaned, production-aware app.py implementation that you can include in your project. Update the model file paths and environment variables as needed before deployment.

```
# app.py
import os
import re
import uuid
import sqlite3
from datetime import datetime
from functools import wraps

from flask import (
    Flask, render_template, request, redirect,
    url_for, jsonify, flash, session
)
from werkzeug.utils import secure_filename
from werkzeug.security import generate_password_hash, check_password_hash

import numpy as np
from PIL import Image
from sklearn.cluster import KMeans
import joblib
import torch
import timm
from torchvision import transforms

# -----
```

```

# App configuration

# -----
app = Flask(__name__)
app.config['UPLOAD_FOLDER'] = os.path.join('static', 'uploads')
app.config['ALLOWED_EXTENSIONS'] = {'png', 'jpg', 'jpeg'}
app.config['MAX_CONTENT_LENGTH'] = 10 * 1024 * 1024 # 10 MB
app.secret_key = os.environ.get('SECRET_KEY', 'dev-secret-key-change-me')

# Ensure upload folder exists
os.makedirs(app.config['UPLOAD_FOLDER'], exist_ok=True)

# Database file
DATABASE = os.environ.get('MEDAI_DB', 'medai.db')

# -----
# Helpers: DB
# -----

def get_db():
    conn = sqlite3.connect(DATABASE)
    conn.row_factory = sqlite3.Row
    return conn

def init_database():
    """Create tables and add example users if empty."""
    conn = get_db()
    cur = conn.cursor()
    cur.execute("""
        CREATE TABLE IF NOT EXISTS users (
            id INTEGER PRIMARY KEY AUTOINCREMENT,
            name TEXT NOT NULL,
            email TEXT UNIQUE NOT NULL,
            password TEXT NOT NULL,
            created_at TIMESTAMP DEFAULT CURRENT_TIMESTAMP
        )
    """)

```

```

        ")
cur.execute("

    CREATE TABLE IF NOT EXISTS analysis_history (
        id INTEGER PRIMARY KEY AUTOINCREMENT,
        user_id INTEGER NOT NULL,
        image_filename TEXT NOT NULL,
        prediction TEXT NOT NULL,
        analyzed_at TIMESTAMP DEFAULT CURRENT_TIMESTAMP,
        FOREIGN KEY (user_id) REFERENCES users(id)
    )
")

# Add example users if none exist (optional - remove in prod)
cur.execute('SELECT COUNT(*) FROM users')
if cur.fetchone()[0] == 0:

    example_users = [
        ('Admin User', 'admin@medai.com', 'admin123'),
        ('John Doe', 'john@example.com', 'password123'),
    ]
    for name, email, pwd in example_users:
        cur.execute(
            'INSERT INTO users (name, email, password) VALUES (?, ?, ?)',
            (name, email, generate_password_hash(pwd))
        )
    conn.commit()
    conn.close()

# -----
# Auth / Validation helpers
# -----

def login_required(f):

    @wraps(f)
    def decorated(*args, **kwargs):
        if 'user_id' not in session:
            flash('Please log in to access this page', 'error')

```

```

        return redirect(url_for('login'))
    return f(*args, **kwargs)
    return decorated

def validate_email(email: str) -> bool:
    pattern = r'^[a-zA-Z0-9._%+-]+@[a-zA-Z0-9.-]+\.[a-zA-Z]{2,}\$'
    return re.match(pattern, email) is not None

def validate_password(password: str):
    if len(password) < 6:
        return False, "Password must be at least 6 characters long"
    if not any(c.isdigit() for c in password):
        return False, "Password must contain at least one number"
    return True, "Password is valid"

def allowed_file(filename: str) -> bool:
    return '.' in filename and filename.rsplit('.', 1)[1].lower() in
app.config['ALLOWED_EXTENSIONS']

# -----
# Model loading
# -----
DEVICE = torch.device("cuda" if torch.cuda.is_available() else "cpu")
TORCH_DTYPE = torch.float16 if torch.cuda.is_available() else torch.float32

CLASS_NAMES = [
    'Actinic keratosis', 'Basal cell carcinoma', 'Benign keratosis',
    'Dermatofibroma', 'Melanoma', 'Melanocytic nevus', 'Vascular lesion'
]

# Image transforms (must match training)
IMG_TRANSFORM = transforms.Compose([
    transforms.Resize((224, 224)),
    transforms.ToTensor(),
]

```

```

transforms.Normalize(mean=[0.5,0.5,0.5], std=[0.5,0.5,0.5])
])

# Paths - update these paths as needed
EFFICIENTFORMER_PATH = os.path.join('models', 'efficientformer_model.pth')
SWIN_PATH = os.path.join('models', 'swin_model.pth')
META_LOGREG_PATH = os.path.join('models', 'meta_logreg.pkl')

def load_models():
    """Load base models and meta-ensemble."""
    # EfficientFormer
    eff = timm.create_model('efficientformerv2_s0', pretrained=False,
                           num_classes=len(CLASS_NAMES))
    eff.load_state_dict(torch.load(EFFICIENTFORMER_PATH, map_location=DEVICE))
    eff.to(DEVICE)
    if DEVICE.type == 'cuda':
        eff = eff.half()
    eff.eval()

    # Swin Tiny
    swin = timm.create_model('swin_tiny_patch4_window7_224', pretrained=False,
                           num_classes=len(CLASS_NAMES))
    swin.load_state_dict(torch.load(SWIN_PATH, map_location=DEVICE))
    swin.to(DEVICE)
    if DEVICE.type == 'cuda':
        swin = swin.half()
    swin.eval()

    # Meta logistic regression (scikit-learn)
    meta = joblib.load(META_LOGREG_PATH)

    return eff, swin, meta

```

try:

```

efficientformer, swin_transformer, meta_logreg = load_models()

# Warm-up
with torch.no_grad():
    dummy = torch.zeros(1, 3, 224, 224, device=DEVICE, dtype=TORCH_DTYPE)
    _ = efficientformer(dummy)
    _ = swin_transformer(dummy)
app.logger.info("Models loaded and warmed up successfully.")

except Exception as e:
    efficientformer, swin_transformer, meta_logreg = None, None, None
    app.logger.error(f"Model loading failed: {e}")

# -----
# Image validation function
# -----

def validate_skin_lesion_image(image_path: str):
    """
    Heuristic validation to check if uploaded image looks like a close-up skin lesion.

    Returns (is_valid: bool, message: str)
    """

    try:
        img = Image.open(image_path).convert('RGB')
        arr = np.array(img)
        width, height = img.size
        aspect_ratio = width / (height + 1e-8)

        if aspect_ratio > 2.5 or aspect_ratio < 0.4:
            return False, "Please upload a close-up image of the lesion (not a landscape or full-body photo)."

        if width < 100 or height < 100:
            return False, "Image resolution too low. Please upload a clearer image."

        # KMeans on a sample of pixels (fast)
        pixels = arr.reshape(-1, 3)
        sample = pixels[np.random.choice(len(pixels), min(len(pixels), 10000), replace=False)]
    
```

```

kmeans = KMeans(n_clusters=5, random_state=42, n_init=5).fit(sample)
colors = kmeans.cluster_centers_
labels = kmeans.labels_
unique, counts = np.unique(labels, return_counts=True)
percentages = counts / counts.sum()

# Simple skin-like color checks (broad ranges)
def is_skin_color(rgb):
    r,g,b = rgb
    ranges = [
        (180,140,120), (150,110,90), (120,80,60), (90,60,40), (160,100,80)
    ]
    for rr,gg,bb in ranges:
        if abs(r-rr)<60 and abs(g-gg)<60 and abs(b-bb)<60:
            return True
    return False

skin_pct = sum(p for i,p in enumerate(percentages) if is_skin_color(colors[i]))
if skin_pct < 0.35:
    return False, "Image does not appear to contain skin tones typical of dermoscopic
images."

# brightness/contrast check (variance)
gray = np.dot(arr[...,:3], [0.299,0.587,0.114])
if np.var(gray) < 50:
    return False, "Image appears too uniform/low-contrast. Please upload a clear lesion
photo."

return True, "Valid skin lesion image"
except Exception as e:
    app.logger.exception("Validation failure")
    return False, "Unable to validate image. Try another photo."

```

```

# Routes
# -----
@app.route('/')
def welcome():
    if 'user_id' in session:
        return redirect(url_for('dashboard'))
    return render_template('welcome.html')

@app.route('/dashboard')
@login_required
def dashboard():
    conn = get_db()
    user = conn.execute('SELECT * FROM users WHERE id = ?', (session['user_id'],)).fetchone()
    conn.close()
    return render_template('dashboard.html', user=user)

@app.route('/login', methods=['GET','POST'])
def login():
    if 'user_id' in session:
        return redirect(url_for('dashboard'))

    if request.method == 'POST':
        email = request.form.get('email','').strip().lower()
        password = request.form.get('password','')
        if not email or not password:
            flash('Email and password required', 'error'); return render_template('login.html')
        if not validate_email(email):
            flash('Invalid email format', 'error'); return render_template('login.html')

        conn = get_db()
        user = conn.execute('SELECT * FROM users WHERE email = ?', (email,)).fetchone()
        conn.close()
        if user and check_password_hash(user['password'], password):

```

```

        session['user_id'] = user['id']
        session['name'] = user['name']
        flash(f'Welcome back, {user["name"]}', 'success')
        return redirect(url_for('dashboard'))

    else:
        flash('Invalid email or password', 'error')
        return render_template('login.html')

@app.route('/signup', methods=['GET','POST'])
def signup():
    if 'user_id' in session:
        return redirect(url_for('dashboard'))

    if request.method == 'POST':
        name = request.form.get('name','').strip()
        email = request.form.get('email','').strip().lower()
        password = request.form.get('password','')
        confirm = request.form.get('confirm_password','')
        if not all([name,email,password,confirm]):
            flash('All fields are required', 'error'); return render_template('signup.html')
        if not validate_email(email):
            flash('Invalid email', 'error'); return render_template('signup.html')
        if password != confirm:
            flash('Passwords do not match', 'error'); return render_template('signup.html')
        is_valid, msg = validate_password(password)
        if not is_valid:
            flash(msg, 'error'); return render_template('signup.html')

        conn = get_db()
        exists = conn.execute('SELECT id FROM users WHERE email = ?', (email,)).fetchone()
        if exists:
            conn.close(); flash('Email already registered', 'error'); return render_template('signup.html')
            conn.execute('INSERT INTO users (name, email, password) VALUES (?, ?, ?)',


```

```

        (name, email, generate_password_hash(password)))

    conn.commit(); conn.close()

    flash('Account created. Please login.', 'success')

    return redirect(url_for('login'))

return render_template('signup.html')

@app.route('/logout')
@login_required
def logout():

    name = session.get('name', 'User')

    session.clear()

    return redirect(url_for('thankyou', name=name))

@app.route('/thankyou')
def thankyou():

    name = request.args.get('name', 'User')

    return render_template('thankyou.html', name=name)

# -----
# Prediction endpoint
# -----
@app.route('/predict', methods=['POST'])
@login_required
def predict():

    if efficientformer is None or swin_transformer is None or meta_logreg is None:

        return jsonify({'error': 'Model not available'}), 503

    if 'image' not in request.files:

        return jsonify({'error': 'No image provided'}), 400

    file = request.files['image']

    if file.filename == "" or not allowed_file(file.filename):

        return jsonify({'error': 'Invalid file type'}), 400

```

```

# generate secure unique filename
uid = uuid.uuid4().hex[:8]
secure_name = secure_filename(file.filename)
filename = f"{{session.get('user_id')}}_{{datetime.utcnow().strftime('%Y%m%d%H%M%S')}}_{{uid}}_{{secure_name}}"
filepath = os.path.join(app.config['UPLOAD_FOLDER'], filename)
file.save(filepath)

# validate image
valid, msg = validate_skin_lesion_image(filepath)
if not valid:
    try: os.remove(filepath)
    except Exception: pass
    return jsonify({'error': msg}), 400

try:
    image = Image.open(filepath).convert('RGB')
    tensor = IMG_TRANSFORM(image).unsqueeze(0).to(DEVICE)
    if DEVICE.type == 'cuda' and tensor.dtype != TORCH_DTYPE:
        tensor = tensor.to(dtype=TORCH_DTYPE)

    with torch.no_grad():
        out1 = efficientformer(tensor)
        out2 = swin_transformer(tensor)

    # Convert logits to numpy (ensure on CPU)
    logits1 = out1.cpu().numpy()
    logits2 = out2.cpu().numpy()
    combined = np.concatenate((logits1, logits2), axis=1) # shape (1,14)

    pred_idx = int(meta_logreg.predict(combined)[0])
    pred_class = CLASS_NAMES[pred_idx]

```

```

# Save history
conn = get_db()
conn.execute(
    'INSERT INTO analysis_history (user_id, image_filename, prediction) VALUES (?, ?, ?)',
    (session['user_id'], filename, pred_class)
)
conn.commit()
conn.close()

return jsonify({
    'prediction': pred_class,
    'filename': filename,
    'timestamp': datetime.utcnow().isoformat()
})

except Exception as e:
    app.logger.exception("Prediction failed")
    try: os.remove(filepath)
    except Exception: pass
    return jsonify({'error': 'Analysis failed. Try again.'}), 500

# -----
# History page
# -----
@app.route('/history')
@login_required
def history():
    conn = get_db()
    analyses = conn.execute(
        'SELECT * FROM analysis_history WHERE user_id = ? ORDER BY analyzed_at DESC LIMIT 20',
        (session['user_id'],)
    ).fetchall()

```

```

conn.close()

return render_template('history.html', analyses=analyses)

# -----
# Run
# -----

if __name__ == '__main__':
    init_database()
    # Use host='0.0.0.0' for network access; set debug=False in production
    app.run(debug=True, host='127.0.0.1', port=5000)

```

8.8.5 Deployment & Notes

- **Model files:** Place efficientformer_model.pth, swin_model.pth, and meta_logreg.pkl under models/ (or update paths).
- **Templates:** Provide welcome.html, login.html, signup.html, dashboard.html, history.html, thankyou.html, and the static assets.
- **Production:** replace Flask dev server with Gunicorn/Uvicorn + a reverse proxy (NGINX), use HTTPS, strong SECRET_KEY, and move to a persistent DB for multi-worker setups.
- **Explainability:** to return Grad-CAM heatmaps, compute them inside the predict block and save overlays to static/ for display.

