

A META-ENSEMBLE DEEP LEARNING APPROACH USING EFFICIENTFORMERV2 AND SWIN TINY TRANSFORMER FOR SKIN LESION CLASSIFICATION

*A Project Report submitted in the partial fulfillment
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

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Project Course 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 of the device | 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

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, enabling more robust feature representation across lesion categories. Experiments show that the Swin Tiny model achieves the highest accuracy ($\sim 90\%$), whereas the logistic-regression ensemble delivers the best balance across classes and strong discrimination capability, 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, overall, the proposed approach demonstrates potential as a reliable, scalable decision- support tool in dermatological practice.

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1. INTRODUCTION

Skin cancer is one of the most serious and rapidly growing forms of cancer, demanding early and accurate detection to ensure effective treatment and improved patient outcomes. These lesions pose significant challenges to healthcare due to their visual diversity, subtle dermoscopic patterns, and varying levels of severity depending on the lesion type, morphological characteristics, and stage of progression. Early identification of malignant lesions—particularly melanoma—is crucial, as timely diagnosis can dramatically increase survival rates, whereas late detection often results in poor prognosis and extensive treatment requirements [1]. Dermoscopy, a non-invasive imaging technique, plays a vital role in examining skin lesions and provides high-quality visualization compared to conventional clinical inspection. However, relying solely on manual interpretation by dermatologists can be time-consuming and inconsistent, and diagnostic decisions may vary based on experience and subjective judgment. These limitations highlight the need for automated systems capable of delivering accurate, fast, and reliable skin lesion classification.

Skin diseases, including skin cancers, are becoming a growing healthcare concern in India, affecting thousands of individuals each year. These lesions can be benign (non-cancerous) or malignant (cancerous) [2], as shown in Fig 1.1, and they occur across all age groups, often going unnoticed until they begin to show visible symptoms. The increasing prevalence of skin cancer in India is associated with factors such as UV exposure, environmental pollution, occupational hazards, genetic predisposition, and insufficient awareness regarding preventive skin care. Despite improvements in medical technology, early recognition of skin cancer remains low in many regions, leading to delays in diagnosis and treatment. According to dermatological studies, a significant proportion of skin cancer cases in India are detected at advanced stages, mainly because individuals fail to seek medical attention during early changes in their skin or lack access to specialized dermatological care [3].

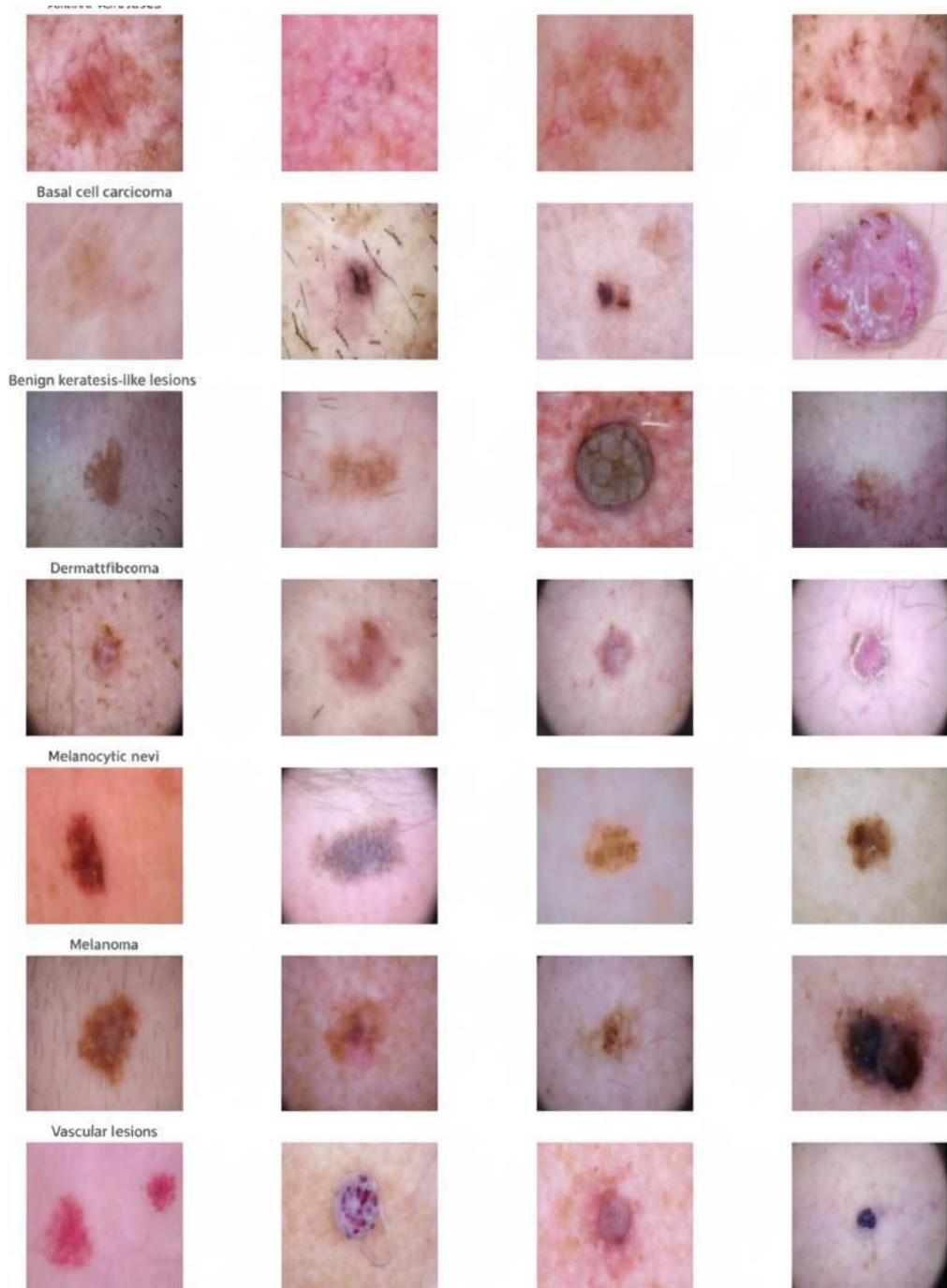


Fig 1.1: Common Dermoscopic Skin Lesion Categories Represented in HAM10000

One of the major challenges in India is the disparity in diagnostic accessibility. While large metropolitan hospitals offer advanced dermoscopic facilities and expert dermatologists, rural and semi-urban regions often lack these resources. Many patients consult general physicians who may not have specialized training in dermoscopy, increasing the likelihood of diagnostic errors. The cost of repeated clinical visits, imaging procedures, and specialized consultations can also be financially burdensome for many families. Additionally, India faces a shortage of dermatologists relative to its population, further

delaying early diagnosis and limiting timely intervention [4]. These barriers demonstrate the importance of affordable, automated diagnostic tools that can assist clinicians in identifying malignant skin lesions at an early stage.

Recent advances in Deep Learning and Artificial Intelligence have shifted the landscape of medical image analysis by introducing automated, efficient, and highly accurate diagnostic solutions. Convolutional Neural Networks (CNNs) [5] have shown exceptional ability in learning hierarchical patterns from dermoscopic images, making them effective for skin lesion classification tasks. Transformer-based architectures have also gained prominence due to their strength in capturing global image relationships and contextual information [6]. By combining these approaches, hybrid systems achieve stronger performance, leveraging the fine-grained feature extraction capabilities of CNNs and the long-range attention modeling of Transformers. Ensemble-based systems further improve reliability and decision-making by integrating the predictions of multiple models, thereby reducing errors and enhancing classification stability [7].

This research proposes a Meta-Ensemble Model that integrates EfficientFormerV2 and Swin Transformer Tiny for accurate multilabel skin lesion classification from dermoscopic images. The system employs several preprocessing techniques—such as resizing, normalization, augmentation, and image enhancement—to improve feature visibility and ensure high-quality inputs. The EfficientFormerV2 model, designed for lightweight and efficient feature extraction, captures localized texture patterns and boundary information within lesions [8]. Meanwhile, the Swin Transformer Tiny utilizes hierarchical attention mechanisms to recognize global structures and contextual variations [6]. The predictions from both models are combined using a logistic regression meta-classifier, enabling the system to achieve a higher level of accuracy, stability, and generalization compared to standalone models [9].

To support practical usability, the proposed system is deployed as a web application using Flask, allowing users to upload dermoscopic images and receive automated classification results instantly. The system includes image validation mechanisms to ensure that only legitimate skin images are analyzed, and provides clear diagnostic outputs that can assist clinicians, researchers, and healthcare workers. With its capability to handle diverse lesion types and provide rapid diagnostic support, the proposed model has the potential to enhance early detection, reduce diagnostic burden, and improve clinical decision-making in

dermatology. As AI continues to advance in healthcare, hybrid ensemble models such as this are expected to play a crucial role in improving accessibility and accuracy in skin cancer diagnosis [10].

1.1 Motivation

Skin cancer remains one of the most challenging dermatological conditions due to its growing prevalence, varying lesion characteristics, and potentially life-threatening outcomes if not detected early [11]. In many cases, individuals fail to recognize early skin changes or do not consider them serious enough to seek immediate medical attention, leading to delayed diagnosis and more complex treatment procedures. The conventional method of dermoscopic analysis, although highly effective in expert hands, is limited by the availability of trained dermatologists and the inherent subjectivity in visual interpretation. Subtle differences between benign and malignant lesions often require years of clinical experience to correctly identify, making early diagnosis difficult for less experienced practitioners or regions with limited access to specialists.

With increasing awareness of skin-related disorders, the reliance on medical imaging has grown substantially, highlighting the importance of automated systems that can support clinicians in analyzing dermoscopic images accurately and efficiently. AI-driven techniques, especially those based on Deep Learning, offer the potential to reduce diagnostic time, minimize human error, and improve overall reliability in identifying suspicious lesions [12]. The motivation for this project arises from the need to develop a robust, accessible, and automated diagnostic tool capable of classifying skin lesions into appropriate categories using advanced ensemble-based learning techniques. By integrating EfficientFormerV2 and Swin Transformer Tiny into a unified diagnostic system, the project aims to assist healthcare professionals, enhance early detection, and ultimately contribute to improved treatment outcomes, particularly in resource-limited clinical settings.

1.2 Problem Statement

Skin lesions, particularly malignant ones, represent a serious health risk due to their ability to progress rapidly and cause severe complications if not detected at an early stage. Accurate classification of skin lesions remains challenging because different lesion types often exhibit similar visual characteristics, including color patterns, texture distribution, and border irregularities. Even experienced dermatologists may face difficulty in distinguishing between benign and malignant lesions when these similarities are subtle. Additionally, dermoscopic images vary significantly due to differences in imaging devices, lighting conditions, the presence of artifacts such as hair or shadows, and variations in patient skin tone, all of which further complicate the diagnostic process.

The challenge is intensified by the class imbalance commonly present in widely used skin lesion datasets such as HAM10000, where certain lesion categories contain significantly fewer samples than others. Traditional single-model deep learning approaches often struggle to learn effective representations for these minority classes, leading to biased predictions and reduced classification performance. Moreover, existing diagnostic practices rely heavily on manual interpretation, which is time-consuming, subjective, and prone to inconsistency across clinicians with varying levels of expertise. These limitations highlight the critical need for a reliable and automated diagnostic system capable of accurately classifying skin lesions. Such a system must effectively address visual similarity, dataset imbalance, and diagnostic variability to support timely clinical decision-making and improve patient outcomes.

1.3 Objectives

The primary objective of this project is to develop an automated, accurate, and efficient skin lesion classification system using a Meta-Ensemble Deep Learning approach. By integrating the strengths of EfficientFormerV2 and the Swin Transformer Tiny, the proposed system aims to achieve improved diagnostic performance on dermoscopic images. The specific objectives of the project are as follows:

- To preprocess dermoscopic images using resizing, normalization, augmentation, and enhancement techniques to ensure consistent image quality and improved feature representation for effective model training.

- To fine-tune EfficientFormerV2 and Swin Transformer Tiny models independently, leveraging their complementary strengths—EfficientFormerV2 for lightweight and efficient local feature extraction, and Swin Transformer Tiny for capturing global and hierarchical contextual patterns.
- To design and implement two ensemble fusion strategies, namely soft voting and a logistic regression-based meta-classifier, to effectively combine model predictions and enhance classification reliability across all skin lesion categories.
- To evaluate the performance of the proposed system using comprehensive metrics such as accuracy, precision, recall, F1-score, confusion matrix, and ROC–AUC, ensuring balanced assessment across both majority and minority classes.
- To deploy the finalized model through a Flask-based web application that allows users to upload dermoscopic images and receive real-time classification results in an accessible and user-friendly manner.
- To assist clinicians and healthcare providers by reducing diagnostic time, minimizing human error, and supporting early detection of skin lesions, thereby improving patient outcomes and expanding access to dermatological diagnostic tools, particularly in underserved regions.

2. LITERATURE SURVEY

2.1 Deep Learning in Medical Image Analysis

Deep learning has reshaped medical image analysis by enabling machines to interpret complex visual data with a level of accuracy that was once achievable only by trained specialists. Unlike traditional image-analysis methods that rely on hand-engineered features, deep neural networks learn representations directly from images, making them particularly powerful for healthcare applications.

Esteva et al. [7] and *Han et al.* [18] demonstrated that Convolutional Neural Networks (CNNs) can achieve performance comparable to expert dermatologists in medical image analysis. Over the past decade, CNNs have played a dominant role in diagnosing diseases such as cancer, diabetic retinopathy, and neurological disorders by providing consistent, reproducible, and high-accuracy results. Their ability to automatically learn hierarchical feature representations from medical images has made them a foundational technique in computer-aided diagnosis systems.

Codella et al. [6] highlighted that the availability of large, well-annotated skin lesion datasets such as HAM10000 has significantly accelerated research in automated dermatological analysis. These datasets enable deep learning models to learn complex visual patterns from thousands of dermoscopic images, improving classification performance and generalization.

