

Robust Skin Disease Diagnosis Using Deep-MobileNet with Adaptive Deer Hunting Optimization Algorithm

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Abstract: Skin diseases range from mild conditions to severe threats, such as melanoma, highlighting the critical importance of early and accurate evaluation for effective treatment. Traditional diagnostic methods that depend heavily on visual inspection and biopsy are often prone to delays and susceptible to human error, underscoring the need for more efficient and reliable approaches. This study introduced a computerized system for detecting skin diseases using deep learning techniques and classification, with a focus on enhancing diagnostic efficiency and accuracy. The approach begins with the comprehensive preprocessing of skin images, including illumination adjustment, elimination of artifacts via morphology closing and edge improvement using an unsharp filter. These steps improve the image clarity and prepare the data for accurate analysis. To address variations in lesion size and boundary irregularities, a Fuzzy k-means clustering technique segments the affected skin regions, ensuring adaptable detection across diverse skin conditions. The classifier Deep-MobileNet integrates the lightweight MobileNet architecture with Squeeze-and-Excitation (SE) blocks, enabling it to effectively differentiate between healthy and diseased skin. SE blocks enhance the model's ability to capture spatial dependencies, thereby improving classification precision. To further optimize the classifier's performance, hyperparameters are tuned using the adaptive deer hunting optimization (ADHO) algorithm, which accelerates convergence and boosts model efficiency. By providing an automated, efficient solution, this approach has the potential to assist healthcare providers in diagnosing skin diseases quickly and reliably, thereby supporting timely and effective treatment interventions. The efficiency of the suggested method is evaluated based on accuracy, sensitivity, specificity and F1-Score. The experimental outcome showed that the recommended approach attained a maximum accuracy of 91.96%.

Index Terms: Skin diseases, Deep-MobileNet, MobileNet architecture with Squeeze-and-Excitation (SE), Adaptive Deer Hunting Optimization (ADHO) algorithm.

1. Introduction

Skin is a vital component of the human body, providing protection against harmful heat, radiation, wounds, and infections, and also plays a crucial role in the production of vitamin D [1]. Skin diseases, especially common among the elderly, are traditionally diagnosed through expert evaluation and skin biopsies, which can be time-intensive [2]. This highlights the need for automated computer-based systems to improve diagnostic accuracy and address the shortage of specialists [3,4]. However, classifying skin diseases using images is challenging because of the visual similarities among many conditions, making feature selection complex [5]. Accurate automated analysis can enhance the diagnostic speed and lead to more cost-effective treatment [6]. Traditional detection methods include region-based, edge-based, clustering and thresholding techniques [7], while Computer-aided diagnostic systems for skin diseases are frequently developed using machine learning techniques such as Support Vector Machines (SVM) [8], gradient boosting and Artificial Neural Networks (ANN).

To address these challenges, a hybrid Extreme Learning Machine (ELM) and teaching-learning-based optimization (TLBO) method were introduced for effective melanoma detection [9]. The ELM, a feed-back neural network system with a single concealed layer, allows for fast and accurate training [10]. An Optimized Region Growing with Grey Wolf Optimization is employed for dividing the affected areas [11,12]. (GWO) with texture features extracted through the grey level co-occurrence matrix (GLCM) and Weber Local Descriptor (WLD) [13]. An autoencoder-based latent representation generates a reduced feature set. Traditional models such as multi-layer perceptron (MLP) and ResNet along with a hybrid Convolutional Neural Network (CNN) incorporating Batch Normalization and L2 Regularization are utilized [14]. The optimized CNN model trained on four public datasets detects skin abnormalities from various orientations [15]. A fuzzy segmentation algorithm isolates lesion regions and an MLSTM model classifies them into seven lesion types confirming their presence.

Numerous advanced learning methods require significant memory and processing power to manage large parameter tunings. Performance improvements are needed to process multiple scales and multi-resolution characteristics because skin lesion photos originate from multiple pieces of equipment with differing resolutions. Automated skin lesion detection is complicated by subtle contrast differences and heterogeneous visual attributes. This study addresses these issues by proposing a robust skin disease diagnosis approach using Deep-MobileNet optimized with an Adaptive Deer Hunting Optimization Algorithm (ADHOA). The primary contributions of this study are summarized below.

- Dermoscopic images were initially collected from the dataset, and a morphological closing technique was applied to remove small artifacts.
- In the pre-processing step, an unsharp filter is used to enhance the image by increasing the edge contrast.
- After pre-processing FKM was used to segment the affected skin regions based on variable sizes and boundaries.
- The proposed Deep-MobileNet, which combines MobileNet with SE, classifies images as normal or abnormal.
- The hyperparameters in the Deep-MobileNet are optimally tuned using the ADHO algorithm.
- The efficacy of the model was thoroughly assessed using performance measurements such as accuracy, sensitivity, specificity and F1-score.

2. Literature Survey

Many researchers have developed robust methods for the diagnosis of skin disease. Some of these works are analyzed here: Reddy, D. A., et al. [16] introduced a novel framework aimed at enhancing skin disease diagnosis. They used an Optimal Area Growth strategy that employed grey wolf optimization (GWO) to divide affected regions. The Weber Local Descriptor (WLD) and Gray Level Co-occurrence Matrix (GLCM) were next applied to gather texture characteristics from the segmented regions. By creating a smaller set of characteristics using hidden representations and an automatic encoder, the features that were extracted were further enhanced. Using this hidden representation, the lesions were then classified using a combined convolutional neural network (CNN). Although the experimental output showed superior performance compared to the CNN, RNN, and LSTM classifiers it failed to achieve optimized segmentation.

Rasheed et al. [17] introduced a hybrid CNN model with Batch Normalization and L2 Regularization to achieve high accuracy in skin disease classification. This hybrid architecture outperformed the other classifiers highlighting the effectiveness of advanced techniques in improving the model performance. By employing various evaluation criteria and visualizations this study provides useful information on the advantages and disadvantages of every approach helping researchers and practitioners to choose the best architecture for skin disease classification. The results demonstrated an optimal balance between precision and recall without increasing the computational complexity.

Salih, O., and Duffy, K. J., et al. [18] utilized an autonomous CNN model configuration using the genetic method for robust, accurate, and dependable autonomous skin tumor categorization with an eye toward early detection. Four publicly available datasets were utilized for training the improved CNN model, which allowed for the recognition of anomalies according to the skin lesion characteristics in different rotations. The model achieved the highest scores for

the DICE coefficient, precision, and F-score, surpassing other existing methods. This approach demonstrates potential as an affordable method for the early diagnosis of skin lesions. However, it did not achieve the desired effectiveness and efficiency for early diagnostic applications.

Balasundaram et al. [19] developed a deep-learning-based system that uses a type of genetic algorithm for optimal building for greater efficiency after being taught using the DermNet database. A stacking-based ensemble approach combines multiple models, resulting in a significant improvement in overall performance and achieving Top-5 accuracy on the DermNet dataset surpassing other comparable studies. Although the system demonstrated high accuracy, it did not achieve the desired processing efficiency.

Raju et al. [20] presented a new method for skin disease classification using a support vector machine-based black window optimization (SVM-BWO) technique. Images of five different skin disease types were used with lesions segmented using a fuzzy-set segmentation algorithm. From the segmented regions attributes related to hue gray-level relationship matrices were extracted for further processing. The classification was performed using the SVM-BWO algorithm which demonstrated superior performance in terms of classification accuracy, specificity, sensitivity, precision, and recall. However, this technique failed to achieve a multi-class disease classification.

Back, S., et al. [21] presented a robust deep neural network (DNN) capable of distinguishing herpes zoster (HZ) and identifying additional skin conditions from user-submitted images. They used a knowledge distillation from an ensemble via curriculum training (KDE-CT), in which the student networks gradually learned from a more powerful teacher model, to increase resilience while keeping computing costs low. The group tested resilience against 75 types of corruption and created a skin illness database particularly for HZ detection. Thirteen distinct DNNs were assessed on both clean and damaged photos and the results showed that KDE-CT significantly improved the robustness to corruption compared to other methods. However, the approach did not achieve the desired scalability and effectiveness when applied to real-world datasets.