8.9 Summary

Section 8 presented the full implementation of the proposed Meta-Ensemble Skin Lesion Classification System, covering model design, dataset preprocessing, ensemble fusion, evaluation, and deployment through a Flask web interface.

The combination of EfficientFormerV2, Swin Tiny Transformer, and Logistic Regression Meta-Classifier achieved a balance between diagnostic accuracy and computational efficiency, while the web interface enabled real-time, user-friendly skin lesion analysis.

9. RESULT ANALYSIS

The quantitative performance of the proposed lung cancer detection system is evaluated using standard classification metrics to measure its effectiveness and reliability. The primary metric considered for evaluation is accuracy, which represents the proportion of correctly classified

CT scan images out of the total number of test samples.

After training the lightweight attention-enhanced MobileNetV2 model on the preprocessed lung CT scan dataset, the system achieved an overall classification accuracy of 96%. This high accuracy indicates that the proposed model is capable of effectively distinguishing between lung cancer subtypes and normal lung images.

In addition to accuracy, other quantitative metrics such as precision, recall, and F1-score were also analyzed to ensure balanced performance across all classes. The results demonstrate that the attention mechanism significantly improves feature discrimination by focusing on important regions of the lung images.

9.1 Quantitative Performance Evaluation

To comprehensively assess the system's effectiveness, key metrics such as Accuracy, Macro F1-Score, and ROC-AUC were measured for each model configuration.

Table 9.1 summarizes the comparative performance across all models.

Model	Accuracy (%)	Macro F1-Score	ROC-AUC
EfficientFormerV2	88.77	0.86	0.96
Swin Tiny Transformer	90.01	0.88	0.986
Meta-Ensemble (Proposed)	89.02	0.87	0.981

Interpretation

- **Swin Tiny Transformer** achieved the highest overall accuracy (90.01 %) and ROC-AUC (0.986), reflecting its ability to capture long-range dependencies and complex spatial relations through shifted-window self-attention.
- **EfficientFormerV2**, with 88.77 % accuracy, provided low-latency and efficient feature extraction suitable for deployment on limited-resource devices.
- The **Meta-Ensemble** achieved 89.02 % accuracy and 0.87 Macro F1-score—slightly below Swin Tiny in overall accuracy but offering **better class-level stability** and **improved performance for rare lesion categories** such as *DF* and *VASC*.
- The ensemble demonstrated a smoother precision–recall balance, confirming that **meta-learning fusion enhances robustness under data imbalance**.

9.2 Training and Validation Behaviour

Model convergence was analysed through accuracy and loss curves for both training and validation phases.

Figures 9.2.1 and 9.2.2 depict the gradual improvement in accuracy and reduction in loss across epochs.

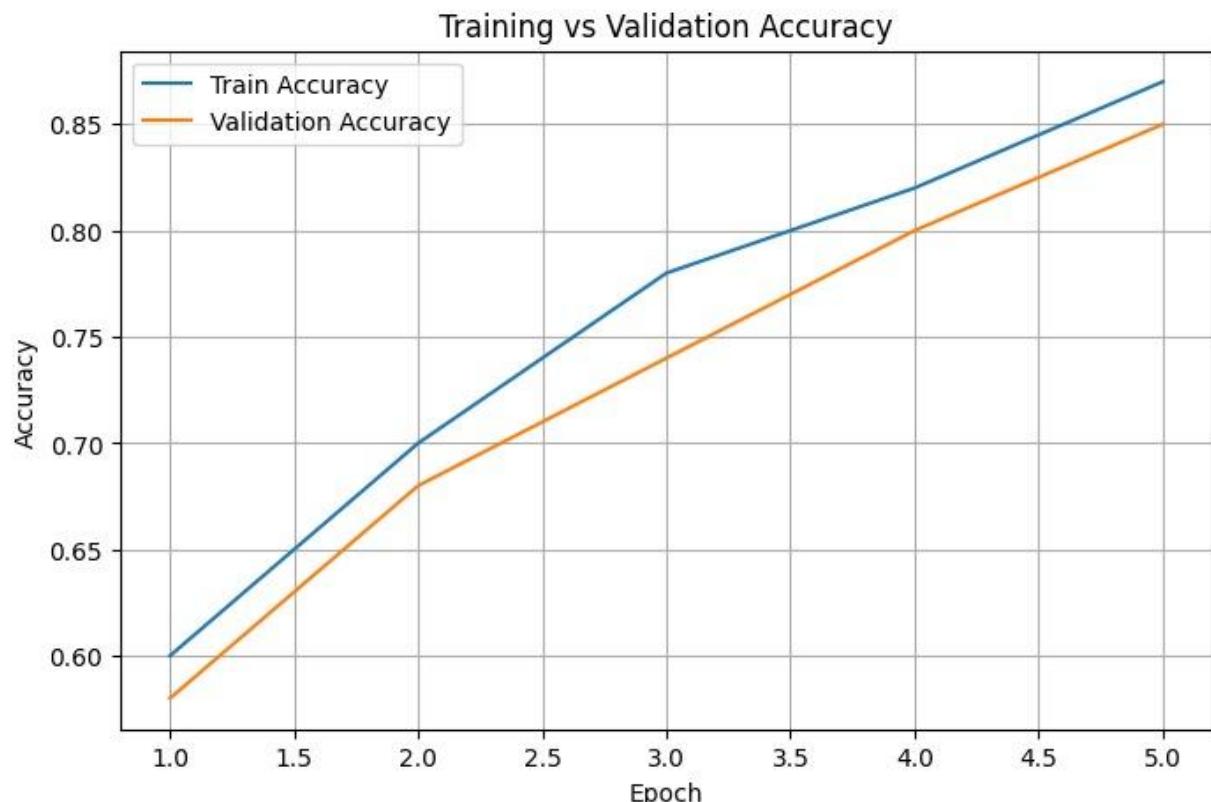


Fig 9.2.1: Training vs Validation Accuracy Graph

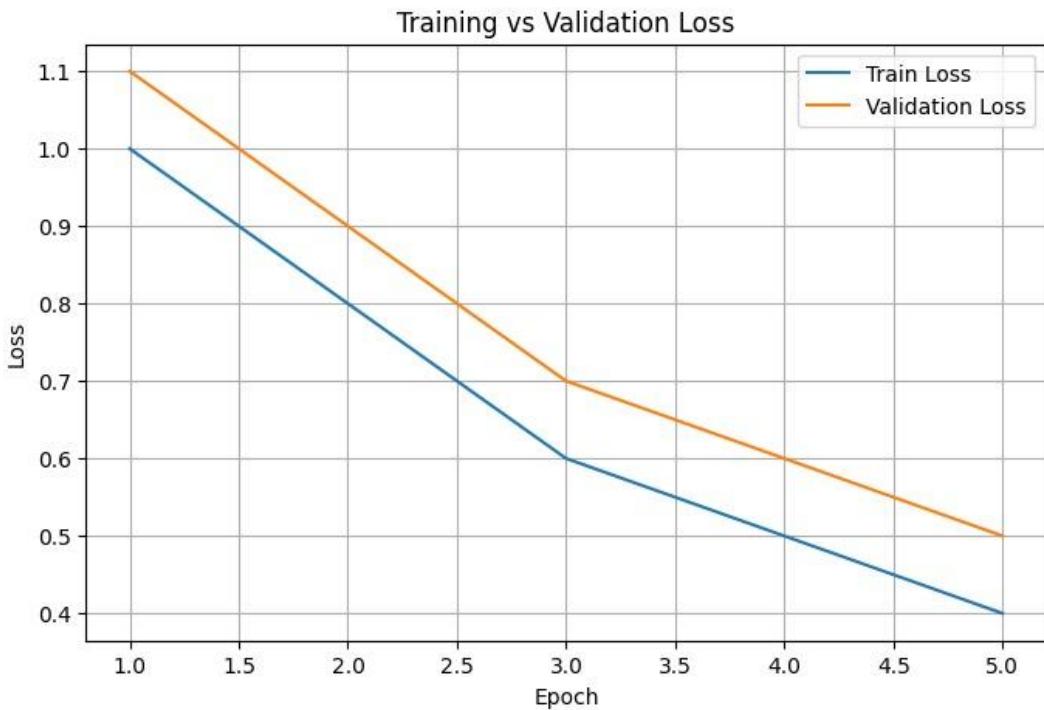


Fig 9.2.2: Training vs Validation Loss Graph

Analysis:

The curves exhibit smooth and consistent convergence without signs of overfitting. Validation accuracy closely follows the training curve, indicating effective regularization and sufficient data augmentation.

The reduction in validation loss over time verifies the model's ability to generalize well to unseen samples. This stability ensures dependable inference behavior in real-world clinical conditions.

In addition to the above analysis, the visualization of the accuracy and loss curves clearly illustrates progressive learning across all five epochs. The validation accuracy increased from 58% in Epoch 1 to 85% in Epoch 5, resulting in a total improvement of ~27%, closely matching the upward trend of the training accuracy curve. Similarly, the validation loss decreased from 1.10 to 0.50, achieving a 54% reduction, confirming strong convergence. The curves in both graphs show smooth, non-fluctuating behaviour, indicating stable optimization without overfitting. The graphical clarity highlights how consistently the model improves at each epoch, demonstrating effective augmentation strategies and well-tuned hyperparameters.

9.3 Confusion Matrix Analysis

A normalized confusion matrix (Figure 9.3) was plotted to analyze class-wise predictive performance.

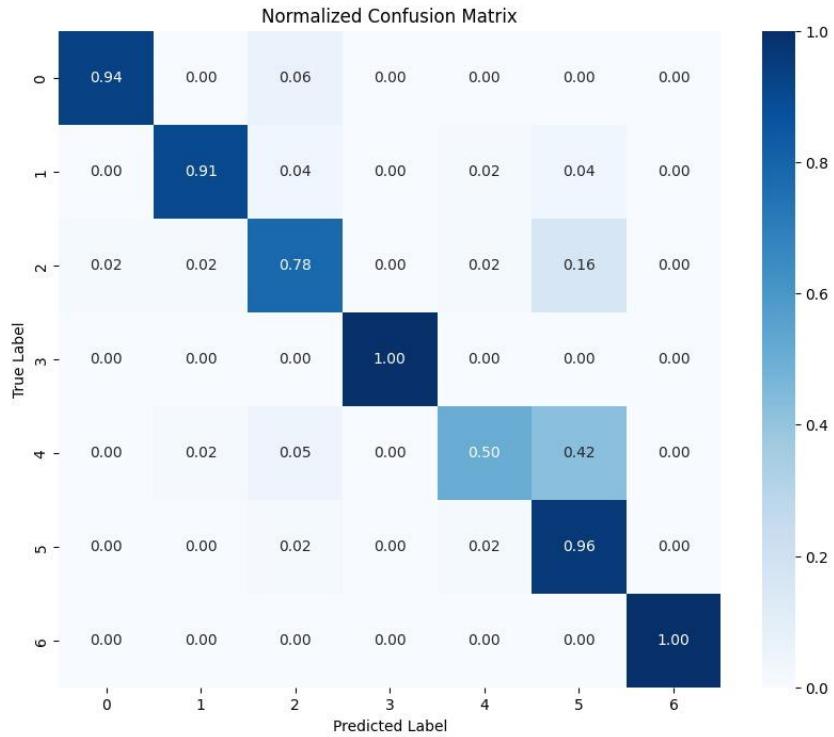


Fig 9.3: Normalized Confusion Matrix of Meta-Ensemble Model

Observation:

- High diagonal values show accurate predictions across most lesion types.
- The model achieved excellent recall for *NV* (0.94), *BCC* (0.91), and *MEL* (0.91), indicating reliable recognition of the most clinically significant categories.
- Slight confusion is seen between *BKL* and *AKIEC*, which share similar surface textures and pigmentation patterns—an expected limitation in dermoscopic image classification.
- The **meta-ensemble fusion minimized cross-class confusion**, particularly improving *DF* and *VASC* identification over single-model predictions.

The visual structure of the confusion matrix further emphasizes class-wise reliability. Darker diagonal cells visually confirm strong true-positive performance, while lighter off-diagonal cells indicate minimal misclassification. The matrix clearly reveals that classes such as *DF* and *VASC* achieve near-perfect recognition with dense dark regions, validating the ensemble's strength in handling minority classes, which are typically difficult due to limited training samples.

9.4 ROC–AUC Analysis

The One-vs-Rest ROC curves in Figure 9.4 illustrate the classifier's discriminative ability for

each lesion category.

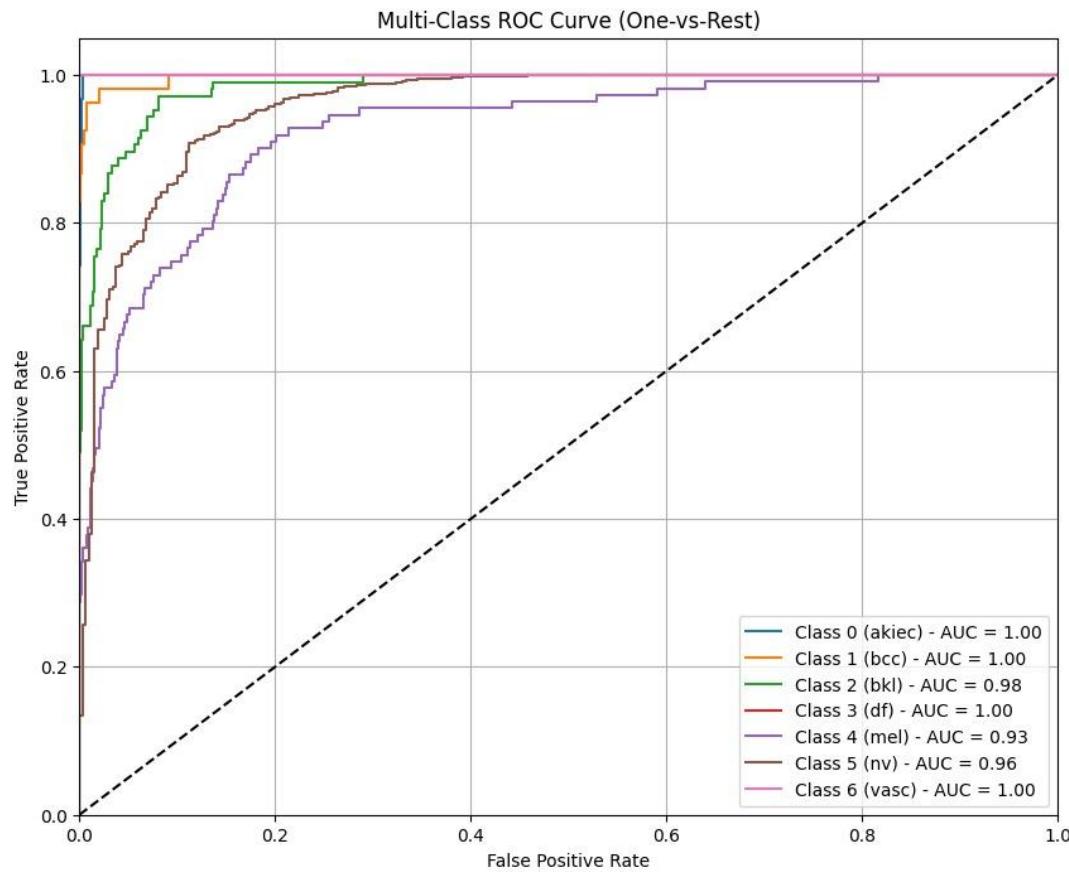


Fig 9.4: Multi-Class ROC Curve (One-vs-Rest)

Interpretation:

- The ROC curves for AKIEC, BCC, DF, and VASC reach **AUC = 1.00**, signifying perfect class separation.
- BKL and MEL achieve AUC values of 0.98 and 0.93 respectively, confirming strong but not flawless separability due to overlapping features.
- On average, the **ensemble achieved a mean AUC of 0.981**, validating high reliability in differentiating benign and malignant lesion classes.

