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Non-Hybrid Machine Learning Techniques for Classifying and Detecting Skin Disease Variants

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Abstract: *Eczema, acne, and psoriasis are all skin diseases that must be diagnosed early on to avoid complications. To detect and classify skin diseases, many researchers have developed a variety of support vector machine (SVM)-based classification models. However, these existing models suffer from imbalanced datasets, irrelevant feature selection, and difficulty in fine-tuning the SVM's hyperparameters. As a result, this study developed "Aquila Optimiser-Support Vector Machine (AO-SVM)" and "Harris Hawk Optimiser-Support Vector Machine (HHO-SVM)" to categorise eight (8) different skin diseases, "Granuloma Annulare (GRA)", "Haemangioma (HEM)", "Herpes (HEP)", "Hidradenitis Suppurativa (HSP)", "Keratocanthoma (KEC)", "Lupus (LUP)", "Sebaceous Hyperplasia (SEH)", and "Sun Damaged Skin (SDS)", using 2,700 photos of skin disease datasets, including 250 photos of each diseased dataset class and 700 photos of normal skin from the Kaggle village datasets. The images were pre-processed, including reducing the size of the images, "digital hair removal using the Black-Hat transformation and inpainting algorithm", and eliminating noise, then the affected area was segmented using the Sobel edge detection method. The Grey Level Spatial Dependence and Colour Moment were then used to extract texture, shape, and colour features, and performance metrics such as false positive rate, specificity, accuracy, precision, and sensitivity were used to compare the efficiency of the two classification models ("AO-SVM" and "HHO-SVM"). The results show that the "AO-SVM and HHO-SVM" classification models perform at 95.99% and 96.56%, respectively. This study adds to the body of knowledge by developing two refined Multiclass Support Vector Machine classification models, "AO-SVM and HHO-SVM", for a subset of skin diseases. These models optimise the SVM classifier parameters (penalty cost, C, and kernel function, γ) to reduce false positives and improve classification accuracy. In conclusion, these two models can be extremely useful in assisting people living in remote areas who have limited access to expert dermatologists in detecting their disease as soon as possible.*

Keywords: AO-SVM, Black-Hat Transformation, Granuloma Annulare, HHO-SVM, Support Vector Machine.

1. INTRODUCTION

Acne, alopecia, decubitus ulcers, pruritus, psoriasis, scabies, urticaria, and other skin and subcutaneous diseases are widespread health issues that contribute significantly to the global disease burden [26]. Skin ailments are caused by "viruses, bacteria, allergies, or fungal infections" and appear as changes in the colour or texture of the skin [5]. A variety of factors can contribute to skin diseases, including genetic predispositions, environmental exposure, infections, autoimmune disorders, and allergies [17]. Granuloma Annulare (GRA), Haemangioma (HEM), Herpes (HEP), Hidradenitis Suppurativa (HSP), Keratocanthoma (KEC), Lupus (LUP), Sebaceous Hyperplasia (SEH), and Sun Damaged Skin (SDS) are some of the types of skin lesions found worldwide based on their symptoms and severity. Many patients suffering from skin disease are unaware of the disease's variants, traits, and phases, making it difficult and expensive to seek treatment from the country's few dermatologists.

However, if skin disease is detected early on, a large number of patients can be successfully treated [2]. As a result, a computerised framework capable of identifying and categorising skin diseases in real time is required to save lives. Many scientists have used "machine learning techniques like support vector machines (SVM) and image processing tools" [33] to develop a machine learning approach for early detection and classification of skin diseases. Authors in [14], [2], [25], [3], [19], [11], [6], and [33] are some of the researchers who use SVM for skin disease detection and classification in their studies.

Moreover, some of these classification models were built on imbalanced datasets, which could have resulted in performance bias towards a specific illness [23]. Similarly, some of these studies address binary classification rather than multiclass classification problems. In addition, in some of these studies, the number of datasets for each class of skin disease and normal skin is not explicitly stated. Furthermore, some of these studies were unable to lessen the size of the extracted features, implying that the addition of extraneous features to the dataset may have increased false positive rates, classification model overfitting, and computational complexity. Moreover, it can be challenging to select an efficient feature selection technique and "choose the best features from a collection of extracted features" [28].

Support vector machine (SVM) is a machine learning technique used for classification tasks, but fine tuning the hyperparameters in the SVM is extremely difficult" [34]. However, some researchers have used optimisation algorithms like "particle swarm optimisation (PSO) and genetic algorithm (GA)" to fine-tune the SVM parameters. Author in [31], [20], and [24] are among the researchers who have used either PSO or GA to fine-tune SVM parameters in their studies. Furthermore, the "No Free Lunch (NLF) theorem" developed by [29] states "that no single algorithm can provide optimal solutions for all problems; thus, new metaheuristic methods are constantly proposed or developed by combining existing algorithms or creating adaptable versions" [29]. As a result, two optimised models (AO and HHO) were developed and used to extract relevant features from the extracted features while also adjusting the support vector machine's hyperparameters. Finally, two non-hybrid multiclass classification models (AO-SVM and HHO-SVM) were created to classify a number of specific skin diseases.

2. LITERATURE REVIEW

Authors in [27] create a classification model for six skin diseases, including "psoriasis, seborrhoeic dermatitis, lichen planus, pityriasis rosea, chronic dermatitis, and pityriasis rubra", which were tested on Dermatology datasets. The dataset was acquired from the "UCI Machine Repository". This dataset has 35 variables, of which 34 are linear and 1 is nominal. The dataset underwent data preprocessing procedures such as variable selection, cleaning, noise removal, and normalisation. Classification models were developed using five "data mining techniques (CART, SVM, DT, RF, and GBDT)", as well as an ensemble of all techniques. The "CART, SVM, DT, RF, and GBDT" models achieved performance accuracy of 94.17%, 96.93%, 93.82%, 97.27%, and 96.25%, respectively. The results also show that the CART, SVM, DT, RF, and GBDT models achieved sensitivity performances of 91.12%, 90.78%, 91.13%, 91.56%, and 92.38%, respectively. The ensemble models had a higher performance accuracy of 98.64%.

Authors in [18] developed "a convolutional neural network-based machine learning classification model for skin disease detection". The proposed system has been evaluated on dermatoscopic photos from the SkinCancer-MNIST dataset (HAM10000), which is publicly available. The dataset contains seven different kinds of skin ailments: "melanocytic nevi, melanoma, benign keratosis, basal cell carcinoma, actinic keratoses, vascular lesions, and dermatofibroma". The collected data was split into training and testing datasets utilising the appropriate ratio. Several data preprocessing procedures were performed, including data cleaning (filling in missing values), data smoothing (identifying and/or removing outliers, noise, and inconsistencies), and data transformation (converting actual values from one representation to the target representation). The collected dataset was used to develop and train a convolutional neural network. According to the results, the model achieved 93.35% performance accuracy at epoch-50 and 93.28% at epoch-20.

Authors in [11] created a skin disease classification model using fuzzy clustering and machine learning techniques. The dataset was collected from 50 hospitalised patients to classify skin disease into two categories: basal and squamous. The collected data were pre-processed using a median filter to remove noise from the images. Fuzzy clustering was used to separate lesions from uninfected part of the image. variables, of which 34 are linear and 1 is nominal. The dataset underwent data preprocessing procedures such as variable selection, cleaning, noise removal, and normalisation. Classification models were developed using five "data mining techniques (CART, SVM, DT, RF, and GBDT)", as well as an ensemble of all techniques. The "CART, SVM, DT, RF, and GBDT" models achieved performance accuracy of 94.17%, 96.93%, 93.82%, 97.27%, and 96.25%, respectively. The results also show that the CART, SVM, DT, RF, and GBDT models achieved sensitivity performances of 91.12%, 90.78%, 91.13%, 91.56%, and 92.38%, respectively. The ensemble models had a higher performance accuracy of 98.64%.

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patients to classify skin disease into two categories: basal and squamous. The collected data were pre-processed using a median filter to remove noise from the images. Fuzzy clustering was used to separate lesions from uninfected part of the image. RGB was used to extract colour features, and SYMLET wavelet analysis was used to extract texture features like mean, standard deviation, entropy, ellipticity, intensity, and coefficient of correlation. The acquired data was divided into 70% for training and 30% for testing. Classification models were created with the "K-Nearest Neighbour (KNN) and Support Vector Machine (SVM)" classifiers. The KNN model achieved 91.2% accuracy, exceeding the SVM's 85% accuracy.