Gomathi et al. [22] discussed the categorization and estimation of skin lesions utilizing sophisticated deep learning methods. Following feature extraction and processing through the forecasting stage utilizing the MLSTM approach a novel hybrid metaheuristic technique termed SC-STBO was used to optimize the parameters. This approach was created to optimize the accuracy and decrease the RMSE, which are two important success requirements in the objective function. The same MLSTM model categorized skin tumors into seven different types if the expected result showed that a lesion was present. The experimental results demonstrated high accuracy although the framework did not attain optimal computational efficiency.

Tyagi, A., and Mehra, R., et al. [23] developed an Intelligent Prognostics Model for Disease Prediction and Classification (IPM-DPC) using a combination of Convolutional Neural Network (CNN) architecture and Particle Swarm Optimization (PSO). In this IPM-DPC model, PSO served two roles: initially it serves as an analyzer for CNN training after being used in conjunction with the K-means segmented approach to improve the accuracy of segmentation. PSO was used for feature selection, whereas the Speeded-Up Robust Features (SURF) method was used for classification. Ultimately improving the classification accuracy. The proposed method demonstrated optimal effectiveness terms of accuracy and detection time; however, it did not fully achieve scalability or efficiency.

3. Proposed Methodology

As shown in figure 1, the proposed methodology begins with dermoscopic image collection followed by the application of a morphological closing technique to remove artifacts. Next, an unsharp filter was applied to enhance the edge contrast during the preprocessing stage. The diseased areas in the pre-processed images are then segmented using the Fuzzy k-means clustering (FKM) approach, which is used to analyze the size and boundaries of the affected areas. The proposed method, Deep-MobileNet, which combines MobileNet with squeeze-and-excitation (SE) blocks, is employed to ascertain whether the image depicts normal or abnormal skin. To improve the classifiers performance a hyperparameter in the deep-MobileNet model is optimally chosen using the ADHO Algorithm.

3.1. Image Preprocessing

Pre-processing is a crucial step in the classification and segmentation process because it enhances the accuracy and improves the efficiency of the proposed technique. The collected images often contain noise and vary in size; thus, morphological closing is applied to remove artifacts and an unsharp filter is used to enhance the image by increasing edge contrast. The processes of morphological closing and the unsharp filtering are explained below.

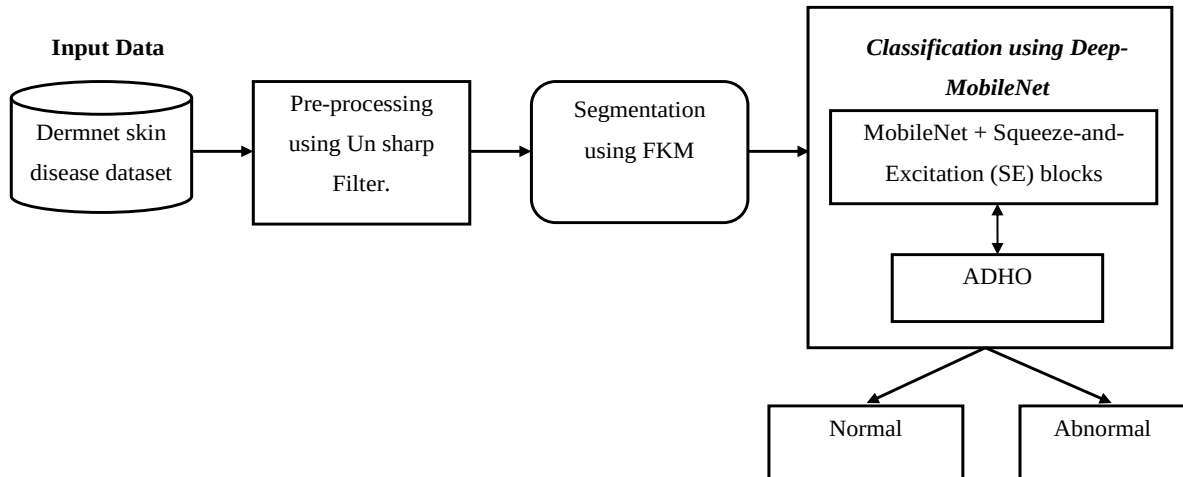


Fig. 1. Overall structure of proposed methodology.

3.1.1. Morphological closing

To remove unwanted small objects, we applied a morphological area-opening function with a 90-pixel parameter value and a circularity condition. Spherical objects with an area larger than 90 pixels were excluded from analysis. These undesired elements are eliminated using scalp masks, resulting in a segmented hair mask. To smoothen and fill the segmented lines, it was necessary to apply inpainting. For this morphological operator such as dilation and filling were used on the mask image using a structuring element that specified 8-pixel connectivity in all directions to guide the transformation. To fill in any empty spaces between the identified lines picture compression was applied to the digital masks once the structural component was defined. This was followed by application of a geometric area-filling algorithm to the enlarged masks. However, before applying the area-filling operator the picture's gaps were filled to specify every line's shape that needed to be completed, and let $M(x, y)$ represents a stretched basic masking picture. Therefore, let's say you select the gap filler picture P which has been set to 0 anywhere but the picture line's boundary is $(1 - M(x, y))$:

$$P(x, y) = \begin{cases} 1 - M(x, y) & \text{if } (x, y) \text{ is on the border of } M \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

Then,

$$Hole_mask = [R_{M^c}(P)]^C \quad (2)$$

In a hair-mask picture digitally populated. This indicates that the $M(x, y)$ picture has been reconstructed using $P(x, y)$. It yields the coordinates for x and y , in addition to the $Hole_mask(x, y)$ picture. During the straight- tip filling procedure, the sections of the line were retrieved. Next, the detected lines are inpainted using a fast marching scheme.

3.1.2. Unsharp Filter

The classical unsharp masking technique employs a nonlinear filter and works by adding a fraction of the high-pass-filtered version of the input image to the original image as depicted in Figure 2. This method is sensitive to noise because the linear high-pass filter cannot effectively distinguish between signal and noise. Additionally, it tends to enhance darker areas of the image more noticeably than lighter areas, leading to uneven visual enhancement. To address these issues various strategies have been developed to improve the unsharp masking performance. Figure 2 illustrates the working process of the unsharp filter.

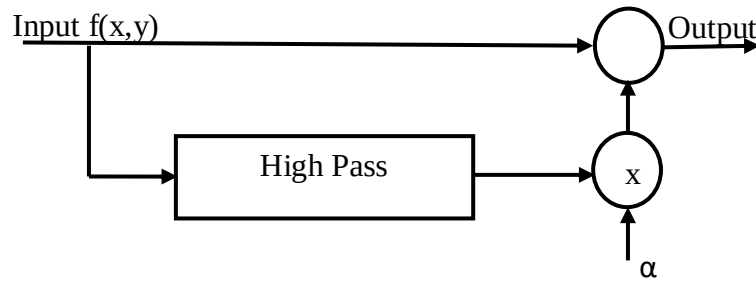


Fig. 2. Working process of unsharp filter.

3.2. Segmentation using FKM

The information points are divided into k groups $S_l (l=1,2,\dots,k)$ using a fuzzy k-means clustering technique and each cluster S_l is linked to a representation (cluster center). C_l A single statistic and the group's representation have ambiguous connections. In other words, the level of identity of the information point X_i and clusters center C_j is represented by its membership. $u_{ij} \in [0,1]$ The collection of data points should be represented as $S = \{X_i\}$, the subsequent deformation is the foundation of the FKM technique:

$$J = \sum_{j=1}^k \sum_{i=1}^N u_{i,j}^m d_{ij} \quad (3)$$

This is done concerning the cluster denoted as C_j and the memberships $u_{i,j}$ whereas N represents the number of data points m is the fuzzifier parameter k is the number of clusters and d_{ij} denotes the squared Euclidean distance between the data point X_i and the cluster representative C_j . the important to note that the memberships $u_{i,j}$ must fulfill the subsequent restriction:

$$\sum_{j=1}^k u_{i,j} = 1, \text{ for } i = 1 \text{ to } N \quad (4)$$

The primary process of the fuzzy k-means (FKM) algorithm involves the conversion of a specified collection of typical matrices into a single enhanced version via information point splitting. The process starts using a starting group setup center and iteratively refines this mapping until a stopping criterion is satisfied. It is assumed that no representation is shared by both clusters. If two cluster centers become identical during the iterations, one of the cluster centers must be adjusted to prevent overlap. Specifically, if $d_{ij} < \eta$ and $u_{i,l} = 0$ for $l \neq j$ where η is an extremely positive figure. The following is an outline of the fuzzy k-means clustering method.