Dosovitskiy et al. [12] and *Liu et al.* [13] introduced transformer-based architectures to computer vision, marking a shift from purely convolutional models. Vision Transformers (ViT) and Swin Transformers gained prominence due to their ability to model long-range dependencies and global contextual relationships within images. Unlike CNNs, which are limited by local receptive fields, transformer-based models capture broader structural information, making them particularly effective for analyzing complex and visually similar skin lesions.

2.2 CNN-Based Approaches for Skin Lesion Classification

Krizhevsky et al. [10] introduced early CNN architectures such as AlexNet, which, along with later models like VGG and ResNet, laid the foundation for automated skin lesion classification. These architectures demonstrated strong capability in extracting hierarchical features ranging from low-level textures to high-level semantic patterns from dermoscopic images, making CNNs the first deep learning models to achieve notable success in this domain.

Esteva et al. [7] conducted a landmark study by training a deep CNN on more than 100,000 skin lesion images, achieving classification performance comparable to that of expert dermatologists. Similarly, *Han et al.* [18] demonstrated that deep CNN models are highly effective in distinguishing benign from malignant lesions with high precision, further strengthening the role of CNN-based approaches in dermatological diagnosis.

Esteva et al. [7] and *Han et al.* [18] identified several key challenges associated with CNN-based skin lesion classification. Their studies reported that CNN models often struggle to distinguish visually similar lesion categories, such as melanocytic nevi and melanoma, as well as benign keratosis and basal cell carcinoma. In addition, severe class imbalance in widely used datasets such as HAM10000—where benign classes dominate while rare categories like dermatofibroma and vascular lesions contain very limited samples—leads to biased learning and reduced sensitivity for minority classes. Furthermore, CNN-based architectures primarily focus on local texture features and may fail to capture broader global contextual and structural information, which is critical for accurate lesion discrimination.

To address these challenges, *Mehta and Aneja* [2], *Mehta and Kundra* [3], *Mohammed et al.* [17], and *Valle et al.* [19] explored enhanced CNN-based strategies. These approaches include hybrid CNN architectures, CNN models combined with Random Forest classifiers, GAN-based data augmentation to improve minority class representation, and ensemble learning techniques. While these methods improved robustness and overall classification performance, achieving consistently balanced accuracy across all seven skin lesion categories remains a persistent challenge. This observation highlights the need for more

advanced hybrid and ensemble-based frameworks that can effectively integrate complementary feature representations.

2.3 Transformer-Based Architectures for Dermatological Imaging

Dosovitskiy et al. [12] introduced Vision Transformers (ViT), marking a major shift in computer vision by replacing local convolutional operations with global self-attention mechanisms. ViT models represent images as sequences of patches and learn relationships across the entire image, enabling improved recognition of structural and contextual patterns. Building on this idea, *Liu et al.* [13] proposed the Swin Transformer, which employs a shifted-window attention mechanism to efficiently capture both local and global information while maintaining computational efficiency.

Ayas [8] evaluated the Swin Transformer on the HAM10000 skin lesion dataset and reported strong multiclass classification performance, demonstrating the model’s ability to capture subtle variations among different lesion types. Further extending this approach, *Paraddy and Virupakshappa* [9] proposed a hybrid architecture that combines CNN-based feature extraction with transformer-based attention mechanisms. Their results showed improved accuracy and prediction stability compared to standalone CNN or transformer models, highlighting the benefits of integrating local and global feature learning in dermatological imaging.

Dosovitskiy et al. [12] and *Liu et al.* [13] reported several limitations of transformer-based architectures when applied to medical imaging tasks. Their studies highlighted that transformer models generally require large, well-annotated datasets to achieve optimal performance, which are often difficult to obtain in clinical environments. In addition, the high computational and memory requirements of transformer architectures pose challenges for real-time deployment and usage in resource-constrained settings.

To address these limitations, *Li et al.* [15] proposed EfficientFormerV2, a lightweight hybrid CNN–Transformer architecture that integrates convolutional operations with efficient attention mechanisms. This design preserves the representational strength of transformer models while significantly reducing computational complexity and memory

overhead. As a result, such lightweight hybrid architectures enable practical deployment of transformer-based solutions in clinical applications, mobile platforms, and real-time dermatological diagnosis systems.

2.4 Ensemble Learning Approaches in Medical Diagnosis

Ensemble learning is a widely adopted machine learning strategy in which multiple models are combined to produce a more accurate and reliable prediction than any single model. By leveraging the diversity among different classifiers, ensemble methods reduce prediction errors, improve robustness, and enhance overall generalization performance.

Mohammed et al. [17] and *Valle et al.* [19] demonstrated that ensemble learning significantly improves diagnostic performance in medical image analysis, particularly under challenging conditions such as limited training data, high inter-class similarity, and severe class imbalance. These conditions are common in medical datasets, where minority disease classes are often underrepresented and visual differences between categories are subtle.

Valle et al. [19] showed that ensembles of CNN-based classifiers improve generalization capability, especially when the available labeled training data is limited. Similarly, *Mohammed et al.* [17] reported that hybrid CNN ensemble approaches achieve higher macro F1-scores than single-model systems, indicating improved balance and reliability across multiple disease categories.

Motivated by these findings, the present work adopts a meta-ensemble framework that integrates EfficientFormerV2, a lightweight CNN–Transformer hybrid architecture, and the Swin Tiny Transformer, a hierarchical self-attention-based model. The outputs of both models are fused using a logistic regression meta-learner, allowing the system to exploit complementary feature representations and achieve balanced classification performance across all seven skin lesion categories.

2.5 Summary of Research and Identified Gaps

Existing research demonstrates that deep learning models, particularly CNNs and transformer-based architectures, have significantly improved automated skin lesion classification. CNNs effectively capture local texture and color features, while transformers model global contextual relationships. Ensemble learning methods further enhance robustness by combining multiple models to reduce prediction errors.

However, several research gaps remain. CNN-based models struggle with visually similar lesion classes due to limited global context awareness, while transformer-based models require large annotated datasets and high computational resources, limiting real-time and clinical deployment. Moreover, many existing ensemble approaches rely on simple fusion techniques that do not adaptively leverage the strengths of individual models.

Additionally, class imbalance in datasets such as HAM10000 continues to negatively impact classification performance, particularly for minority lesion categories. There is limited research on meta-learning-based ensembles that integrate lightweight CNN–Transformer hybrids with hierarchical transformer architectures to achieve balanced performance and computational efficiency.

To address these gaps, this project proposes a Meta-Ensemble Deep Learning framework that combines EfficientFormerV2 and the Swin Tiny Transformer using a logistic regression meta-learner. The proposed approach aims to improve classification accuracy, handle class imbalance effectively, and enable efficient deployment for practical dermatological diagnosis.

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 building CNN and Transformer architectures

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

NumPy & Pandas – Data manipulation and pre-processing

Torchvision & OpenCV – Image transformations and augmentation

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.

2.7 Consolidated Comparison Table of Prior Research

Table 2.1: Consolidated Comparison Table of Prior Research

| Study / Approach | Model Type | Dataset | Strengths | Limitations | Reference |
|----------------------------------|---------------------|------------------------------|--|--------------------------------------|-----------|
| CNN-based large-scale classifier | CNN | 100k+ images | High accuracy; dermatologist-level results | Struggles with rare classes | [7] |
| Deep CNN for tumor detection | CNN | Dermoscopic images | Strong benign–malignant separation | Limited global context | [18] |
| CNN–GAN hybrid | CNN + GAN | Dermatology datasets | Augmentation improves minority class performance | GANs are hard to train | [3] |
| Hybrid CNN–RF method | CNN + Random Forest | Skin lesion datasets | Improves decision boundaries | Limited scalability | [2] |
| EfficientN -et scaling | CNN | Natural and medical datasets | High accuracy through compound scaling | Heavy computation on larger versions | [14] |
| Vision Transform -er (ViT) | Transformer | Benchmark image datasets | Captures long-range dependencies | Needs large datasets | [12] |

| | | | | | |
|--------------------------------|--|-----------------------------------|---|--|-------------------|
| Swin Transform -er | Hierarchical Transformer | HAM10000 and other datasets | Strong multiclass performance | Computationally demanding | [8], [9], [13] |
| EfficientF -ormerV2 | Lightweight CNN– Transformer hybrid | Vision datasets | Fast and efficient; low memory footprint | Not deeply explored in dermatology | [15] |
| Meta- learning ensembles | Meta-learner with multiple backbones | Medical datasets | Improves stability and balance | Limited research in dermatology | [17], [19] |

3. SYSTEM ANALYSIS

3.1 Existing System

Skin lesion detection and classification have traditionally depended on the manual evaluation of dermoscopic images by dermatologists. While specialists can often diagnose lesions accurately through years of clinical experience, this manual approach is:

- Time-consuming,
- Subjective, and
- Prone to variability between different experts.

Dermoscopy involves observing subtle patterns such as color gradients, border shapes, asymmetry, and textural irregularities. Because these features can differ only slightly between benign and malignant lesions—including melanoma—manual interpretation becomes challenging, especially in early stages. As a result, misdiagnosis or delayed identification of cancerous lesions is common, which increases patient risk and affects treatment outcomes.

To address these limitations, earlier automated systems used traditional Machine Learning algorithms such as:

- Support Vector Machines (SVM)
- Random Forests (RF)
- Decision Trees
- k-Nearest Neighbors (k-NN)

These models depended on handcrafted features, manually extracted from images. Such features typically included:

- Color histograms
- Texture descriptors
- Shape indexes
- Geometric features

Although these methods achieved moderate performance, they suffered from major drawbacks:

- Manual feature extraction required domain expertise
- Models failed to generalize to new datasets
- Image quality variations significantly affected outcomes

- Class imbalance caused models to become biased

The advancement of Deep Learning and Convolutional Neural Networks (CNNs) transformed medical image analysis. CNNs such as VGG16, ResNet, Inception-V3, and DenseNet outperformed traditional ML methods by learning complex patterns directly from dermoscopic images. CNNs significantly improved classification accuracy, yet they introduced their own challenges:

- Large annotated datasets were needed for optimal training
- Small or imbalanced datasets resulted in overfitting
- CNNs struggled to capture global structural context due to their localized receptive fields
- The models required high computational power and GPU resources

To reduce data dependency, transfer learning was widely adopted, where pretrained deep learning models were fine-tuned on dermoscopic image datasets. As illustrated in Figure 3.1 , this approach enabled CNNs to reuse learned low-level and mid-level features, leading to improved classification accuracy compared to training models from scratch. Standalone CNN architectures continued to face challenges in multi-class skin lesion classification, particularly in distinguishing lesion categories with highly similar visual characteristics.

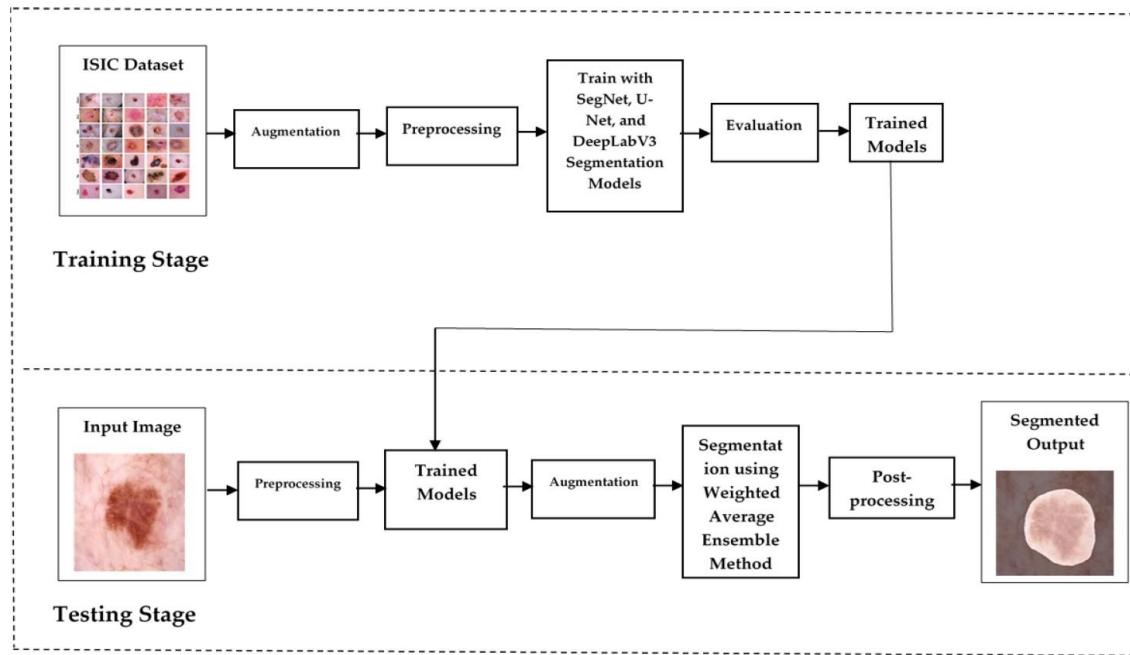


Fig 3.1: Flow chart of existing system for skin lesion classification

The traditional skin lesion classification workflow generally includes four main stages:

1. Preprocessing

Enhances image quality by removing noise, correcting illumination, and improving contrast.

2. Segmentation

Separates the lesion region from surrounding skin, forming the base for further analysis.

3. Feature Extraction

Identifies important lesion characteristics such as asymmetry, color variations, texture, and border patterns.

4. Classification

Uses ML or CNN-based methods to assign the lesion to a specific diagnostic category.

While effective in controlled laboratory conditions, these systems still struggle with inconsistent lighting, dermoscopic artifacts (hair, reflections, shadows), and high variability in lesion appearance, limiting their real-world reliability.

3.1.1 DISADVANTAGES OF EXISTING SYSTEM

Despite technological improvements, existing automated skin lesion classification systems suffer from several critical limitations:

➤ Dependence on Large Annotated Datasets

Deep learning models need thousands of labeled images, but medical image annotation requires dermatologists, making datasets expensive and time-consuming to produce.

➤ High Computational Requirements

State-of-the-art CNNs, including ResNet, DenseNet, and VGG, require powerful GPUs, limiting deployment in rural or resource-constrained clinics.

