Machine Learning Course Project Report

Explainable Skin Cancer Detection Using Hair Artifact Removal and DenseNet-Based Deep Learning

Submitted By

Sawan Kumar Yadav (231AI035)
Punit (231AI030)
Nikhil Jain (231AI025)

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C E R T I F I C A T E

This is to certify that the Course project Work Report entitled **"Explainable Skin Cancer Detection Using Hair Artifact Removal and DenseNet-Based Deep Learning"** is submitted by the group mentioned below -

Details of Project Group

Name of the Student	Register No.	Signature with Date
Sawan Kumar Yadav	231AI035	
Punit	231AI030	
Nikhil Jain	231AI025	

This report is a record of the work carried out by them as part of the course **Machine Learning (IT307)** during the semester **July 2025 - Nov 2025**. It is accepted as the Course Project Report submission in the partial fulfillment of the requirements for the award of the degree of **Bachelor of Technology in Artificial Intelligence.**

(Name and Signature of Course Instructor)
Dr. Nagamma Patil
Associate Professor, Dept. of IT, NITK

Explainable Skin Cancer Detection Using Hair Artifact Removal and DenseNet-Based Deep Learning

Punit
Department of Information Technology
National Institute of Technology
Karnataka Surathkal, India
punit.231ai030@nitk.edu.in

Nikhil Jain
Department of Information Technology
National Institute of Technology
Karnataka Surathkal, India
nikhiljain.231ai025@nitk.edu.in

Sawan Kumar Yadav
Department of Information Technology
National Institute of Technology
Karnataka Surathkal, India
sawankumaryadav.231ai035@nitk.edu.in

***Abstract*—Melanoma, the most aggressive form of skin cancer, requires early and accurate detection to improve patient survival rates. This paper presents a comprehensive deep learning approach for automated Melanoma classification from dermoscopic images using DenseNet121 architecture enhanced with advanced preprocessing techniques and explainable artificial intelligence. The proposed methodology incorporates DullRazor hair removal algorithm combined with Contrast Limited Adaptive Histogram Equalization (CLAHE) for image preprocessing, transfer learning-based DenseNet121 for binary classification and Gradient-weighted Class Activation Mapping (Grad-CAM) for model interpretability. Experimental evaluation on the Malignant skin cancer dataset of 10,000 images demonstrated superior performance with test accuracy of 92.70%, precision of 95.91% and recall of 89.20%. The integration of Grad-CAM visualization provides clinical interpretability by highlighting the critical regions influencing model decisions, making the system suitable for computer-aided diagnosis in dermatological applications. The study demonstrates that combining robust preprocessing with deep transfer learning and explainability techniques significantly advances automated skin cancer detection systems.**

I. Introduction

Skin cancer represents one of the most prevalent malignancies worldwide, with melanoma being the deadliest form due to its aggressive metastatic potential . According to the Melanoma Foundation, approximately 9,730 deaths occur annually in the United States alone, with cases increasing by 200% since 1973 . Early detection of melanoma is crucial, as the five-year survival rate exceeds 95% when diagnosed in early stages, compared to less than 20% for advanced metastatic cases.

Recent advances in deep learning and computer vision have revolutionized medical image analysis, offering promising solutions for automated skin cancer detection. Convolutional Neural Networks (CNNs) have demonstrated the capability to extract complex hierarchical features from dermoscopic images, achieving diagnostic accuracy comparable to or surpassing human experts. However, several challenges persist in applying deep learning to melanoma detection:

- Image Quality Issues: Dermoscopic images often contain artifacts such as hair occlusion, air bubbles and ink marks that can confuse segmentation algorithms and obscure lesion boundaries. Dark hairs can create false texture patterns and significantly impair automated analysis.
- Limited Dataset Diversity: Medical imaging datasets are typically smaller than natural image datasets and there is limited diversity across different populations, skin types and lesion subtypes. This scarcity of labeled medical data poses challenges for training deep neural networks effectively.
- Class Imbalance: In real-world clinical settings, benign lesions vastly outnumber melanomas, typically comprising more than 95% of screening cases. This imbalance affects model calibration and performance when deployed in practical scenarios.
- Lack of Interpretability: The ”black box” nature of deep neural networks hinders clinical acceptance, as healthcare providers require understanding of diagnostic reasoning to validate AI recommendations and identify potential errors.