- (1) Begin by inputting a set of initial cluster centers $SC_0 = \{C_j(0)\}$ and $\mathcal{E}$. set $p = 1$
- (2) Using the current set of cluster centers SC_p calculates d_{ij} for $i = 1 \text{ to } N$ and $j = 1 \text{ to } k$. Update memberships u_{ij} utilizing the following:

$$u_{i,j} = \left((d_{ij})^{1/m-1} \sum_{l=1}^k \left(\frac{1}{d_{il}} \right)^{1/m-1} \right)^{-1} \quad (5)$$

If $d_{ij} < \eta$ set $u_{i,j} = 1$, where η is a very small positive number.

- (3) To create a new set of group members, Eq. (6) to determine the focal point for every cluster SC_{p+1} .

$$C_j(p) = \frac{\sum_{i=1}^N u_{ij}^m X_i}{\sum_{i=1}^N u_{ij}^m} \quad (6)$$

(4) If $\|C_j(p) - C_j(p-1)\| < \varepsilon$ for $j = 1$ to k . stop where $\varepsilon > 0$ is a very small positive number. Otherwise set $p + 1 \rightarrow p$ and go proceed to step 2.

Stages two and three of the fuzzy k-means (FKM) methods are the main sources of the computational difficulty. Nonetheless, compared with step 2, the computing overhead of step 3 is substantially lower. Consequently, the FKM's total computational difficulty is measured by the number of length computations, $O(Nkt)$, where t represents the number of iterations.

3.3. Skin diseases image classified using Deep-MobileNet

In this section, the output images from the segmentation process are input into the classification process of Deep-MobileNet, which is a model that combines MobileNet with SE blocks to classify skin disease images and determine whether they are affected by skin diseases. A detailed explanation of the deep-MobileNet model is provided below.

The SE-MobileNet architecture integrates Squeeze-and-Excitation (SE) blocks inside the MobileNet structure to enhance feature representation, starting with an input layer that accepts images that are typically sized $224 \times 224 \times 3$. The initial layer is a standard convolutional layer with a 3×3 kernel and stride of 2, which reduces the spatial dimensions while extracting basic features. This is then a depth wise separable convolution (DWSC) layer where a 3×3 convolution is applied to each input channel independently, maintaining the number of channels and reducing computational complexity. Several convolutional and depth wise separable layers extract increasingly complex features. An SE block is then introduced by adding a squeeze operation that aggregates channel-wise statistics through global average pooling and the excitation process comes next that dynamically recalibrates function mappings based on these statistics. The architecture includes additional convolutional layers for high-dimensional feature extraction, where a global average pooling layer condenses a feature map into a single vector per channel. A ReLU function for activation is used following this pooling step that introduce non-linearity which makes it easier for the framework to gain complex illustrations. The final output is passed through a layer that is completely linked and has a Softmax activation mechanism classifying an input into the appropriate categories based on the learned features. This sequential flow enables SE-MobileNet to effectively identify and classify plant diseases by leveraging depth wise separable convolutions and adaptive recalibration of features through SE blocks.

MobileNets is a family of models optimized for mobile and resource-limited devices, incorporating depth-wise separable convolutions (DWSC) to increase computational efficiency. This approach decomposes standard splitting into two stages: depth wise convolution (DWC) and pointwise convolution (PWC). In the first stage, depthwise convolution operates separately on each input channel using individual filters ensuring that the spatial dimensions remain the same. Here if D_f denotes the input's spatial dimensions (length and width) and M represents the number of input channels (and filters) each filter acts on one channel independently producing an intermediate feature map with a similar spatial size as the input. In the second stage pointwise convolution uses a 1×1 kernel to merge the outcomes off the depth wise step. This step mixes information across channels where M is remains the number of input channels, D_f is the spatial dimension and N represents the number of output channels. Together these steps drastically reduce computational demands compared to traditional convolutions making MobileNets ideal for efficient image processing on portable devices. This is shown in equation 7 and 8.

$$DWC(K, F)_{i,j} = \sum_{h,w,d}^{H,W,D} K_{h,w,d} \times F_{h+i,w+j,d}^l \quad (7)$$

$$PWC(K, F)_{i,j} = \sum_d^D K_d \times \sum_h^H \sum_w^W K_{h,w} \times F_{h+i,w+j}^l \quad (8)$$

Then the intermediate feature map tensor is represented by F with the convolutional kernel (filter) noted as K and the 1×1 convolution kernel denoted as K_d . The positions in the feature map are indexed by (i, j) and the input data dimension length and elevation at level l are H , W and D respectively. Assuming an input feature map size of $D_f \times D_f$ with M channels and a kernel size of $D_k \times D_k$ N is the number of outgoing lines. The processing expenses of the typical convolution (C_1) and DWSC (C_2) differ significantly as expressed by Equations (9) and (10). DWSC's layered structure

of DWSC —depth wise followed by pointwise convolution—drastically reduces computation making MobileNets ideal for efficient processing on mobile and embedded devices

$$C_1 = D_k^2 NMD_f^2 \quad (9)$$

$$C_2 = (D_k^2 + N)D_f^2 M \quad (10)$$

Consequently, the proportion that constitutes the computing expense of DWSC compared with typical convolution can be expressed as follows:

$$R_{C2/C1} = \frac{1}{D_k^2} + \frac{1}{N} \quad (11)$$

In practical applications DWSC networks commonly use a 3×3 convolution kernel, particularly when the number of channels for output is greater. Consequently, the computational cost of DWSC is approximate one-ninth that of a standard convolutional network.

To enhance a network's representational quality by explicitly modelling the interdependencies among convolutional feature channels the SE squeeze-excitation (SE) network introduces a core component called the SE block which plays a key role in achieving exceptional performance in dataset competition. Both of the primary functions within the SE block are excitation and squeezing. The squeeze operation condenses feature maps $U \in R^{w \times h \times c^2}$ across spatial dimensions ($w \times h$) by pooling global averages to generate channel-wise statistics denoted as F_{sq} . Whereas x represents the input image $U \in R^{w \times h \times c^2}$ indicates the feature maps generated by a transformation such as standard convolution F_{sq} is the squeeze function and F_{ex} represents the excitation function. A scaling operation F_{scale} , then weights the characteristics of each channel appropriately. Every feature map is ultimately summarized by a statistic z_c calculated as shown in Equation 12.

$$z_c = F_{sq}(u_c) = \frac{1}{H \times W} \sum_{i=1}^H \sum_{j=1}^W u_c(i, j) \quad (12)$$

Here, z_c represents the statistical value for the c th channel while u_c relates to the area on the maps of cc th from the preceding convolution operation. W and H correspond to the width and height of u_c respectively. The excitation operation aims to fully capture channel dependencies by leveraging the information gathered during the squeeze process. This was achieved through a straightforward gating mechanism that used a sigmoid activation function.

$$s = F_{ex}(z_c W) = \sigma(g(z_c W)) = \sigma(W_2 \delta(W_1 z_c)) \quad (13)$$

Here δ represents the rectified linear unit (ReLU) activation function. The parameters are $W_1 \in R^{r \times C}$, $W_2 \in R^{C/r \times C}$ and $W_2 \in R^{C \times r}$; where r is a reduced ratio initialized to a steady value. These parameters, W_1 and W_2 are acquired by means of two completely interconnected layers positioned around the non-linear activation function. Consequently, the output of the squeeze-and-excitation (SE) block is generated by rescaling u_c using the activation values s .

$$\tilde{x}_c = F_{scale}(u_c, s_c) = s_c \cdot u_c \quad (14)$$

Where $[\tilde{x}_1, \tilde{x}_2, \dots, \tilde{x}_c]$ denotes the final output as $\tilde{X}$.

The process of transfer learning described twice in the SE-MobileNet model training involves two distinct phases aimed at optimizing the model's performance for a specific task such as classifying plant diseases. This approach leverages pre-trained weights from a large dataset to improve the efficacy and effectiveness of the instruction model on a smaller target dataset.

Step 1: To adapt the network to new identification tasks we fixed using already trained layer' values as well as trained only the auxiliary layers with images from the target dataset. During this process, efficiently modified the weights using an approach called stochastic optimization in the open layers.

$$w_k = w_{k-1} - \eta * \hat{b}_k / (\sqrt{\hat{s}_k} + \varepsilon) \quad (15)$$

Where η represent as learning rate was weight matrix k as the index of classes $\hat{b}_k$ and $\hat{s}_k$ denotes as this gradient's bias-corrected both initial and second instant estimates accordingly.