➤ Overfitting on Small or Imbalanced Datasets

Public datasets such as HAM10000 often contain highly imbalanced classes. This causes:

Biased learning

Low sensitivity for rare lesion types

Weak generalization to new data

➤ **Difficulty Capturing Global Contextual Patterns**

CNNs excel at extracting local texture but struggle to understand global lesion structures, affecting classification of lesions with subtle boundary or shape differences.

➤ **Sensitivity to Artifacts**

Dermoscopic images often contain:

- Hair
- Shadows
- Reflections
- Blur
- Uneven illumination

These degrade model performance and reduce reliability.

➤ **Poor Adaptability Across Imaging Devices**

Variation in dermoscopy equipment (resolution, lighting, magnification) results in inconsistent model performance.

➤ **Suboptimal Segmentation Accuracy**

Traditional segmentation techniques struggle with:

- Irregular lesion shapes
- Indistinct borders
- Complex backgrounds

This negatively impacts downstream feature extraction and classification.

Together, these issues highlight the urgent need for a robust, scalable, and accurate system capable of handling real-world dermatology challenges.

3.2 Proposed System

The proposed system introduces a Meta-Ensemble Deep Learning Framework for multi-class skin lesion classification, as shown in *Figure 3.2*. The framework integrates two complementary architectures: EfficientFormerV2, a lightweight hybrid CNN–Transformer model optimized for efficient local feature extraction, and Swin Transformer Tiny, a hierarchical transformer architecture capable of capturing global and long-range contextual dependencies. The integration of these models enables improved classification performance, stability, and generalization.

The processing pipeline begins with a preprocessing stage in which dermoscopic images undergo resizing to ensure uniform input dimensions, normalization to stabilize learning, and data augmentation to address dataset imbalance. Additional enhancement techniques, including adaptive gamma correction, contrast enhancement, and median filtering, are applied to improve lesion boundary visibility and reduce noise, resulting in consistent and high-quality inputs.

Following preprocessing, a segmentation or region-of-interest extraction step identifies the primary lesion area for focused analysis. Feature extraction is then carried out independently by the two backbone models. EfficientFormerV2 focuses on learning discriminative local textural features while enabling fast inference suitable for resource-constrained environments. In parallel, Swin Transformer Tiny captures global structural information such as lesion shape, symmetry, and border irregularities through hierarchical self-attention mechanisms.

The predictions produced by both models are subsequently fused using ensemble strategies such as soft voting or a logistic regression-based meta-classifier, which serves as a high-level decision-making module. This fusion strategy improves classification robustness and accuracy across all seven skin lesion categories, particularly for visually similar lesion types.

Advantages of the Proposed System

- **High Accuracy and Robustness**

Ensemble fusion enhances prediction stability and reduces classification errors.

- **Better Generalization**

Hybrid features from CNNs and Transformers allow better performance across diverse skin tones, lighting conditions, and lesion appearances.

- **Improved Preprocessing Quality**

Techniques such as gamma correction and contrast enhancement highlight important lesion patterns.

- **Reduced Overfitting**

The use of multiple models and a meta-classifier reduces reliance on any single architecture.

- **Scalable and Extensible**

The system can be extended to additional lesion types or other dermatological

imaging tasks.

➤ Deployment Ready

Integrated into a Flask-based web application, enabling real-time image uploads and instant classification results.

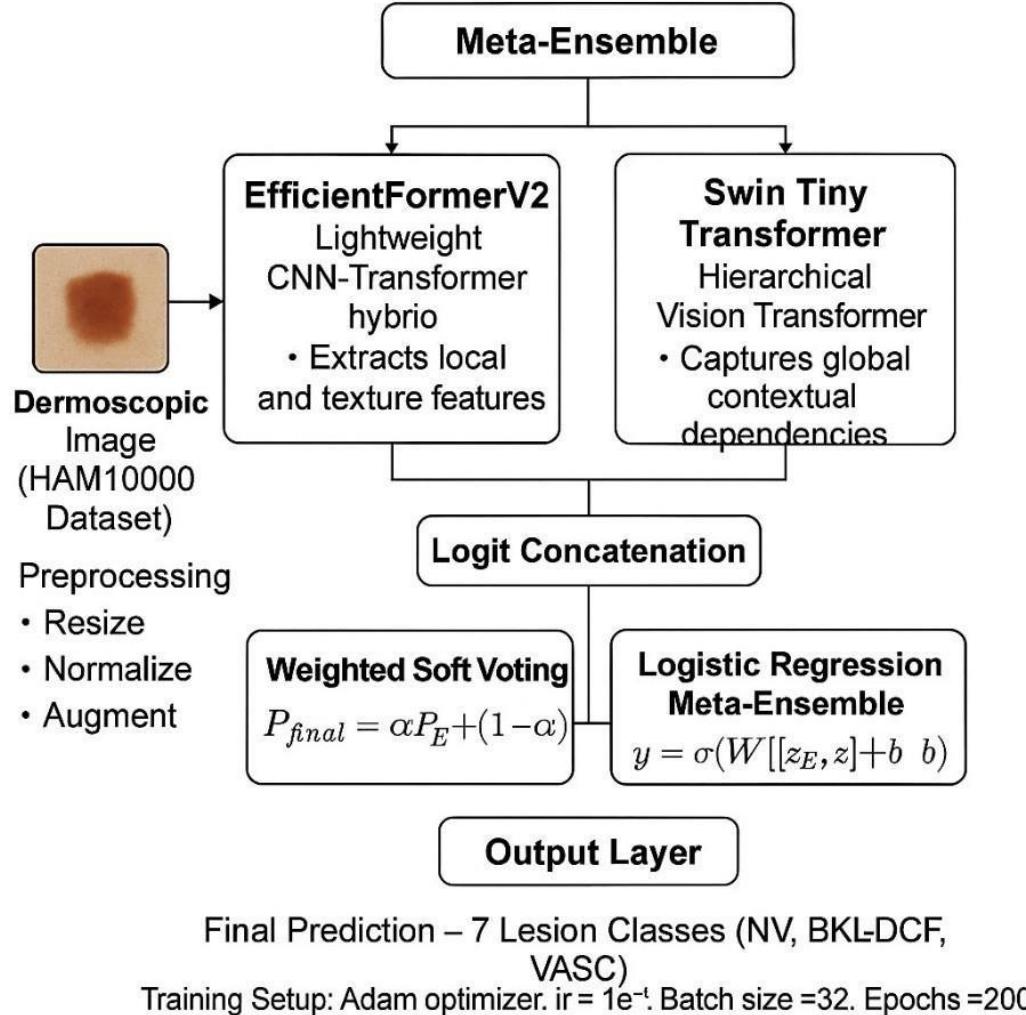


Fig 3.2: Flow chart of proposed system

3.3 Feasibility Study

The feasibility of the proposed system is analyzed across Technical, Operational, and Economic aspects.

1. Technical Feasibility

- **Automated Feature Extraction:**

EfficientFormerV2 and Swin Transformer Tiny eliminate the need for manual feature engineering.

- **Accurate and Robust Classification:**
Ensemble fusion creates strong decision boundaries and reduces misclassification.
- **Reduced Overfitting:**
Data augmentation and meta-classification significantly improve generalization.
- **Scalable Architecture:**
The system can incorporate additional lesion types or extend to other medical imaging domains.
- **Efficient Transfer Learning:**
Pretrained weights reduce training time and achieve high accuracy even with limited data.

2. Operational Feasibility

- **Ease of Integration:**
A Flask-based web interface allows dermatologists to upload images and obtain predictions instantly.
- **High User Acceptance:**
Confidence scores and interpretable predictions help build trust among clinical users.
- **Low Maintenance Requirements:**
Updating or retraining only the meta-classifier is simple and efficient.
- **Support for Non-Expert Users:**
The system provides accurate diagnostic assistance without requiring specialized dermatological expertise.

3. Economic Feasibility

- **Cost-Effective Development:**
Transfer learning reduces computational and data-related costs.
- **Optimized GPU Usage:**
EfficientFormerV2 delivers high performance reducing computational overhead.

- **Reduced Diagnostic Costs:**

Automated early screening reduces manual workload and speeds up diagnosis.

- **Long-Term Benefits:**

Early detection leads to reduced treatment expenses and improved patient outcomes.

4. SYSTEM REQUIREMENTS

4.1 Software Requirements

1. **Operating System** : Windows 11 (64-bit)
2. **Hardware Accelerator** : CPU (GPU optional but recommended for training)
3. **Programming Language** : Python
4. **Python Environment / Tools** : Google Colab Pro, Flask
5. **Browser** : Any latest browser (e.g., Google Chrome, Firefox, Edge)

4.2 Requirement Analysis

The Skin Lesion Classification system is designed to build an efficient, accurate, and automated deep learning-based solution capable of identifying seven skin lesion categories using dermoscopic images. The system integrates EfficientFormerV2 and Swin Transformer Tiny in a meta-ensemble architecture to improve robustness and classification accuracy.

The application allows users to upload dermoscopic images through a web interface, where the system performs input validation to ensure only valid skin lesion images are processed. The uploaded images undergo preprocessing techniques such as resizing, normalization, augmentation, and enhancement to improve clarity and overall model performance. The system then performs inference using the ensemble models and displays the predicted class along with confidence levels.

The backend is implemented in Python using the Flask framework, responsible for handling image processing, model inference, and communication with the frontend. The frontend utilizes HTML, CSS, Bootstrap, and JavaScript to provide a clean, responsive, and user-friendly interface.

Non-functional requirements focus on the system's performance, usability, security, and reliability. The application must be fast, capable of producing predictions within seconds, and should handle invalid inputs gracefully by providing user-friendly error messages.

Training and model development require frameworks such as TensorFlow/Keras, scikit-learn, and OpenCV, along with sufficient computational resources for processing dermoscopic images.

A well-labeled skin lesion dataset (such as HAM10000) is essential for training, validating, and testing the model. The system can be deployed locally or on a cloud server, enabling access through any standard web browser. To ensure accessibility, the application is designed to be intuitive even for users with minimal technical background.

4.3 Hardware Requirements

1. **System Type** : 64-bit Operating System, x64-based processor
2. **Cache Memory** : 4 MB
3. **RAM** : 16 GB
4. **Hard Disk** : 8 GB free space
5. **GPU** : Intel® Iris® Xe Graphics (sufficient for inference; training recommended on cloud GPU)

4.4 Software Description

The Skin Lesion Classification project is built using a powerful combination of software tools, frameworks, and technologies intended to ensure high accuracy, efficiency, and scalability.

The recommended platform is Windows 11, 64-bit OS, ensuring compatibility with modern development tools and supporting stable execution of machine learning workflows. The primary computation is performed on a CPU for inference, while training is conducted using Google Colab Pro, which provides access to GPUs and faster processing capabilities. The core development uses Python, chosen for its rich ecosystem of machine learning and deep learning libraries. Google Colab Pro is used for model training, experimentation, and evaluation. The final trained model is integrated into a Flask-based backend, which handles image uploads, preprocessing, classification, and communication with the user interface.

The frontend uses:

- HTML5, CSS3, and Bootstrap for an intuitive and responsive interface

- JavaScript for interactive elements and smooth user experience

The system runs seamlessly on any latest web browser such as Chrome, Firefox, or Edge.

For machine learning and deep learning tasks:

- **TensorFlow/Keras** is used to build and train EfficientFormerV2 and Swin Transformer Tiny models
- **scikit-learn** is used for implementing the Logistic Regression meta-classifier and evaluation metrics
- **OpenCV** performs preprocessing operations like resizing, format validation, and noise removal
- **NumPy** supports fast numerical computations

Visualization tools such as **Matplotlib** and **Seaborn** are used to plot accuracy, loss curves, and confusion matrices during model evaluation.

Together, these tools enable a robust, scalable, and high-performance skin lesion classification system suitable for practical deployment.

5. SYSTEM DESIGN

5.1 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.

5.2 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. 5.1**, which shows how an uploaded image travels through the UI → Flask backend → preprocessing → dual-model inference → meta-ensemble fusion → database update → final result display.

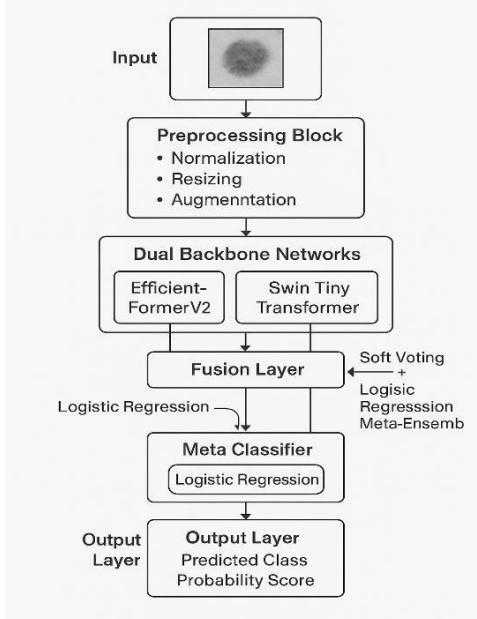


Fig. 5.1: System Architecture of the Meta-Ensemble Skin Lesion Classification System

5.3 Functional Modules

Table 5.1: 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. |

5.4 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

Fig. 5.2 depicts the complete activity flow:

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

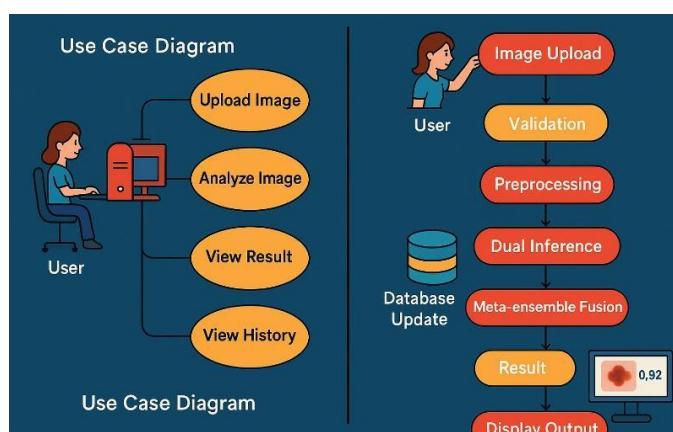


Fig:5.2: Activity Flow Diagram

5.5 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.