Authors in [3] use "machine learning and image processing techniques" to create classification models for skin diseases. The authors gathered 377 images from four disease categories: "acne, cherry angioma, melanoma, and psoriasis from the Dermnet NZ and Atlas Dermatologico databases". The acquired images were pre-processed by first resizing to 250X250 and then applying the median filter to reduce noise. Furthermore, Otsu's thresholding was used to segment the image, texture features were extracted using Gabor and Entropy techniques, and edge features were extracted using the Sobel method. Three models based on "SVM, RF, and K-NN" were trained and tested with the acquired dataset, and the results show that SVM outperforms the other models in terms of the study's performance evaluation metrics.

Author in [12] used a "hybrid feature-optimised multiclass support vector machine (MSVM)" classification model to create a "skin cancer" detection system. The dataset for this study was obtained from the freely available HAM10000 database, which contains 10,015 dermatoscopic images. To reduce unwanted noise, a median filter (MF) is employed. The Fuzzy C-Means method is used to separate homogeneous clusters. Following feature extraction, the Grey Wolf Optimisation (GWO) method was used to select the optimal features. The "Hybrid Feature-Optimized MSVM" classifier is used to distinguish between cancerous and non-cancerous images. The "hybrid feature-optimise-MSVM" achieved 98.0% accuracy, 97.2% specificity, and 96.2% sensitivity.

Authors in [10] developed a deep learning-based classification model for predicting skin diseases. This study utilised the HAM-10000 Dataset, a widely used and publicly available dataset in dermatology research. The HAM-10000 Dataset contains 10,000 images of various skin conditions, including "nevi, melanoma, benign keratosis, basal cell carcinoma, actinic keratoses, vascular lesions, and dermatofibromas". The dataset contains images of varying resolutions and sizes. Images are resized to a standard size, typically 224x224 pixels, as part of the data preprocessing steps to ensure unified input sizes for the convolutional neural network (CNN). To ensure a fair assessment of the model's efficacy, the input data is split into three sections: training, validation, and test. The splitting is stratified to ensure that each set contains a proportional representation of various skin ailments. The training set trains the model, the validation set tunes hyperparameters and chooses models, and the test set assesses the model's final performance. The outcomes show that the suggested approach achieves an accuracy of 97.05%.

Authors in [16] used the "Wolf Antlion Neural Network (WALNN) technique to develop a classification model for detecting and classifying skin diseases". The proposed method classifies carcinoma of the skin using the "ISIC archive dataset" as input. This dataset contains 2,750 dermoscopy images. 2000 people were employed as instructors, 600 for development and 150 for confirmation. These practical instances from each Data application for a general audience back up the segmentation technique. The photos in the classification challenge are divided into three categories: "nevi, seborrhoeic keratosis, and melanoma (1372, 254, and 374)". During pre-processing stage, "a wavelet denoising, bilateral filtering, and histogram equalisation" were used to remove noise, improve edges, and increase contrast. Following that, an improved thresholding approach is used for segmentation, and the Grey Level Co-occurrence Matrix is used to extract texture features like contrast, mean, energy, and homogeneity. Finally, a classification model based on the Wolf AntLion Neural Network (WALNN) is used to identify cancerous skin lesions. The results show that the WALNN model achieved 98.34% specificity, 99.12% sensitivity, 98.98% precision, and 99.01% accuracy.

Authors in [13] developed a skin illness classification framework using "sophisticated image processing techniques and an attention-based vision approach to assist dermatologists in solving classification problems". The dataset is first collected, and then the images are subjected to a variety of preprocessing techniques, including "adaptive histogram equalisation (AHI), binary cross-entropy with implicit averaging (BCEI), gamma correction, and contrast stretching". The pre-processed images are subsequently fed into a deep-learning framework built around vision transformers (ViT). The enhanced images are then classified using an attention-based approach that relies on the encoder part of the transformers and multi-head attention. Extensive experimentation is conducted to collect various results from two publicly available datasets, confirming the robustness of the proposed approach. The suggested method performs competitively on two freely accessible datasets in comparison to a cutting-edge approach.

Authors in [8] proposes a "Hybrid Deep Transfer Learning Method (HDTLM) that combines DenseNet121 and EfficientNetB0" to improve dermatological illness prediction. The suggested hybrid approach leverages "DenseNet121's" dense connectivity to capture intricate patterns, as well as "EfficientNetB0's "computational efficiency and scalability. To train and validate, a dataset of 19,171 images representing 19 skin conditions was used. Accuracy, precision, recall, and F1-score were among the performance metrics used to evaluate the model. A comparison was also made with cutting-edge models such as "DenseNet121, EfficientNetB0, VGG19, MobileNetV2, and AlexNet". The suggested HDTLM achieved a

precision of 0.95, recall of 0.96, F1-score of 0.95, and overall accuracy of 98.18%, consistently outperforming baseline models. The findings indicate that the hybrid model has a better ability to generalise across multiple skin disease categories.

3. METHODOLOGY

This system's algorithms include image resizing, RGB to grayscale image conversion, bi-histogram equalisation, a Black-Hat transformation and inpainting algorithm to remove digital hair, adaptive median filtering, Sobel operator, GLCM algorithm, AO-SVM classification model and HHO-SVM classification model, all designed using MATLAB software. Figures 1 and 2 show a block diagram of the proposed classification model's methodology, as well as a flowchart for the trained and tested skin image datasets using AO-SVM or HHO-SVM.

3.1 Image Acquisition

Two thousand seven hundred images of skin comprise eight different skin diseases and normal skin taken from the Kaggle village collection. An equal number of datasets from the original dataset were randomly selected for each of the diseased datasets to prevent an unbalanced dataset for class labelling. The dataset is divided into nine categories: seven hundred (700) normal skin, two hundred and fifty (250) each for granuloma annulare (GRA), haemangioma (HEM), herpes (HEP), hidradenitis suppurativa (HSP), keratocanthoma (KEC), lupus (LUP), sebaceous hyperplasia (SEH), and sun damaged skin (SDS). Figure 3 depicts a sample of each class of diseased datasets and normal skin datasets.

3.2 Image Preprocessing and Segmentation

During the preprocessing phase, the RGB images were resized using MATLAB's image resize toolbox to remove unnecessary pixel information and improve the classification model efficiency. Bi-histogram equalisation was used to improve contrast, and RGB images were converted to greyscale. A Black-Hat transformation and an inpainting algorithm were used to remove digital hair. The images were then denoised using the adaptive median filtering method prior to image segmentation processing. To achieve the necessary segregation, the proposed model divides the affected and unaffected regions of a leaf using the Sobel edge detection algorithm.

3.3 Feature Extraction

Following the segmentation procedure, the three features of colour, shape, and texture were extracted. To extract shape and texture features, the Gray-Level Spatial Dependence Matrix was used, while colour features were extracted using the Colour Moment. The four colour moments extracted were medium, standard deviation, asymmetry, and kurtosis. The Haralick model was used to extract five texture attributes: energy, contrast, homogeneity, correlation, and entropy. Six shape features were identified: eccentricity, area, solidity, rectangularity, equidimeter, and perimeter. To fuse all three features, the linear combination method was used.

3.4 Formulation of Aquila Optimiser (AO) and Harris Hawk Optimiser (HHO) Models

Algorithms 1 and 2 are used to formulate the model for AO and HHO used in this study.

Algorithm 1: Aquila Optimiser Model

Algorithm 1: Pseudocode of Aquila Optimiser (AO)
Input: size of population (N), maximum number of iterations (Q)
Initialisation phase:
Initialise the Aquila Optimizer's parameters (i.e., *S, q, Q, K, α, β, V, g, h, S_1, r_1, γ,* and *ω*).
Outputs: Solution to the problem
WHILE (end condition is not encountered) do
Evaluate the objective function values.
$C_{Be}(q)$= Determine the most optimal obtained solution based on the objective values.
for (i = 1,2…, N) do
Revise the current solution's mean value C_{Me}(q).
Revise the *x, y,* P_1, P_2, *LV(DI), UF(q),* C_{ME}, *μ*
if $q \leq (\frac{2}{3}) \times Q$ Then
if $rmd \leq ½$

Step 1: Expanded Exploration (C_1)

The existing solution can be revised using Equations (1) and (2)

$$C_1(q+1) = C_{Be}(q) \times \left(1 - \frac{q}{Q}\right) + (C_{Me}(q) - C_{Be}(q) \times rmd) \quad (1)$$

where $C_1(q+1)$ indicates the outcome of the subsequent iteration at time q, C_{Be} (q) is the optimal solution generated by the algorithm through repetition q. It depicts the estimated target spot. The rmd is an arbitrary integer within range of zero and one; q and Q represent the present and ultimate number of repetitions, respectively. The term $\left(1 - \frac{q}{Q}\right)$ is used to control the number of instances in the expanded search (exploration) and C_{Me} (q) represent the mean spot of the present solution within q^{th} repetition, which is expressed in Equation (2).