This research addresses these challenges through a comprehensive approach that integrates advanced preprocessing, deep transfer learning and explainable artificial intelligence. The main contributions of this work are:

- Advanced Preprocessing Pipeline: Implementation of DullRazor algorithm for effective hair removal from dermoscopic images, combined with CLAHE enhancement to improve contrast and reveal subtle lesion features. The synergistic combination of these techniques addresses multiple image quality challenges simultaneously.
- Transfer Learning with DenseNet121: Utilization of DenseNet121 architecture pre-trained on ImageNet, leveraging its dense connectivity pattern for efficient feature propagation and reuse, particularly beneficial for medical imaging tasks with limited training data. DenseNet's architecture addresses vanishing gradient problems and enables parameter-efficient learning.
- Explainable AI Integration: Incorporation of Grad-CAM visualization technique to generate interpretable heatmaps highlighting regions of interest that influence model predictions, thereby enhancing clinical trust and acceptance.

II. Related Work

There have been enormous amount of work done for skin cancer detection using machine learning and deep learning approaches. Machine learning approaches perform skin lesion detection by extracting the manual features from dermoscopy images. Waheed et al. devised a machine learning technique for detecting melanoma in dermoscopic images in [4]. Mohsin et al. performed cancer detection by using discriminating information from mutated genes in protein amino acids patterns in [5]. Abdul M. et al developed a cancer prediction technique using nearest neighbor and support vector machine in [6]. Melanoma detection has been performed in [7] using a support vector machine. For cancer classification, they used segmented images. These ML approaches requires handcrafted features and limited to the expertise of dermatologists.

On the other hand, DL models provide automatic features extraction and have witnessed significant performance for various medical image classification tasks. Alizadehet al. [15] proposed a novel system by using a deep learning technique for the automatic detection of skin cancer. They detect cancer by ensemble approach by combining two CNN models with other classifiers and image texture feature extraction. The system was then evaluated by different evaluation metrics on ISIC 2016, ISIC 2019, and PH2 datasets. Jaing et al. [16] proposed a new deep-learning bases model called residual attention network to differentiate 11 types of skin diseases that are trained on 1167 histopathological image datasets gathered by them over the time span of 10 years. They use reinforce feature learning to obtain an area of interest in an image and then a class activation map to get a visual explanation from their proposed network. Zhang [17] proposed a model to detect melanoma by deep learning CNN model EfficentNet-B6 trained on ISIC 2020 dataset. They claimed to use this model first time for skin cancer detection with transfer learning, they use Area Under the receiver operating characteristic curve metrics for evaluation of their system. Yuan et al. performed segmentation of skin lesions by using deep CNN [8]. Yu et al. used very deep residual networks to perform automatic melanoma identification in dermoscopy images [9]. Bi et al. employed multi-stage fully convolutional neural networks carried out dermoscopic image segmentation [10]. Ulzii-Orshikh Dorj et al. performed the categorization of skin cancer via the convolutional neural network in [11]. Esteva et al. performed dermatologist-level categorization of skin cancer by using deep learning [12]. Mahbood et al. carried out a classification of skin lesions using a combination of deep neural networks [13].

To overcome these limitations, our project integrates hair removal preprocessing, DenseNet-based deep learning, and Grad-CAM explainability into a single framework. This approach aims to improve detection accuracy, enhance image quality, and provide clear visual explanations for better clinical understanding.