5.6 Model Building

The proposed Meta-Ensemble model combines:

- **EfficientFormerV2**
- **Swin Tiny Transformer**

Each model processes dermoscopic images independently and learns complementary features.

EfficientFormerV2

- Lightweight
- Faster inference
- Extracts local texture and border-level details

Swin Tiny Transformer

- Uses hierarchical window-based attention
- Captures global structural patterns

- Handles variations in color distribution and shape

The outputs (logits) of both models are fused via:

Meta-Ensemble Fusion

- **Weighted Soft Voting**
- **Logistic Regression Classifier**

This combination reduces class imbalance issues and strengthens the decision boundary between visually similar lesion classes.

5.7 Classification

The final classification stage takes the fused predictions from both models and outputs one of the seven lesion categories.

The classification process includes:

- Softmax probability distribution
- Meta-classifier decision refinement
- Confidence score generation

This hybrid classification strategy ensures improved model reliability, reduced false positives, and more accurate lesion identification—critical for early diagnosis.

The ensemble model outperforms individual architectures such as VGG, ResNet, Random Forest, FCNN, and ANN, due to the combination of local-global feature extraction and strong decision boundary formation.

6. METHODOLOGY

The methodology of this project is built around a carefully designed, multi-stage deep learning pipeline aimed at accurately classifying dermoscopic images into the seven diagnostic categories of the HAM10000 dataset. Given the complex visual nature of skin lesions—where many benign and malignant types share overlapping color patterns, textures, and borders—the system adopts a dual-backbone approach that leverages the complementary strengths of both convolution-based and attention-based architectures.

To achieve this, the framework integrates EfficientFormerV2, a lightweight CNN–Transformer hybrid optimized for fast inference, with the Swin Tiny Transformer, a hierarchical attention model capable of capturing long-range contextual relationships within images. Individually, these models have demonstrated strong performance in dermatological imaging, but when combined, they offer a richer and more balanced feature representation. This duet of architectures allows the system to simultaneously learn fine-grained local patterns—such as pigment networks and lesion edges—and global structures, such as asymmetry and overall lesion morphology. Such combined learning has been shown to enhance diagnostic precision, especially in visually similar skin lesion classes.

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. Overall, the methodology is structured to ensure consistency, robustness, and clinical applicability. It consists of the following sequential stages:

1. **Dataset preparation and augmentation**, ensuring image uniformity and diversity;
2. **Independent training of EfficientFormerV2 and Swin Tiny Transformer** backbones;
3. **Construction of ensemble fusion mechanisms** (soft voting and meta-learning);
4. **Inference pipeline development**, enabling reliable, real-time predictions.

This integrated framework ultimately provides a strong foundation for developing an AI-assisted dermatology tool capable of improving diagnostic accuracy and supporting clinicians in early skin cancer detection.

6.1 Dataset

The dataset used in this project is the HAM10000 (Human Against Machine with 10,000 training images) Skin Lesion Dataset, a widely recognized and publicly available collection of dermoscopic images commonly used for skin lesion classification research. The dataset consists of dermoscopic images belonging to seven distinct skin lesion categories, representing real-world dermatological variations in lesion shape, color, texture, and structural characteristics.

The HAM10000 dataset is publicly available on Kaggle and can be accessed at:

<https://www.kaggle.com/datasets/kmader/skin-cancer-mnist-ham10000>

The images were collected from multiple clinical sources and correspond to specific dermatological conditions, including melanoma, melanocytic nevus, benign keratosis, basal cell carcinoma, dermatofibroma, and vascular lesions. This diversity enables the learning of complex visual distinctions required for accurate multi-class skin lesion classification.

All images are provided in JPEG and PNG formats, ensuring compatibility with modern deep learning frameworks. The dataset exhibits substantial variability in lesion size, border irregularity, pigmentation, and visual appearance, presenting realistic diagnostic challenges and promoting robust generalization to unseen samples. Figure 6.1 illustrates representative sample images from each lesion category.



Fig.6.1: Sample images from each category

Before model training and inference, all images undergo preprocessing steps such as resizing, normalization, data augmentation, and contrast enhancement. These procedures ensure uniform input representation and reduce variability caused by differences in lighting conditions, dermoscopic devices, and image acquisition settings.

The dataset includes thousands of high-quality dermoscopic images collected from multiple clinical sources. Each class corresponds to specific dermatological conditions such as melanoma, melanocytic nevus, benign keratosis, basal cell carcinoma, dermatofibroma, vascular lesions, etc. These classes allow the model to learn complex visual distinctions required for multilabel classification.

All images in the dataset are stored in JPEG/PNG format, ensuring compatibility with deep learning frameworks. The dataset also includes varying lesion sizes, border structures, and pigmentation patterns, providing realistic diagnostic challenges. This diversity helps the model generalize better across unseen samples.

Before feeding images into the model, preprocessing techniques—including resizing, normalization, augmentation, and contrast enhancement—ensure uniformity and reduce variability caused by lighting conditions or dermoscopic devices.

6.1.1 Dataset Preparation

Before training and evaluation, the dermoscopic images undergo a series of preprocessing and augmentation steps, as illustrated in *Figure 6.2*, to ensure consistent input representation, enhance discriminative feature learning, and reduce variability arising from differences in imaging devices and lighting conditions.

Preprocessing Steps

The following preprocessing operations are applied uniformly to all images:

1. **Resizing to 224×224 pixels**

All images are resized to a fixed resolution of 224×224 pixels to ensure compatibility with both EfficientFormerV2 and Swin Tiny Transformer architectures, which require fixed-size inputs.

2. **Color Normalization**

Pixel values are normalized using predefined mean and standard deviation values to stabilize training and reduce the impact of illumination variations across dermoscopic images.

3. **Tensor Conversion (ToTensor)**

Images are converted into PyTorch tensor format to enable efficient GPU-accelerated computation during model training and inference.

Augmentation Techniques

Before training and evaluation, the dermoscopic images undergo a series of preprocessing and augmentation steps to ensure consistency, improve feature representation, and reduce variability caused by differences in imaging devices and lighting conditions.

Preprocessing Steps

The following preprocessing operations are applied uniformly to all images:

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Pixel values are normalized using predefined mean and standard deviation values to stabilize training and reduce the impact of illumination variations across dermoscopic images.

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Images are converted into PyTorch tensor format to enable efficient GPU-accelerated computation during model training and inference.

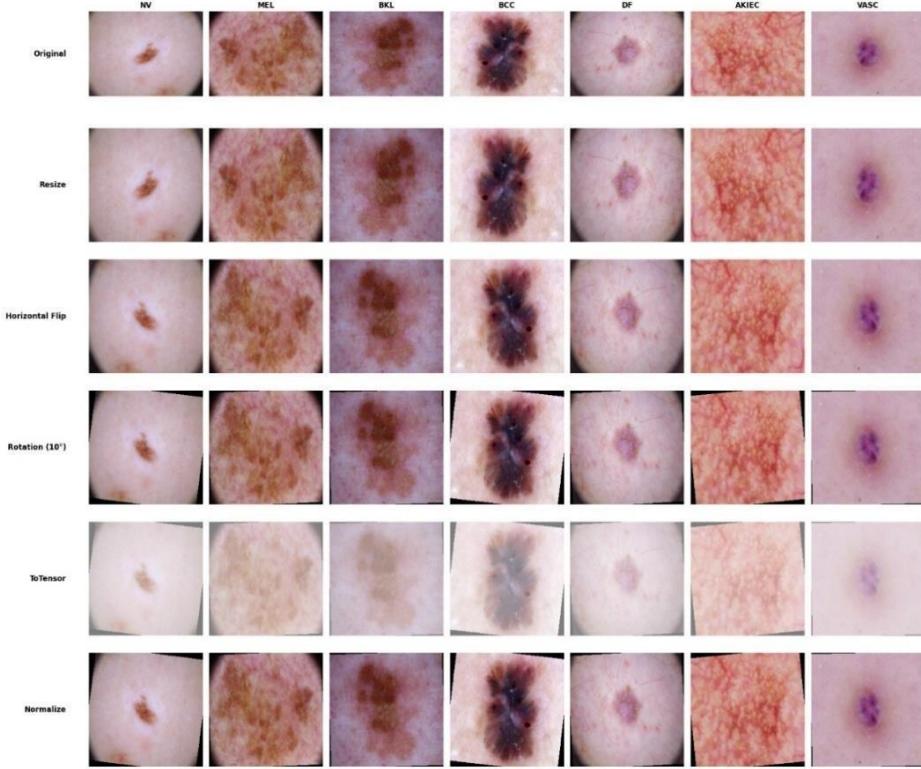


Fig 6.2: Sample Preprocessing and Augmentation Pipeline Applied to HAM10000 Images

6.2 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.

6.2.1 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.

6.2.2 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.

6.3 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].

6.4 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].

6.5 Inference Workflow

The inference stage represents the final step of the proposed system, where a new dermoscopic image is analyzed and classified into one of the seven HAM10000 lesion categories, as illustrated in *Figure 6.3*. This stage closely mirrors the training pipeline, ensuring consistent and reliable model behavior during real-world deployment. When a user submits an image—either from the dataset or through the 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].

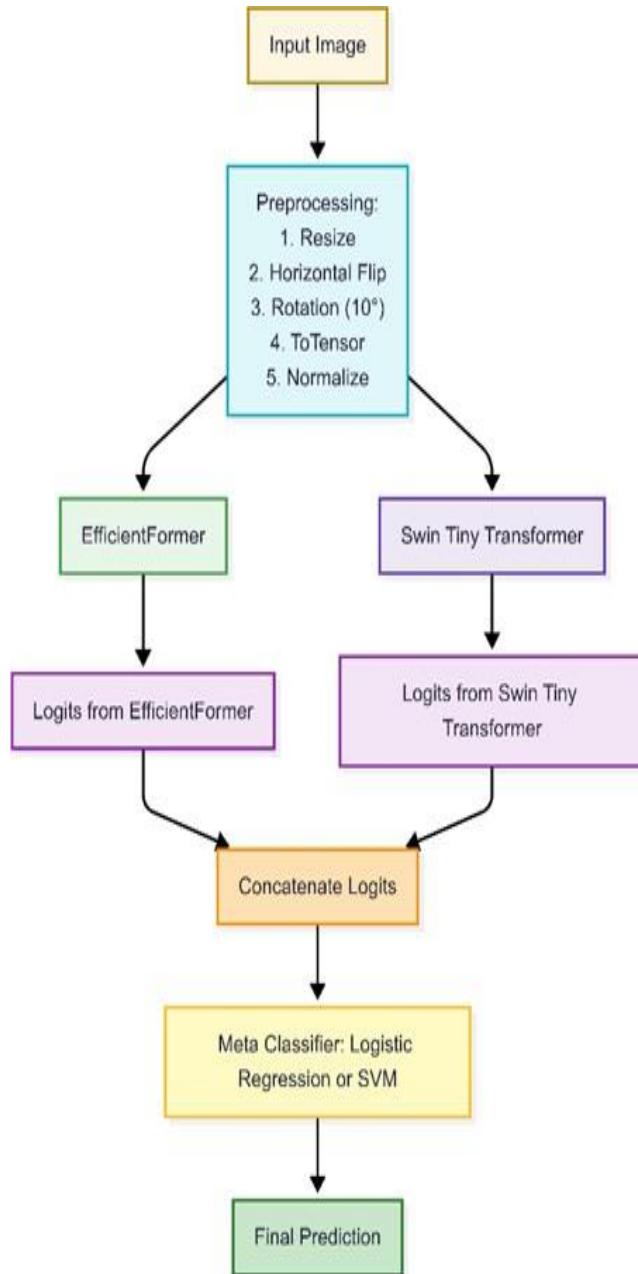


Fig 6.3: Proposed Meta-Ensemble Classification Workflow

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

6.6 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].

7. 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.

7.1 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')
```

7.2 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']
```

7.3 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)

```

7.4 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

```

7.5 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

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

Meta-ensemble fusion

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

7.6 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)')
```

7.7 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)
    logit_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)

```

7.8 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.

7.8.1 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.

7.8.2 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.

7.8.3 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.

7.8.4 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. RESULT ANALYSIS

The performance evaluation of the proposed Meta-Ensemble Skin Lesion Classification Framework was conducted using the HAM10000 dataset, which contains 10,015 dermoscopic images categorized into seven diagnostic classes: Melanocytic Nevi (NV), Melanoma (MEL), Benign Keratosis (BKL), Basal Cell Carcinoma (BCC), Actinic Keratoses (AKIEC), Dermatofibroma (DF), and Vascular Lesions (VASC).

The dataset's inherent class imbalance and visual similarity among lesions posed a significant challenge for accurate and reliable classification, making it an ideal benchmark for evaluating ensemble-based deep learning frameworks.

The proposed approach integrates two complementary architectures—EfficientFormerV2 and Swin Tiny Transformer—and fuses their outputs using a logistic regression meta-learner. This hybrid ensemble strategy aims to combine the computational efficiency of lightweight convolutional networks with the contextual awareness of hierarchical transformers.

8.1 Quantitative Performance Evaluation

To comprehensively assess the effectiveness of the proposed framework, standard classification metrics derived from the confusion matrix were used, including Accuracy, Precision, Recall, F1-Score, and ROC–AUC.

Let TP, TN, FP, and FN denote True Positives, True Negatives, False Positives, and False Negatives, respectively.

Evaluation Metrics

Accuracy measures the overall correctness of the model:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

Precision indicates the reliability of positive predictions:

$$\text{Precision} = \frac{TP}{TP + FP}$$

Recall (Sensitivity) measures the ability to correctly identify actual positive samples:

$$\text{Recall} = \frac{TP}{TP + FN}$$

F1-Score is the harmonic mean of Precision and Recall:

$$\text{F1-Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

ROC–AUC evaluates the model’s discriminative capability across different thresholds, where:

$$\text{TPR} = \frac{TP}{TP + FN}, \text{FPR} = \frac{FP}{FP + TN}$$

For multi-class classification, ROC–AUC is computed using a One-vs-Rest strategy and averaged across all classes.

Table 8.1 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

As shown in *Table 8.1*, the 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 relationships through shifted-window self-attention. EfficientFormerV2, with an accuracy of 88.77%, demonstrated low-latency and efficient feature extraction, making it suitable for deployment in resource-constrained environments.