$$C_{Me}(q) = \frac{1}{N} \sum_{q=1}^{N} C_i(q), \forall N = 1,2,\ldots,S \quad (2)$$

where N is the number of possible solutions and S is the problem's dimension size (population size).

if Objective ($C_1(q+1)$) < Objective ($C(q)$) then
$C(q)$ =($C_1(q+1)$)
if Objective ($C_1(q+1)$) < Objective ($C_{Be}(q)$) then

$C_{Be}(q) = C_1(q+1)$
endif
endif
else

Step 2: Narrowed Exploration (C_2)

The present solution can be updated by using Equation (3).

$$C_2(q+1) = C_{Be}(q) \times LV(DI) + C_R(q) + (y - x) \times rmd \quad (3)$$

where C_R (q) is a generic solution in the range [1, N] at the i^{th} iteration as in [1]. $C_2(q+1)$ indicates the outcome for the subsequent iteration at time q. LV (DI) is mathematically expressed in Equation (4). Equations (6), (7), (8), (9) and (10) can be used to compute both y and x, which model the spiral flight trajectory in the search.

$$LV(DI) = K \times \frac{g \times \mu}{|h|^{\frac{1}{\alpha}}} \quad (4)$$

where K is a constant value of 0.01, g and h are arbitrary numbers that vary from 0 to 1, α is a constant value of 1.5, μ and is determined by employing Equation (5).

$$\mu = \frac{rmd(1+\alpha) \times Sin\left(\frac{\pi \times \alpha}{2}\right)}{rmd\left(\frac{1+\alpha}{2}\right) \times \alpha \times 2\left(\frac{\alpha-1}{2}\right)} \quad (5)$$

$$x = rmd \times Cos(\theta) \quad (6)$$

$$y = rmd \times Sin(\theta) \quad (7)$$

where rmd and θ can be determined using Equations (8), (9) and (10).

$$rmd = rmd_1 + V \times S_1 \quad (8)$$

$$\theta = -\omega \times S_1 + \theta_1 \quad (9)$$

$$\theta_1 = \frac{3 \times \pi}{2} \quad (10)$$

where rmd_1 refers to an integer indicating the search cycles between 1 and 20 as in [36], V is a modest value, fixed at 0.00565, ω equal to 0.005, and S_1 denotes the random integer from the range of 1 to the dimensions as in [1].

if Objective ($C_2(q+1)$) < Objective ($C(q)$) then
$C(q) = (C_2(q+1))$
if Objective ($C_2(q+1)$) < Objective ($C_{Be}(q)$) then
$C_{Be}(q) = C_2(q+1)$
endif
endif
endif
else
if rmd ≤½

Step 3: Expanded Exploitation (C_3)

The present solution can be updated by using Equation (11).

$$C_3(q+1) = (C_{Be}(q) - C_{Me}(q)) \times \beta - rmd + ((upp - low) \times rmd + low) \times \gamma \quad (11)$$

where $C_3(q+1)$ indicates the outcome for the subsequent iteration at time q, $C_{Me}(q)$ indicates the mean position in the i^{th} generation, $C_{Be}(q)$ is the best Aquila position obtained in this iteration, rmd is an arbitrary generated number within range of [0, 1], β and γ are valuable utilisation adjustment parameters set at a fixed value of 0.1 used to control exploitation search space, and upp and low refer to the upper and lower boundaries as in [1].

if Objective ($C_3(q+1)$) < Objective ($C(q)$) then
$C(q) = (C_3(q+1))$
if Objective ($C_3(q+1)$) < Objective ($C_{Be}(q)$) then
$C_{Be}(q) = C_3(q+1)$
endif
endif
else

Step 4: Narrowed Exploitation (C_4)

Reverse the current solution using Equations (12), (13), (14), and (15).

$$C_4(q+1) = UF \times C_{Be}(q) - (P_1 \times C(q) \times rmd) - P_2 \times LV(DI) + rmd \times P_1 \quad (12)$$

$$UF(q) = q \times \frac{2 \times rmd - 1}{(1-r)^2} \quad (13)$$

$$P_1 = 2 \times rmd - 1 \quad (14)$$

$$P_2 = 2 \times \left(1 - \frac{q}{Q}\right) \quad (15)$$

where $C_4(q+1)$ indicates the subsequent iteration's outcome at time q, UF. represents a quality function that helps to stablise search strategies. P_1 stands for the various initiatives of the Aquila optimiser when monitoring target during elusion. P_2 is a value that drops from 2 to 0, indicating the gradient of the flight utilised by the Aquila optimiser to monitor target during elusion from the first to the last position. $C(q)$ is the present outcome in the qth iteration, according to authors in [1] and *LV (DI)* represents the Levy flight distribution function.

if Objective ($C_2(q+1)$) < Objective ($C(q)$) then
$C(q) = (C_2(q+1))$
if Objective ($C_2(q+1)$) < Objective ($C_{Be}(q)$) then
$C_{Be}(q) = C_2(q+1)$
endif
endif

endif
endif
endfor
endwhile
Return Optimal solution (C_{Be})

ALGORITHM 2: PSEUDOCODE OF HARRIS HAWK OPTIMISATION (HHO)

Input: size of population (N), maximum number of iterations (Q)
Initialisation phase:
Initialise the parameters of the Harris Hawk Optimizer (i.e., *DI, q, Q, ρ, VI, SE, υ*, low, upp, and t).
Initialise H_i i=1, 2, …, M
Outputs: Outcome to the problem
While (q < Q) do

Determine the objective function values for every hawk, H_i. Identify the prime instance (target position)
Check if it is beyond bounds.
For every hawk (H_i)

Execute Transition from Exploration Phase to Exploitation Phase

Reverse the convergence factor with Equation (16) as in [9].

$$\mathrm{ES} = 2 \times ES_0 \times \left(1 - \frac{q}{Q}\right) \tag{16}$$

where ES is the convergence factor, q is the present repetition number, Q is the ultimate repetition number, and ES_0 stand for initial energy of the target which can be expressed mathematically using Equation (17).

Reverse the initial energy of target using Equation (17).

$$ES_0 = 2 \times rmd_5 - 1 \tag{17}$$

Calculate the exploration range of the target with Equation (18).

$$J = 2 \times (1 - rmd_6) \tag{18}$$

J represents the random jump strength of the target and $rmd_6$is an equally distributed random number in (0,1), If (|ES| ≥ 1) then

Execute Exploration Phase

Update hawk position using Equation (19) as in [9].

$$H(q+1) = \begin{cases} H_{rand}(q) - rmd_1 |H_{rand}(q) - 2 \times rmd_2 \times H(q)|, & t \geq 0.5 \\ (H_{prey}(q) - H_{Me}(q)) - rmd_3 \times ((low + rmd_4 \times (upp - low)), & t < 0.5 \end{cases} \tag{19}$$

where rmd1, rmd2, rmd3, rmd4, and t are stochastic value within the range [0,1]. A hawk spot at the current iteration and subsequent iterations are denoted by H(q) and H(q+1), respectively. $H_{prey}(q)$ and $H_{rand}(q)$ stand for optimal spot and stochastically selected hawk spot, respectively. $H_{Me}(q)$ stands for mean value of the spots in the present candidate solution calculated with Equation (20) as in [9].

$$H_{Me}(q) = \frac{1}{M}\sum_{i=1}^{M} H_i(q) \tag{20}$$

where M is the population size
Endif
Elseif (|ES| < 1) then
If (rmd ≥½ and |ES|≥½)

Execute Soft Besiege to Siege the Prey

Update hawk position using Equation (21).

$$H(q+1) = \Delta H(q) - ES|J \times H_{prey}(q) - H(q)| \tag{21}$$
$$\Delta H(q) = H_{prey}(q) - H(q)$$

where $\Delta H(q)$ stands for the location difference between the present location of the target and the present location, $H_{prey}(q)$ stands the location of the prey, and $H(q)$ is the present location.

