IAES International Journal of Artificial Intelligence (IJ-AI)
Vol. 13, No. 4, December 2024, pp. 4822~4832
ISSN: 2252-8938, DOI: 10.11591/ijai.v13.i4.pp4822-4832

Transfer-learning based skin cancer diagnosis using fine-tuned AlexNet by marine predators algorithm

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Article Info

Article history:

Received Jan 16, 2024
Revised Mar 3, 2024
Accepted Mar 21, 2024

Keywords:

AlexNet
Convolutional neural network
Marine predators algorithm
Skin cancer
Transfer learning

ABSTRACT

Melanoma represents one of the most dangerous manifestations of skin cancer. According to statistics, 55% of patients with skin cancer have lost their lives as a result of this disease. Early diagnosis of this condition will significantly reduce mortality rates and save lives. In recent years, deep learning methods have shown promising results and captured the attention of researchers in this field. One common approach is the use of pre-trained deep neural networks. In this work, a pre-trained AlexNet networks, which are networks with specified architecture and weights is used to automatic skin melanoma diagnosis. In the transfer learning phase, by reducing the learning rate, the pre-trained network is trained to recognize skin cancer, which is called fine-tuning. In addition, hyperparameters of the AlexNet network have been optimized by the marine predators algorithm (MPA) algorithm to enhance the network performance. Experimental findings show the satisfactory efficiency of the presented approach, with an accuracy rate of 98.47%. The outcomes demonstrate the effectiveness of the suggested approach in contrast to alternative existing methods.

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1. INTRODUCTION

The human body comprises various organs, with one of the most prominent being the skin, which serves as the body's largest organ, encompassing its entirety [1]–[5]. A skin ailment pertains to any condition that impacts the human skin [6]–[9]. Skin diseases, including skin cancer, are regarded as among the most widespread contagious conditions globally. Skin cancer, specifically, is a prevalent type of cancer that impacts numerous individuals globally. It is identified by the abnormal proliferation of cells. Early detection is crucial for effective treatment, as late-stage skin cancer can spread to other organs and potentially lead to death. Identifying skin cancer in its initial phases is typically more successful. In the past, skin cancer diagnosis involved using a dermo scope, which was expensive and required the expertise of a trained dermatologist. Skin diseases can be caused by viruses, bacteria, allergies, fungal infections, and genetic factors. Typically, these illnesses target the epidermis, the top layer of the skin, and their visibility can lead to psychological distress and physical injuries [10]–[15]. Different varieties of skin lesions are present, including actinic keratosis (AK), basal cell carcinoma (BCC), benign keratosis (BKL), dermatofibroma (DF), melanoma (MEL), melanocytic nevus (NV), squamous cell carcinoma (SCC), and vascular lesion (VASC). The symptoms and severity of these lesions vary, with certain ones being permanent while others are temporary. They can also vary in terms of pain levels. Melanoma is regarded as the most perilous among these skin conditions and potentially deadly.

Detecting skin diseases early is crucial, as around 95% of patients can recover if the condition is identified in its initial stages. Leveraging an automated computer-aided system can be advantageous in precisely categorizing skin diseases [11], [16]–[20]. There is frequently a considerable disparity between dermatologists and skin disease patients since many individuals lack awareness of the various kinds, symptoms, and phases of skin diseases. Delayed onset of symptoms can further complicate the situation, emphasizing the importance of early detection. However, accurately diagnosing skin diseases to identify their type and stage can be challenging and costly. Fortunately, the development of automatic computer-aided systems utilizing machine learning techniques have enabled this possibility to achieve more accurate and rapid detection of skin disease types. This advancement has the potential to bridge the gap and improve outcomes for patients.

Over the past 30 years, skin disease classification has been a significant area of research and has become a popular topic. Despite the considerable effort put into researching skin disease detection and classification, there remains an existing gap that requires attention and resolution. Past research endeavors have predominantly concentrated on a single disease., indicating a need for additional research and development to enhance the precision and utility of skin disease classification systems across a broader range of skin diseases [21]–[24]. The existing research in this field is insufficient for effectively classifying multiple classes of skin diseases. The task of classifying multiple classes is particularly challenging due to the similarities in behavior exhibited by different skin diseases. With the advancement of computational technology, particularly machine learning and computer vision, disease classification has improved. Imaging technologies are beneficial due to their lower cost, ease of use, and non-invasiveness procedure. When machine learning and computer vision are combined, the classification of skin lesions and selected features significantly impacts classification results. convolutional neural networks (CNN), a recently technology based on deep learning, enable image classification without the need for human detection and feature segmentation. This paper introduces an innovative approach to skin cancer diagnosis leveraging an improved AlexNet network enhanced by the marine predators algorithm (MPA). The research aims to increase the accuracy of the proposed method in comparison with other past studies in the field of skin cancer detection. In summary, the primary contributions of our research are outlined below:

- In this work, we have used pre-trained AlexNet networks, which are networks with specified architecture and weights. In the transfer learning phase, by reducing the learning rate, we train the pre-trained network to recognize skin cancer, which is called fine-tuning.
- The advantages of the fine-tuning method used in this work is the high learning ability on limited input images, as well as the ability to decrease the diagnosis error.