The proposed Meta-Ensemble model achieved 89.02% accuracy and a Macro F1-score of 0.87. Although its overall accuracy was slightly lower than that of the Swin Tiny Transformer, the ensemble provided better class-level stability and improved performance for rare lesion categories such as DF and VASC. Furthermore, the ensemble exhibited a smoother precision–recall balance, confirming that meta-learning–based fusion enhances robustness under severe class imbalance conditions.

8.2 Training and Validation Behaviour

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

Figures 8.1 and 8.2 depict the gradual improvement in accuracy and reduction in loss across epochs.

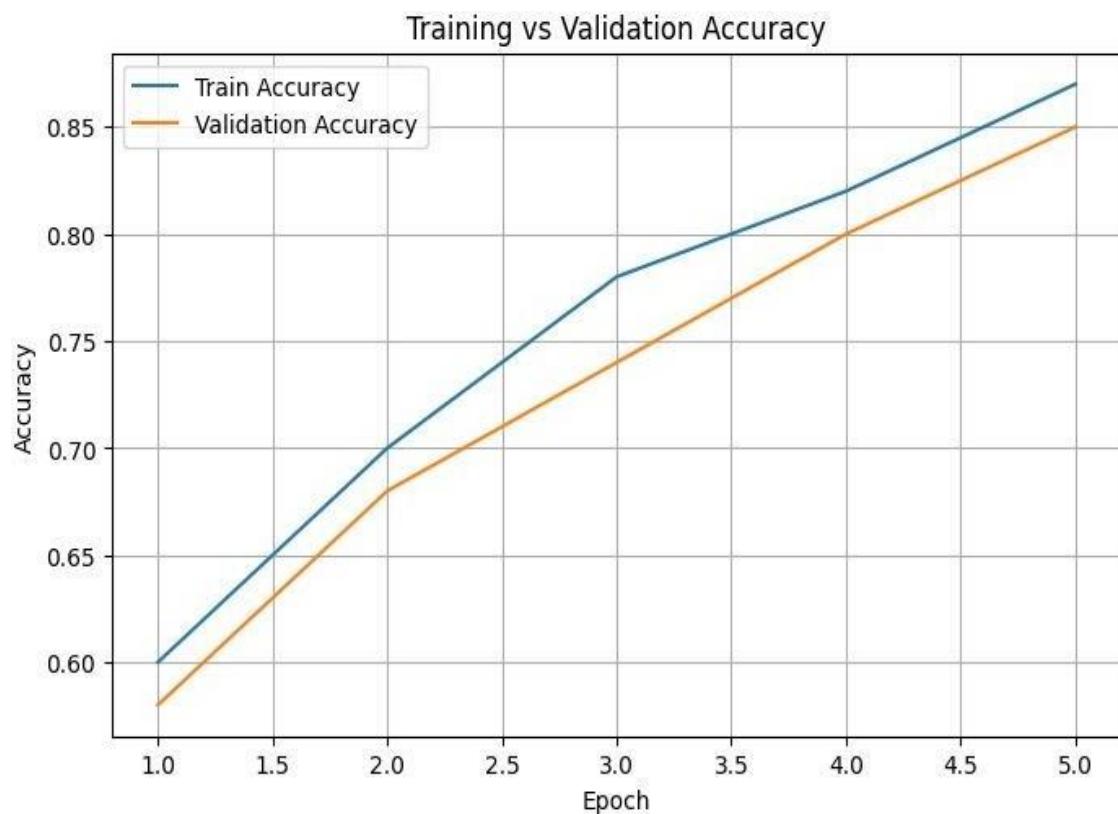


Fig 8.1: Training vs Validation Accuracy Graph



Fig 8.2: 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.

8.3 Confusion Matrix Analysis

A normalized confusion matrix (Figure 8.3) was plotted to analyze class-wise predictive performance.

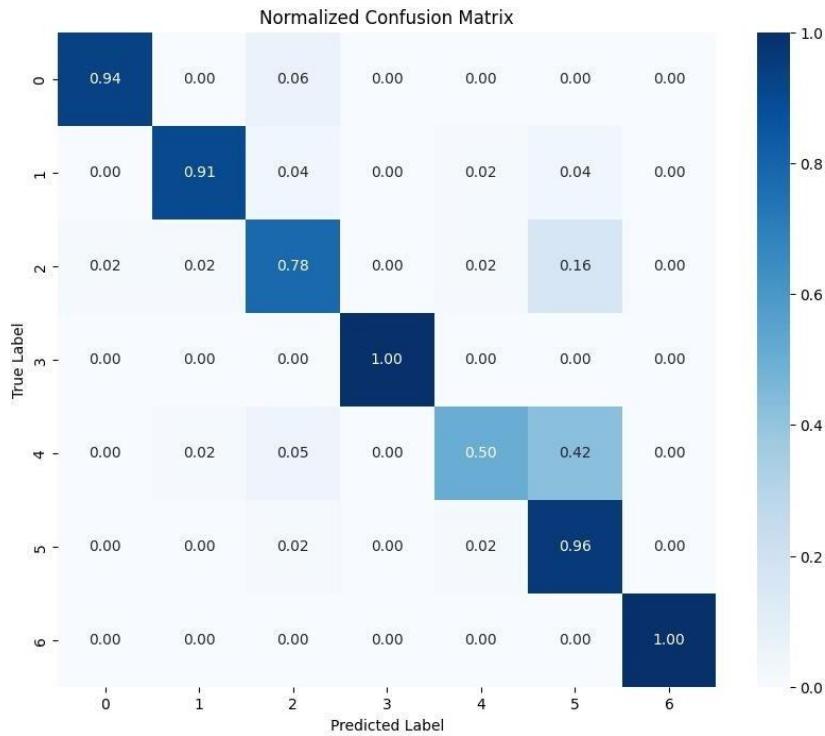


Fig 8.3: Normalized Confusion Matrix of Meta-Ensemble Model

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.

8.4 ROC–AUC Analysis

The One-vs-Rest ROC curves in Figure 8.4 illustrate the classifier's discriminative ability for each lesion category.

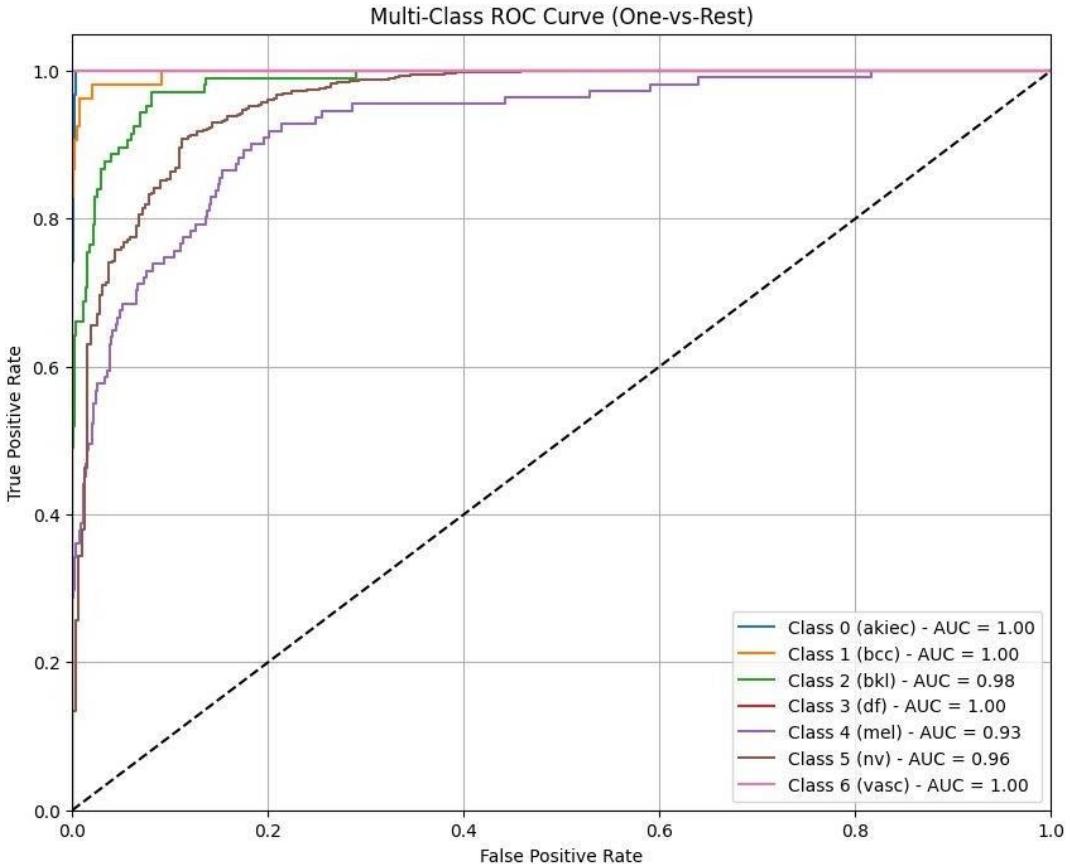


Fig 8.4: Multi-Class ROC Curve (One-vs-Rest)

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.

8.5 Qualitative Visualization of Preprocessing

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

Figure 8.5 showcases these transformations.

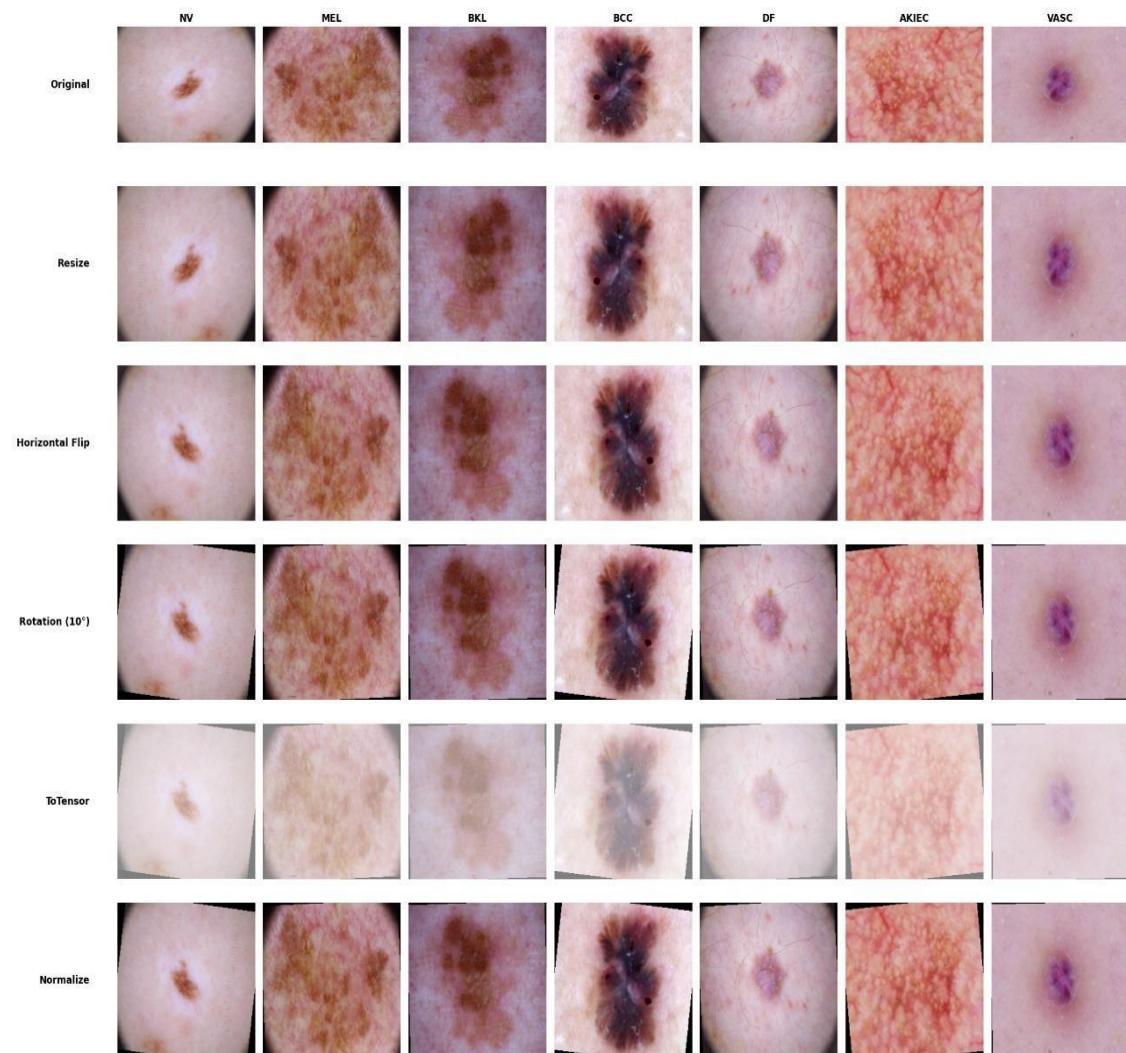


Fig 8.5: Dataset Preprocessing and Augmentation Results on HAM10000

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.

8.6 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.

8.7 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.

Table 8.2 Functional Test Summary Table

| Test Case ID | Test Scenario | Input / Action | Expected Output | Actual Output | Status |
|--------------|--------------------------------|---|---|---------------|--------|
| 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 |

9. Output Screens

This section presents the output screens of the developed Skin Cancer Analysis System, which collectively demonstrate how the user interacts with the application from authentication to diagnosis and logout. Each screen represents a specific step in the operational workflow and highlights how deep learning-based medical analysis is made intuitive and accessible through an interactive web interface. The displayed outputs reflect both the technical functionality and usability considerations implemented during system development.

The user interface (UI) has been designed following modern design principles to ensure clarity, accessibility, and visual balance. A dark-themed layout was adopted to reduce visual strain, maintain professional aesthetics, and provide high contrast for image visibility—an essential factor when viewing dermatological images. Consistent use of typography, spacing, and color gradients enhances readability, while responsive design ensures the application adjusts seamlessly across different screen sizes and devices. Each functional component, from login panels to result displays, has been aligned with clinical interface standards, ensuring that the system appears reliable, professional, and easy to use for both medical practitioners and general users.