Endif
If (rmd ≥½ and |ES|<½)

Execute Hard Besiege to Siege the Prey

Update hawk position using Equation (22).

$$H(q+1) = H_{prey}(q) - ES|\Delta H(q)| \tag{22}$$

Endif
If (rmd <½ and |ES|≥½)

Execute Soft Besiege with Progressive Rapid Dives to Siege the Prey

Update hawk position using Equations (23), (24), (25), (26), and (27).

$$A = H_{prey}(q) - ES|J \times H_{prey}(q) - H(q)| \tag{23}$$

$$B = A + SE \times LVY(DI) \tag{24}$$

where DI is the magnitude to resolve the issue, SE is an arbitrary vector whose dimension is DI and LVY is the levy flight function defined as in Equation (25).

$$LVI(DI) = \frac{0.01 \times \vartheta\delta}{|VI|^{\frac{1}{\rho}}} \tag{25}$$

$$\left(\frac{rmd \times (1+\rho) \times Sin\left(\frac{\pi \times \rho}{2}\right)}{rmd\left(\frac{1+\rho}{2}\right) \times \rho \times 2 \times \left(\frac{\rho-1}{2}\right)}\right)^{\frac{1}{\rho}} \tag{26}$$

where $\vartheta, VI \in (0,1)$, ρ is a constant of 1.5 as in [9].

$$H(q+1) = \begin{cases} A & IF\ F(A) < F(H(q)) \\ B & IF\ F(B) < F(H(q)) \end{cases} \tag{27}$$

where A and B is the next position for the new iteration
Endif

If (rmd <½ and |ES|<½)

Execute Hard Besiege with Progressive Rapid Dives to Siege the Prey

Update hawk position using Equations (28), (29), and (30).

$$A = H_{prey}(q) - ES|J \times H_{prey}(q) - H_{Me}(q)| \quad (28)$$

$$B = A + SE \times LVY(DI) \quad (29)$$

$$H(q+1) = \begin{cases} A & IF\ F(A) < F(H(q)) \\ B & IF\ F(B) < F(H(q)) \end{cases} \quad (30)$$

Endif

Endif

Endfor

Q=q+1

End while

Output the best solution H_{prey} and its fitness value

3.4 Formulation of Aquila Optimiser Model and Harris Hawk Optimiser Model for Optimising Support Vector Machine Parameters

Algorithms 3 and 4 were used to formulate the model for AO for the optimisation of support vector machine parameters and HHO for the optimisation of support vector machine parameters in this study.

Algorithm 3: AO Model for Optimizing SVM Parameters

1: Input: The datasets, which include both the train and test datasets
2: Subset the training and testing datasets using 10-fold cross-validation.
3: Setting the AO parameters and particle initialisation: Create the first particles with the feature mask C and ϒ combined. As in Algorithm 1, set the AO parameters that include the low and upp represent lower and upper bound of the problem, M represent total number of potential solutions, s represent population size, q and Q represents both initial and maximum iterations, rmd random value range between 0 and 1, V small value assigned with 0.00565, α unchangeable value assigned with 0.01, ω fixed value at 0.005 and π at 3.142.
4: Set the iteration count to v + 1.
5: while (v < V) do
6: Use the chosen feature subset to train the SVM model
   a) Preprocessing of training sets: choose input features for training datasets based on the feature mask that is shown in a particle's first part.
   b) SVM classifier accuracy calculation: considering (C, γ) that is depicted in the subsequent and third base components of a particle, use Equation (31) to get the average classification accuracy (*CLA*).

$$CLA = \frac{ACL}{ACL+NACL} \times 100\% \quad (31)$$

where the *ACL* and *NACL*, respectively, represent how many instances were accurately and inaccurately classified by the SVM classifier.

   (c) Regarding the (C, γ) and the entire training set T_r, the trained model's classification accuracy can be evaluated using Equation (31).
7: Apply Equation (32) to evaluate the Fitness Function (FitFuc) as defined by authors in [4].

$$FitFuc = \rho \times (1 - \frac{E_d}{F}) + \sigma \times \frac{SA_d}{N} \quad (32)$$

8: Set up potential solutions by utilising Equation (33).

$$C_{i,j} = rdm \times (upp_j - low_j) + low_j, i = 1,2,3,4,\ldots M_j = 1,2,3,4,\ldots S \quad (33)$$

where rdm stand for arbitrary number, low_j and upp_j stand for the j^{th} minimum bound and j^{th} maximum bound of the given problem, respectively. M is the aggregate of feasible outcomes and S represents the number of instances
9: for v = 1 to V do
10: To update potential solutions $C_{i,j}$, use Equations (1), (2), (3), (4), (5), (6), (7), (8), (9), (10), (11), (12), (13), (14), and (15)
11: Assess the Fitness Function (FitFuc) of the updated potential solutions using Equation (32)
12: end for
13: Training and Testing the SVM classifier
End while
14: Proceed to step 15 if the stopping criteria are met (i.e., v > V); if not, proceed to step 3.
15: Output: Obtain the optimal value for C and γ from the optimal solution

Algorithm 4: HHO Model for Optimizing SVM Parameters

1: Input: The datasets, which include both the train and test datasets
2: Subset the training and testing datasets using 10-fold cross-validation.
3: Setting the HHO parameters and particle initialisation: Create the first particles with the feature mask C and ϒ combined. As in Algorithm 2, set the HHO parameters, which include the rmd, the random number range from 0 to 1, ϑ and VI fixed number range from 0 to 1, ρ

constant value at 1.5, upp and loo represent lower and upper bound of the problem, o represents fixed value range from 0 to 1, and σ represents position deviation of the dung beetle at fixed value of -1 or 1, the iteration v=0,

4: Set the iteration count to v + 1.
5: while (v < V) do
6: Use the chosen feature subset to train the SVM model
   a. Preprocessing of training sets: choose input features for training datasets based on the feature mask that is shown in a particle's first part.
   b. SVM classifier accuracy calculation: considering (C, γ) that is depicted in the subsequent and third base components of a particle, use Equation (31) to get the average classification accuracy (*CLA*).
   c. Regarding the (C, γ) and the entire training set T_r, the trained model's classification accuracy can be evaluated using Equation (31).
7: Apply Equation (32) to evaluate the Fitness Function (FitFuc) as defined by authors in [4].
8: for v = 1 to V do
9: To update potential solutions $C(q)$, use Equations (16), (17), (18), (19), (20), (21), (22), (23), (24), (25), (26), (27), (28), (29), and (30)
10: Assess the Fitness Function (FitFuc) of the updated potential solutions using Equation (32)
11: end for
12: Training and Testing the SVM classifier
End while
13: Proceed to step 14 if the stopping criteria are met (i.e., v > V); if not, proceed to step 3.
14: Output: Obtain the optimal value for C and γ from the optimal solution