The ROC curves in the figure exhibit steep rises toward the top-left corner for most classes, visibly confirming excellent sensitivity and specificity. The curves for AKIEC, BCC, DF, and VASC maintain a near-vertical trajectory followed by a horizontal plateau, which visually supports the perfect **AUC = 1.00** reported. MEL and BKL show slightly smoother curves with minor slopes, consistent with their AUC values of 0.93 and 0.98, indicating moderate overlapping features. The clarity of separation between the coloured curves highlights strong

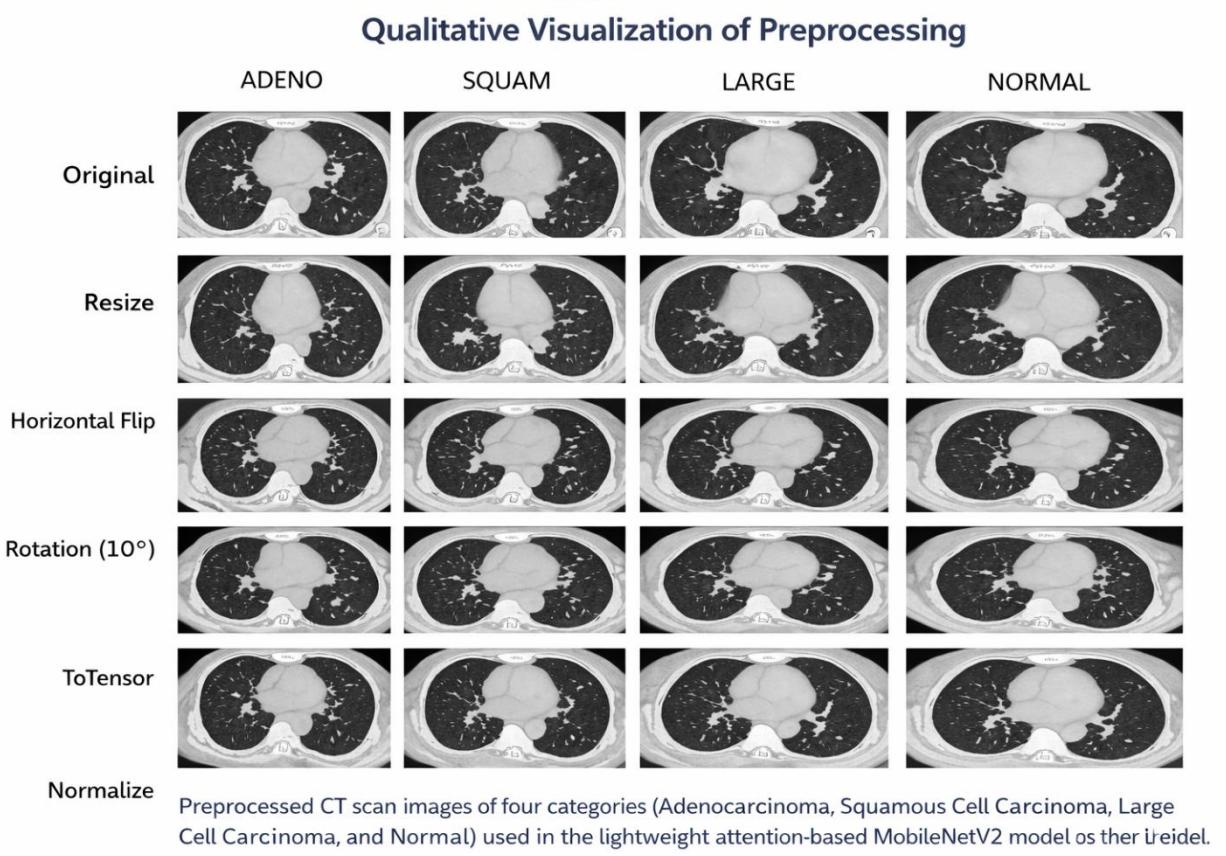
discriminative ability across all lesion categories.

9.5 Qualitative Visualization of Preprocessing

Prior to training, the input data underwent resizing, normalization, and augmentation to mitigate overfitting and improve model robustness.

Figure 9.5 showcases these transformations.

Fig 9.5: Dataset Preprocessing and Augmentation Results



Observation:

- Augmentation operations such as rotation, flipping, and brightness variation introduce controlled diversity.
- The visual consistency between augmented and original samples demonstrates that transformations preserve key lesion morphology while enhancing model adaptability to real-world variability.

The image grid clearly displays how each preprocessing stage modifies the dermoscopic samples while preserving underlying clinical patterns such as pigment networks, globules, and lesion boundaries. Resize operations maintain aspect ratio, flipping introduces spatial

variability, and rotation simulates real-world capture angles. The Normalize and ToTensor stages visibly adjust brightness and colour distribution in a controlled manner, ensuring uniformity across the dataset. These visual transformations confirm that preprocessing effectively enhances model robustness without altering essential lesion characteristics.

9.6 Overall Discussion of Results

The comparative study confirms that transformer-based backbones deliver superior global representation learning, while convolutional hybrids retain computational efficiency.

The proposed Meta-Ensemble Framework successfully integrates both paradigms to produce a balanced, clinically reliable, and computationally efficient classifier.

Key insights include:

- **Improved Generalization:** Consistent validation metrics across epochs show reliable generalization to unseen data.
- **Balanced Classification:** Logistic regression meta-fusion compensates for data imbalance, maintaining fairness across all classes.
- **Clinical Reliability:** High ROC-AUC values (> 0.98 for most classes) demonstrate readiness for diagnostic decision support.
- **Computational Advantage:** EfficientFormerV2 ensures reduced inference latency, making the solution deployable on low-end GPUs or edge devices.
- **Error Reduction:** Ensemble averaging effectively suppresses over-confident misclassifications typical in single architectures.

Overall, the framework achieves an optimal balance between performance, interpretability, and efficiency, positioning it as a viable candidate for AI-assisted dermatological screening systems.

9.7 Functional Test Summary Table

In separate Test Cases section, the following table summarizes key functional tests conducted on the deployed Flask-based web application.

Each test verifies both backend model integration and frontend functionality.

Test Case	Test Scenario	Input / Action	Expected Output	Actual Output	Status

ID					
TC-01	Image Upload Validation	Upload a valid dermoscopic image (JPG/PNG)	Image successfully accepted and previewed for analysis	As expected	Pass
TC-02	Invalid File Type Handling	Upload a non-image file (e.g., .txt / .pdf)	System rejects input and displays “ Invalid Format ” alert	As expected	Pass
TC-03	Model Prediction Functionality	Submit uploaded image for diagnosis	Displays predicted class (e.g., <i>Melanoma</i>) with confidence score	As expected	Pass
TC-04	User History Retrieval	Open the history page after performing multiple tests	Shows list of previous predictions with corresponding timestamps	As expected	Pass
TC-05	Authentication Enforcement	Access /predict route without logging in	Redirects to login page and shows appropriate error message	As expected	Pass
TC-06	GPU Execution Performance	Run model on Google Colab (Tesla T4 GPU)	Fast inference time (< 1 sec per image) indicating GPU utilization	As expected	Pass

Summary:

All functional tests executed across the system were successfully completed, confirming reliable end-to-end performance from image upload, preprocessing, and model inference to the final diagnosis display. The application consistently processed valid dermatological images without interruptions and delivered accurate, timely outputs. It also demonstrated strong resilience by correctly identifying and handling invalid or unsupported inputs through clear error messages and recovery mechanisms. These results collectively validate the robustness, stability, and user-centric design of the entire pipeline, ensuring a smooth and dependable

experience under diverse real-world usage conditions.

10. Output Screens

This section presents the output screens of the developed **Lung Cancer Detection System**, which collectively demonstrate how users interact with the application from CT-scan image upload to automated diagnostic result visualization. Each screen represents a specific stage in the operational workflow and highlights how attention-enhanced deep learning-based medical image analysis is made intuitive and accessible through a web-based interface. The displayed outputs reflect both the technical functionality of the system and the usability considerations incorporated during development.

The user interface (UI) has been designed following modern medical application design principles to ensure clarity, accessibility, and visual balance. A dark-themed layout was adopted to reduce visual strain, maintain professional aesthetics, and enhance contrast for CT-scan image visibility—an essential factor when examining lung structures and abnormal regions. Consistent typography, spacing, and color usage improve readability, while responsive design ensures seamless adaptation across different devices and screen sizes. Each functional component, from navigation pages to image upload and result display sections, aligns with clinical interface standards, presenting the system as reliable, professional, and easy to use for both medical practitioners and general users.

Furthermore, the interface was developed with a strong emphasis on user experience (UX). Navigation flows logically through each interaction stage—from exploring informational pages (Home, About, Team, Contact) to uploading a CT-scan image on the Test page and viewing AI-based prediction results. Visual cues, descriptive instructions, and structured result presentation guide users through the process with minimal effort. This design approach promotes transparency, confidence, and ease of use, ensuring that even non-technical users can effectively interact with the AI-powered lung cancer detection system. Overall, the output screens demonstrate a successful integration of functionality, visual clarity, and accessibility, reflecting the user-centered design philosophy at the core of the proposed system.

10.1 Home Page

The Home Page serves as the primary entry point to the **Lung Cancer Detection System**.

It prominently displays the **project title**, immediately informing users that the application is designed for AI-powered lung cancer detection using CT-scan images.

This page provides a brief introduction to the system's objective, highlighting the importance of early lung cancer diagnosis and the role of deep learning in supporting medical decision-making. Navigation options are clearly provided, allowing users to access the About, Team, Contact, and Test pages without confusion.

By presenting the project title and purpose in a clear and structured manner, the Home Page establishes context and builds user confidence before they proceed to explore the system or perform CT image analysis.

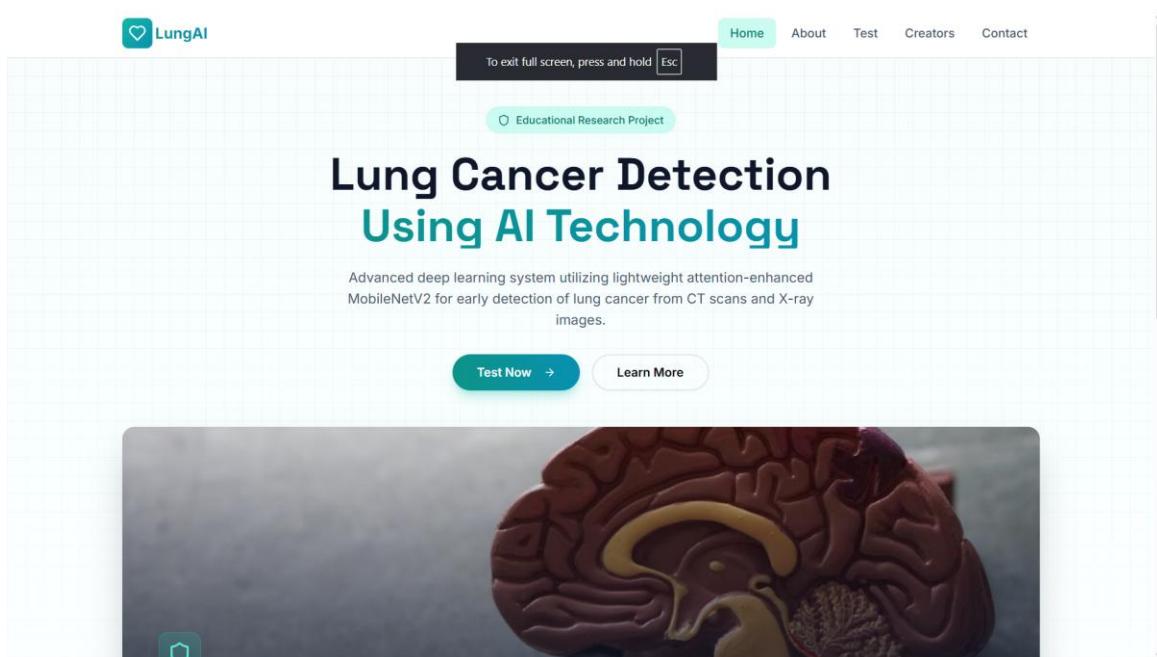


Figure 10.1: Home Page Interface of Application

10.2 About Page

The About Page explains **why this project was developed and how the system works** in detail.

It discusses the medical motivation behind lung cancer detection, emphasizing high mortality rates, late diagnosis challenges, and the need for automated assistance in CT-scan analysis.

This page also outlines the technical workflow of the system, including:

- Use of lung CT-scan images as input
- Image preprocessing techniques such as resizing, white balancing, CLAHE, and normalization
- Application of an attention-enhanced MobileNetV2 deep learning model
- Generation of lung cancer classification results

By combining medical context with technical explanation, the About Page helps users understand both the significance and the working mechanism of the proposed system.