Moreover, the interface was developed with a strong focus on user experience (UX). Navigation flows logically through each stage of interaction—from signing in, uploading an image, and viewing AI-based predictions, to reading the condition details and recommendations, and finally logging out. Visual cues, descriptive text prompts, and consistent iconography guide users through the process with minimal effort. The design promotes transparency, comfort, and confidence, ensuring that even non-technical users can effectively access AI-powered skin lesion analysis. Overall, the output screens demonstrate a successful blend of functionality, aesthetics, and accessibility, embodying the user-centered approach at the core of the system.

9.1 Home Page

The Home Page serves as the entry point to the system.

It introduces the platform's main objective — AI-powered skin cancer detection for early diagnosis and prevention.

From this screen, users can either sign in to access their dashboard or create a new account.

The home screen highlights key attributes such as:

- **Average Analysis Time:** Less than 3 seconds
- **Number of Detectable Conditions:** 7
- **Core Features:** High accuracy, medical reliability, and secure AI-based diagnosis

The detectable skin conditions displayed are:

Actinic Keratosis, Basal Cell Carcinoma, Benign Keratosis, Dermatofibroma, Melanocytic Nevus, Melanoma, and Vascular Lesion.

This concise and informative landing page provides users with an overview of the platform's diagnostic capabilities before proceeding.

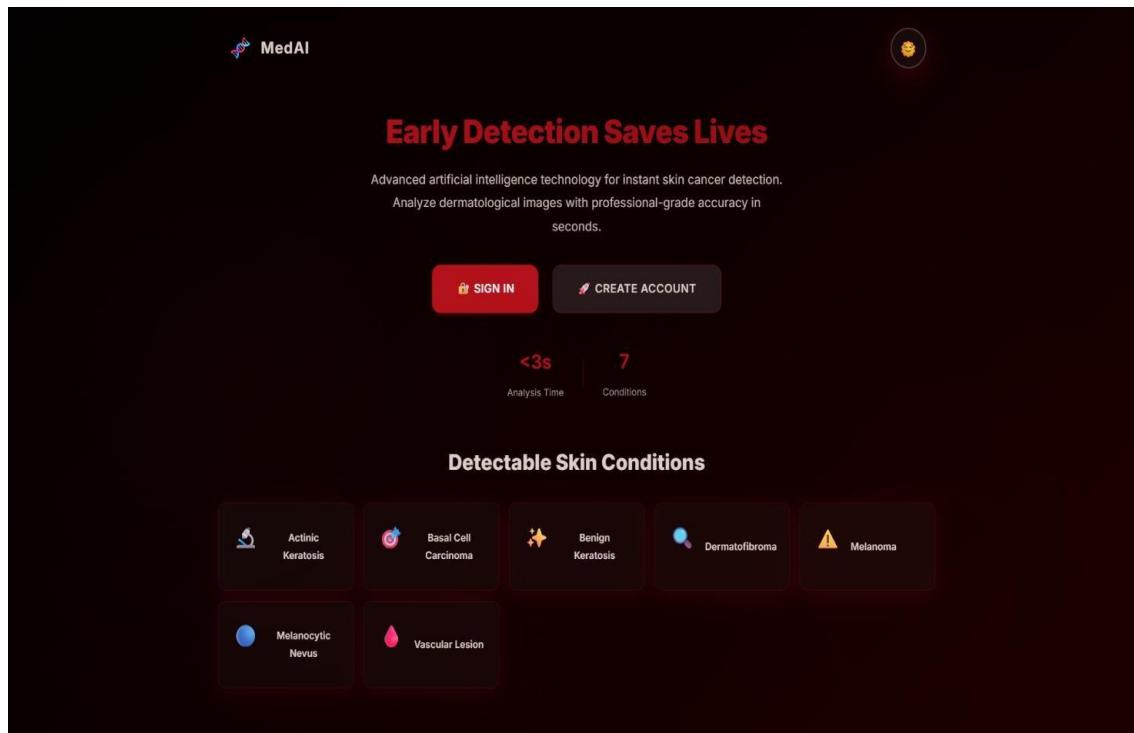


Figure 9.1: Home Page Interface of Application

9.2 Sign In Page

The Sign In Page allows registered users to log in securely to their personalized dashboard.

The screen features a clean dual-panel layout:

- The left panel contains input fields for the user's email address and password.
- The right panel describes the AI-powered diagnostic system, emphasizing its rapid analysis time and reliability.

The design ensures that user authentication is both secure and straightforward, while the minimalist interface enhances focus and usability.

Encryption is implemented to ensure confidentiality and session protection.

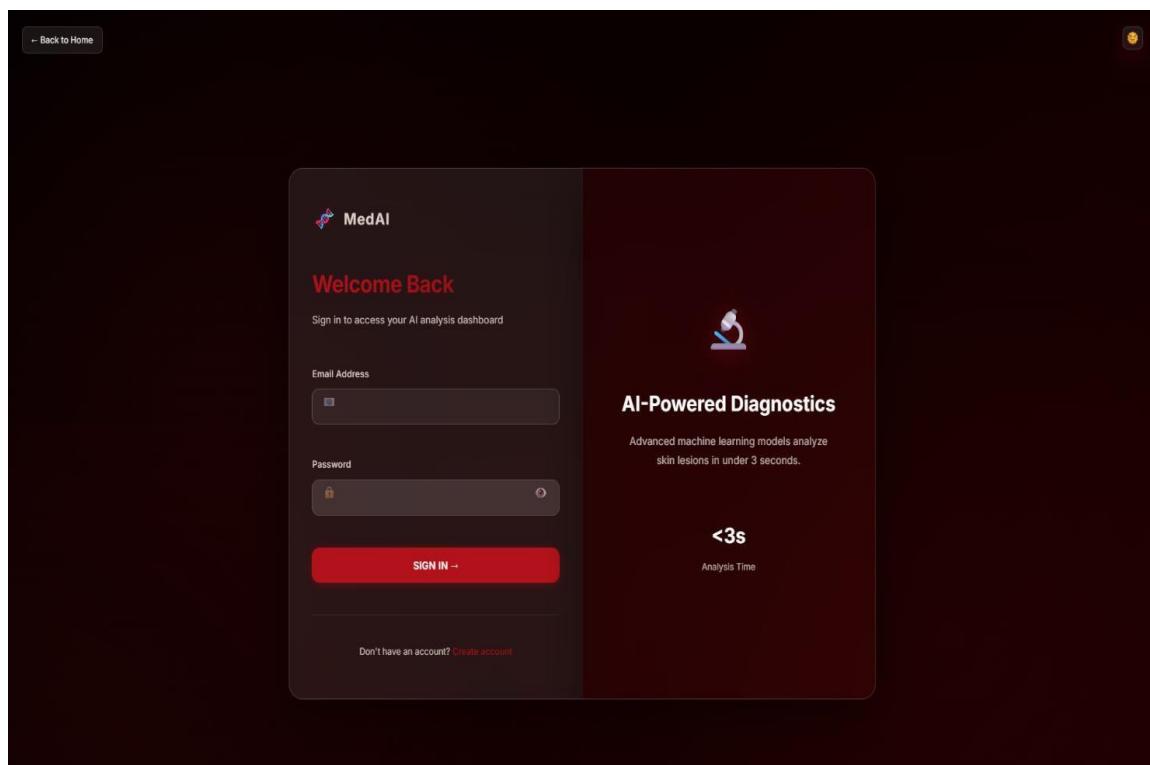


Figure 9.2: Sign In Page of Application

9.3 Create Account Page

The Create Account Page facilitates new user registration.

Users are prompted to enter their Full Name, Email Address, Password, and Confirm Password fields to set up a secure account.

A side panel provides reasons to choose :

- **Lightning Fast:** Results in under 3 seconds
- **Highly Accurate:** Powered by advanced deep learning models
- **Secure & Private:** HIPAA-compliant data protection
- **Track Progress:** Maintains a complete history of previous analyses

This interface promotes trust and ensures easy onboarding for first-time users.

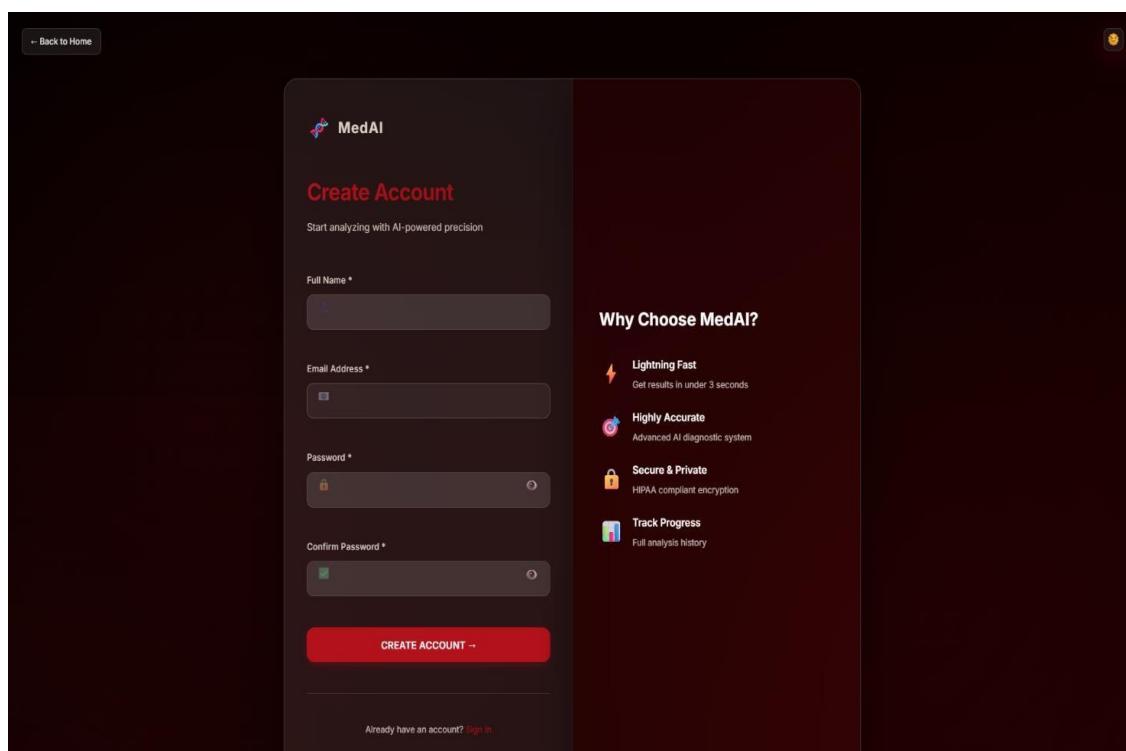


Figure 9.3: User Registration Interface of System

9.4 Upload Image Page

Once logged in, users are directed to the Upload Image Page, the core functional area of the system.

Here, they can upload dermatological images for AI-based analysis either by drag-and-drop or manual selection.

Key features include:

- Support for JPG, PNG, and JPEG formats
- Maximum file size of 10 MB
- A clearly visible “**Analyze Image**” button for initiating processing

The interface displays a thumbnail preview of the uploaded image before analysis, minimizing user error.

The dark interface ensures contrast and highlights the uploaded image effectively.

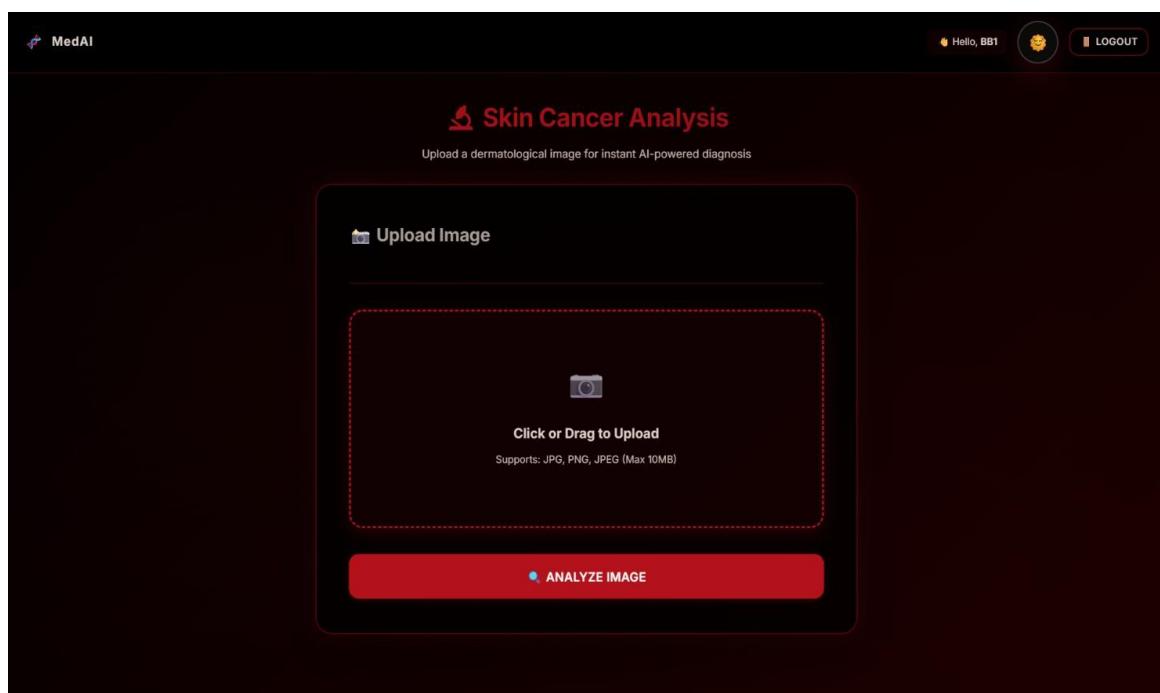


Figure 9.4: Image Upload Interface before Analysis

9.5 Image Analysis Result Page

After the image is uploaded and processed, the Analysis Result Page displays the prediction generated by the AI model.

The layout is divided into two panels:

- Left: Displays the uploaded skin image.
- Right: Displays the detected skin condition predicted by the AI.

The detected condition appears in bold red text for immediate visibility, accompanied by an option to analyze another image for further evaluation.