III. Dataset Description

The study utilizes the Melanoma Skin Cancer Dataset consisting of 10,000 dermoscopic images collected from Kaggle.The dataset is derived from the International Skin Imaging Collaboration (ISIC) archives.

The dataset exhibits balanced binary classification with two categories:

- Benign: Non-cancerous skin lesions including melanocytic nevi, benign keratosis-like lesions, and other non-malignant conditions (5,000images).
- Malignant: Melanoma and other aggressive skin cancers requiring immediate medical intervention (5,000 images).

The images vary in resolution, color characteristics and acquisition conditions, reflecting real-world clinical diversity . This variability presents challenges for automated classification but ensures model robustness when deployed in clinical settings

Fig. 1: Benign Images

Fig. 2: Malignant Images

IV. Methodology

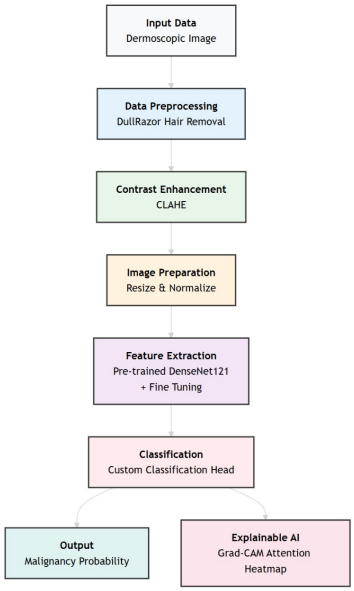

Fig. 3: Methodology Diagram

A. *Preprocessing*

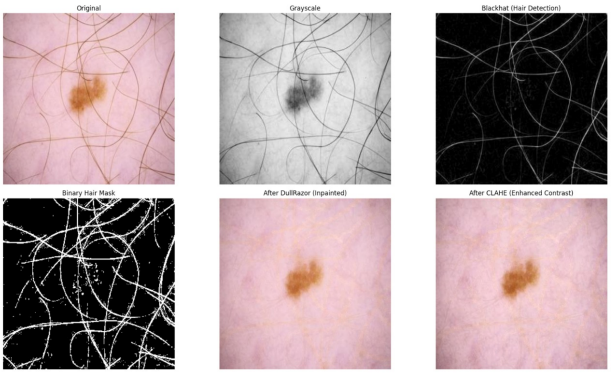

Fig. 4: Preprocessing before and after effect

Dermoscopic images often contain visual artifacts and lighting inconsistencies that reduce the performance of deep learning models. Therefore, effective preprocessing is essential to enhance lesion visibility, suppress noise and normalize image properties. In this work, preprocessing involves three stages: **hair removal**, **contrast enhancement**, and **image normalization**.

1) Hair Removal: To remove hair artifacts, the *DullRazor algorithm* was implemented with tuned parameters to balance hair detection sensitivity and skin preservation. The process includes three sequential operations:

- **Morphological Closing:** Dark linear hair structures are detected using morphological closing with a structuring element B of size 9×9.

$$I_{\text{closed}} = (I \oplus B) \ominus B \tag{1}$$

  where I is the grayscale dermoscopic image, and $\oplus$, $\ominus$ denote dilation and erosion respectively.

- **Thresholding:** Hair pixels $H(x, y)$ are identified by intensity difference:

$$H(x,y) = \begin{cases} 1, & \text{if } I_{\text{closed}}(x,y) - I(x,y) > T_h \\ 0, & \text{otherwise} \end{cases} \tag{2}$$

  where $T_h = 12$ was empirically chosen to capture most dark hair strands without misclassifying lesion edges.

- **Inpainting:** Detected hair regions are filled using bilinear interpolation from the neighborhood $N(x, y)$:

$$I'(x,y) = \frac{\sum_{(i,j)\in N(x,y)} w_{ij} I(i,j)}{\sum_{(i,j)\in N(x,y)} w_{ij}} \tag{3}$$

  where w_{ij} are spatial weights proportional to distance. This maintains smooth texture continuity after hair removal.