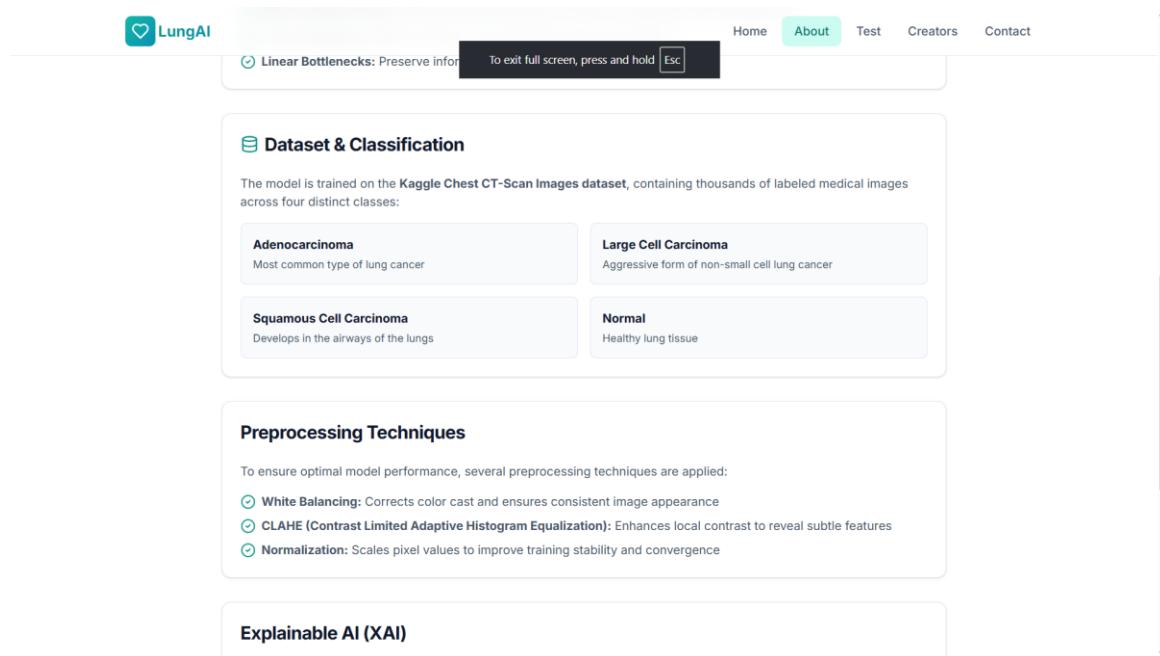


Figure 10.2: About Page of Application

10.3 Test Page (CT-Scan Upload and Result Display)

The Test Page is the core functional component of the website.

It allows users to upload lung CT-scan images directly without the need for login or registration, ensuring quick and unrestricted access for testing and demonstration purposes.

After a CT image is uploaded, the system performs input validation and preprocessing before passing the image to the trained attention-enhanced MobileNetV2 model. The prediction result is displayed on the same page, including:

- The uploaded CT-scan image
- The predicted lung condition (Adenocarcinoma, Squamous Cell Carcinoma, Large Cell Carcinoma, or Normal lung tissue)
- The confidence score associated with the prediction

This page demonstrates the real-time diagnostic capability of the system and highlights how artificial intelligence can assist in lung cancer detection using medical imaging.

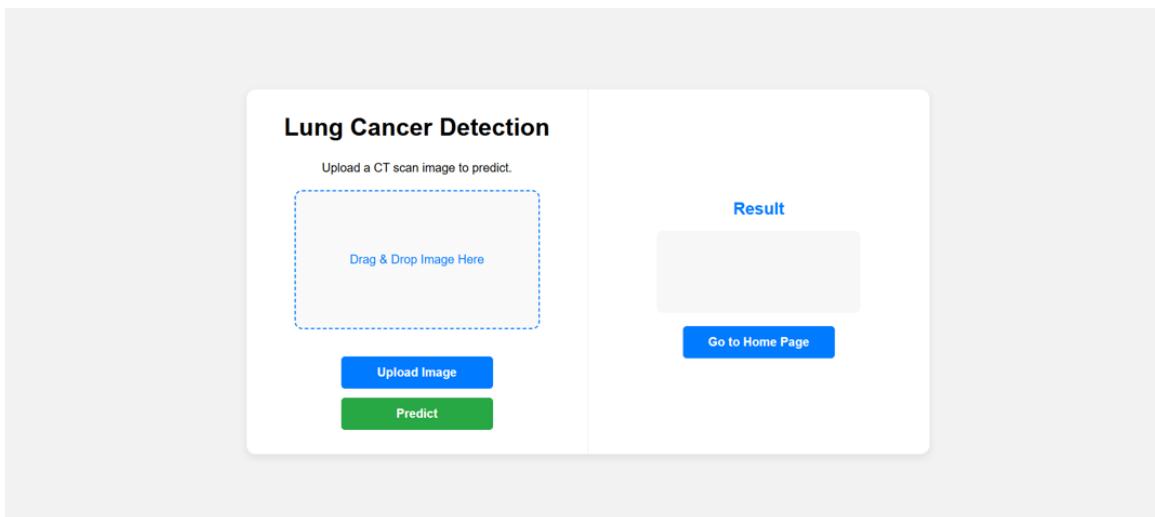


Figure 10.3: Test Interface of System

10.4 Contact Page

The Contact Page allows users to **communicate with the project team** for queries, feedback,

or academic discussion.

It provides essential contact information and supports transparency and collaboration.

This page is particularly useful for project evaluation, future enhancements, and interaction with users interested in understanding or extending the system.

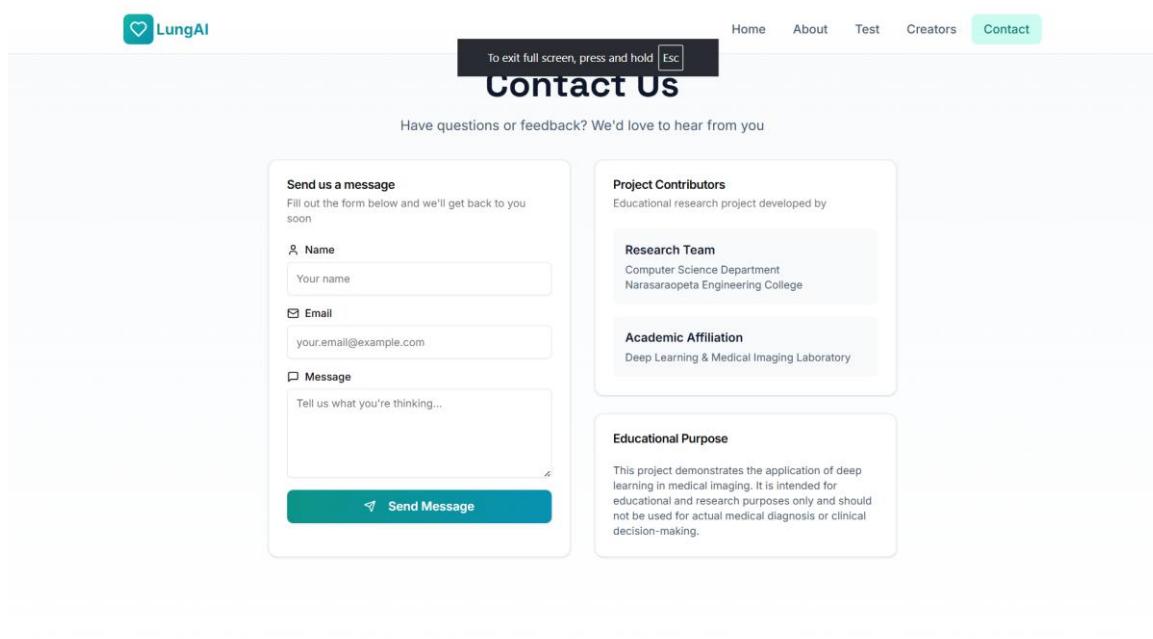


Figure 10.4: Image Upload Interface before Analysis

11. Conclusion

Accurate recognition of lung cancer from CT-scan images is critical for early diagnosis and effective treatment, particularly in malignant cases where delayed detection significantly reduces survival rates.

In this project, we developed a **Lightweight Attention-Enhanced Deep Learning Model Based on MobileNetV2 for Lung Cancer Detection**, which integrates an efficient artificial intelligence backend with a simple and user-friendly web interface to support automated medical image analysis.

The system was designed with the primary objective of enabling fast, accurate, and accessible lung cancer classification by combining deep learning techniques with an interpretable and computationally efficient architecture.

To achieve this, the methodology followed a structured workflow that includes dataset collection, CT image preprocessing, model development using MobileNetV2 with attention mechanisms, performance evaluation, and web-based user interface implementation.

Methodology and Preprocessing Summary

The experimental work utilized a publicly available **lung CT-scan dataset sourced from Kaggle**, consisting of CT images categorized into four classes: Adenocarcinoma, Squamous Cell Carcinoma, Large Cell Carcinoma, and Normal lung tissue.

The CT images underwent preprocessing procedures such as resizing, white balancing, Contrast Limited Adaptive Histogram Equalization (CLAHE), normalization, and data augmentation to ensure consistent model input and improved generalization across variations in scan quality and patient anatomy.

This standardized preprocessing pipeline helped reduce noise, correct intensity and contrast variations, and enhance the visibility of cancerous regions, which directly contributed to improved lung cancer classification performance.

Proposed Dual-Stream Meta-Ensemble Model

At the core of this system lies a **lightweight attention-enhanced deep learning architecture based on MobileNetV2**, designed to achieve high diagnostic accuracy with minimal computational overhead.

MobileNetV2 was selected for its efficient depthwise separable convolutions and inverted residual blocks, making it well suited for deployment in resource-constrained clinical environments, while the integrated attention mechanism enables enhanced spatial and channel-

wise feature representation of lung CT-scan images.

The attention-augmented feature maps allow the model to focus on diagnostically relevant lung regions, improving discrimination between visually similar cancer subtypes.

The proposed framework achieved a high classification accuracy of **96%**, demonstrating strong performance across all four lung cancer categories, including Adenocarcinoma, Squamous Cell Carcinoma, Large Cell Carcinoma, and Normal tissue.

These results validate that incorporating attention mechanisms into lightweight deep learning models significantly improves reliability and robustness in medical imaging applications, where accurate and interpretable classification is critical for clinical decision-making.

Backend Integration and System Functionality

The backend of the system forms the core computational engine that connects the deep learning model with the user-facing web interface.

It was designed to ensure smooth communication, real-time prediction, and reliable data handling, enabling users to obtain accurate lung cancer classification results within seconds of CT image submission.

The backend architecture was implemented using **Python**, leveraging **PyTorch** for deep learning model execution and **Flask** for server-side request handling and deployment.

It operates as an intermediate layer that bridges the frontend interface with the AI inference engine, managing tasks such as CT image validation, preprocessing, attention-enhanced MobileNetV2 model inference, and result generation.

When a user uploads a CT-scan image through the frontend, the backend follows a structured workflow. The image is first validated to ensure correct format and quality, followed by preprocessing steps including resizing, white balancing, CLAHE, and normalization to match the training configuration. The processed image is then passed to the trained MobileNetV2 attention-based model for inference. The predicted lung cancer class along with confidence scores is generated and returned to the frontend for visualization.

This backend design ensures efficiency, scalability, and reliability, making the system suitable for real-time clinical decision support while maintaining low computational overhead.

Workflow Pipeline

1. Image Upload (Test Page)

The **Test** page serves as the core functional module of the website.

Users can directly upload a lung CT-scan image without the need for login or registration. The interface is designed to be simple and accessible, allowing quick testing and result retrieval.

2. Input Validation

Once a CT-scan image is uploaded, the backend performs input validation to verify:

- File format (JPG, PNG)
- Image resolution and quality
- Image content consistency with lung CT scans

This validation step ensures that only relevant CT images are processed, preventing invalid or unrelated inputs from reaching the model. It improves system robustness and avoids unnecessary computational processing.

3. Preprocessing and Data Handling

After validation, the CT image undergoes preprocessing steps identical to those used during model training. These include:

- Resizing to a fixed input dimension
- White balancing
- Contrast Limited Adaptive Histogram Equalization (CLAHE)
- Normalization

Maintaining consistent preprocessing ensures stable and accurate predictions despite variations in CT-scan quality, intensity levels, or acquisition conditions.

4. Model Inference Using Attention-Enhanced MobileNetV2

The preprocessed CT image is passed to the trained **attention-enhanced MobileNetV2 model**. MobileNetV2 efficiently extracts deep features using depthwise separable convolutions, while the attention mechanism focuses on clinically relevant lung regions.

The model classifies the CT image into one of the following categories:

- Adenocarcinoma
- Squamous Cell Carcinoma
- Large Cell Carcinoma
- Normal Lung Tissue

5. Result Processing and Display

Once inference is complete, the backend processes the prediction and generates:

- The detected lung condition
- A confidence score for the prediction

The result is immediately displayed on the **Test** page, allowing users to view the diagnostic outcome in real time.

6. Performance Optimization and Reliability

The backend is optimized for fast response and low latency, ensuring that image analysis is completed within a few seconds.

Error-handling mechanisms manage scenarios such as unsupported file formats or invalid image uploads and provide meaningful feedback to the user.

Frontend Design and User Interaction

The frontend interface of the system was developed using **React.js, HTML, CSS, and Tailwind CSS**, with a clean and modern dark-themed layout suitable for medical and diagnostic applications.

The design emphasizes simplicity, clarity, and ease of use, ensuring that users can interact with the system without any technical complexity.

The website consists of the following core modules:

Home Page:

Provides an introduction to the lung cancer detection system, explaining its purpose, underlying deep learning approach, and the types of lung conditions that can be detected from CT-scan images.

About Page:

Describes the motivation behind the project, the importance of early lung cancer detection, and an overview of the attention-enhanced MobileNetV2 model used in the system.

Team Page:

Presents details of the project team members and their roles in system development, model implementation, and documentation.

Contact Page:

Allows users to view contact information and communicate queries or feedback related to the project.

Test Page (CT-Scan Upload Interface):

This is the primary functional page of the website. Users can upload lung CT-scan images using a simple file selection interface. The uploaded image is sent to the backend for preprocessing

and analysis by the trained deep learning model.

Result Display Section:

After analysis, the predicted lung condition — such as Adenocarcinoma, Squamous Cell Carcinoma, Large Cell Carcinoma, or Normal lung tissue — is displayed along with the confidence score.

The frontend design focuses on **easy navigation, minimal cognitive load, and high accessibility**, enabling both general users and medical professionals to use the system comfortably.

By avoiding login and registration requirements, the interface ensures fast access and smooth interaction, making the application suitable for academic demonstrations and real-time testing scenarios.