This two-pane display ensures clarity, efficiency, and professional presentation of diagnostic results.

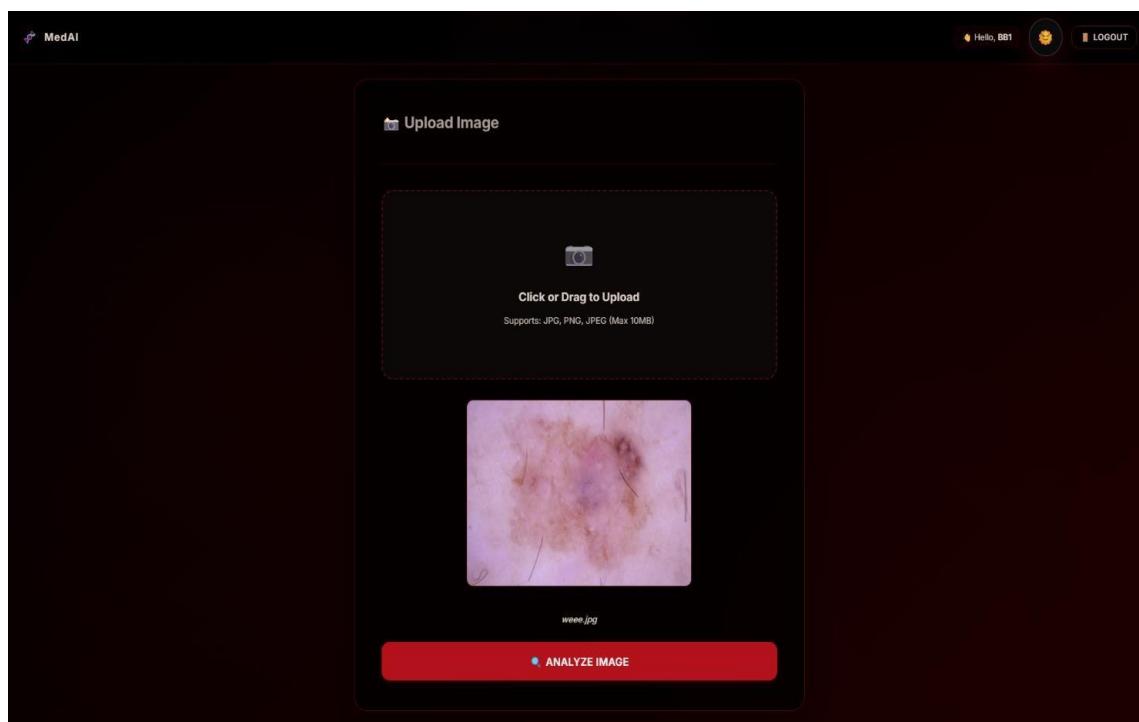


Figure 9.5.1: Sample Upload Image Display

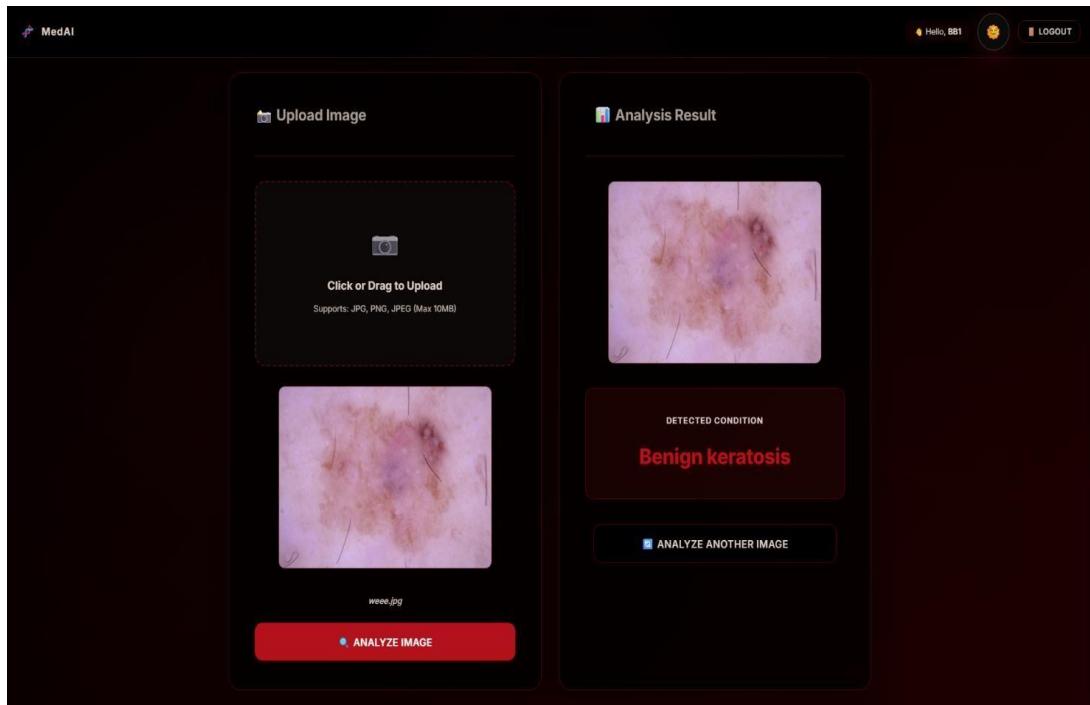


Figure 9.5.2:Prediction Result Display for Benign Keratosis

9.6 Condition Details and Medical Recommendations

Following diagnosis, the system automatically generates a Condition Details and Recommendations section.

This section provides both an explanation of the detected condition and practical medical advice to the user.

For instance, if Benign Keratosis is detected:

- **Condition Description:**

Non-cancerous skin growth resembling moles or warts, common in adults, and harmless unless irritated.

- **Medical Recommendations:**

- No treatment required unless for cosmetic reasons.
- Consult a dermatologist if irritation or bleeding occurs.
- Possible removal options include cryotherapy or shave excision.
- Regular skin self-checks are encouraged.
- Sunscreen use helps prevent new lesions.

At the end, a warning note reminds users:

“This AI analysis is for informational purposes only. Always consult a qualified dermatologist for proper diagnosis and treatment.”

This maintains ethical compliance and reinforces the supportive role of AI in medical decision-making.

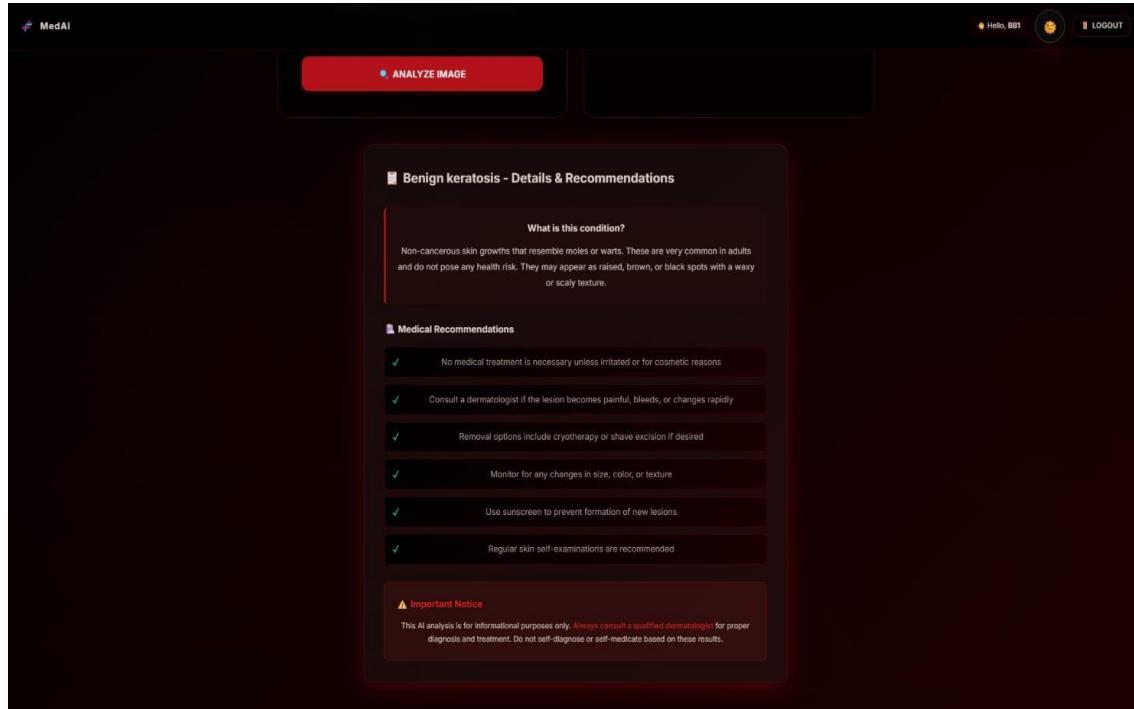


Figure 9.6: Condition Details and Medical Recommendations Page

9.7 Invalid Image Detection (Validation Feature)

One of the crucial features of the system is its robust image validation mechanism, implemented to ensure that only relevant and medically valid dermatological images are analyzed.

This is a vital step in maintaining the accuracy, reliability, and integrity of the AI model's predictions.

When a user uploads an image, the system first performs a pre-analysis validation check to determine whether the uploaded file appears to contain a genuine skin lesion.

This process helps prevent the model from attempting to classify irrelevant images (such as abstract designs, artistic visuals, landscapes, or objects) that could lead to incorrect or meaningless outputs.

If the uploaded file does not meet the expected dermatological characteristics, the system immediately displays a warning message to the user:

“Error: Image does not appear to be a skin lesion. Please upload a medical image showing skin.”

This validation occurs before processing begins, saving computation time and avoiding false predictions.

It enhances the overall user experience by guiding the user to provide valid input while maintaining professional clarity in feedback.

Key aspects of this feature include:

- **Input Verification:** Ensures uploaded images meet minimum dermatological quality standards.
- **Error Prevention:** Protects the model from analyzing irrelevant or distorted images.
- **User Guidance:** Provides clear, user-friendly feedback for corrective action.
- **Model Stability:** Maintains prediction consistency by filtering out non-medical data.
- **Time Efficiency:** Prevents unnecessary computation on invalid inputs.

By implementing this validation step, the system demonstrates strong defensive design principles, a hallmark of dependable AI-driven healthcare software.

It ensures that each analysis is performed on accurate and meaningful data, leading to more trustworthy diagnostic outcomes.

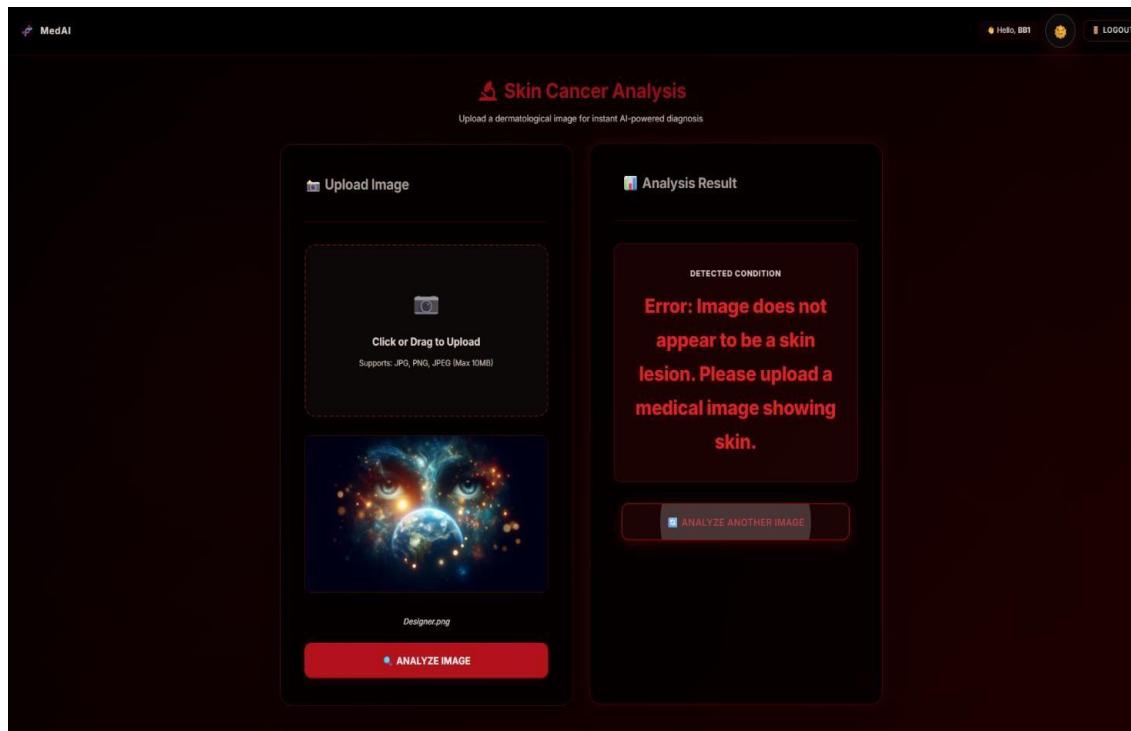


Figure 9.7: Invalid Image Detection and Validation Handling Screen

9.8 Workflow Summary

The complete operational flow of the system can be summarized as follows:

1. **User Authentication:** Secure login or new user registration.
2. **Image Upload:** Dermatological image is uploaded in supported format.
3. **AI Analysis:** The image is processed by the trained model in under 3 seconds.
4. **Result Display:** Condition and recommendations are shown to the user.
5. **Error Handling:** Non-skin images trigger a validation alert.
6. **Logout:** Ends the session securely, redirecting to the Thank You page.

This workflow ensures a fast, accurate, and intuitive user experience.

9.9 Thank You Page

When a user clicks the **Logout** button, they are redirected to the **Thank You Page**, marking the end of their session.

This page serves as a polite acknowledgment of the user's engagement with the platform.

The screen features:

- A celebratory emoji icon  to symbolize session completion
- A personalized greeting, for example, "Thank You, BB1!"

A '**Return to Home**' button to navigate back to the main screen

This final interface closes the user session in a positive and professional manner.

It reinforces the platform's commitment to user satisfaction and health awareness while maintaining consistency in tone and design across the entire application.