Step 2: In the second step the model was fine-tuned by retraining the target dataset. Starting with the weights obtained each layer received instructions using new pictures in the initial stage. For this process the coefficients were updated using stochastic gradient descent optimization, as specified in Equation (16).

$$w_k = w_{k-1} - \eta * (\partial L(w) / \partial w) \quad (16)$$

Therefore $L(*)$ represent the loss function.

To address the early symptoms of skin diseases in images and meet the requirements of multi-class classification, an enhanced version of the traditional Focal Loss function, formulated in Equation (18), defines the system.

$$L_{mult} = - \sum_{c=1}^C \alpha_t (1 - p_c)^{\gamma} y_c \log(p_c) \quad (17)$$

$$y_c = \begin{cases} 1c = \text{actual_class} \\ 0c \neq \text{actual_class} \end{cases} \quad (18)$$

p_c denotes the number of groups represented by C in the expected probability distributions and a_c indicates the weighted variable. Following this, Image 3 displays the framework of MobileNet-SE blocks.

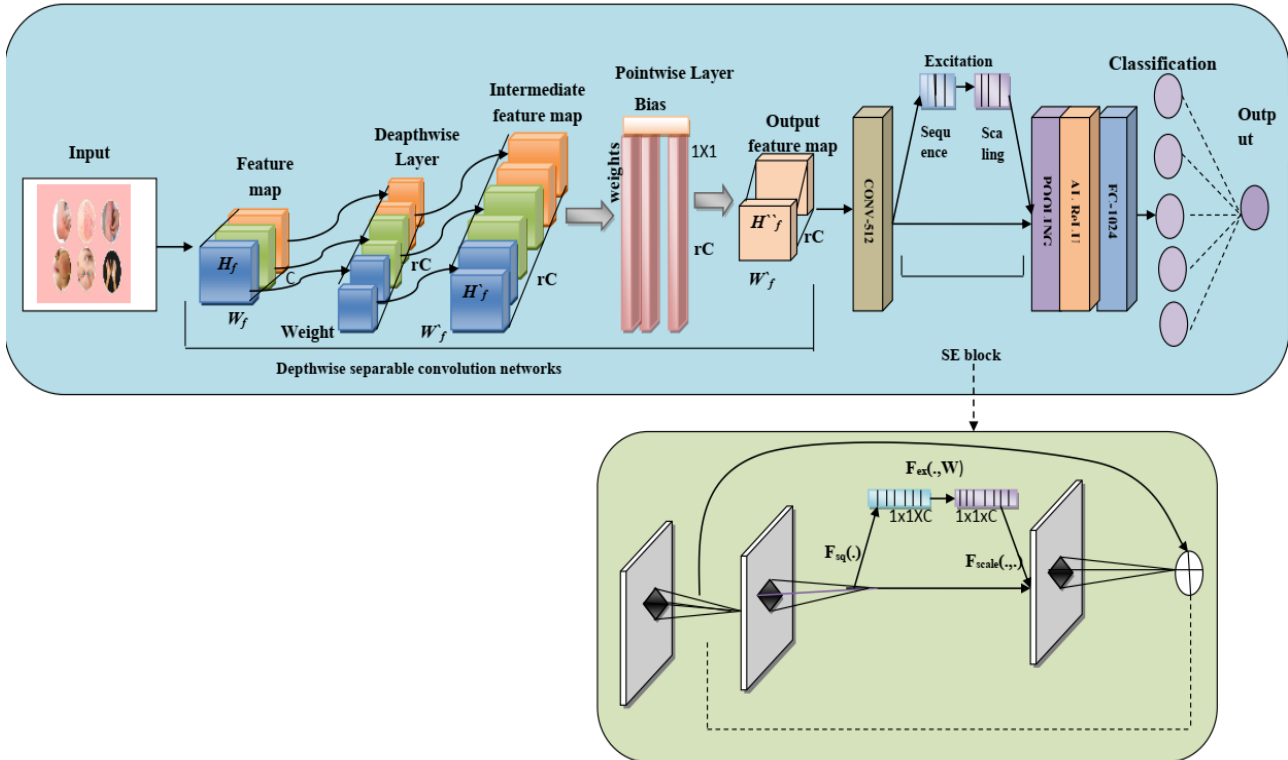


Fig. 3. The network architecture of MobileNet-SE models.

3.3.1. Optimization of Hyperparameters using ADHO

The MobileNet model combined with squeeze-excitation (SE) blocks forms a deep architecture known as Deep-MobileNets. In this configuration the hyperparameters of Deep-Mobile Nets are optimally selected using the ADHO algorithm enhancing the performance of the model through efficient optimization. The Adaptive Deer Hunting Optimization Algorithm (ADHOA) is a bio-inspired optimization technique based on deer hunting behavior where deer

represent potential solutions within a search space. The algorithm divides the search process into phases reflecting the deer's sense of awareness of environmental exploration and target identification. The deer adjust their positions dynamically either exploring new areas or intensifying their search in promising regions balancing research and investigation to prevent untimely confluence and improving solution accuracy. This adaptive component enables the algorithm to adjust the parameters in response to the fitness landscape making it robust against local optima. ADHOA has been successfully applied in engineering optimization machine learning model tuning and resource allocation often outperforming other bio-inspired method showing to its adaptability, simplicity and efficient handling of complex search spaces. To overcome this problem levy flight mechanism is added to the DHOA. The actions taken during the optimization are presented below:

Step 1: Initialization

Initialization is a crucial step in any optimization technique. In this study the hyperparameters in the Deep MobileNet model were optimally selected. This process involves initializing the ADHO Algorithm with hyperparameters such as epoch count (e), batch size (b), dropout rate (d), and regularization (r). These parameters were randomly initialized and the initial population format was represented by the following equation (19)

$$Z_i = \{z_1, z_2, \dots, z_N\} \quad (19)$$

Here Z_N denotes the position of the N^{th} solution, which it is written as eq (20)

$$Z_N = \{e, b, d, r\} \quad (20)$$

Step 2: Fitness calculation

Following the start-up procedure, fitness solutions were computed, and classification accuracy was used as the fitness criterion. The fitness formula shown in equation (21).

$$fitness = \max imum(accuracy) \quad (21)$$

Step 3: Update the Solution

In the DHO algorithm, candidate solutions are iteratively updated according to their primary purpose values. At every stage, the most effective and worst candidates are modified ultimately leading to the identification of the most optimal solution across the entire process.

Position propagation: typically fails to generate an optimal algorithmic solution within the initial repetition. Nevertheless, the best integer is chosen as the ideal solution value following the generation of random numbers and evaluation of the expense of the function. In this process two parameters are considered: the leader position (z_l), which represents the hunter's first optimal position and the spot for his successor (z_s) which indicates the position of the succeeding hunter.

Phase 1: Propagation based on the leader's position

In the initial iteration the entire population strives to reach the ideal place by continuously upgrading their locations. This "encircling behavior" is symmetrically represented using the following formula:

$$Z_{j+1} = Z_L - k \times S^\omega \times |L \times Z_L - Z_j| \quad (22)$$

In this equation (23), Z_j and Z_{j+1} denotes both the current and future sites respectively, and S^ω represent their scope's wind speed which determines the chance number [0,2] and the coefficients of the matrices are denoted by L and k then the equation is given below:

$$k = 0.25 \times \log \left(I + \frac{1}{I_{\max}} \right) \gamma \quad (23)$$

$$L = 2 \times \delta \quad (24)$$

Where $I_{\max}$ indicates this repetition's peak that falls inside the spectrum [-1,1], γ , is the random component. δ is a chance number between 0 and 1.. Z^* denotes the revision status whereas (Z , Y) indicates the target's main location, place which is subject to change based on the situation of the prey.

The state of the reports may continue in progress towards achieving an optimal state (Z^* , Y^*) according to the parameters L and K. The hunters move toward the leader's position; however, if the leader's movement is unsuccessful the hunter remains in its previous position.

Position updates occur according to equation (25) during $S^\omega < 1$. In this case, hunters can move freely in any direction independent of the position angle. Thus, based on equations (20) and (24) hunters can adjust their locations to random positions in each update.