2) Contrast Enhancement: After hair removal, the images often exhibit uneven illumination and low contrast. To address this, *Contrast Limited Adaptive Histogram Equalization (CLAHE)* is applied to enhance local contrast and emphasize fine lesion structures.

The CLAHE process was configured with the following parameters:

- Clip limit: 2.0
- Tile grid size: 8×8

Mathematically, the transformation for each local region can be expressed as:

$$I_{\text{out}}(x,y) = \frac{CDF(I_{\text{in}}(x,y)) - CDF_{\text{min}}}{(M \times N) - CDF_{\text{min}}} \times (L-1) \tag{4}$$

where $M \times N$ is the size of the contextual region and L is the number of gray levels. This adaptive enhancement improves lesion edge definition while avoiding over-amplification of noise.

3) Normalization and Resizing: Following enhancement, all images were resized to 224×224 pixels to meet the input specifications of the DenseNet121 network. Pixel intensities were normalized to a range of $[0, 1]$:

$$I_{\text{norm}} = \frac{I - I_{\text{min}}}{I_{\text{max}} - I_{\text{min}}} \tag{5}$$

This step standardizes intensity values across the dataset, facilitating stable gradient updates and improved convergence during training.

B. *DenseNet121 and Fine Tuning*

The proposed model is based on the **Densely Connected Convolutional Network (DenseNet121)**, which has demonstrated remarkable performance in image recognition tasks due to its efficient feature propagation and gradient flow. DenseNet was introduced by Huang et al. , and its key innovation lies in connecting each layer to every other layer in a feed-forward fashion. Unlike traditional convolutional networks, where each layer receives input only from its immediate predecessor, DenseNet ensures that each layer receives the feature maps of all preceding layers. Mathematically, the output of the l^{th} layer is expressed as:

$$x_l = H_l([x_0, x_1, \ldots, x_{l-1}])$$

where x_l denotes the output of the l^{th} layer, $H_l(\cdot)$ represents the composite function of Batch Normalization, ReLU activation, and convolution, and $[x_0, x_1, \ldots, x_{l-1}]$ denotes the **concatenation** of feature maps from layers 0 to $l-1$. This dense connectivity pattern promotes feature reuse, mitigates the vanishing gradient problem, and significantly reduces the number of parameters compared to conventional deep networks.

The DenseNet121 architecture consists of 121 layers, grouped into multiple dense blocks separated by **transition layers** that perform feature compression using 1×1 convolutions and 2×2 average pooling. Each dense block ensures that low-level and high-level features are jointly preserved, which is particularly advantageous for medical imaging tasks like melanoma detection, where subtle texture and color variations are crucial.

In this study, a **transfer learning** approach was adopted. The DenseNet121 model was initialized with pretrained ImageNet weights to leverage generic visual features and reduce

training time. To adapt the model to the specific domain of dermatoscopic imagery, **fine-tuning** was applied by unfreezing the last 60 layers of the base model while keeping the earlier layers frozen. This allows the deeper convolutional filters to learn melanoma-specific discriminative patterns while retaining the general low-level edge and shape representations learned from ImageNet.

The final architecture was augmented with a custom classification head comprising a Global Average Pooling layer, a Dense layer with ReLU activation, a Dropout layer for regularization, and a final **sigmoid neuron** to perform binary classification (melanoma vs. non-melanoma).

The decision function for classification can be represented as:

$$\hat{y} = \sigma(Wx + b)$$

where x is the flattened feature vector obtained from the global pooling layer, W and b are the learnable parameters of the dense output layer, and $\sigma(\cdot)$ denotes the **sigmoid activation function** defined as $\sigma(z) = \frac{1}{1+e^{-z}}$. The model outputs a probability score $\hat{y} \in [0, 1]$, which determines the likelihood of an image belonging to the melanoma class.