In the proposed method, the MPA is used to optimally adjust the hyperparameters of the model, which prevents overfitting of the network. The subsequent sections of this study are organized in the following manner: section 2 delves into the relevant literature. The suggested method is denoted in section 3. Section 4 provides the datasets utilized in this study, along with the corresponding experimental results. In conclusion, section 5 summarizes the research findings and outlines future prospects.

2. RELATED WORKS

Dorj *et al.* [2] employed dermoscopy pictures and digital pictures to distinguish skin disorders. Authors utilized CNN in feature extraction phase, wherein support vector machine (SVM) is employed as the classification method. It should be noted that in order to accurate skin diseases recognition from dermoscopy pictures, the expertise of a dermatologist is required. The authors employed Gaussian channels for hair removal and segmentation to isolate the affected areas. SVM was then utilized to classify the different types of skin diseases. However, additional investigation is required to expand and enhance the skin diseases classification specifically from dermoscopy pictures. Hosny *et al.* [25] suggested technique underwent assessment utilizing a dataset called HAM10000. Authors attained enhanced test and training accuracy through the using of SVM algorithm. However, analyzing the images posed challenges due to problematic elements such as reflections of light from the skin surface and variations within the images.

The analysis of skin lesions model proposed in [13] focuses on the automated image analysis module, that comprises stages including: image capturing, hair detection and elimination, lesion delineation, feature derivation, and characterization. However, it is important to note that this framework specifically focuses on identifying a single type of skin cancer and does not aim to distinguish between different types of skin tumors. Shanthi *et al.* [26] introduced a model based on computer vision for diagnosing four main skin ailments. Their methodology involved employing CNN networks with eleven layers, encompassing activation, convolutional, fully connected, pooling, and soft-max layers. The evaluation of the model utilized images sourced from the DermNet database, covering a range of skin disorders. However, the authors concentrated solely on four class of skin disorders: urticaria, eczema herpeticum, keratosis, and acne, with a restricted number of samples (30 to 60 samples per class). This research primary constraints entail the limited number of images and the narrow focus on only four classes of skin diseases.

Bhavani *et al.* [27] proposed an approach based on computer vision to detect various dermatological skin disorders. They utilized 3 deep learning-based methods, namely Resnet, Mobilenet, and Inception v3 for feature extraction from medical images. Logistic regression, a ML technique, was utilized for training and evaluating the medical images. The authors found that integrating of the three CNN models enhanced the overall performance of diagnosis system. However, it should be noted that the method employed in the study needed high computationally demanding. Also the dataset was used included just three forms of skin disorders. As a result, the architecture that used in this work may not be ideally suited for scenarios that involve multiclass classification.

Albawi *et al.* [28] presented a novel method for effectively identifying three specific skin diseases, namely nevus, melanoma, and atypical. To preprocess skin images, authors utilized an adaptive filtering technique to eliminate noise. Following that, they employed an adaptive region growing method to precisely localize and extract the regions of interest (ROI) corresponding to the affected areas. For extracting relevant features, they employed a hybrid approach that combined two-dimensional discrete wavelet transform with texture features and geometric. This combination allowed them to capture important information. Lastly, they implemented CNN on the international skin imaging collaboration (ISIC) dataset. The suggested method yielded remarkable results, achieving a classification accuracy of 96.768% for the identified diseases.

Ahammed *et al.* [29] introduced a digital hair removal technique that makes use of morphological filteration methods, such as black-hat transformation and an inpainting technique. They also applied Gaussian filteration to address image blurring or noise. The automatic Grabcut segmentation technique was utilized for accurate lesion segmentation. For extracting relevant patterns associated with images of skin, the authors employed techniques like statistical features and gray level co-occurrence matrix (GLCM). Ramachandro *et al.* [30] focused on classifying skin images, specifically targeting 4 types of skin tumors. They employed models based on deep learning, particularly transfer learning, utilizing pretrained deep neural networks such as DenseNet and CNN models. Additionally, they incorporated machine learning methods inclusing SVM and random forest (RF) classifier in their analysis.

3. METHOD

The objective of the research is to provide an effective model for detection of skin cancer using deep neural networks. Deep neural networks excel in image-related tasks due to their depth and the efficiency of convolutional filters. In this study, we employed the AlexNet deep neural network for this purpose. However, a significant challenge in enhancing the operation of neural networks is the precise tuning of the parameters. To address this challenge, we utilized the MPA algorithm for the optimal tuning of AlexNet network parameters. The schematic representation illustrating the presented method is depicted in Figure 1.