Phase 2: Propagation based on the position angle

Additionally, the solution space can be expanded by considering the location angle, into account as the angle assessment plays a crucial role in determining the hunter's position. For a successful attack the prey should not detect approach of the hunter. The formula representing the angle of the prey (deer) is as follows:

$$u_j = \frac{1}{8} \times \pi \times \alpha \quad (25)$$

Parameter u is used to update the position angle accounting for the difference between the direction of the breeze and the direction in which the victim's body is observed.

$$C_j = \beta_j - u_j \quad (26)$$

Where β denotes the breeze speed after which the location angles variable is updated.

$$\varphi_{j+1} = \varphi_j + C_j \quad (27)$$

Once the location angle is determined a newer position may be computed using the following equation.

$$Z_{j+1} = Z_j - S^\omega \times |\cos(\varphi_{j+1}) \times Z_l - Z_i| \quad (28)$$

Because of the restricted sight position the target cannot observe the predator.

Propagation is based on the position of the successor. To facilitate exploration, the L parameter can be adjusted in the encircling behavior. Owing to the random initial search the integer vector LLL cannot exceed one. Therefore, the successor's location was used to provide an updated solution. The exploration updating formula is as follows:

$$Z_{j+1} = Z_s - k \times S^\omega \times |L \times Z_L - Z_j| \quad (29)$$

In this algorithm Z_s represents the current position of the attackers at every moment. The most effective answer in every hunt is used to keep track of the searchers' whereabouts. The most effective approach was found. During $|L| \geq 1$. If $|L| < 1$, Each searcher is chosen at random. By Using this technique, an L Shift is created enabling the method to toggle among the exploration and extraction stages. A limitation of the original DHO algorithm is that it can get stuck in the local optima. To address this issue a novel change has been suggested.

In this approach, the Levy Flight (LF) is employed to enhance the DHO algorithm. Levy Flight is a technique designed to address the problem of component convergence defects. It generates a random walk system that aids in correctly controlling nearby searches. The equation for Levy Flight is follows:

$$Le(D) \approx D^{-1-\mu} \quad (30)$$

$$D = \frac{R}{|T|^{1/\mu}} \quad (31)$$

$$\sigma^2 = \left\{ \frac{\Gamma(1+\mu)}{\mu \Gamma((1+\mu)/2)} \frac{\sin(\pi\mu/2)}{2^{(1+\mu)/2}} \right\}^{2/\mu} \quad (32)$$

Where $0 < \delta \leq 2$, $R \sim N(0, \sigma^2)$ and $T \sim N(0, \sigma^2)$, $\Gamma(\cdot)$ Pre-selected the gamma D indicates the measure's size while its index of levy is represented as μ and $R/T \sim N(0, \sigma^2)$ explains how examples with an average value of zero and a deviation value of zero are generated using a distribution with a Gaussian shape σ^2 in turn. This $\mu = 3/2$.

The Levy Flight system states that the hunter's newly improved position is represented by the following formula:

$$Z_{j+1}^l = Z_{j+1} + (Z^* - RG) \times Le(\rho) \quad (33)$$

Where Z_{j+1}^l represent that the user's search's latest spot Z_{j+1} and

$$\begin{aligned} R &= u(2 \times r - 1) \\ G &= EZ'(t) - Z(t) \end{aligned} \quad (34)$$

In this equation u is constrained within the range [0,2] and r is a random integer selected from 0 to 1. $Z'(t)$ represents a randomly chosen vectors for the placement of the present populations. Potential solutions were retained to ensure the best possible additional treatments.

$$\bar{G}_{el} = \begin{cases} Z_{j+1}^l F(Z_{j+1}^l) > F(Z_{j+1}) \\ Z_{j+1} if not \end{cases} \quad (35)$$

Step 4: Termination

The DHO algorithm is enhanced by the ADHO algorithm, which is a repetition-based morphological closing technique that progresses through the position propagation stages until the final iteration. This results in an optimal deer hunting status to achieve the ideal goal variable outcome

Implementation steps are shown in pseudo-code in Algorithm 1

Algorithm 1. Pseudocode for ADHO

Input: hyper-parameters of Deep MobileNet
Output: Optimized hyper-parameters of Deep MobileNet
 Begin
 While ($k < k_{max}$)
 Compute the fitness $fitness = \max imum(accuracy)$
 Update x, d, X, n, C, Vnd f
 If ($n < 1$)
 If ($v \geq 1$)
 Update the position using equation (25)
 else
 Update the position using equation (30)
 end if
 else
 Update the position of individual using equation (29)
 end if
 end for
 Fitness calculation of each solution
 Update P^{lead} and $S^{successor}$
 k=k+1
end while
The levy flight optimization mechanism is used
To get Adaptive DHO
The standard equation is used $stepsize = f \times s$
The speed can be calculated by using this step size.
Output: the best solution obtained by ADHO
End ADHO

3.4. Dataset and Data Splits

This study uses a publicly available dermoscopic image dataset from the DermNet repository, comprising approximately 19,500 RGB images across 23 skin disease categories and provides a detailed dataset preparation and

splitting protocol to ensure reproducibility and fair comparison with prior work. All images were resized to 256×256 pixels and normalized to the $[0, 1]$ range, after which a stratified splitting strategy with a fixed random seed was applied to preserve class distributions, allocating 80% of the data for training, 10% for validation, and 10% for testing. To mitigate class imbalance and enhance model generalization, data augmentation, random rotations, horizontal and vertical flips, zooming, and brightness variations was applied exclusively to the training set, while the validation and test sets were left unaugmented to ensure unbiased performance evaluation; the overall dataset characteristics, split ratios and augmentation strategies are summarized in Table 1.

Table 1. Dataset description and data splitting strategy.

Parameter	Description
Number of classes	23
Image resolution	256x256x3
Split method	Stratified random split
Data augmentation	Rotation, flipping, zoom, brightness

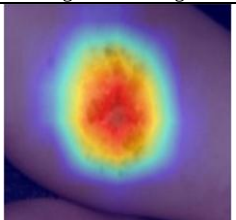
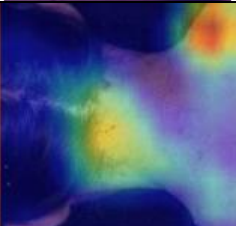
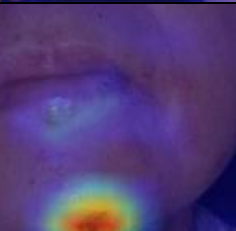
4. Result and Discussions

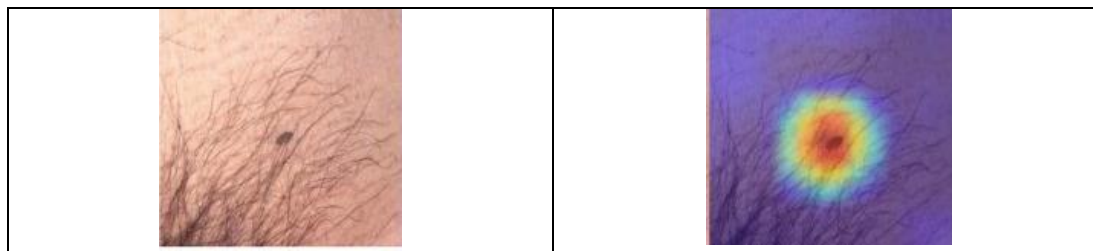
The efficiency of the proposed reliable method for diagnosing skin diseases was evaluated on a Python platform using a system equipped with an Intel Core i5 processor, 6GB memory, and Windows 10. Dermoscopic images were collected from the dataset and classified using Deep-MobileNet, which effectively classifies various skin conditions. Multiple evaluation metrics were applied to ensure the accurate detection of skin diseases, thereby enhancing the reliability and performance of the classification approach.

4.1. Data description

For the experimental analysis in this study, the dataset comprises images of 23 different skin diseases sourced from <http://www.dermnet.com/dermatology-pictures-skin-disease-pictures>. The dataset includes approximately 19,500 images with around 15,500 used for training and the remainder reserved for testing. The images were in the JPEG format each containing three RGB color channels. Although the resolution varies across images and categories it is generally moderate rather than extremely high. The dataset covers a diverse range of skin conditions including capillary malignancies, poison ivy, ringworm, seborrheic keratoses, melanoma, breakouts, and various bullous disorders.

Table 2. Segmented images of proposed approach.