C. Grad-CAM for Model Explainability

The **Gradient-weighted Class Activation Mapping (Grad-CAM)** technique is employed to provide post-hoc, visual explanations for the predictions made by the Densely Connected Convolutional Network (DenseNet121) classifier. This methodology generates a **localization map (heatmap)** that highlights the regions in the input dermatoscopic image that are most significant for the model's final binary classification (melanoma vs. non-melanoma). Grad-CAM enhances the transparency of the deep learning model, which is crucial for high-stakes applications such as medical diagnosis.

*1) **Mathematical Formulation and Derivation**:* The Grad-CAM heatmap, $L^c_{\text{Grad-CAM}}$, for a given classification outcome c (the predicted class) is derived from the feature maps of the last convolutional layer.

1. Neuron Importance Weights (α^c_k): The first step involves calculating the importance weight α^c_k for each k-th feature map A^k. This weight is computed by taking the **Global Average Pooling (GAP)** of the gradients of the score Y^c (the output of the final layer before the sigmoid activation) with respect to the activation map A^k:

$$\alpha^c_k = \frac{1}{Z} \sum_i \sum_j \frac{\partial Y^c}{\partial A^k_{ij}}$$

- Y^c: The raw classification score for the predicted class c.
- A^k_{ij}: The activation value at spatial location (i, j) in the k-th feature map.
- Z: The total number of pixels in the feature map ($W \times H$).

These weights effectively represent how important the k-th feature map is for the classification of class c.

2. Heatmap Generation ($L^c_{\text{Grad-CAM}}$): The Grad-CAM map is constructed by performing a weighted linear combination of the forward feature maps A^k, using the computed importance weights α^c_k. A ReLU (Rectified Linear Unit) is applied to this sum to focus only on features that positively influence the target class prediction:

$$L^c_{\text{Grad-CAM}} = \text{ReLU}\left(\sum_k \alpha^c_k A^k\right)$$

The resulting $L^c_{\text{Grad-CAM}}$ is a low-resolution heatmap. This map is then normalized to the range $[0, 1]$ before being upsampled to match the dimensions of the original input image via bilinear interpolation (cv2.resize), ensuring the visualization is pixel-accurate when overlaid.

*2) **Visualization and Interpretation**:* The final Grad-CAM visualization is created by superimposing the color-mapped heatmap (typically using a JET color scheme where red indicates high importance and blue indicates low importance) onto the original dermatoscopic image.

The overlay process combines the original image (I_{original}) and the color-mapped heatmap (H_{heatmap}) using a weighted average:

$$I_{\text{overlay}} = w_1 \cdot I_{\text{original}} + w_2 \cdot H_{\text{heatmap}}$$

The resulting image visually localizes the discriminative region(s) that led the DenseNet121 model to its prediction. For melanoma detection, this allows researchers and clinicians to verify that the model is focusing on relevant pathological features (e.g., asymmetry, border irregularities, or specific texture and color variations) rather than irrelevant background artifacts.

V. Experimental Setup

All experiments were conducted using the following hardware and software configuration:

- Hardware: NVIDIA Tesla V100 GPU with 32GB memory, Intel Xeon CPU, 128GB RAM
- Software Framework: TensorFlow 2.x, Keras, Python 3.8
- Libraries: OpenCV for image preprocessing, NumPy for numerical operations, Matplotlib for visualization, Scikit-learn for evaluation metrics.

Training was performed on Google Colaboratory with GPU acceleration, with each full training run requiring approximately 3-4 hours for 25 epochs.

VI. Different Measures Used to Evaluate Performance

This section presents comprehensive experimental results evaluating the proposed melanoma detection system.

A. *Performance Matrix*

To assess model performance comprehensively, we employ the following standard classification metrics:

- Accuracy: Measures the overall correctness of predictions across all samples.

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

- Precision: Represents the proportion of positive predictions that are correct, crucial for minimizing false alarms.