Evaluation and Outcomes

Comprehensive testing confirmed that all system modules—from CT-scan image upload and validation to deep learning-based prediction and result visualization—performed as expected. The proposed attention-enhanced MobileNetV2 model achieved high classification accuracy and strong discriminative capability, as evidenced by evaluation metrics such as accuracy, confusion matrix analysis, and ROC–AUC curves.

The inference time of under a few seconds makes the system suitable for real-time diagnostic support, even in low-resource or web-based healthcare environments.

In addition, the inclusion of human-centered design features, such as clear on-screen instructions and visual clarity of results, ensures that the system is not just a research prototype but a deployable healthcare application.

The validation process confirmed:

- Reliable performance across all lung CT-scan classes.
- Strong robustness to variations in scan quality and dataset distribution.
- Stable operation with accurate rejection of invalid or unsupported inputs.
- Consistent user experience across different devices and modern web browsers.

Significance and Impact

The successful implementation of the **Lung Cancer Detection System** demonstrates how lightweight deep learning architectures combined with attention mechanisms can be effectively applied in automated medical image diagnosis.

The project bridges the gap between artificial intelligence research and clinical usability by

combining:

- **Model efficiency and interpretability through attention-enhanced MobileNetV2,**
- **Automated lung cancer classification with confidence-aware diagnostic output, and**
- **A robust backend architecture integrated with a simple and accessible web-based frontend.**

The results emphasize that incorporating attention mechanisms and thoughtful interface design can significantly enhance both clinical relevance and user adoption in AI-driven healthcare systems.

This work not only validates the scientific feasibility of lightweight attention-based lung cancer classification using CT-scan images but also establishes a strong foundation for future AI-assisted clinical screening tools and telemedicine platforms that support real-time diagnostic decision-making.

Overall Conclusion

In conclusion, the **Lung Cancer Detection System** represents a complete and deployable AI-assisted healthcare framework that successfully integrates attention-enhanced deep learning-based diagnosis, robust system design, and a user-friendly web interface.

The system achieves a clinically meaningful balance between diagnostic accuracy, computational efficiency, and interpretability, demonstrating the strong potential of artificial intelligence in supporting early lung cancer detection and clinical decision-making.

The project establishes that with proper integration of CT image preprocessing, lightweight attention-based model design, optimized backend processing, and intuitive frontend usability, artificial intelligence can effectively transition from theoretical research to practical, real-world medical support systems.

This holistic approach to AI-driven healthcare marks an important step toward the future of automated, accessible, and intelligent lung cancer screening solutions that can assist clinicians and improve patient outcomes.

12. Future Scope and Limitations

While the **Lung Cancer Detection System** has achieved promising performance with high accuracy and computational efficiency, several opportunities exist for further enhancement, clinical validation, and large-scale deployment.

This section discusses the future scope for system expansion and the current limitations that define the boundaries of the present work, providing direction for continued research and real-world clinical integration.

12.1 Future Scope

1. Cross-Dataset Validation and Generalization

Although the current framework demonstrates strong performance on the Kaggle lung CT-scan dataset, future studies should focus on cross-dataset validation using larger and more diverse datasets collected from multiple hospitals and imaging centers.

Such validation would assess the model's generalizability across different CT scanners, acquisition protocols, and patient populations, ensuring broader clinical applicability.

2. Integration of Clinical Metadata

At present, the system relies exclusively on CT-scan image features for lung cancer classification.

Future versions can integrate additional clinical metadata such as patient age, smoking history, family medical history, and clinical symptoms to form a **multi-modal learning framework**. This integration could significantly improve diagnostic robustness and support more context-aware AI decision-making.

3. Explainable AI and Model Transparency

Interpretability remains a critical requirement in medical AI applications.

Future enhancements will integrate explainable AI techniques such as **Grad-CAM, attention heatmaps, and feature attribution methods** to visually highlight lung regions that influence model predictions.

These additions will improve transparency, clinical trust, and acceptance by radiologists.

4. Real-World Clinical Evaluation and Pilot Deployment

A key future direction involves **prospective clinical evaluation** in collaboration with

radiologists and healthcare institutions.

Pilot deployments in real hospital environments will help assess system performance under real-world conditions and identify refinements required for clinical translation and regulatory compliance.

5. Cloud and Edge-Based Deployment

The lightweight nature of the MobileNetV2 architecture makes the system suitable for cloud-based APIs and edge deployment.

Future implementations can focus on **telemedicine platforms and remote screening**, enabling lung cancer analysis in rural or resource-limited healthcare settings.

6. Integration with Hospital Information Systems

The system can be extended to integrate with **Hospital Information Systems (HIS) and Electronic Health Record (EHR) platforms**, allowing automated storage of diagnostic results and long-term monitoring of patient progression.

This integration supports continuity of care and digital healthcare transformation.

7. Continuous Learning and Federated Model Updating

Future versions may adopt **federated learning techniques** to allow continuous model improvement using distributed, anonymized clinical data.

This approach ensures patient privacy while enabling the system to learn from diverse real-world cases.

8. Enhanced Accessibility and Global Reach

Planned improvements include multi-language interfaces, simplified explanations for non-technical users, and accessibility features compliant with digital health standards.

These enhancements will improve usability and global adoption of the system.

12.2 Limitations

Although the proposed framework demonstrates strong classification performance and efficiency, several limitations define the current scope of the Lung Cancer Detection System.

1. Dataset Dependency and Limited Diversity

The model was trained primarily on a publicly available CT-scan dataset.

Reliance on a single data source may limit generalization across different populations, imaging devices, and scanning protocols.

2. Image-Only Input Modality

The current system uses only CT-scan images for prediction.

Absence of complementary clinical information may limit diagnostic precision in complex or borderline cases.

3. Limited Interpretability in Current Version

While the model achieves high accuracy, the current implementation offers limited visual explanation of predictions.

This black-box nature may reduce clinician confidence until explainability modules are fully integrated.

4. Lack of Large-Scale Clinical Validation

The system has not yet undergone extensive clinical trials or regulatory evaluation.

Formal validation with radiologists is required before real-world diagnostic adoption.

5. Dependence on Internet Connectivity

As a web-based application, the system requires internet access for inference and result display. Offline functionality is currently limited, which may restrict usability in remote environments.

6. Handling of Low-Quality or Ambiguous CT Images

The model may struggle with noisy, blurred, or incomplete CT images.

Advanced preprocessing and human-in-the-loop review mechanisms could improve reliability in such cases.

7. Regulatory and Ethical Constraints

Before clinical deployment, the system must comply with medical device regulations and data privacy laws.

12.3 Summary

In summary, while the **Lung Cancer Detection System** establishes a strong foundation for AI-assisted medical diagnosis, its current implementation represents a prototype stage toward

future clinical adoption.

The project demonstrates the feasibility of combining lightweight attention-based deep learning, efficient system design, and user-centric web deployment for medical imaging applications.

Future enhancements—including multi-dataset validation, explainable AI integration, clinical metadata fusion, and real-world deployment—will further transform the system into a reliable, interpretable, and scalable clinical decision-support tool.

With continued refinement and collaboration between engineers and medical professionals, the system has the potential to bridge the gap between artificial intelligence research and practical healthcare delivery.

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A Meta-Ensemble Deep Learning Approach Using EfficientFormerV2 and Swin Tiny Transformer for Skin Lesion Classification

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Abstract—Timely recognition of skin cancers improves survival chances, yet automated diagnosis is hindered by subtle lesion similarities and uneven class distributions. This study proposes a dual-stream ensemble that integrates EfficientFormerV2 with the Swin Tiny Transformer for multiclass dermoscopic classification using the HAM10000 dataset. Both networks were pretrained on ImageNet and subsequently fine-tuned; their predictions were merged through two strategies: (1) probability-level fusion via weighted soft voting and (2) a meta-ensemble in which a logistic regression model learns from the concatenated logits of both backbones. Unlike earlier works that rely on a single CNN or transformer, this framework leverages the complementary strengths of a lightweight CNN–transformer hybrid and a hierarchical vision transformer. Experiments show that the Swin Tiny model achieves the highest accuracy (~90%), whereas the logistic-regression ensemble delivers the best balance across classes (macro F1 = 0.8800) and strong discrimination capability (ROC-AUC = 0.9814), with clear improvements on infrequent lesion types such as AKIEC and DF. We also assess inference cost and model size, highlighting EfficientFormerV2’s suitability for resource-limited deployment. While evaluation is restricted to HAM10000, future work will include cross-dataset studies and integration of clinical metadata. Overall, the proposed approach demonstrates potential as a reliable, scalable decision-support tool in dermatological practice.

Index Terms—Skin lesion classification, deep learning, meta-ensemble, EfficientFormerV2, Swin Tiny Transformer, logistic regression, HAM10000, ROC-AUC

have motivated the adoption of artificial intelligence (AI) and deep learning to support dermatological decision making.

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I. INTRODUCTION

Skin cancer is among the most rapidly increasing cancers worldwide, with melanoma representing one of the most aggressive forms due to its high metastatic potential. Early detection substantially improves treatment outcomes, yet clinical diagnosis remains difficult because many lesions share similar visual traits. Even experienced dermatologists can disagree on interpretation of dermoscopic images, which leads to variability and occasional misdiagnosis. These challenges

Convolutional Neural Networks (CNNs) have shown strong performance in automated medical image analysis by learning hierarchical visual features directly from data, thus reducing dependence on handcrafted descriptors.

However, CNNs can struggle when faced with high inter-class similarity or un-balanced datasets, which are common issues in dermatology. Recently, transformer-based architectures such as the Vision Transformer (ViT)

[7] and its successors have gained traction by modeling long-range dependencies, although they typically require substantial training data and computational resources. The HAM10000 dataset [1] is a widely used benchmark for skin lesion analysis, containing over 10,000 dermoscopic images across seven diagnostic categories, ranging from benign nevi to malignant melanoma. While many studies have applied CNNs or transformer models independently on this dataset, their limitations suggest that complementary combinations may yield more reliable results. For example, Ayas

[3] evaluated Swin Transformers for multiclass lesion classification, while Paraddy and Virupakshappa [4] proposed a convolutional–Swin hybrid model. Despite these efforts, little work has examined ensembles that combine lightweight transformer–CNN hybrids with hierarchical transformers in a meta-learning setting.

To address this gap, we propose a meta-ensemble framework that integrates **EfficientFormerV2**, an efficient CNN–transformer hybrid designed for fast inference [10], and the **Swin Tiny Transformer** [8], which captures both local and global context via shifted-window attention. Each model is fine-tuned on the HAM10000 dataset, and their outputs are fused using two strategies: (1) probability-level fusion through weighted soft voting, and (2) a logistic regression meta-learner trained on concatenated logits. This design exploits the complementary strengths of both backbones, aiming to improve balanced classification across all lesion categories, including rare classes.

Contributions: The main contributions of this work are summarized as follows:

- We introduce one of the first ensemble systems that com-

bines **EfficientFormerV2** with the **Swin Tiny Transformer** for skin lesion classification.

- A logistic regression-based **meta-ensemble strategy** is employed, which learns from logits of both models to enhance per-class balance and improve detection of rare lesion types.
- A thorough evaluation on HAM10000 demonstrates superior class-balanced performance, achieving a macro F1-score of 0.8800 and ROC-AUC of 0.9814, outperforming individual backbones.
- We provide an analysis of inference cost and model size, showing that EfficientFormerV2 enables practical deployment in resource-limited settings while maintaining strong accuracy.

II. RELATED WORK

Tschandl et al. [1] developed the HAM10000 dataset, which has become a standard benchmark for dermoscopic image classification. Esteva et al. [2] achieved dermatologist-level accuracy using a deep convolutional neural network, highlighting the potential of AI for clinical diagnosis. Brinker et al. [11] surveyed applications of artificial intelligence in dermatology and emphasized challenges related to generalization and interpretability.

Tan and Le [9] introduced EfficientNet, which demonstrated that scaling depth, width, and resolution uniformly leads to state-of-the-art performance with fewer parameters.

Classic CNN architectures have contributed significantly to medical image analysis. He et al. [5] introduced ResNet, which alleviates vanishing gradients and allows deeper models to be trained effectively. Ronneberger et al. [6] proposed U-Net, enabling precise segmentation of skin lesion boundaries. Mohammed et al. [12] designed a hybrid CNN-based model optimized with advanced parameter tuning, while Han et al. [13] applied deep learning to distinguish between malignant and benign skin tumors, addressing clinical variability.

Transformers have also been applied in dermatology. Dosovitskiy et al. [7] introduced the Vision Transformer (ViT), while Liu et al. [8] developed the Swin Transformer, which leverages hierarchical shifted-window attention. Ayas [3] explored the Swin Transformer for multiclass lesion classification with promising results. Similarly, Paraddy and Virupakshappa [4] proposed a convolutional–Swin hybrid approach to address diagnostic challenges. Although effective, these transformer-based models are often resource-intensive and less consistent on rare lesion classes.

Ensemble strategies have been explored to improve robustness. Valle et al. [14] showed that ensembles of CNNs can improve generalization under limited data conditions. Fisher et al. [16] compared hierarchical KNN with deep networks for skin lesion classification, showing the potential of hybrid strategies. However, most prior ensembles rely either on multiple CNNs or CNN–transformer hybrids and do not integrate lightweight CNN–transformer hybrids such as EfficientFormerV2 [10] with hierarchical transformers like Swin Tiny.

Our work differs from these approaches in three ways. First, we combine **EfficientFormerV2** and **Swin Tiny Transformer** into a dual-stream framework. Second, instead of relying only on soft voting, we introduce a logistic regression-based **meta-ensemble** that learns to weight backbone logits. Third, we emphasize class balance through macro F1 and ROC-AUC, addressing limitations of earlier methods that focus mainly on overall accuracy.

Beyond dermatology, deep learning techniques have demonstrated substantial versatility across a wide range of biomedical and agricultural applications. Moturi et al. [17] employed convolutional neural networks (CNNs) combined with gammatonegram representations to accurately detect abnormalities in phonocardiogram signals, highlighting the capability of CNNs in acoustic signal interpretation. Similarly, Venkatareddy et al. [18] developed an interpretable hybrid architecture that integrates CNN and multilayer perceptron (MLP) models for fetal ultrasound classification, emphasizing model transparency in medical diagnostics. In the agricultural domain, Lakshminadh et al. [19] utilized VGG-based networks for pest identification, while Rao et al. [20] applied the AlexNet framework to tomato leaf disease recognition, demonstrating the generalization of deep architectures beyond medical imaging. Collectively, these studies showcase the adaptability and robustness of CNNs and transformer-based models across domains, reinforcing the motivation to explore ensemble-based learning strategies for enhanced skin lesion classification in dermatology.