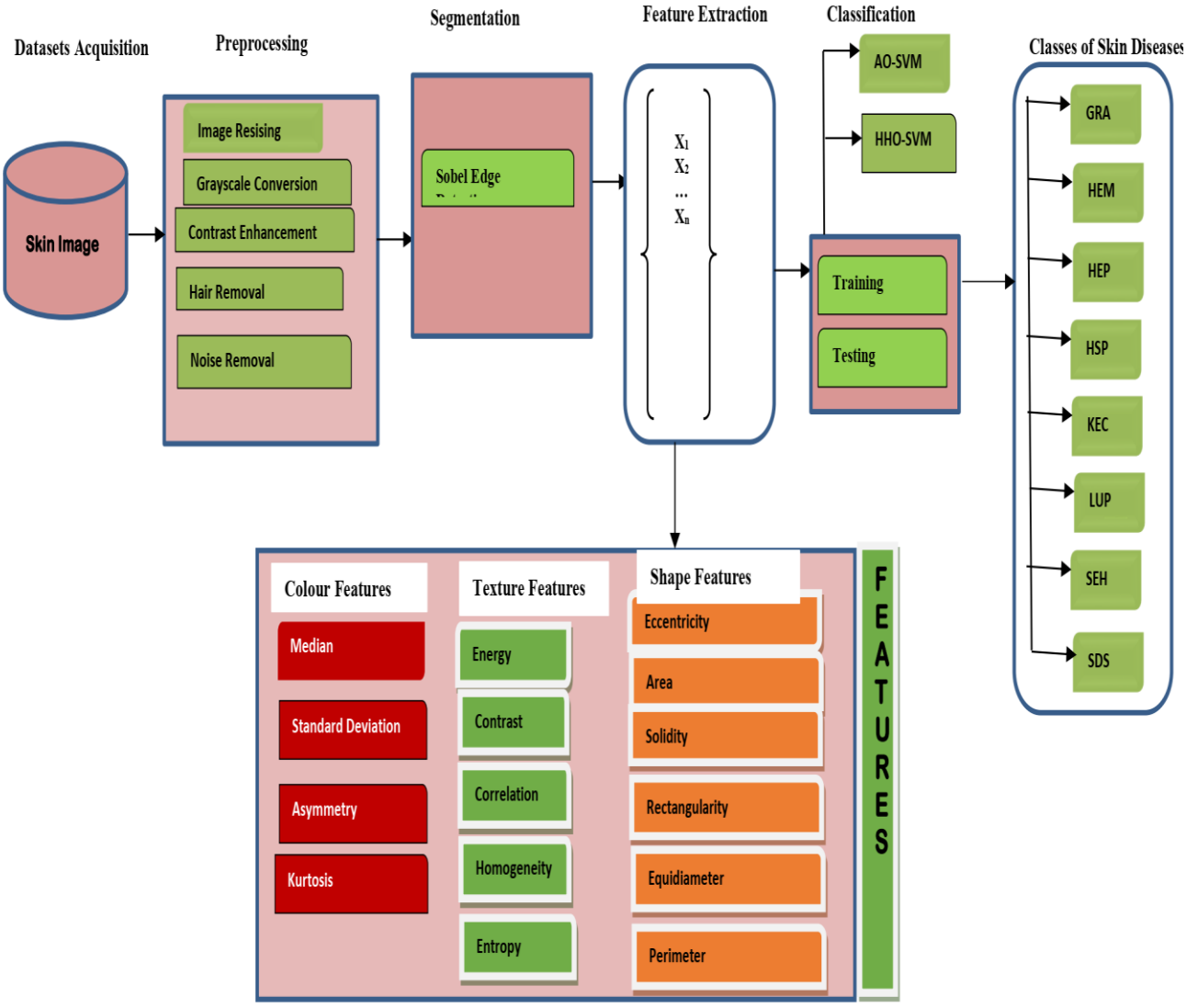

Figure 1: A block diagram of the developing skin diseases classification models

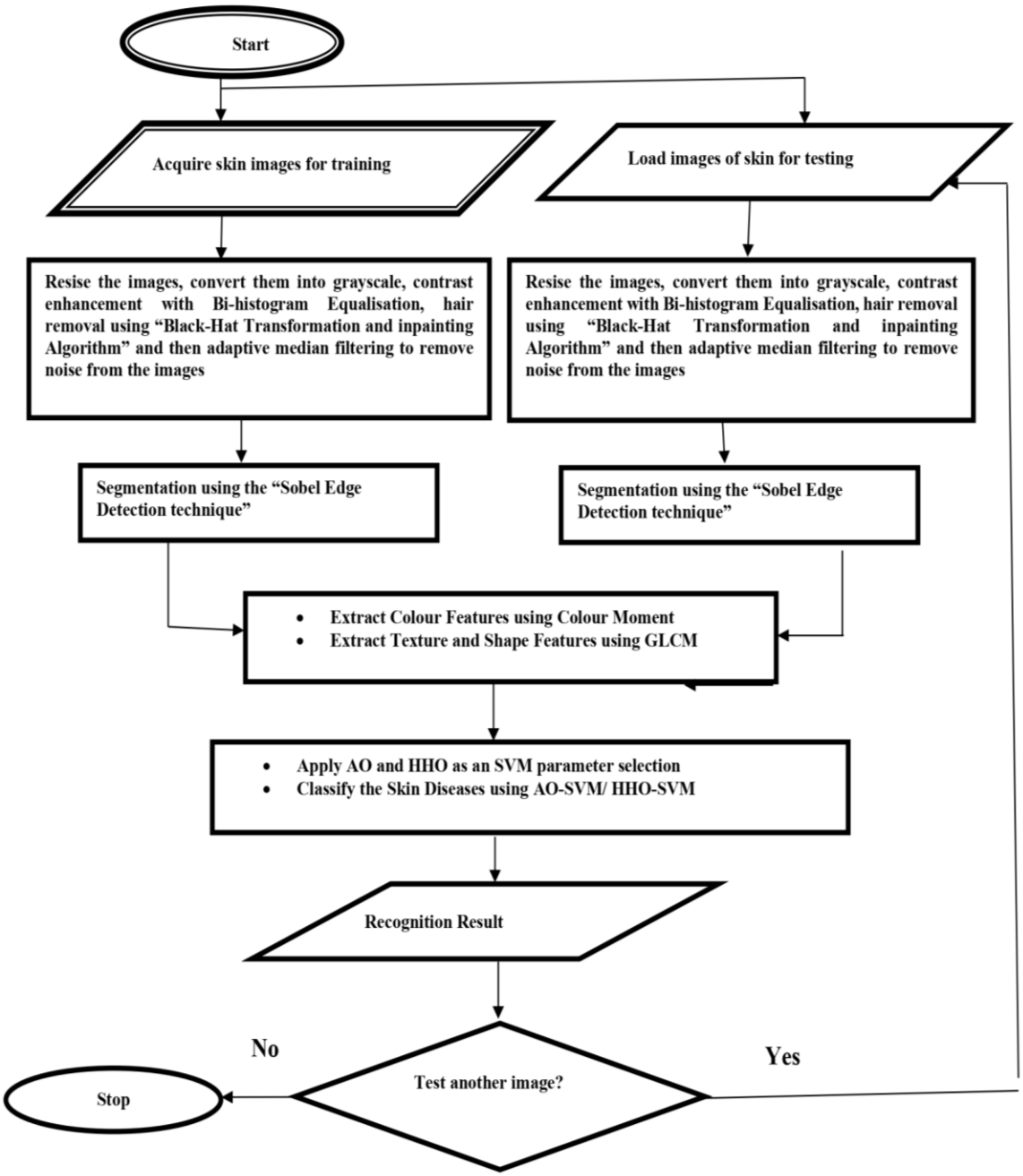

Figure 2: Flowchart showing trained and tested skin images datasets with AO-SVM and HHO-SVM classification model