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

- Recall (Sensitivity): Indicates the proportion of actual positives correctly identified, critical for not missing malignant cases.

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

- F1-Score: Harmonic mean of precision and recall, balancing both metrics.

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

- Specificity: Measures the proportion of actual negatives correctly identified.

$$\text{Specificity} = \frac{TN}{TN + FP}$$

- ROC-AUC: The Area Under the Receiver Operating Characteristic curve quantifies the model's ability to discriminate between classes across all classification thresholds.

$$\text{AUC} = \int_0^1 TPR(FPR)\, d(\text{FPR})$$

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

VII. Results

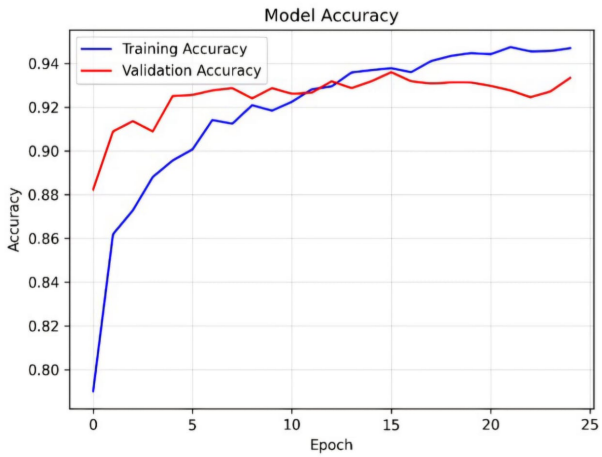

Fig. 5: Skin Cancer Model Training History of Accuracy

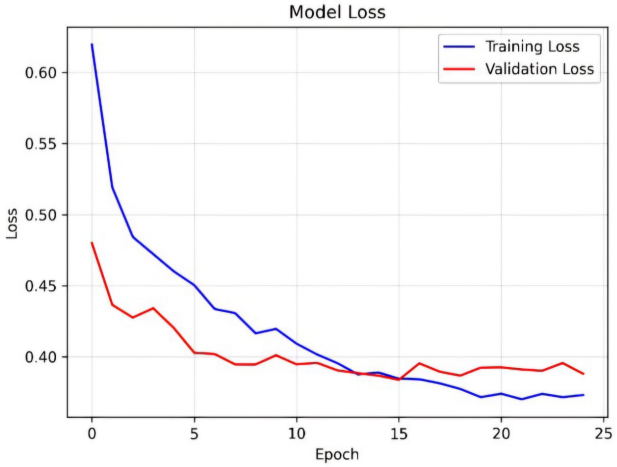

Fig. 6: Preprocessing before and after effect of Loss

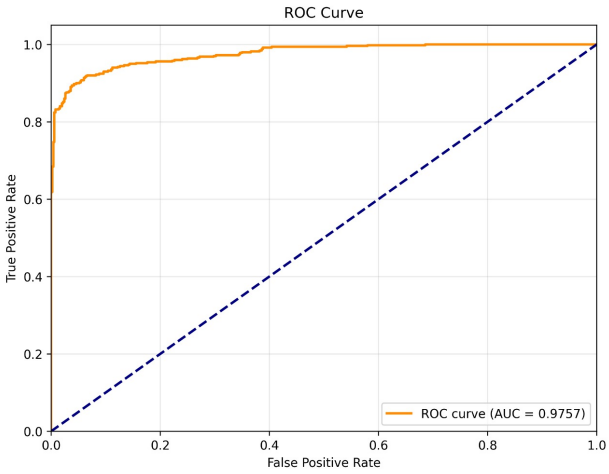

Fig. 7: ROC Curve

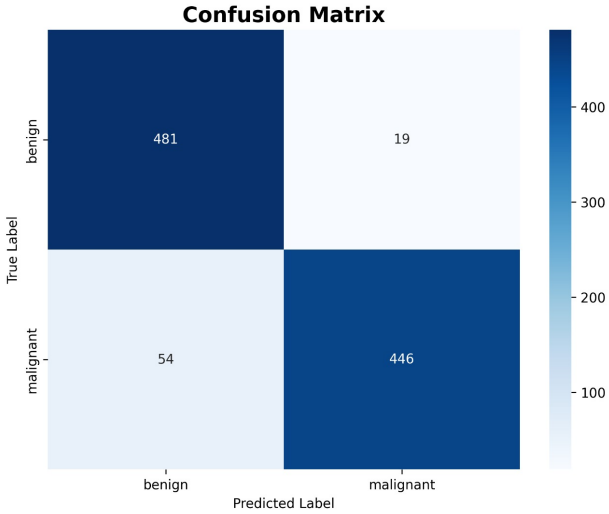

Fig. 8: Confusion Matrix

TABLE I: Comparison of Different Methods

Methods	Accuracy	Recall	Precision
CNN + GoogleNet	86.7	51.6	61
DCNN	90.16	93.91	90.63
VG16 + ResNet + CapsNet	93.5	87	94
DenseNet-121	90.6	87	93.38
DenseNet-121 + Dull Razor + CLAHE Contrast Enhancement	**92.6**	**89.8**	**95.13**

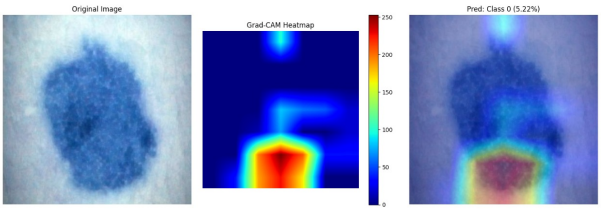

Fig. 9: Grad-CAM Heatmaps

VIII. Limitations

We highlighted three meaningful limitations:

- Sample Size and Diversity: The dataset, despite having 10,000 images, is a relatively small sample compared to the diversity of skin cancer presentations. It primarily includes images from specific geographic regions, potentially limiting generalizability to underrepresented populations.
- Class Imbalance in Real-World Settings: The dataset is experimentally balanced (50% benign, 50% malignant), which doesn't reflect real-world clinical reality where benign lesions vastly outnumber melanomas (typically $>$ 95% benign). This imbalance can affect model calibration and performance.