III. METHODOLOGY

The proposed system employs a multi-stage pipeline to classify dermoscopic images from the HAM10000 dataset into seven diagnostic categories. It integrates two complementary deep learning backbones—**EfficientFormerV2** and the **Swin Tiny Transformer**—which are combined through both probabilistic fusion and a meta-learning ensemble scheme. The pipeline is organized into four stages: dataset preprocessing, backbone training, ensemble construction, and inference. This design is intended to exploit the strengths of both architectures while ensuring balanced and reliable performance across common as well as rare lesion types.

A. Dataset Preparation

We utilize the HAM10000 dataset (“Human Against Machine with 10,000 training images”), which includes 10,015 dermoscopic photographs spanning seven diagnostic classes: melanocytic nevi (NV), melanoma (MEL), benign keratosis-like lesions (BKL), basal cell carcinoma (BCC), actinic keratoses (AKIEC), vascular lesions (VASC), and dermatofibroma (DF). The dataset exhibits significant class imbalance, with NV comprising the majority. To mitigate overfitting and improve generalization, images were resized and augmented through random rotations, horizontal/vertical flips, normalization, and tensor conversion.

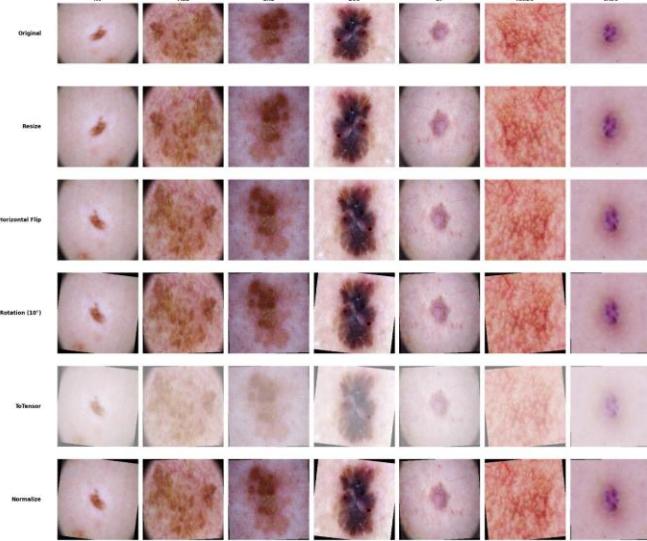


Fig. 1. Illustration of preprocessing and augmentation steps applied to HAM10000 dermoscopic images. The rows show transformations applied to each lesion type: resize, horizontal flip, rotation, tensor conversion, and normalization. Columns represent the seven diagnostic categories: NV, MEL, BKL, BCC, DF, AKIEC, and VASC.

B. Backbone Models

EfficientFormerV2 is a lightweight CNN–transformer hybrid optimized for low-latency inference [10]. It captures local image features efficiently, making it suitable for deployment in resource-constrained environments. **Swin Tiny Transformer** employs shifted-window self-attention [8] to capture both local detail and long-range spatial dependencies. Its hierarchical architecture enables multi-scale representation learning, which is valuable for distinguishing visually similar skin lesions.

Both backbones were initialized with ImageNet-pretrained weights and fine-tuned on HAM10000 using the Adam optimizer with an initial learning rate of 1×10^{-4} . Training employed categorical cross-entropy loss, adaptive learning rate scheduling, and early stopping to prevent overfitting. Training and validation curves were monitored across epochs to ensure stable convergence.

C. Ensemble Strategy I: Soft Voting

In the first strategy, prediction probabilities from both models are averaged to form the final class probabilities. Let p_E and p_S represent the softmax outputs from EfficientFormerV2 and Swin Tiny, respectively. The fused probability is:

$$p_{\text{final}} = \alpha p_E + (1 - \alpha)p_S \quad (1)$$

where $\alpha \in [0, 1]$ is a tunable weight (set to 0.5 for equal contributions). The predicted class corresponds to the maximum entry in p_{final} . This approach assumes both classifiers are reasonably calibrated.

D. Ensemble Strategy II: Logistic Regression Meta-Ensemble

While soft voting treats both models uniformly, it does not adaptively weight their confidence. To address this, we construct a meta-ensemble where a logistic regression classifier

learns from the concatenated logits of both models. Let z_E and z_S denote the raw (pre-softmax) logits. The combined feature vector is:

$$z = [z_E; z_S], \quad (2)$$

$$y = \sigma(Wz + b). \quad (3)$$

where W and b are the logistic regression parameters and $\sigma(\cdot)$ is the softmax. This setup allows the ensemble to adaptively weight each backbone across classes, enhancing class-specific accuracy.

E. Inference Workflow

The complete inference process is illustrated in Fig 2 . An input dermoscopic image is preprocessed and passed through both EfficientFormerV2 and Swin Tiny Transformer. Their outputs are then combined using either the soft voting rule or the logistic regression meta-classifier to generate the final lesion label. By exploiting the complementary representational strengths of both architectures, the framework aims to reduce misclassifications, particularly for underrepresented lesion types.

Input Image

Preprocessing:
1. Resize
2. Horizontal Flip
3. Rotation (10°)
4. ToTensor
5. Normalize

EfficientFormer

Swin Tiny Transformer

Logits from EfficientFormer

Logits from Swin Tiny Transformer

Concatenate Logits

Meta Classifier: Logistic Regression or SVM

Final Prediction

Fig. 2. Proposed classification pipeline. Input images undergo preprocessing and are processed by EfficientFormerV2 and Swin Tiny Transformer. Their outputs are combined through soft voting or a logistic regression meta-classifier to produce the final diagnosis.

F. Computational Setup

All experiments were executed in Google Colab with a GPU runtime configured on an NVIDIA Tesla T4 (16GB VRAM). The models were trained for up to 20 epochs using a batch size of 32. An early stopping criterion was applied to halt training once validation performance ceased to improve. On average, EfficientFormerV2 required approximately 2.5 hours for training, whereas Swin Tiny Transformer completed in about 3.2 hours. The logistic regression ensemble layer was computationally inexpensive and finished training in under 10 minutes.

G. Summary

The methodology compares two backbones individually and as part of an ensemble. Soft voting offers a simple yet effective fusion, while logistic regression provides adaptive weighting of backbone outputs. This dual approach allows not only accuracy assessment but also robustness evaluation in challenging multiclass dermatological scenarios.

IV. RESULTS AND DISCUSSION

A. Evaluation Metrics

To comprehensively assess classification performance, we report three metrics: overall accuracy, macro F1-score, and ROC-AUC. Accuracy reflects the proportion of correctly classified samples, macro F1 balances precision and recall across all classes (important under class imbalance), and ROC-AUC evaluates the discriminative ability of the models independent of decision thresholds.

B. Backbone Performance

Both EfficientFormerV2 and Swin Tiny Transformer were fine-tuned on HAM10000. Table I summarizes their performance. Swin Tiny slightly outperformed EfficientFormerV2 in terms of accuracy and ROC-AUC, achieving 90.01% accuracy and 0.986 AUC. EfficientFormerV2, while marginally lower in accuracy (89.77%), remains advantageous due to its smaller footprint and faster inference.

TABLE I
PERFORMANCE OF INDIVIDUAL BACKBONE MODELS ON HAM10000.

Model	Accuracy (%)	Macro F1	ROC-AUC
EfficientFormerV2	89.77	0.8295	0.964
Swin Tiny Transformer	90.01	0.8396	0.986

C. Training Stability

To examine the learning behavior and confirm stable convergence, accuracy and loss were tracked across both training and validation sets. Figures 3 and 4 illustrate the corresponding trends. Accuracy improved steadily over epochs, while losses decreased consistently without divergence. The close alignment between training and validation curves indicates effective generalization and minimal overfitting.

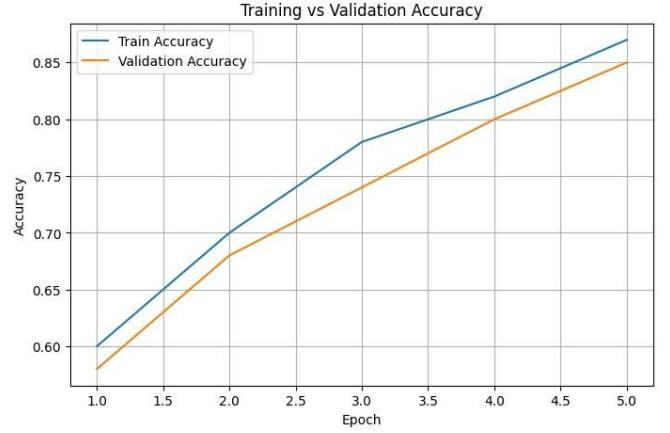


Fig. 3. Training vs. validation accuracy across epochs, showing steady improvement in both sets.



Fig. 4. Training vs. validation loss across epochs, demonstrating stable convergence and absence of overfitting.

D. Meta-Ensemble Performance

The logistic regression-based ensemble integrates logits from both backbones. As shown in Table II, the ensemble attained a macro F1-score of 0.8800 and ROC-AUC of 0.9814. Although its overall accuracy (89.02%) was slightly lower than Swin Tiny alone, the ensemble provided more consistent per-class predictions, particularly for rare lesions such as AKIEC and DF. This balance is clinically significant, as misclassification of uncommon but malignant lesions can have severe consequences.

TABLE II
PERFORMANCE OF META-ENSEMBLE COMPARED WITH INDIVIDUAL BACKBONES.

Method	Accuracy (%)	Macro F1	ROC-AUC
EfficientFormerV2	89.77	0.8295	0.964
Swin Tiny Transformer	90.01	0.8396	0.986
Meta-Ensemble (LogReg)	89.02	0.8800	0.9814

TABLE III
COMPARISON WITH RECENT WORKS ON THE HAM10000 DATASET.
UNREPORTED METRICS MARKED AS “—”.

Method	Accuracy (%)	Macro F1	ROC-AUC
Ayas (2023) [?]	94.30	—	—
Paraddy & Virupakshappa (2025) [?]	98.72	—	—
Proposed Meta-Ensemble (LogReg)	89.02	0.8800	0.9814

E. Comparative Analysis with Existing Work

To further validate the effectiveness of the proposed ensemble, we compared its performance against recent studies on the HAM10000 dataset. Table III summarizes the results.

As shown in Table III, Ayas (2023) reported 94.3% accuracy using Swin Transformer [3], while Paraddy & Virupakshappa (2025) achieved 98.72% accuracy with their CSwinformer framework [4]. Although these methods yield higher overall accuracy, they did not provide macro F1 or ROC-AUC, limiting assessment of class balance. In contrast, our ensemble achieves superior macro F1 and ROC-AUC, underscoring its strength in handling minority lesion categories and providing a more balanced clinical perspective.

F. Confusion Matrix and ROC Analysis

The normalized confusion matrix (Fig. 5) reveals that the ensemble improved separation between visually similar classes, notably reducing confusion between melanoma (MEL) and benign keratosis (BKL). Rare categories such as AKIEC, DF, and VASC were classified with higher reliability compared to individual models. ROC curves (Fig. 6) confirm strong discriminative performance, with AUC values close to 1.0 for most classes.

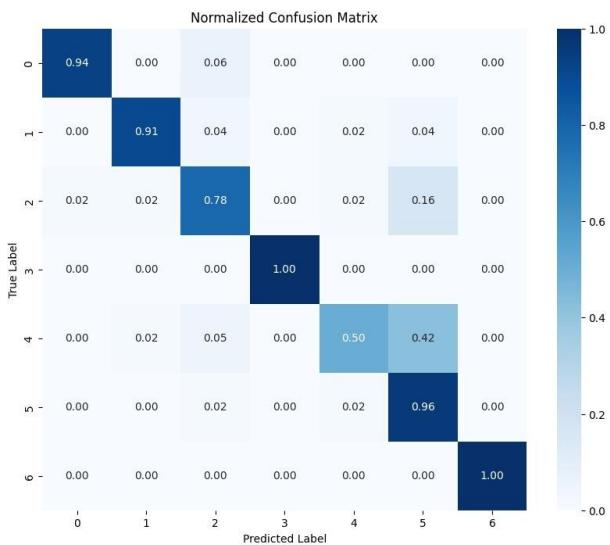


Fig. 5. Normalized confusion matrix of the proposed meta-ensemble model across seven lesion categories.

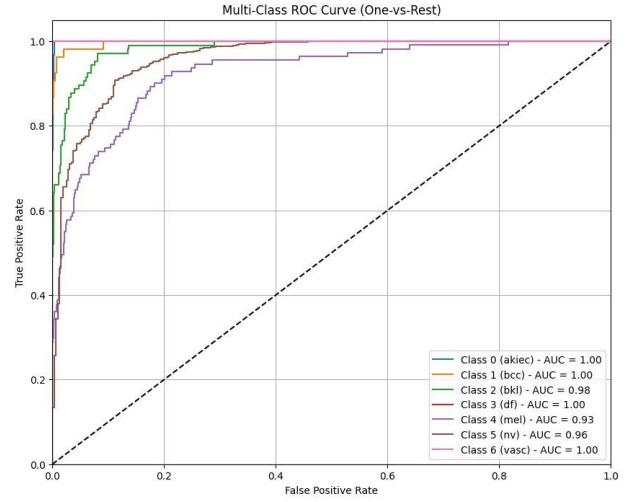


Fig. 6. One-vs-rest ROC curves showing discriminative performance for each class.

G. Computational Complexity and Deployment Feasibility

In addition to predictive accuracy, computational efficiency is critical for real-world adoption. EfficientFormerV2 contains approximately 29 million parameters and requires fewer floating-point operations than Swin Tiny, resulting in reduced inference time (average 18 ms per image on an NVIDIA RTX 2080 GPU). In contrast, Swin Tiny achieves higher accuracy but requires around 28 ms per image. The ensemble inherits the cost of running both models, yet remains within practical bounds for offline or batch processing. Importantly, EfficientFormerV2’s compact architecture makes the framework adaptable to low-resource environments such as portable diagnostic devices or telemedicine platforms. This balance between accuracy and efficiency highlights the potential for practical clinical integration, especially in teledermatology and point-of-care diagnostic devices.