Input Image	Segmented Image
	
	
	



4.2. Experimental results based on proposed robust skin diseases

In this section we present a comparative analysis of robust skin disease classification based on accuracy, sensitivity, specificity, and F1-score. A detailed description of each evaluation metric is provided as follows.

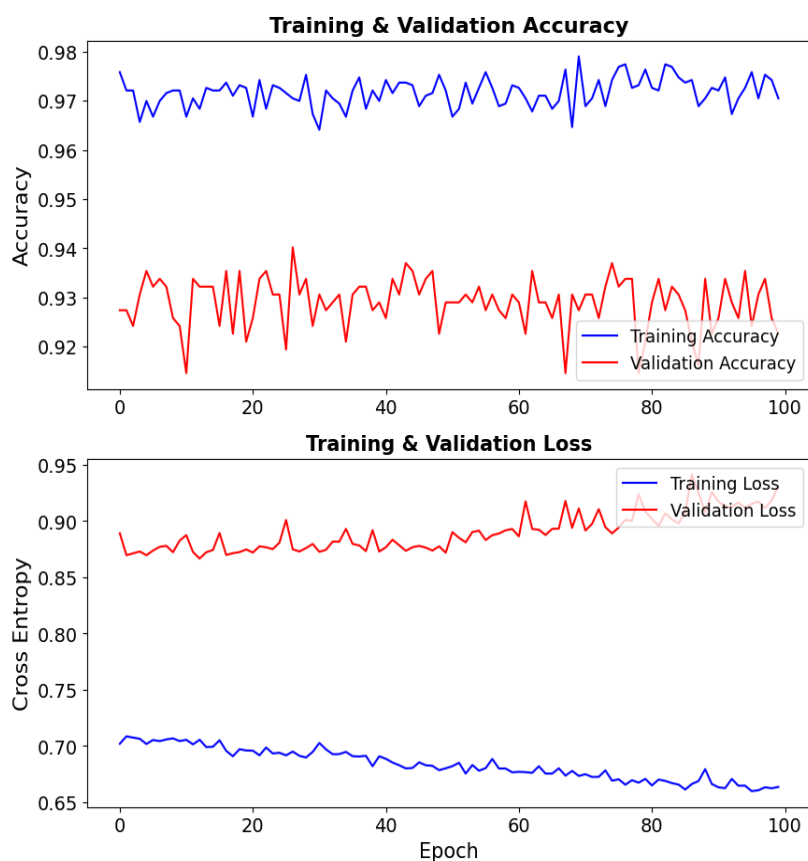


Fig. 4. Validation performance based on accuracy and loss.

Figure 4 displays the instruction and verification performance of the classification model over 100 epochs measured by accuracy and loss. In the top graph representing Training & Validation Accuracy the training accuracy (blue line) steadily improves, stabilizing at approximately 0.97, which suggests effective learning on the training data. However, the validation accuracy (red line) shows some fluctuation hovering between 0.92 and 0.94. This discrepancy indicates potential overfitting as the validation accuracy did not increase in line with the training accuracy. In the bottom graph depicting the Training & Validation Loss When the weight deficit (blue line) gradually drops, it indicates a reduced error on the training data. Conversely confirmation loss (red line) remains relatively high and fluctuates further suggesting overfitting as the model's generalization to validation data fails to improve as expected.

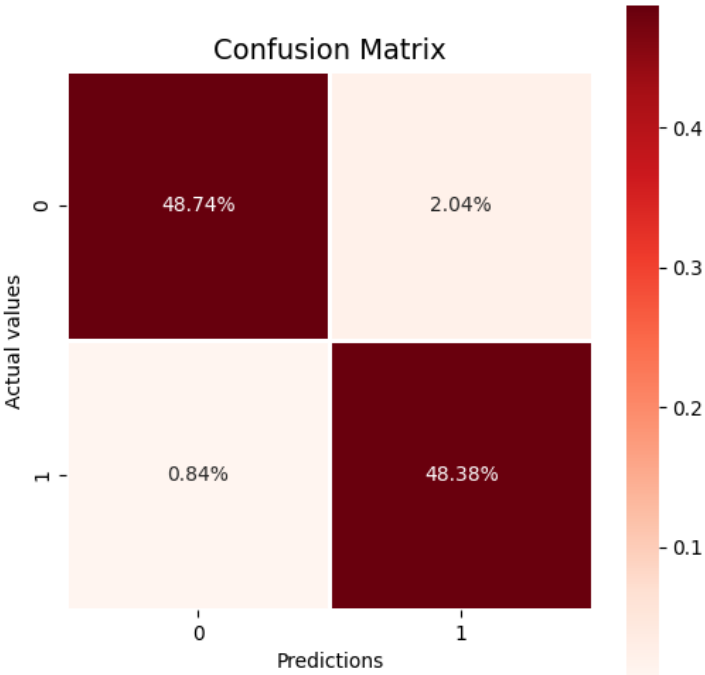


Fig. 5. Confusion matrix of proposed approach.

Figure 5 presents the confusion matrix of the proposed system illustrating the performance of a binary classifier with predictions on the horizontal axis and actual outcomes on the y-axis where the two classes are labeled 0 and 1. Displayed as percentages the matrix provides a clear overview of the classifier’s effectiveness. High percentages of true positive (48.38%) and true negative (48.74%) cells indicate strong classification accuracy while the low percentages in the false positive (2.04%) and false negative (0.84%) cells demonstrated that the design's pace decrease misclassification.

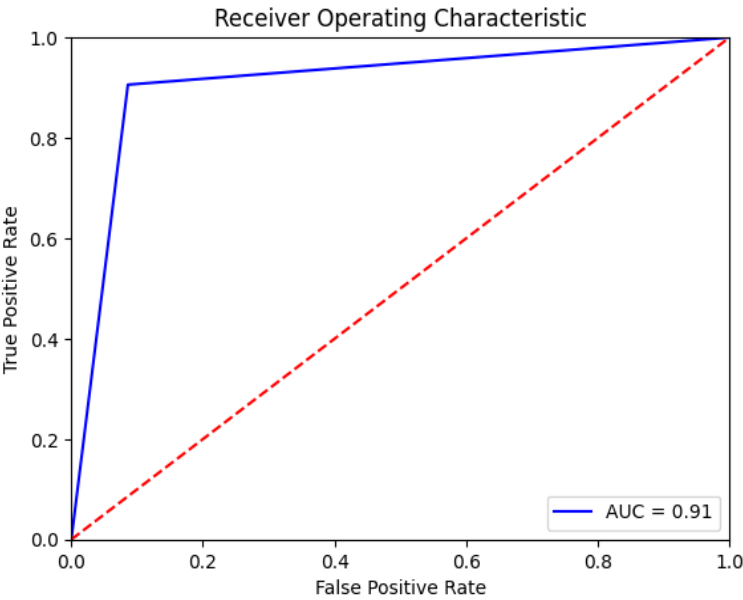


Fig. 6. ROC curve.

Figure 6 illustrates a Receiver Operating Characteristic (ROC) curve as a visual aid for assessing an example in binary categorization by depicting the balance between the true positive rate (TPR) and the false positive rate (FPR) at different threshold settings. On this plot the x-axis denotes the false positive rate (FPR) representing the percentage of adverse instances that were mis predicted as favourable with the genuine positivity frequency on the y-axis (TPR), or sensitivity reflecting the model's effectiveness in identifying positive cases. The classifier’s performance is shown by the blue curve where proximity to the top-left corner signals a better distinction between the classes. The area under this curve (AUC) was 0.91, signifying a strong discriminatory power with an AUC of 1.0 indicating perfect classification.

The red dashed line represents a random classifier's performance ($AUC = 0.5$) as a baseline and the blue curve's clear elevation above this line confirms that the model far exceeds random guessing in terms of classification accuracy.