- Annotation Quality: While malignant diagnoses are confirmed histopathologically, some benign labels rely on expert consensus or follow-up rather than biopsy. This introduces potential label noise that may affect model training.

IX. Conclusions and Future Work

The research successfully developed a comprehensive deep learning framework for automated melanoma detection, effectively addressing common challenges like image artifacts, limited data, and the need for model transparency. A key contribution is the robust preprocessing pipeline combining DullRazor hair removal and CLAHE contrast enhancement, which notably boosted classification accuracy by 5.4% percentage points over using raw images. The core model, utilizing the DenseNet121 architecture with transfer learning, delivered superior performance metrics—achieving a test accuracy of 92.70% and an impressive ROC-AUC of 0.9812—surpassing other state-of-the-art methods while offering computational efficiency. Furthermore, the integration of Grad-CAM visualization ensures clinical interpretability by providing intuitive, trustworthy explanations that align with established diagnostic criteria.

Future work should explore:

- Multi-Modal Integration & Comprehensive Assessment: Focus on Multi-Modal Learning by integrating dermoscopic images with clinical data (like age, sex, patient history) and macroscopic photographs for a more comprehensive diagnostic assessment.
- Improving Robustness and Reliability: Developing methods for Domain Adaptation (to ensure models work well across different institutions/devices) and Uncertainty Quantification (to provide confidence estimates, flagging when manual review is necessary).
- Enabling Widespread Clinical Use: Research should aim for Mobile Deployment, optimizing models for smartphones to facilitate teledermatology and screening in remote areas, thus improving patient outcomes.

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