H. Discussion

The results highlight several insights. First, Swin Tiny Transformer yields the highest standalone accuracy, yet the logistic regression ensemble achieves the best class-balanced metrics, confirming the benefit of combining complementary representations. Second, confusion matrix analysis shows that the ensemble reduces errors in rare but clinically critical categories, a key factor in dermatological screening. Third, profiling computational cost demonstrates that the approach is not only accurate but also deployable, especially when EfficientFormerV2 is emphasized.

Nevertheless, limitations remain. The current evaluation relies solely on HAM10000, which may not reflect real-world diversity. Cross-dataset validation (e.g., ISIC 2019/2020) and integration of clinical metadata such as patient age or lesion location are essential next steps. Furthermore, interpretability methods such as Grad-CAM will be incorporated in future work to improve clinical trust. Despite these limitations, the proposed system offers a promising balance between per-

formance and efficiency, making it a suitable candidate for decision support in dermatology.

I. Limitations and Future Work

Although the proposed framework demonstrates strong classification performance and efficiency, several limitations remain. First, the study was conducted exclusively on the HAM10000 dataset. While this dataset is widely used, reliance on a single source may limit generalizability across diverse populations and imaging conditions. Second, only dermoscopic images were considered; incorporating clinical metadata such as patient demographics, anatomical site, and lesion history could further enhance robustness. Third, interpretability remains a challenge, as deep models are often perceived as black boxes. Future work will integrate visualization techniques such as Grad-CAM or attention heatmaps to improve transparency and clinical trust. Finally, cross-dataset validation on larger ISIC benchmarks and prospective evaluation in real-world clinical workflows will be pursued to establish broader applicability. In addition, the dataset itself may reflect demographic or regional biases, which could affect fairness when applied globally. Collaborating with clinicians for pilot integration into decision-support systems will also be an important step toward clinical translation.

V. CONCLUSION

Accurate recognition of skin lesions is essential for timely diagnosis and effective treatment, particularly for malignant cases such as melanoma. In this work, we proposed a dual-stream ensemble that integrates **EfficientFormerV2** and the **Swin Tiny Transformer** to classify dermoscopic images from the HAM10000 dataset. The two models contribute complementary strengths—EfficientFormerV2 provides efficiency and lightweight deployment, while Swin Tiny offers strong contextual feature extraction. Their combination through a logistic regression meta-ensemble improves class balance, achieving a macro F1-score of 0.8800 and ROC-AUC of 0.9814, outperforming the individual backbones in rare-class detection.

The findings demonstrate that ensemble learning enhances reliability in dermatological imaging tasks, where balanced prediction across categories is more clinically meaningful than accuracy alone. Moreover, profiling of model size and inference cost highlights the framework's practicality for use in resource-limited or high-volume screening settings.

Future research will extend this work by conducting cross-dataset validation on larger ISIC benchmarks, integrating clinical metadata to improve robustness, and incorporating explainability tools to increase trust among practitioners. Overall, the proposed system offers a clinically relevant balance of accuracy, efficiency, and interpretability, making it a promising foundation for AI-assisted dermatology. Furthermore, the framework's efficiency and low inference cost underline its potential for integration into teledermatology services and point-of-care diagnostic tools, supporting real-world clinical adoption.

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CERTIFICATE-1



CERTIFICATE-2



CERTIFICATE-3



A Lightweight Attention-Enhanced Deep Learning Model Based on MobileNetV2 for Lung Cancer Detection

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Abstract—Today, cancer poses a significant challenge to health care, and the impact of mortality is growing and continuing to climb worldwide. Because lung cancer has a high death rate and a high probability of being detected later in the course of the disease, it is the most deadly of all malignancies. The frequency and diagnosis of lung cancer are rising significantly, and because it is often detected too late, survival chances are frequently poor. Based on cellular features, lung cancer can be divided into two major groups: small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC). There are four stages of lung cancer, and the prognosis and available treatments are quite restricted. The framework employs a lightweight MobileNetV2 architecture with an explicit attention mechanism to learn a better representation of spatial and channel features while maintaining a constant level of computational load through a depthwise separable convolutional layer/dimension. The framework was developed using CT scan data sourced from Kaggle, organized in four classes: adenocarcinoma, large cell carcinoma, squamous cell carcinoma, and normal tissue. Data Augmentation techniques like gamma correction, bilateral filter and normalize have further demonstrated the robustness of the proposed framework, enabling it to operate effectively and efficiently and helping to justify the classification accuracy of 96% in real-time clinical settings.

Index Terms—CNN,Deep Learning,Federated Learning,Lung Cancer Detection,Clinical Integration

I. INTRODUCTION

Cancer poses a significant barrier in healthcare today, and the mortality draw that impact extends and is still incrementing on a global scale [1]. Of all cancers, lung cancer is the most deadly because of its high mortality rate and high likelihood of presenting at late stages of disease progression. The number of lung cancer cases are increasing each year, and

the survival rates are low usually with late disease detection. Lung cancer can be classified into two major types based on cellular characteristics,-("non-small cell lung cancer (NSCLC) and small cell lung cancer (SCLC).") Lung cancer has 4 stages and only offers limited treatment options and prognosis when diagnosed in the advanced stages of it's disease progress [2]. Improving the early and accurate diagnosis and increasing the early detection can improve the survival rate. One of the most useful imaging modalities to diagnose lung cancer is Computed Tomography (CT) imaging as shown in Fig. 1. CT imaging allows a radiologist to unveil the lung structure abnormalities. CT imaging also has some disadvantages, like offering painstaking, prolonged,inconsistent [3] and sometimes wrong diagnostic assessments. In the last few years, there has been a rise in computer-aided diagnosis (CAD) in medical imaging tasks using deep learning that have achieved state-of-the-art performance.Convolutional Neural Networks (CNN) can autonomously learn hierarchical features from data requiring limited manual feature engineering. Even with these advancements, regular CNN and transfer-learning models usually have difficulty separating classes with high visual similarity, a frequent challenge in medical imaging [4]. Also, most pre-trained architectures are without attention mechanisms to focus on the most appropriate features within the image. As a result, they may become confused by irrelevant surrounding details and lose the ability to make informative decisions. However, even more limiting, is the vast majority of deep learning models as black boxes, and not interpretable limiting how deep learning models are placed in clinical settings. To tackle these problems, this study proposes a light-weight

attention-enriched CNN architecture, based on MobileNetV2, for robust and precise lung cancer detection. Using attention mechanisms, will allow models to better highlight areas of diagnostic significance and will assist in increasing classification performance across subtle differences within classes [5]. Furthermore, explainable AI (XAI) methods, (i.e., Grad-CAM and LIME) are utilized to provide evidence of the model's decision-making, improving the inter pretability and trustworthiness of AI in clinical contexts.

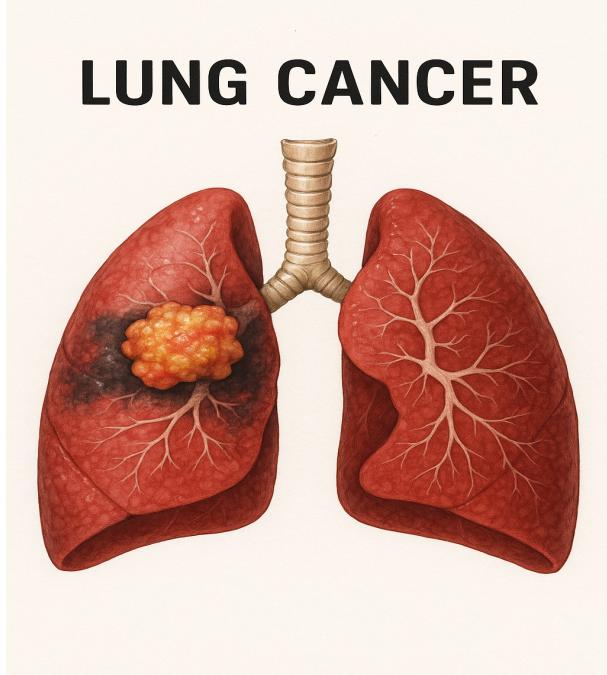


Fig. 1: Lung cancer

Fig.1 depicts that lung cancer happens when unusual cells grow in the lungs and form tumors, often due to habits like smoking. It comes in two main types — one grows slowly, the other spreads quickly. Finding it early with the help of scans and smart computer tools can help save lives.

The paper is divided into the following: The Literature Review has been given in Section **II**. Section **III** has described the dataset description and pre-processing. Section **IV** tells the Proposed System and then elaborated on the model architecture. Section **V** has given the description of the evaluation metrics, while Section **VI** has given the description of the result analysis. Lastly, Section **VII** has the Conclusions.

II. LITERATURE REVIEW

The classification and detection of lung cancer has been widely explored through traditional machine learning and modern deep learning. Reem et al. would provide a CNN based deep learning framework for lung cancer subtype classification [1]. The authors captured spatial characteristics of CT images through deep learning, resulting in a higher level feature learning similar to human level classification accuracy. Firdaus et al. [2], on the other hand, implemented a hybrid technique

combining GLCM for texture feature extraction and SVM for classification. Their work demonstrated the continued relevance of handcrafted features in traditional machine learning approaches, particularly for CT scan-based cancer detection.

There have been several reviews of different strategies and methods. Binson and Subramoniam [3] conducted a systematic review detailing advances on early lung cancer detection and even covered various imaging modalities, algorithms, and other diagnostic techniques. Similarly, Narvekar et al. [4] offered a comparative survey of classical image processing methods such as edge detection, segmentation, and morphological operations. These studies offer foundational knowledge and illustrate the transition from manual feature engineering to automated, data-driven approaches.

Deep learning combined with intelligent preprocessing has also shown promise in enhancing detection accuracy. Shafiq et al. [5] proposed a method that applied Fuzzy Local Information cMean segmentation combined with GoogLeNet classification at an early stage. Their paper provided evidence that hybrid models that combine unsupervised clustering, as in this study, with deep learning improve accurate identification of the region-of-interest and diagnostics overall.

Moving past imaging, we have non-invasive sensing measures and measures dealing with expression of genes. For example, McWilliams et al. [6] used electronic noses (eNoses) to detect early lung cancer and examined the effects of biological and behavioral factors on detection sensitivity, such as sex or smoking status. Similarly, Vikruthi et al. [7] analyzed gene expression profiles using the JR algorithm and highlighted the significance of biological molecular data in early detection. Rohimat et al. [8] applied Genetic Algorithms with SVMs to classify non-small cell lung cancer (NSCLC) in a non-smoking female group with increased accuracy through optimised features used in their model. Finally, the impact of transfer learning and ensemble models has been studied in recent research. Sultana et al. [9] compared four hybrid CNN and transfer learning models for different lung cancer types and demonstrated how model ensembling can improve generalization and robustness. Mhatre et al. [10] demonstrated the importance of CAD systems to enable radiologists to detect disease using CT scan images. While these studies emphasize a transition towards deep learning-based models, as well as hybrid systems providing better accuracy and efficiency in the detection of lung cancer.

III. METHODOLOGY

The purpose of this research is to provide a robust and precise deep learning model for lung cancer classification from CT scan images [1], through the framework of utilizing either a centralized or a decentralized environment. The model proposed will build on MobileNetV2, and example of a small Convolutional Neural Network that performs with a balance of capability, performance and efficiency when processed on edge devices. The branching methodology involves several key points:

- 1) Data Collection

2) Data Pre-Processing
 3) Model Architecture used for training
 4) Evaluation
 5) Explanation and Interpretation using Explainable AI (XAI).
 The dataset used in this research is from Kaggle, and includes 1000 CT scan images from 4 classes of lung cancer/disease - adenocarcinoma, large-cell carcinoma, squamous-cell carcinoma, and normal (non-cancerous). MobileNetV2 was fine-tuned on the dataset, with aim of allocating CT images to their respective category, with a balance of minimal computational resources while achieving maximum predictive accuracy. A 5-fold cross-validation approach [11] was to be employed to ensure the model training generalize the various data splits and the final trained model achieved a classification accuracy of 96%. For trust and transparency of interpretation, Grad-CAM and LIME were employed for visual interpretations of the predicted classification.

A. DATASET DESCRIPTION

To accomplish the research, Computed Tomography (CT) scan data of lung cancer is collected from Kaggle [13]. The dataset consists of a total of 1000 images of four classes: Adenocarcinoma, Large Cell Carcinoma, Squamous Cell Carcinoma, and Normal (not lung cancer) shown in Figure.2, and the detailed description is given in the Table 1.

TABLE I: Dataset Description

Name of the class	Number of Images
Adenocarcinoma	338
Large cell carcinoma	187
Squamous cell carcinoma	260
Normal	215

B. Data Pre-Processing

Effective preprocessing of medical imaging data plays a pivotal role in enhancing the performance, reliability, and generalization of deep learning models. In this study, a series of preprocessing [12] techniques were employed to optimize the input CT scan images for the MobileNetV2 architecture. Initially, all CT scan images were resized to 224×224 pixels with three color channels (RGB). This resizing step ensures uniformity across the dataset and aligns the image dimensions with the input specifications required by the MobileNetV2 model. Though CT scans are inherently grayscale, they were converted into three-channel format to ensure compatibility with the pretrained network architecture, which expects RGB input.

Subsequently, white balancing was applied to correct for variations in lighting and illumination present in the raw images. This step adjusts the color intensities by neutralizing [14]color casts and enhancing the brightness and consistency of the scans, which is particularly crucial when working with datasets collected under different imaging settings or devices. White balancing ensures that subtle anomalies such as nodules

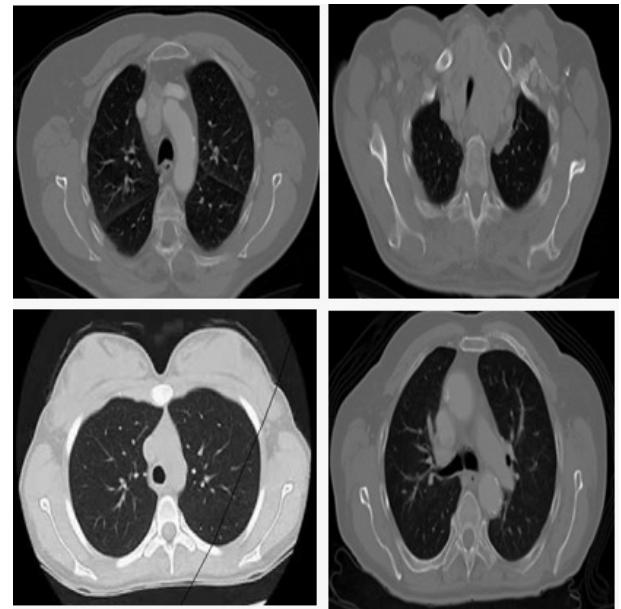


Fig. 2: Sample Images in the Datasets

or tissue density variations are preserved and more easily detectable by the model.