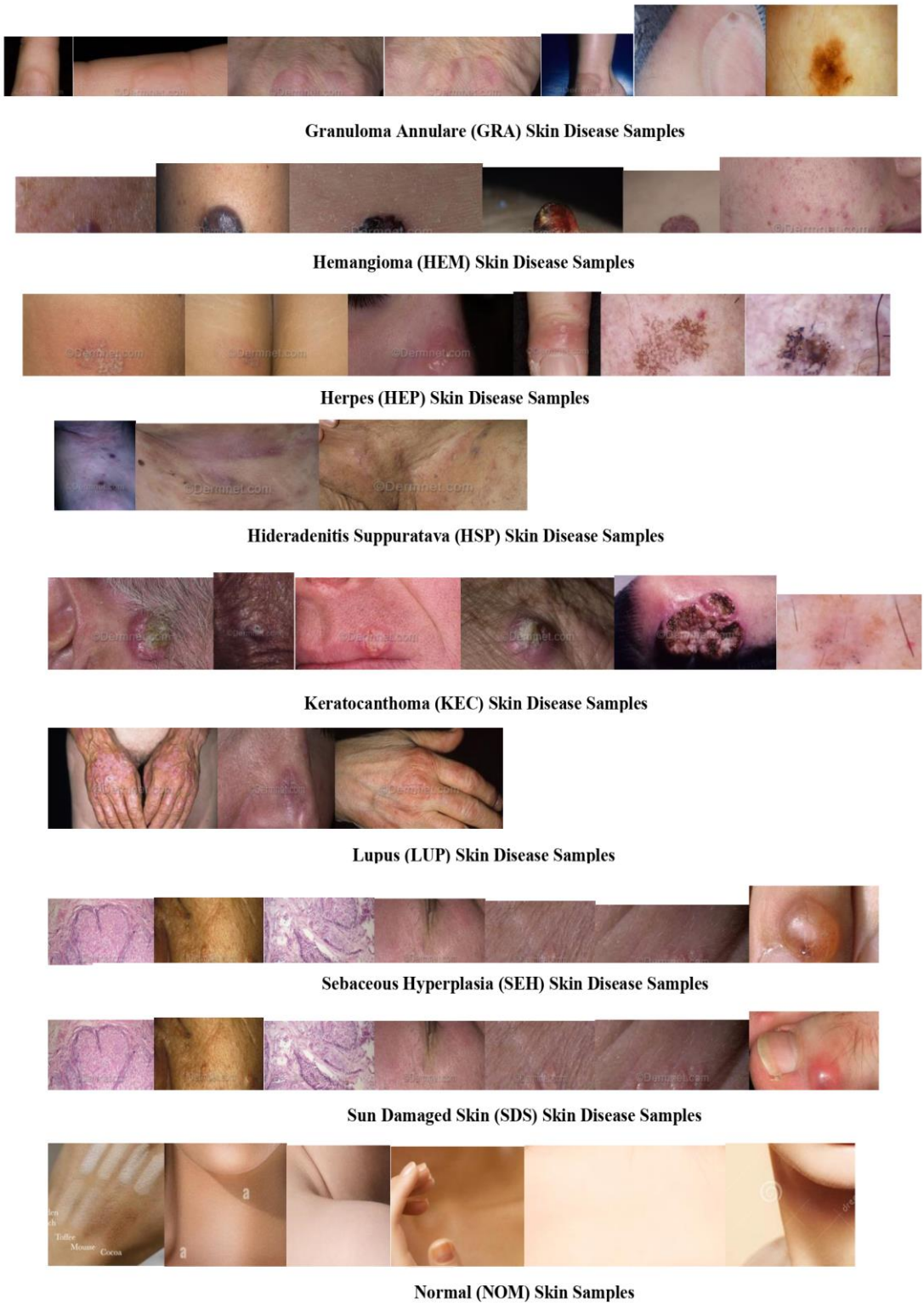

Figure 3: Sample of each class of diseased datasets and normal skin datasets

3.5 Classification of Skin Diseases using Multiclass Classification Models (AO-SVM and HHO-SVM)

Selected disease segment images from the skin classified using classification models in connection with a Directed Acyclic Graph Support Vector Machine (DAGSVM), which can classify more than two data classes. Multiclass SVM is reduced to a two-class classification problem in this research. In the study, the training dataset, SE = $(g_a; h_b)^t{}_{b=1}$, where the class label is $h_a \epsilon \{0,1\}$and the feature vector is $g_a \epsilon R^n$. The linear classifier creates a decision function (*df*) using Equation (34).

$$df(g) = vec^k g + e \quad (34)$$

where e is the bias and *vec* = (vec_1, vec_2..., *vecn*) is the weight vector. If d*f (g)*> 0, the prediction label is +1; if not, it is -1. The convex optimisation problem with maximal margin 2/||vec||^2 and minimal training errors is represented by Equation (35), which the created standard Support Vector Machine (SVM) solved through the identification of a region of space *df (g) = 0* between two classes.

$$\min_{vec,e\varphi}\left[\frac{1}{2}\sum_{b=1}^{n}\|vec\|^2 + c\sum_{a=1}^{k}\sum_{u\neq h_a}\varphi_b^u\right] \quad (35)$$

Subject to the constraints

$$vec_{ha}\cdot G_b + e_{hb} \geq Vec_u \cdot G_b + e_u + 2 - \varphi_b^u \quad (36)$$

for

and,

$$\varphi_b^u \geq 0 \qquad \text{for } b = 1,\ldots,k \quad (37)$$

where $h_b \in \{1,\ldots,X\}$ the multiclass labels of the data vectors and $u \in \{1,\ldots,X\} \setminus h_b$ the multiclass labels excluding h_b are allowed by φ the training error loss function for possibly non-linearly separable data. The specified parameter C controls the amount of misclassification on the training set of data by balancing the margin and losses.

Authors in [35] discovered that a large C corresponds to giving the errors a higher penalty, which lowers the margin, while a small C allows for more errors and increases the margin. In this study, K = 8 movements were categorised using the DAG method. There is a total of K (K-1)/2 binary classifiers, or 28 binary classifiers for skin-related diseases, that are involved in this classification process. In the training phase, one binary classifier is assigned to each pair of movements. The soft margin strategy is necessary to keep the classes apart because there is a chance that the data for the two distinct classes will overlap during each binary classifier's training. However, the training step involves using inequality constraints to solve the quadratic optimisation problem given in Equation (35) to train 28 different binary classifiers for the classification of skin diseases in the dataset. The constant C's value and the kernel value were utilised for mapping the input feedback.

Optimisation Problem Formulation of AO-SVM

The AO algorithm searches for the best combination of SVM hyperparameters as shown in Equation (38).

$$\text{Objective:} \quad \min_{C,\gamma} \rho = 1 - Accuracy_{CV}(C,\gamma) \quad (38)$$

where C is regularization parameter, γ is the kernel coefficient (for RBF kernel), ρ is loss (or fitness function), and $Accuracy_{cv}$ is classification accuracy via cross-validation.

Each candidate solution (search agent) is a vector of hyperparameters as shown in Equation (39).

$$X_i=[C_i,\gamma_i] \quad (39)$$

Each candidate solution is evaluated using an SVM model, trained with the parameters from AO. A 10-fold cross-validation is typically used to measure the generailisation ability represented by Equation (40).

$$\text{Fitness-1-mean}Accuracy_{CV} \quad (40)$$

Optimization Problem Formulation of HHO-SVM

The HHO algorithm searches for the best combination of SVM hyperparameters represented by Equation (41).

$$\text{Objective:} \quad \min_{C,\gamma} \rho = 1 - Accuracy_{CV}(C,\gamma,selected\ features) \quad (41)$$

Each candidate solution (search agent) is a vector of hyperparameters shown in Equation (42).

$$X_i= [C_i,\gamma, f_1, f_2, \ldots, f_d] \quad (42)$$

$f_j \in \{0,1\}$: binary indicator for selecting the j^{th} feature
d: total number of features

Search Process

1. Initialise population: Randomly generate N sets of [C,γ]
2. Evaluate fitness: For each, train SVM and compute CV accuracy
3. Update population: Using AO or HHO strategy
4. Select best: Keep the best solution found so far
5. Iterate: Repeat for a number of iterations or until convergence

4. RESULTS AND DISCUSSION

Table 1 shows performance measures of the experimental outcomes of the proposed models, while Table 2 compares their performance measures to that of existing classification models.

4.1 Performance Evaluation Metrics of the Developed Classification Models (AO-SVM and HHO-SVM)

The AO-SVM model achieved FPR performance of 2.86, 3.14, 3.57, 2.57, 2.71, 3.00, 2.57, and 3.29% and the HHO-SVM model achieved FPR performance of 2.43, 2.71, 3.14, 2.14, 2.29, 2.57, 2.14%, and 2.86 on the diseased dataset for each class comprising GRA, HEM, HEP, HSP, KEC, LUP, SEH, and SDS, respectively. Also, the AO-SVM model achieved specificity performance of 97.14, 96.86, 96.43, 97.43, 97.29, 97.00, 97.43, and 96.71% and the HHO-SVM model achieved specificity performance of 97.57, 97.29, 96.86, 97.86, 97.71, 97.43, 97.86, and 97.14% for each class comprising GRA, HEM, HEP, HSP, KEC, LUP, SEH, and SDS, respectively. More so, the AO-SVM model achieved sensitivity performance of 92.80, 91.60, 90.40, 93.20, 94.00, 92.00, 93.20, and

91.20% and the HHO-SVM model achieved sensitivity of 94.00, 92.80, 91.60, 94.40, 95.20, 92.80, 94.40, and 92.40% on the diseased dataset for each class GRA, HEM, HEP, HSP, KEC, LUP, SEH, and SDS, respectively. Furthermore, the AO-SVM model achieved precision performance of 92.06, 91.24, 90.04, 92.83, 92.52, 91.63, 92.83, and 90.84% and HHO-SVM model achieved precision performance of 93.25, 92.43, 91.24, 94.02, 93.70, 92.80, 94.02, and 92.03% on the diseased dataset for each class comprising GRA, HEM, HEP, HSP, KEC, LUP, SEH, and SDS, respectively. Finally, the AO-SVM model achieved performance accuracy of 96.00, 95.47, 94.84, 96.32, 96.42, 95.68, 96.32, and 95.26% and HHO-SVM model achieved performance accuracy of 96.63, 96.10, 95.47, 96.95, 97.05, 96.21, 96.94, and 95.89% on the diseased dataset for each class comprising GRA, HEM, HEP, HSP, KEC, LUP, SEH, and SDS, respectively shown in Table 1.

The results in Table 1 show that the HHO-SVM multiclass classification model outperforms the AO-SVM multiclass classification model in all performance metrics. However, HHO model is very strong in exploitation search behaviour but very weak in exploration search behaviour whereas, AO model is very week in exploitation search behaviour but very strong in exploration search behaviour. The “No Free Lunch (NFL) theorem states that an algorithm’s performance on one problem category does not assurance its performance on other categories” [30]. As a result, the effectiveness and superiority of HHO-SVM across AO-SVM in this study is heuristic. Nonetheless, "it is clear that the efficacy of any type of algorithm, including a nature-inspired optimisation algorithm (NIOA), is profoundly influenced by the algorithm's design viewpoint, such as optimal mixing of exploration and exploitation" [21].