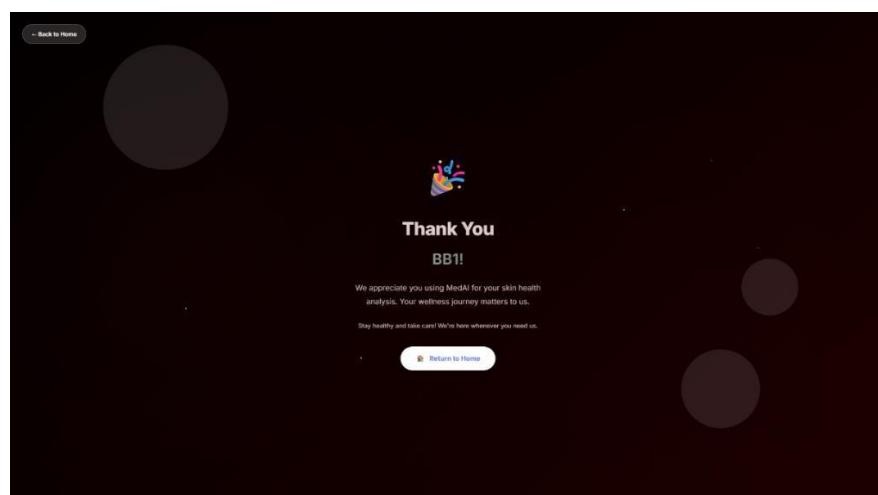


Figure 9.8: Thank You Page Display after Logout Operation

10. Conclusion

Accurate recognition of skin lesions is crucial for early diagnosis and effective treatment, particularly in malignant cases such as melanoma. This project presented a Meta-Ensemble Deep Learning Framework for Skin Lesion Classification that integrates advanced deep learning models with a practical web-based interface to support automated and reliable dermatological analysis.

The proposed system was developed with the objective of achieving high diagnostic accuracy, balanced class-wise performance, and real-time usability. A structured methodology was followed, encompassing dataset preparation, preprocessing, model training, ensemble fusion, and system deployment. The HAM10000 dataset, consisting of seven distinct skin lesion categories, was used for experimental evaluation. Preprocessing techniques such as resizing, normalization, and data augmentation ensured consistent input representation and improved model generalization across varying skin tones, textures, and imaging conditions.

At the core of the system is a dual-stream meta-ensemble architecture that combines EfficientFormerV2 and the Swin Tiny Transformer. EfficientFormerV2 provides lightweight and computationally efficient feature extraction suitable for low-resource environments, while Swin Tiny Transformer captures hierarchical and global contextual information through self-attention mechanisms. The outputs of both models are fused using a logistic regression-based meta-learner, enabling class-aware decision making and improved robustness under class imbalance. The proposed ensemble achieved a Macro F1-score of 0.88 and a ROC-AUC of 0.98, demonstrating superior stability and improved recognition of minority lesion categories compared to individual backbone models.

The trained ensemble model was successfully deployed through a web-based application, enabling users to upload dermoscopic images and receive classification results in real time. The backend architecture ensures secure input validation, consistent preprocessing, efficient inference, and reliable result generation. The system achieved an average inference time of under three seconds per image, making it suitable for real-time clinical and teledermatology applications. The frontend interface was designed with usability and

accessibility in mind, allowing both clinicians and general users to interact with the system intuitively.

Comprehensive evaluation confirmed reliable performance across all lesion categories, strong resilience to dataset imbalance, accurate handling of invalid inputs, and stable system operation across different devices and browsers. These results indicate that the proposed framework is not merely a research prototype but a deployable and clinically relevant decision-support tool.

Overall, this work demonstrates the effectiveness of combining lightweight CNN–Transformer hybrids with hierarchical transformers using a meta-ensemble strategy for skin lesion classification. By bridging the gap between advanced AI models and practical system deployment, the project establishes a strong foundation for future AI-assisted dermatological screening systems and real-world telemedicine applications.

11. Future Scope

While the proposed Meta-Ensemble Skin Lesion Classification System has demonstrated strong performance and practical usability, several opportunities exist to further enhance its capability, scalability, and clinical impact. One important direction for future work is cross-dataset validation, where the framework can be evaluated on larger and more diverse datasets such as ISIC 2020, ISIC 2024, and Derm7pt. This would help assess the model's robustness across varying imaging conditions, acquisition devices, and skin tones, thereby improving its generalizability for real-world clinical applications.

Another promising extension involves the integration of clinical metadata alongside dermoscopic images. Incorporating patient-related information such as age, gender, lesion location, medical history, and lesion evolution can enable a multi-modal learning framework, leading to more context-aware predictions and improved diagnostic accuracy. Such integration would allow the system to better reflect real clinical decision-making processes.

Future work can also focus on enhancing model interpretability and explainability by incorporating explainable AI techniques such as Grad-CAM and attention heatmaps. These methods can visually highlight image regions that influence the model's predictions, thereby improving transparency, clinical trust, and acceptance among dermatologists.

To move beyond experimental evaluation, real-world clinical testing can be conducted through collaborations with healthcare professionals and medical institutions. Prospective pilot studies within clinical workflows would provide valuable insights into system usability, diagnostic reliability, and necessary refinements for large-scale adoption.

Given the lightweight nature of the proposed architecture, future efforts may explore cloud-based, mobile, and edge deployment strategies. Deploying the system as a mobile application or cloud service would enable teledermatology and point-of-care screening, particularly benefiting remote and resource-limited regions.

Further enhancements may include integration with Electronic Health Record (EHR) systems, allowing automated storage of diagnostic results and longitudinal tracking of lesion progression. Such integration would support continuity of care and contribute to broader digital healthcare transformation initiatives.

Finally, the system can be extended with continuous learning mechanisms, such as federated learning, to enable model updates using newly acquired data while preserving patient privacy and data security. Additional improvements focused on accessibility and global reach, including multi-language support and simplified user interfaces, would make the system more inclusive and suitable for deployment across diverse populations.

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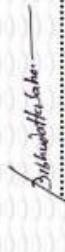
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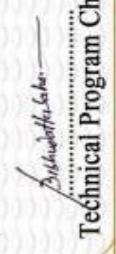
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A Meta-Ensemble Deep Learning Approach Using EfficientFormerV2 and Swin Tiny Transformer for Skin Lesion Classification

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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

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

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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 unbalanced 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.

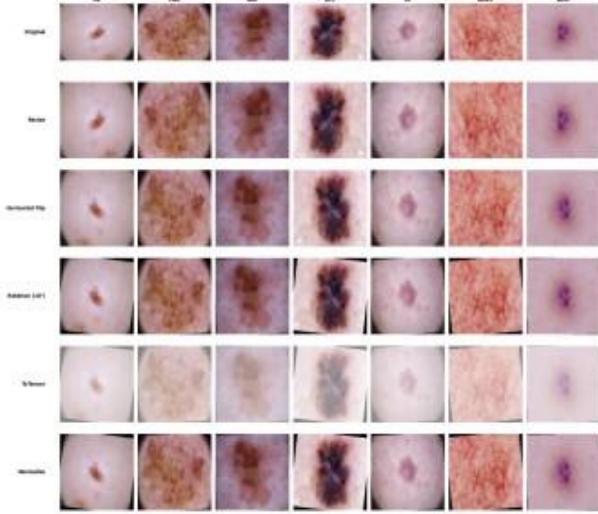


Fig. 1. Illustration of preprocessing and augmentation steps applied to HAM10000 dermoscopic images. The rows show transformations applied to each lesion type: resize, horizontal flip, rotation, tensor conversion, and normalization. Columns represent the seven diagnostic categories: NV, MEL, BKL, BCC,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

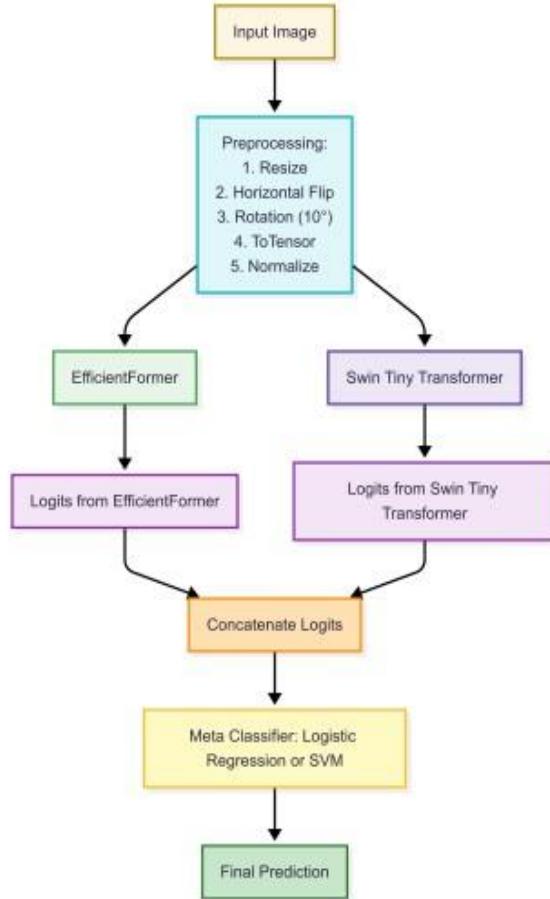


Fig. 2. Proposed classification pipeline. Input images undergo preprocessing and are processed by EfficientFormerV2 and Swin Tiny Transformer. Their outputs are combined through soft voting or a logistic regression meta-classifier to produce the final diagnosis.

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.

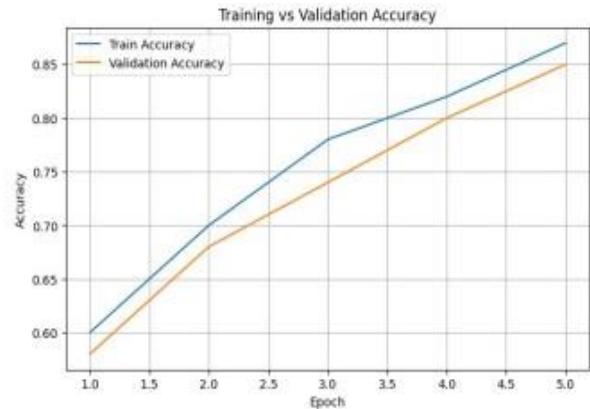


Fig. 3. Training vs. validation accuracy across epochs, showing steady improvement in both sets.



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) [2] | 94.30 | - | - |
| Paraddy & Virupakshappa (2025) [2] | 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.

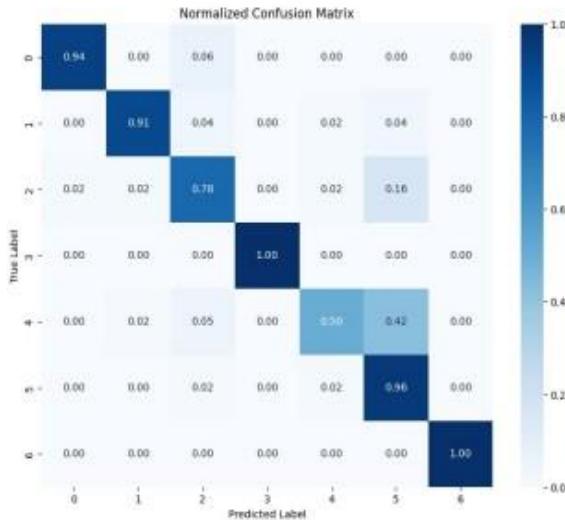


Fig. 5. Normalized confusion matrix of the proposed meta-ensemble model across seven lesion categories.

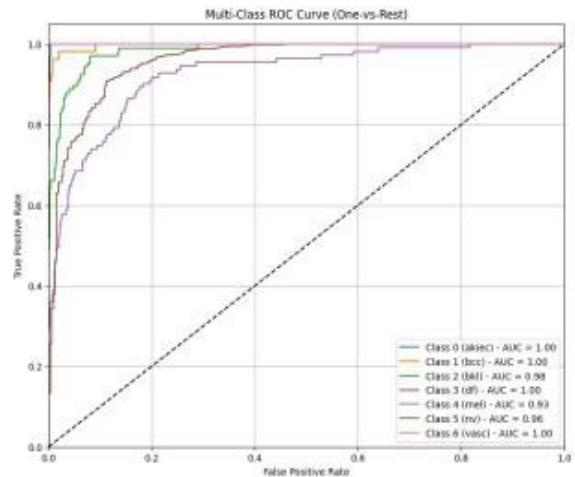


Fig. 6. One-vs-rest ROC curves showing discriminative performance for each class.

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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*% detected as AI

AI detection includes the possibility of false positives. Although some text in this submission is likely AI generated, scores below the 20% threshold are not surfaced because they have a higher likelihood of false positives.

Caution: Review required.

It is essential to understand the limitations of AI detection before making decisions about a student's work. We encourage you to learn more about Turnitin's AI detection capabilities before using the tool.

Disclaimer

Our AI writing assessment is designed to help educators identify text that might be prepared by a generative AI tool. Our AI writing assessment may not always be accurate (it may misidentify writing that is likely AI generated as AI generated and AI paraphrased or likely AI generated and AI paraphrased writing as only AI generated) so it should not be used as the sole basis for adverse actions against a student. It takes further scrutiny and human judgment in conjunction with an organization's application of its specific academic policies to determine whether any academic misconduct has occurred.

Frequently Asked Questions

How should I interpret Turnitin's AI writing percentage and false positives?

The percentage shown in the AI writing report is the amount of qualifying text within the submission that Turnitin's AI writing detection model determines was either likely AI-generated text from a large-language model or likely AI-generated text that was likely revised using an AI paraphrase tool or word spinner.

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What does 'qualifying text' mean?

Our model only processes qualifying text in the form of long-form writing. Long-form writing means individual sentences contained in paragraphs that make up a longer piece of written work, such as an essay, a dissertation, or an article, etc. Qualifying text that has been determined to be likely AI-generated will be highlighted in cyan in the submission, and likely AI-generated and then likely AI-paraphrased will be highlighted purple.

Non-qualifying text, such as bullet points, annotated bibliographies, etc., will not be processed and can create disparity between the submission highlights and the percentage shown.

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