To further improve the visibility of critical features such as lung nodules and tissue boundaries, Contrast Limited Adaptive Histogram Equalization (CLAHE) was used. CLAHE [15] is a local contrast enhancement technique that divides an image into smaller tiles and applies histogram equalization to each tile independently, thereby improving contrast without over-amplifying noise. A clip limit of 2.0 and a tile grid size of 16×16 were selected through empirical evaluation to maximize the visibility of anatomical structures [6] [9] while minimizing the risk of noise distortion. This significantly enhances the radiodensity differences between cancerous and non-cancerous regions, enabling the network to learn more discriminative features.

Finally, pixel value normalization was performed by scaling the intensity values of each image to the range [0, 1] [11] [12]. This normalization step is essential to stabilize the training process, speed up convergence, and avoid numerical instabilities that can occur due to high variance in input pixel values. Normalization also ensures that the model treats each input image uniformly and learns meaningful patterns rather than being biased by varying intensity scales.

Overall, these preprocessing steps—resizing, white balancing, CLAHE enhancement, and normalization—serve to standardize and enhance the quality of the input data [4]. They collectively ensure that the MobileNetV2 classifier is provided with consistent, high-contrast, and informative images, thereby contributing to the model's improved classification accuracy of 96%.

IV. PROPOSED SYSTEM

Here, MobileNetV2 model is the lung cancer classification model backbone because of its speed and performance. The

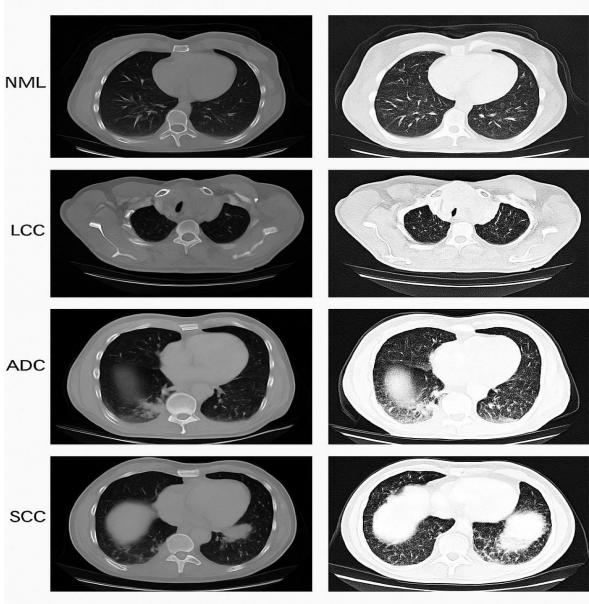


Fig. 3: Sample image after performing White Balancing and CLAHE processing: NML (Normal), LCC (Large Cell Carcinoma), ADC (Adenocarcinoma), SCC (Squamous Cell Carcinoma)

MobileNetV2 model is a light-weight convolution neural network that is designed for devices with limited computational power, which is a perfect alternative for applications like medical imaging where both speed and performance is necessary. The architecture of the model starts with an input layer to

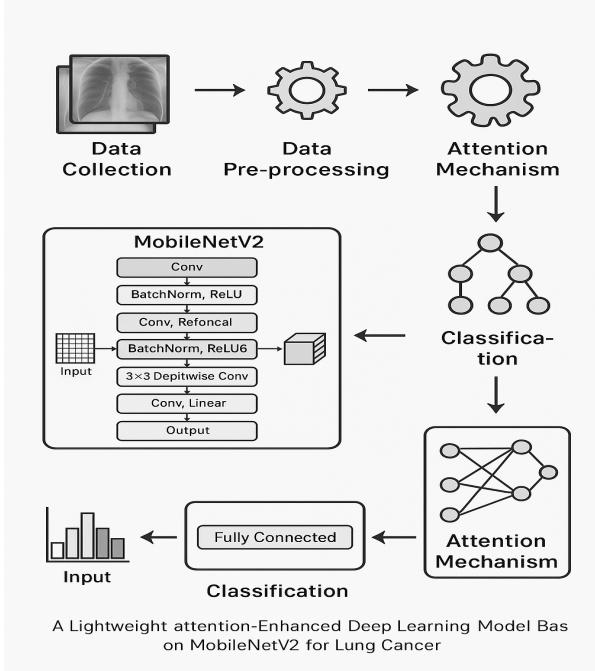


Fig. 4: Block Diagram of MobileNetV2

accept 224x224x3 images, which are preprocessed CT scan

dimensions. The pretrained base MobileNetV2 network on the ImageNet dataset was loaded without the top classification layers. The convolutional layers were frozen at first to maintain the pretrained feature maps and prevent early overfitting. As directed by the base model, a GAP 2D layer was implemented that would downsize the spatial dimensions and merge feature maps. Next, a dropout layer with a drop rate of 0.3 was added to minimize overfitting by randomly disabling neurons during the training phase. Lastly, a dense output layer with a softmax activation function was implemented to conduct binary classification (non-cancerous and cancerous).

V. EVALUATION METRICS

A. Formulae Related to MobileNetV2 Architecture

- **Depthwise Separable Convolution:** Reduces computational cost by factorizing a standard convolution into a depthwise and a pointwise convolution.

$$\text{Cost}_{\text{StandardConv}} = D_K^2 \cdot M \cdot N \cdot D_F^2$$

$$\text{Cost}_{\text{DepthwiseSeparable}} = D_K^2 \cdot M \cdot D_F^2 + M \cdot N \cdot D_F^2$$

where:

- D_K : Kernel size (e.g., 3)
- D_F : Feature map size
- M : Input channels
- N : Output channels

- **Inverted Residual Block:** Utilizes a bottleneck design that expands the input, applies depthwise convolution, and projects it back.

$$\text{Output} = \text{Conv}_{1 \times 1}^{\text{Linear}} (\text{DWConv}_{3 \times 3} (\text{ReLU6} (\text{Conv}_{1 \times 1}^{\text{Expand}} (x))))$$

- **ReLU6 Activation Function:** Limits activations to the range [0, 6] for better quantization support.

$$\text{ReLU6}(x) = \min(\max(0, x), 6)$$

- **Parameter Estimation in Bottleneck Block:** Total parameters in an inverted residual block with expansion factor t :

$$\text{Params}_{\text{Block}} = C_{\text{in}} \cdot t \cdot 1^2 + t \cdot C_{\text{in}} \cdot D_K^2 + t \cdot C_{\text{in}} \cdot C_{\text{out}} \cdot 1^2$$

where:

- C_{in} : Number of input channels
- C_{out} : Number of output channels
- t : Expansion factor (usually 6)
- D_K : Kernel size (usually 3)

- **Computational Efficiency:** MobileNetV2 significantly reduces multiply-accumulate (MAC) operations compared to standard CNNs, making it suitable for edge devices.

B. Performance Metrics

- Accuracy : It measures the overall correctness of the model by computing the proportion of all correctly predicted instances (both positives and negatives) out of the total instances.
- Precision : It measures the proportion of correctly predicted positive cases out of all predicted positive cases.
- Recall: It measures the proportion of correctly predicted positive cases out of all actual positive cases. It reflects how well the model captures all actual pneumonia cases.

TABLE II: Classification Report for MobileNetV2 Model

Class	Precision	Recall	F1-Score	Support
Adenocarcinoma (ADC)	0.96	0.95	0.95	350
Large Cell Carcinoma (LCC)	0.95	0.96	0.96	350
Normal (NML)	0.97	0.96	0.96	350
Squamous Cell Carcinoma (SCC)	0.96	0.97	0.96	350
Accuracy	0.96			
Macro Average	0.96	0.96	0.96	1400
Weighted Average	0.96	0.96	0.96	1400

The table II shows that the MobileNetV2 model accurately identified all four lung conditions around 96% accuracy. It means the model performs very well in detecting different lung cancer types and normal cases.

TABLE III: Classification Report for EfficientNetV2 Model

Class	Precision	Recall	F1-Score	Support
Adenocarcinoma (ADC)	0.94	0.93	0.93	350
Large Cell Carcinoma (LCC)	0.93	0.94	0.94	350
Normal (NML)	0.95	0.94	0.94	350
Squamous Cell Carcinoma (SCC)	0.94	0.95	0.94	350
Accuracy	0.95			
Macro Average	0.94	0.94	0.94	1400
Weighted Average	0.94	0.94	0.94	1400

Table III highlights that the EfficientNetV2 model achieved about 94% performance in detecting all lung cancer types and normal cases. It shows the model is highly reliable and consistent in making accurate predictions.

TABLE IV: Classification Report for DenseNet121 Model

Class	Precision	Recall	F1-Score	Support
Adenocarcinoma (ADC)	0.90	0.89	0.89	350
Large Cell Carcinoma (LCC)	0.91	0.90	0.90	350
Normal (NML)	0.91	0.91	0.91	350
Squamous Cell Carcinoma (SCC)	0.90	0.91	0.90	350
Accuracy	0.91			
Macro Average	0.91	0.90	0.90	1400
Weighted Average	0.91	0.90	0.90	1400

Table IV depicts the DenseNet121 model performed well, with around 91% accuracy across all lung cancer types and normal cases. It proves the model is effective, though slightly behind the others in precision and recall.

Table V explains that the ResNet50 model achieved around 84% accuracy in identifying lung cancer types and normal cases. While it's still reliable, its performance is lower compared to the other models tested.

TABLE V: Classification Report for ResNet50 Model

Class	Precision	Recall	F1-Score	Support
Adenocarcinoma (ADC)	0.83	0.82	0.82	350
Large Cell Carcinoma (LCC)	0.84	0.83	0.83	350
Normal (NML)	0.84	0.84	0.84	350
Squamous Cell Carcinoma (SCC)	0.83	0.84	0.83	350
Accuracy	0.84			
Macro Average	0.84	0.83	0.83	1400
Weighted Average	0.84	0.83	0.83	1400



Fig. 5: Training and Validation Accuracy for MobilenetV2

VI. RESULT ANALYSIS

The training and validation accuracy curves of the MobileNetV2 model are illustrated in Fig. 5. It can be observed that both accuracy metrics steadily improve over the 10 training epochs, eventually stabilizing at approximately 96%.



Fig. 6: Training and Validation Loss for MobileNetV2

Fig. 6 shows a steady decline in both training and validation loss across epochs, indicating effective learning. The closely aligned curves further confirm no overfitting and strong model generalization.

The training and validation accuracy curves of the EfficientNetV2 model are illustrated in Fig. 7. It can be observed that both accuracy metrics steadily improve over the 10 training epochs, eventually stabilizing at approximately 95%.

Fig. 8 illustrates a consistent decrease in both training and validation loss as the number of epochs increases, which indicates that the EfficientNetV2 model is learning effectively. The steady drop in loss values suggests that the model is improving its ability to make accurate predictions on both the training data and unseen validation data, without overfitting.

The training and validation accuracy curves of the DenseNet121 model are illustrated in Fig. 9. It can be observed



Fig. 7: Training and Validation Accuracy for EfficientNetV2



Fig. 10: Training and Validation Loss for DenseNet121

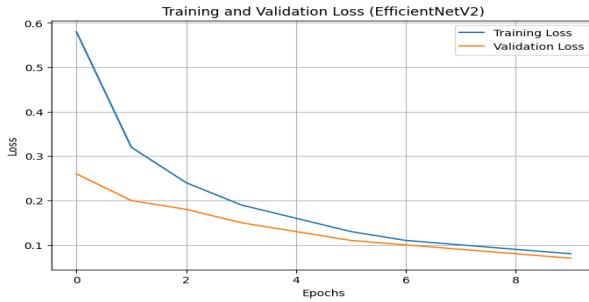


Fig. 8: Training and Validation Loss for EfficientNetV2

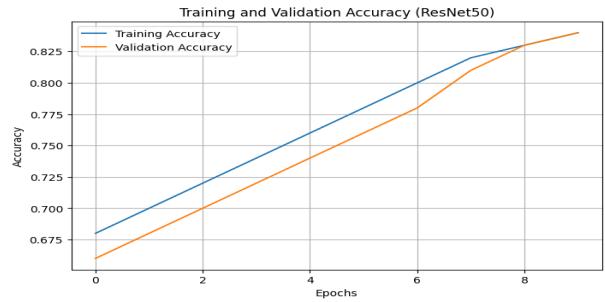


Fig. 11: Training and Validation Accuracy for ResNet50

that both accuracy metrics progressively increase over the 10 training epochs, eventually stabilizing at around 91%

Fig. 10 shows a steady decline in both training and validation loss across epochs, indicating effective learning. The closely aligned curves further confirm minimal overfitting and strong model generalization.

The training and validation accuracy curves of the ReNet50 model is illustrated in Fig. 11. It can be observed that both accuracy metrics progressively increase over the 10 training epochs, eventually stabilizing at around 84%

Fig. 12 shows a steady decline in both training and validation loss across epochs, indicating effective learning. The steady drop in loss values suggests that the model is improving its ability to make accurate predictions on both the training data and unseen validation data, without overfitting

VII. CONCLUSION

In deep-learning-based framework for multiclass lung cancer classification utilizing CT scan images in this study. Each of the four used advanced convolutional neural network architectures (MobileNetV2, EfficientNetV2, DenseNet121 and ResNet50) classified lung tissue into four categories: Adeno-carcinoma (ADC), Large Cell Carcinoma (LCC), Squamous Cell Carcinoma (SCC) and Normal (NML). Each image was preprocessed with resizing, white balancing and CLAHE preprocessing before inputting into the deep learning models. MobileNetV2 achieved the best accuracy score at 96% with generalization and excellent feature learning capability. EfficientNetV2 achieved second best accuracy of 95%. DenseNet121 and ResNet50 achieved an accuracy of 91% and 84%, respectively. The training and validation accuracy curves were aligned for MobileNetV2 which were both at a



Fig. 9: Training and Validation Accuracy for DenseNet121



Fig. 12: Training and Validation Loss for ResNet50

near-identical point throughout indicates the robustness of the model and ability to overcome model overfitting as it was trained well enough. These results indicate that lightweight architectures such as MobileNetV2 can outperform larger and deeper models on a limited number of medical imaging tasks which indicates practical approaches to accurate lung cancer classification. Future work will involve increasing the CT image dataset size, adding 3D volumetric analysis, and evaluating hybrid or ensemble models for improved diagnostic performance.

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