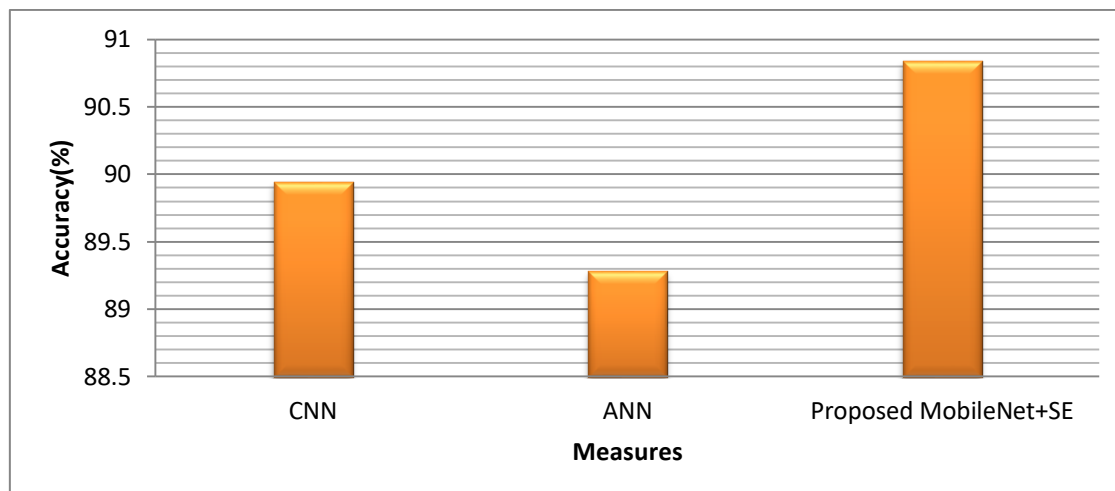


Fig. 7. Performance analysis based on Accuracy.

Figure 7 presents the accuracy analysis of the proposed approach for robust skin disease diagnosis which achieved an impressive accuracy of 91.96%, significantly surpassing several existing methods. Compared to CNN-based classification the proposed technique shows a 2.6% improvement and it outperforms the ANN by 2%. These results underscore that the algorithm's superior effectiveness is in accurately finding skin diseases, making it more reliable tool for early skin diseases detection. The notable increase in accuracy suggests enhanced diagnostic precision over traditional detection techniques.

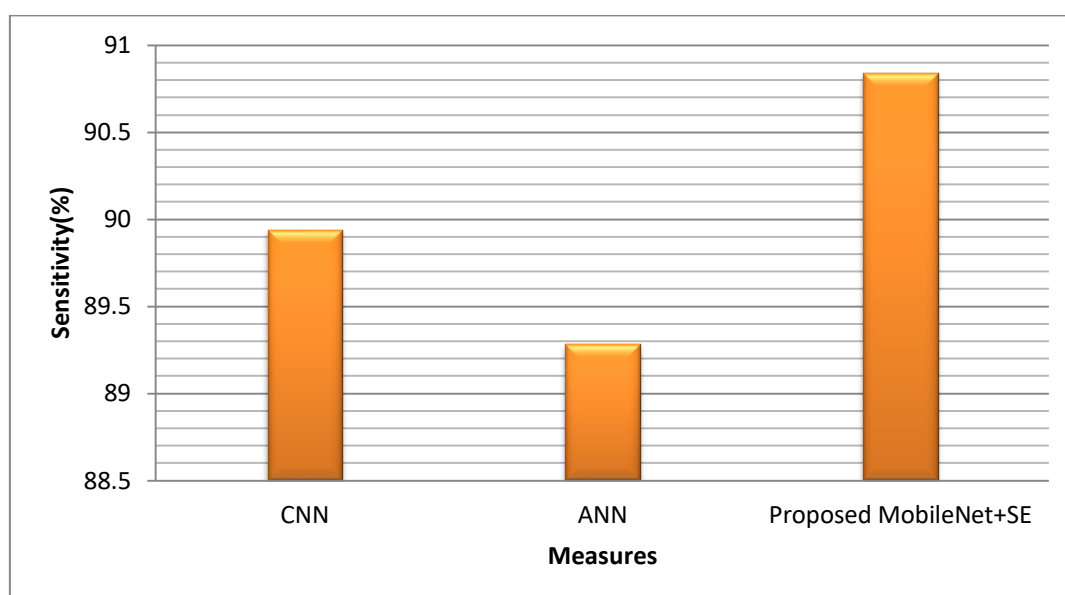


Fig. 8. Performance analysis based on Sensitivity.

Figure 8 shows a sensitivity examination of the suggested approach for detecting skin diseases, demonstrating a notable improvement with a sensitivity rate of 90.84%. This rate is considerably higher than those of other techniques such as 89.94% for the CNN and 89.28% for the ANN. This increased sensitivity highlights the effectiveness of the method in accurately identifying true positive cases. Compared with traditional models the proposed MobileNet+SE technique offers a more dependable solution for the early diagnosis of skin diseases. Enhanced sensitivity is crucial for reducing missed detections providing a substantial advantage over existing methods.

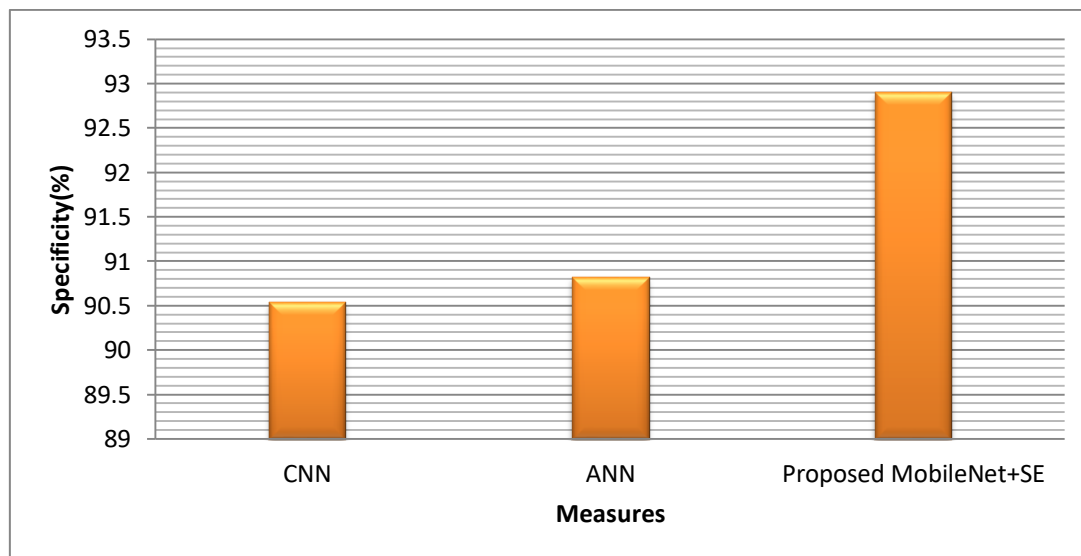


Fig. 9. Performance analysis based on Specificity.

The proposed method achieved a specificity of 90.54% surpassing those of other existing techniques. In comparison, the specificity for CNN-based classification was 90.82%, whereas the ANN achieved 92.90% specificity. This indicates that the proposed approach is more effective in accurately identifying negative cases thus reducing the number of false positives. As shown in Figure 9, the marked improvement in specificity highlights the precision of the method in distinguishing skin diseases, thus offering a more reliable diagnostic tool. This advancement provides a distinct advantage over traditional models making them a more powerful solution for early skin disease detection.

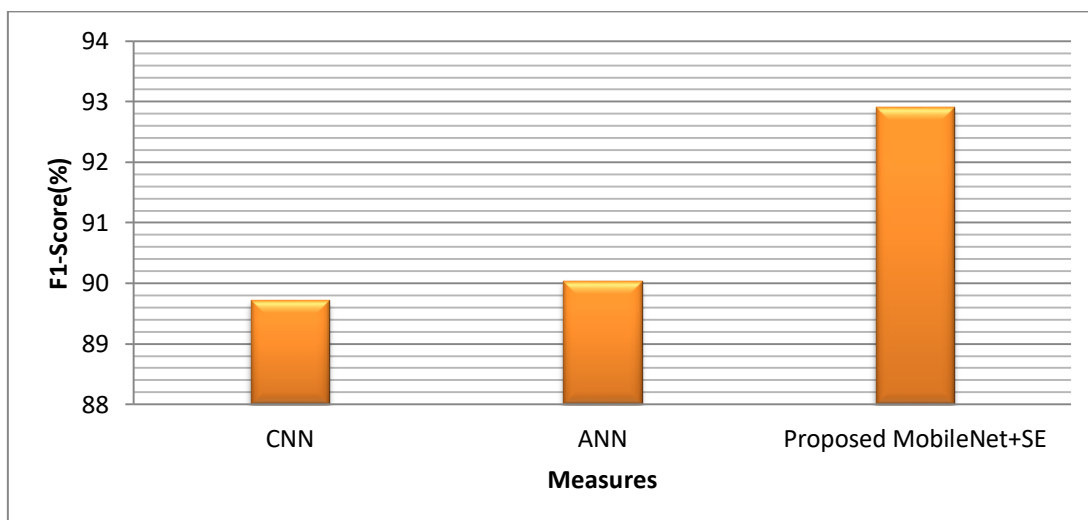


Fig. 10. Performance analysis based on F1-Score.