4.2 Performance Evaluation Metrics Comparison of the Developed Classification Models with the Existing Classification Models in Skin Diseases Classification

This study's findings are consistent with previous research on skin disease detection and classification algorithms. Table 2 compares the results of the suggested classification models to other developed multiclass support vector machine classification models and currently available classification models. This study, however, bears similarities to studies conducted by [22] that optimise support vector machine with fruit fly optimisation (FSO-SVM) and [16] that optimise neural network with Wolf antlion optimiser (WALNN). Regarding the performance evaluation metrics used, as shown in Table 2, the developed models (AO-SVM and HHO-SVM) outperformed some of the existing models.

In light of the experiment's outcomes, the developed multiclass classification models (AO-SVM) and (HHO-SVM) is more sensitive, specific, and accurate. Furthermore, the correctness of the (AO-SVM) and (HHO-SVM) models are further validated by their false positive rate result. The two models thus offered improved specificity, sensitivity, accuracy, and precision along with a reduction in calculation time and false positive rate. The performance evaluation results of the (AO-SVM and HHO-SVM) models are thus comparable to those of the other existing conventional infected skin diseased classification models.

Table 1: Performance evaluation metrics of the developed multiclass support vector machine classification models on skin datasets

	All Diseased Datasets	GRA	HEM	HEP	HSP	KEC	LUP	SEH	SDS	AVE
False Positive Rate (FPR) (%)										
AO-SVM	4.57	2.86	3.14	3.57	2.57	2.71	3.00	2.57	3.29	**3.14**
HHO-SVM	4.14	2.43	2.71	3.14	2.14	2.29	2.57	2.14	2.86	**2.71**
Specificity (%)										
AO-SVM	95.43	97.14	96.86	96.43	97.43	97.29	97.00	97.43	96.71	**96.86**
HHO-SVM	95.86	97.57	97.29	96.86	97.86	97.71	97.43	97.86	97.14	**97.29**
Sensitivity (%)										
AO-SVM	98.30	92.80	91.60	90.40	93.20	94.00	92.00	93.20	91.20	**92.97**
HHO-SVM	98.45	94.00	92.80	91.60	94.40	95.20	92.80	94.40	92.40	**94.01**
Precision (%)										
AO-SVM	98.40	92.06	91.24	90.04	92.83	92.52	91.63	92.83	90.84	**92.49**
HHO-SVM	98.55	93.25	92.43	91.24	94.02	93.70	92.80	94.02	92.03	**93.56**
Accuracy (%)										
AO-SVM	97.56	96.00	95.47	94.84	96.32	96.42	95.68	96.32	95.26	**95.99**
HHO-SVM	97.78	96.63	96.10	95.47	96.95	97.05	96.21	96.94	95.89	**96.56**

Note: Granuloma Annulare (GRA), Hemangioma (HEM), Herpes (HEP), Hidradenitis Suppurativa (HSP), Keratocanthoma (KEC), Lupus (LUP), Sebaceous Hyperplasia (SEH), Sun Damaged Skin (SDS), Average (AVE), Aquila Optimiser-Support Vector Machine (AO-SVM), Harris Hawk Optimiser-Support Vector Machine (HHO-SVM

Table 2: Performance evaluation metrics comparison of developed classification models with the existing classification models in skin disease classification

Author(s) and Models	False Positive Rate (%)	Specificity (%)	Sensitivity (%)	Precision (%)	Accuracy (%)
		[2]			
"Support Vector Machine (SVM)"	-	-	97.57	97.71	97.00
'K-Nearest Neighbour (KNN)"	-	-	95.57	95.71	95.00
"Decision Tree (DT)"	-	-	95.14	95.14	95.00
		[32]			
"Random Forest (RF)"	-	-	94.00	94.00	87.00
"Decision Tree (DT)"	-	-	74.00	75.00	68.00
"Logistic Regression (LR)"	-	-	55.00	56.00	58.00
"Support Vector Machine (SVM)"	-	-	50.00	54.00	53.00
"K-Nearest Neighbour (KNN)"	-	-	50.00	54.00	48.00
		[3]			
"Support Vector Machine (SVM)"	-	-	90.80	91.00	90.70
"Random Forest (RF)"	-	-	84.20	84.80	84.20
"K-Nearest Neighbour (KNN)"	-	-	67.10	72.80	67.10
		[12]			
"Hybrid Features Optimised MSVM"	-	97.26	96.20	-	98.00
		[22]			
"Fruit Fly Optimization-Support Vector Machine (FOA-SVM)"	-	96.00	98.50	-	98.80
		[16]			
"Wolf AntLion Neural Network (WALNN)"	-	98.34	99.12	98.98	99.01
Developed Models					
AO-SVM	**3.14**	**96.86**	**92.97**	**92.49**	**95.99**
HHO-SVM	**2.71**	**97.29**	**94.01**	**93.56**	**96.56**

Note: Histogram Oriented Gradient (HOG), Aquila Optimiser-Support Vector Machine (AO-SVM), Harris Hawk Optimiser-Support Vector Machine (HHO-SVM)

5. CONCLUSION

Skin disease has been the most common health problem facing many countries and varies accordingly from symptom and severity. Skin disease may be permanent, temporary, painful or painless based on the affected disease. However, many skin diseases are life-threatening, which need prompt and continuous monitoring to provide proper treatment and ensure faster recovery must be diagnosed and treated early to avoid severe consequences. This study uses clinical and histopathological attributes to classify ESD, such as Granuloma Annulare, Hemangioma, Herpes, Hidradenitis Suppurativa, Keratocanthoma, Lupus, Sebaceous Hyperplasia, and Sun Damaged. We created two non-hybridized models (AO and HHO) to fine-tune the support vector machine's hyperparameters. The research project was carried out in several stages, beginning with dataset collection from the Kaggle.com, followed by data preprocessing and segmentation, and finally feature extraction. The classification was done, and the effectiveness of the techniques was evaluated using False Positive Rate (FPR), specificity, sensitivity, precision and accuracy. Based on the findings, the base models achieved different accuracies in classifying the 8 different skin diseases, and HHO-SVM achieved the highest performance accuracy with 96.56% compared to AO-SVM with 95.99%. As a result, the developed models were highly effective at identifying and categorising common dermatological conditions. Such models, when combined with technology such as telemedicine, can be extremely beneficial in assisting people living in sparsely populated areas with limited access to specialised dermatological care in detecting disease early and then taking timely measures to cure the disease and prevent the spread of communicable skin disease.

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REFERENCES

[1] Abualigah, L., Yousri, D., Abd Elaziz, M., Ewees, A.A., Al-qaness, M.A. and Gandomi, A.H. (2021) Aquila optimizer: a novel meta-heuristic optimization algorithm. *Computer and Industrial Engineering*, 157(11), 1-16.

[2] Ahammed, M., Mamun, A. and Uddin, M.S. (2022). A machine learning approach for skin disease detection and classification using image segmentation. *Healthcare Analytics*, 2(4), 1-16. https://www.sciencedirect.com/science/article/pii/S2772442522000624/pdfft?md5=d9203351df584

04d9b41aed9cd3c814fandpid=1-s2.0-S2772442522000624-main.pdf

[3] AlDera, S.A. and Othman, M.T.B. (2022). A model for classification and diagnosis of skin disease using machine learning and image processing techniques. *International Journal of Advanced Computer Science and Applications*, 13(5), 253-259. https://thesai.org/Downloads/Volume13No5/Paper_31-A_Model_for_Classification_and_Diagnosis_of_Skin_Disease.pdf

[4] Al-Shourbaji, I., Helian, N., Sun, Y., Alshathri, S. and Abd Elaziz, M. (2022). Boosting ant colony optimization with reptile search algorithm for chun prediction. *Mathematics*, 10(7), 1-21. https://www.mdpi.com/2227-7390/10/7/1031/pdf?version=1648450940

[5] Md. Al Mamun and Uddin, M.S. (2021). A survey on a skin disease detection system, *International Journal of Healthcare Information Systems and Informatics*, 16 (4),1-17.

[6] Bordoloi, D., Singh,V., Kaliyaperumal, K., Ritonga, M., Jawarneh, M., Kassanuk, T. and Quinonez-Choquecota, J. (2023). Classification and detection of skin disease based on machine learning and image processing evolutionary models. *Computer Assisted Methods in Engineering and Science*, 30(2), 247-256.

[7] Cho, M. and Hoang, T. T. (2017). Feature selection and parameters optimization of SVM using particle swarm optimization for fault classification in power distribution systems. *Computational Intelligence and Neuroscience*, 2017(4135465), 1-9. https://pmc.ncbi.nlm.nih.gov/articles/PMC5525094/pdf/CIN2017-4135465.pdf

[8] Gulzar, Y., Agarwal, S., Soomro, S., Kandpal, M., Turaev, S., Onn, C.W., Saini, S. and Bounsiar, A. (2025). Next-generation approach to skin disorder prediction employing hybrid deep Transfer learning. *Frontiers in Big Data*, 8(1503883), 1-15. https://pmc.ncbi.nlm.nih.gov/articles/PMC11879938/pdf/fdata-08-1503883.pdf

[9] Hong, L., Mo, Y., Bao, D. and Gong, R. (2022). Chaos elite harris hawk optimization algorithm to solve chemical dynamic optimization problems. *IEEE Access*, 10(65833), 1-21.