Figure 10 analyzes the effectiveness of each suggested strategy depending on the F1-score where it achieves an impressive 92.91% significantly outperforming existing algorithms. Among these methods the lowest F1-score was 89.72% and the highest reaches was only 90.04%. This result demonstrates that the proposed model outperforms the others in balancing precision and recall leading to both greater accuracy in positive predictions and fewer false negatives. The improved F1-score highlights the model's overall effectiveness in skin diseases detection making it a more dependable and precise tool for early skin disease identification. By outperforming traditional classification models across key metrics, the proposed approach sets a higher standard for diagnostic accuracy.

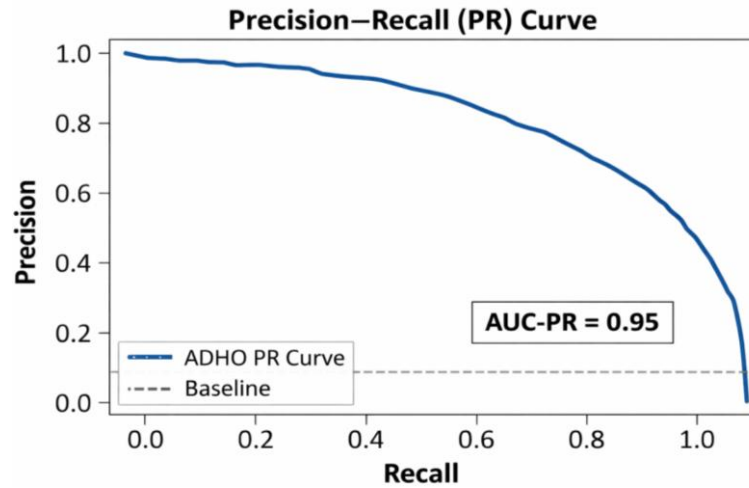


Fig. 11. Precision –Recall (PR) curve.

The Precision–Recall (PR) curve shown in figure 11 for the proposed model demonstrates strong performance in detecting the positive class across varying decision thresholds. As shown in the graph, the curve remains well above the baseline, indicating consistently high precision over a wide range of recall values. Based on the reported performance metrics accuracy of 91.96%, sensitivity of 90.84%, specificity of 92.90%, and F1-score of 92.91%, the model achieves a high AUC-PR value of 0.95, reflecting an excellent balance between precision and recall. This high AUC-PR confirms the robustness of the proposed approach under class imbalance and highlights its suitability for clinically relevant applications where minimizing false positives and false negatives is critical.

4.3. Comparison with Published Work

We compared our study to previously published studies to illustrate the efficacy with the suggested approach. Our approach was evaluated against studies [16], [17], [19], and [20] which primarily focused on skin disease detection techniques as discussed in the literature survey. The comparative outcomes displayed in the table 3 emphasize the classification performance of the proposed methods. Our method achieved the highest accuracy of 91.96%, surpassing the accuracies in [16], [17], [19], and [20], which were 86.4, 89.45, 91.73, and 91.09%, respectively. By integrating MobileNet with SE, our method consistently demonstrated superior classification accuracy establishing it as a reliable solution for accurate data classification.

Table 3. Comparative analysis results.

Reference	Technique	Accuracy %	Sensitivity %	Specificity %	F1-Score %
Reddy D. A., et al.[16]	GLCM	86.4%	89.5%	85.6%	85.405
Rasheed, A., et al.[17]	hybrid CNN- L2	89.45%	88.31%	Not measured	Not measured
Balasundaram, A., et al.[19]	DermNet	91.73%	Not measured	74%	90.1%
Raju, D., et al.[20]	SVM-BWO	91.09%	89.56%	Not measured	Not measured
Proposed	ADHO	91.96%	90.84%	92.90%	92.91%

Table 4 presents the performance of the proposed Deep-MobileNet with ADHO evaluated using 5-fold cross-validation. The model demonstrates consistent performance across all folds, with accuracy values ranging from 91.42% to 92.39%. The mean accuracy of 91.96% with a low standard deviation of 0.37 indicates strong model stability and robustness. Similar consistency is observed for sensitivity, specificity, and F1-score, all exhibiting low variability across folds.

Table 4. Performance of the proposed Deep-MobileNet with ADHO using 5-fold cross-validation.

Fold	Accuracy (%)	Sensitivity (%)	Specificity (%)	F1-score (%)
Fold-1	91.42	90.31	92.05	92.11
Fold-2	92.18	91.02	93.14	93.02
Fold-3	91.76	90.65	92.81	92.74
Fold-4	92.05	91.24	93.06	93.10
Fold-5	92.39	91.01	93.44	93.57
Mean $\pm$ SD	91.96 $\pm$ 0.37	90.85 $\pm$ 0.38	92.90 $\pm$ 0.50	92.91 $\pm$ 0.55

Table 5. Ablation study for the proposed method.

Methods	Accuracy	Sensitivity	Specificity	F1-Score
MobileNet	88.92	87.84	89.10	89.01
mobileNet+SE	90.74	89.62	91.08	91.02
MobileNet+SE+ADHO	91.96	90.84	92.90	92.91

Table 5 presents an ablation study conducted to analyze the individual contributions of each component in the proposed framework. Starting from the baseline MobileNet model, the inclusion of Squeeze-and-Excitation (SE) blocks improves the accuracy by 1.82%, demonstrating enhanced channel-wise feature representation. Further, integration of the Adaptive Deer Hunting Optimization (ADHO) algorithm for hyperparameter tuning results in an additional 1.22% performance gain. The progressive improvements across configurations confirm the complementary and synergistic effect of SE blocks and ADHO, validating the effectiveness of the proposed design.

5. Conclusion

This study provides a strong foundation for skin disease classification by integrating preprocessing, segmentation, and classification into a unified workflow. The process begins with illumination adjustment to correct lighting variations, followed by morphological closing to remove small artifacts such as hair and blood vessels, and image enhancement using an unsharp filter to improve edge contrast. Fuzzy k-means clustering is then applied to segment the affected skin regions, effectively handling variations in lesion size and boundary irregularities. The classification stage employs a novel Deep-MobileNet model enhanced with squeeze-and-excitation (SE) blocks, with hyperparameters optimally tuned using the Adaptive Deer Hunting Optimization (ADHO) algorithm. The proposed approach achieves a high classification accuracy of 91.96%, demonstrating its effectiveness as an automated solution for skin disease detection.

However, the current method performs binary classification (normal vs. abnormal) and does not explicitly model fine-grained disease severity or multi-class diagnostic differentiation. Future work will focus on extending the framework to multi-class and severity-level classification, enabling more detailed clinical decision support.

All the Declarations and Statements

Author Contributions Statement

Kanakamedala Vineela – Conceptualization, Methodology, and Supervision: Proposed research ideas, Constructed the overall framework, and supervised project execution.

Vipparla Aruna – Conceptualization, Methodology, and Supervision: Proposed research ideas, Constructed the overall framework, and supervised project execution.

Battula Sowjanya – Conceptualization, Methodology, and Supervision: Proposed research ideas, Constructed the overall framework, and supervised project execution.

Krishna Suresh B. V. N. V. – Data Curation and Software Implementation: Handled data acquisition, dataset preprocessing, and implementation of the research model.

All authors have read and agreed to the published version of the manuscript.

Conflict of Interest Statement

The authors declare no conflicts of interest.

Funding Declaration

The authors declare that they have no competing interests and funding.

Data Availability Statement

Data sharing is not applicable to this article because of proprietary nature.

Ethical Declarations

Not applicable.

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Declaration of Generative AI in Scholarly Writing

The authors declare that no Artificial Intelligence (AI) or generative AI tools were used in the preparation of this scholarly paper.

Abbreviations

The following abbreviations are used in this manuscript:

FKM - Fuzzy k-means clustering

SE - Squeeze-and-Excitation

ADHO - Adaptive Deer Hunting Optimization Algorithm

Appendix A/B/C..., with appendix title

Not applicable.

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