[10] Jadhav, A., Hardade, S., Phadtare, V., Mhetre, A. and Tikait, R. (2023). Skin disease prediction using deep learning. *International Journal of Research Publication and Reviews*, 4(5), 5526-5530. https://ijrpr.com/uploads/V4ISSUE3/IJRPR10736.pdf

[11] Jagdish, M., Gualán Guamangate Guamangate, S.P., García López, M.A., De La Cruz-Vargas, J.A. and Roque Camacho, M.E. (2022). Advance study of skin diseases detection using image processing methods. Natural Volatiles and Essential Oils, 9(1), 997-1007.

[12] Kumar, A. (2023). A melanoma skin cancer diagnosis using hybrid feature-optimized MSVM classification model on dermotoscopic images. *GLIMPSE Journal of Computer Science*, 2(1), 19-24. https://www.akgec.ac.in/wp-content/uploads/2024/01/Jan-June2024_2.pdf

[13] Noor, M.N., Haneef, F., Ashraf, I. and Masud, M. (2025). Enhanced skin disease classification via dataset refinement and attention-based vision approach. *Bioengineering*, 12(275), 1-17. https://www.mdpi.com/2306-5354/12/3/275/pdf?version=1741678039

[14] Pranjal, P., Utkarsha, P., Sanyukta, W. and Bidve, V.S. (2021). Skin disease using svm. *International Journal of Advance Scientific Research and Engineering* Trends, 6(5), 171-175. https://www.ijasret.com/VolumeArticles/FullTextPDF/835_40.SKIN_DISEASE_USING_SVM.pdf

[15] Putra Asana, M.D., Ari Oka, D.G., Widyantara, M.O. and Sandhiyasa, M.S. (2024). Improved SVM Classification Using Particle Swarm Optimization for Student Completion Prediction System. *JUITA: Jurnal Informatika,* 12(2), 217-225.

[16] Rajeswari, R., Kalaiselvi, K., Jayshri, N., Lakshmi, P. and Muthusamy, A. (2024). Meta-heuristic-based melanoma skin disease detection and classification using Wolf Antlion Neural Network (WALNN) model. *International Journal of Intelligent Systems and Application in Engineering (IJISAE)*, 12(9s), 87-95.

[17] Rao, T.K., Chamanthi, P., Kumar, N.T., Amulya, R.L. and Sagar, M.U. (2022). Skin disease detection using machine learning. *IJFANS International Journal of Food and Nutritional Sciences*, 11(12), 1593-1604. https://ijfans.org/uploads/paper/155c01557c3eb20004a45795b59f3a41.pdf

[18] Rao, K.S., Yelkar, P.S., Pise, O.N. and Borde, S. (2021). Skin disease detection using machine learning. *International Journal of Engineering Research and Technology (IJERT)*, 9(3), 64-68. https://www.ijert.org/research/skin-disease-detection-using-machine-learning-IJERTCONV9IS03016.pdf

[19] Reddy, S.V., Shitole, V.N., Dhanawade, M., Ware, R. and Kadam, M. (2022). Skin disease detection using support vector machine algorithm. *International Journal of Scientific Research in Engineering and Management*, 1-5.

[20] Saleh, H., Mostafa, S., Ismail, A.H., Srivastava, S. and Alsamhi, S.H. (2024). Swin-pso-svm: A novel hybrid model for monkeypox early detection. *IEEE Access*, 4, 1-21.

[21] Sasmal, B., Hussein, A.G., Das, A. and Dhal, K.G. (2023). A comprehensive survey on aquila optimizer. *Archives of Computational Methods in*

Engineering,30,4449-4476. https://link.springer.com/content/pdf/10.1007/s11831-023-09945-6.pdf

[22] Sonia, R., Joseph, J., Kalaiyarasi, D., Kalyani, N., Gupta, A.S.A.J.G., Ramkumar, G., Almoallim, H.S., Alharbi, S.A. and Raghavan, S.S. (2023). Segmenting and classifying skin lesions using fruit fly optimization algorithm with a machine learning framework. *Journal for Control, Measurement, Electronics, Computing and Communications*, 65(1), 217-231.

[23] Tasci, E., Zhuge, Y., Camphausen, K. and Krauze, A.V. (2022). Bias and class imbalance in oncologic data Towards inclusive and transferrable AI in large scale oncology data sets. *Cancer*, 14(12), 1-16. https://pmc.ncbi.nlm.nih.gov/articles/PMC9221277/pdf/cancers-14-02897.pdf

[24] Tapak, L., Afshar, S., Afrasiabi, M., Ghasemi, M.K. and Alirezaei, P. (2021). Application of Genetic Algorithm-based support vector machine in identification of gene expression signatures for psoriasis classification: A hybrid model. *Hindawi BioMed Research International*, 2021(5520710), 1-10. https://pmc.ncbi.nlm.nih.gov/articles/PMC8443357/pdf/BMRI2021-5520710.pdf

[25] Thamizhvani, T.R., Aparna, K. A., Sannidhya, V., Hemalatha, R.J. and Chandrasekaran, R. (2022). Psoriasis skin disease identification using support vector machine (SVM) image classification and determining the growth rate. *Journal of Physics: Conference Series,* 2318 (2022), 1-11. https://iopscience.iop.org/article/10.1088/1742-6596/2318/1/012034/pdf

[26] Urban, K., Chu, S., Giesey, R.L., Mehrmal, S., Uppal, P., Delost, M.E. and Delost, G.R. (2021). Burden of skin disease and associated socioeconomic status in Asia: a cross-sectional analysis from the Global Burden of Disease Study 1990-2017. *JAAD International*, 2,40-50. https://pmc.ncbi.nlm.nih.gov/articles/PMC8362322/pdf/main.pdf

[27] Verma, A.K., Pal, S. and Kumar, S. (2019). Classification of skin disease using ensemble data mining techniques. *Asian Pacific Journal of Cancer Prevention*, 20(6), 1887-1894. https://pmc.ncbi.nlm.nih.gov/articles/PMC7021628/pdf/APJCP-20-1887.pdf

[28] Vishnoi, V. K., Kumar, K. and Kumar, B. (2021). A comprehensive study of feature extraction techniques for plant leaf disease detection. *Multimedia Tools and Applications*, 80(2), 1-54. https://www.researchgate.net/publication/354507540_A_comprehensive study of_ feature_extraction_techniques_for_plant_leaf_disease_detection

[29] Wolpert, D. H. and Macready, W. G. (1997). No free lunch theorems for optimization. *IEEE Transactions on Evolutionary Computation*, 1(1), 67-82.

[30] Yang, X.S. (2012). Free lunch or no free lunch: that is not just a question? *International Journal of Artificial Intelligence Tools*, 21(3), 1-13.

[31] Zeng, W., Liao, Y., Chen, Y., Diao, Q., Fu, Z. and Yao, F. (2023). Research on classification and recognition of the skin tumors by laser ultrasound using support vector machine based on particle swarm optimization. Optics Laser Technology, 158(6), 1-10.

[32] Shetty, B., Fernandes, R., Rodrigues, A.P., Chengoden, R., Bhattacharya, S. and Lekshmanna, K. (2022). Skin lesion classification of dermoscopic images using machine learning and convolutional neural network. *Scientific Reports*, 12(18134), 1-11.

[33] Raju, S.M. and Shobha, K.B. (2025). Automated skin cancer detection using support vector machines: A comprehensive approach. *Heritage Research Journal*, 73(3), 1-8.

[34] Saradhi, T.V. (2025). A study on hyperparameter tuning in support vector machines nd its impact on model accuracy. *Global Journal of Engineering Innovations and Interdisciplinary Research*, 5(1), 1-6.

[35] Gonzalez-Mendoza, M., Ibarra Orozco, R. E., Garcia Gamboa, A. L., Hernandez-Gress, N., Mora-Vargas, J. and Lopez-Pimentel, J. C. (2014). Quadratic optimization fine tuning for the support vector machine learning phase. *Expert Systems with Application*, 41(3), 886-892.

[36] Gopi, S. and Mohapatra, P. (2024). Fast random opposition-based learning aquila optimization algorithm. *Heliyon*, 10(2024), 1-31.