3.1. Data preprocessing

During the preprocessing phase, the image size is initially adjusted. As mentioned in the database description, the image size in the database is 600×450 pixels. However, the input image size for the AlexNet neural network is 227×227 pixels. Therefore, the image size is first resized to these dimensions. Subsequently, the data is segmented into test and training sets. In our work, 70% of the dataset is considered for training, and 30% for evaluating the network. The training set is applied to perform the training operation and update weights of the neural network. The test data is utilized to assess the network efficacy based on accuracy and generalization capabilities. The steps of the presented model are explained as follows.

3.2. AlexNet deep neural network

In this research, the AlexNet deep neural network is deployed for skin cancer detection. The proposed architecture of AlexNet includes a set of pooling layers, convolutional layers, fully connected layers, and a softmax layer. Structure of this network is depicted in Figure 2. This network is described as follows:

- Input layer: Images are provided to the network as input in this layer. Prior to entering the AlexNet network, preprocessing is applied. This process involves resizing the images to the dimensions required by the network and normalizing pixel values to a standardized scale (e.g., [0,1]).
- Convolutional layers: AlexNet comprises several convolutional layers that act as filters moving across images, detecting various features such as edges, enhancers, and different objects. These layers extract lower-level features like lines and shapes.
- Pooling layers: In the proposed architecture, pooling layers are placed after each convolutional layer. Pooling layers compress features and use essential information for subsequent stages. These layers help to reduce the spatial dimensions of the image.

- Fully connected layers: The extracted features enter these layers, subsequent to the pooling and convolutional layers. The fully connected layers are typically connected to a deeper neural network, capturing higher-level features and more complex combinations in the images.
- Activation function: In the hidden neural layers, activation functions like rectified linear unit (ReLU) are used. Activation functions nonlinearly transform the network's performance and extract nonlinear features from images.
- Output layers: The final result of this stage in the AlexNet network includes predicted labels for each image. These labels determine the detected class for each image.

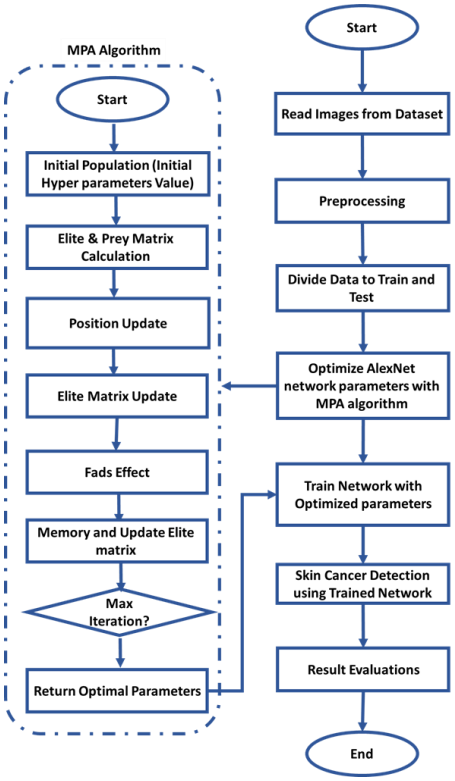

Figure 1. The diagram of the presented model

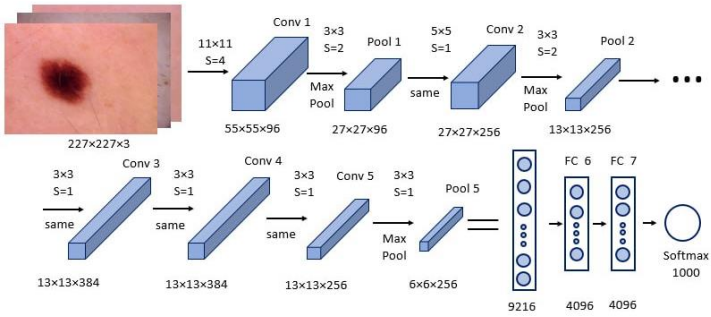

Figure 2. AlexNet deep neural network architecture

3.3. Fine-tuning AlexNet hyperparameters using marine predators algorithm

Utilizing deep CNN such as AlexNet for skin cancer detection can offer an effective solution with high accuracy. However, the challenge with using neural network models lies in the issues of overfitting or poor performance, often stemming from suboptimal parameter tuning. In the presented study, the MPA algorithm is employed to achieve optimal hyperparameter tuning for the AlexNet neural network, aiming to overcome challenges in the learning process. The hyperparameters of the AlexNet network, which were optimized based on this algorithm, are outlined in Table 1.

Table 1. The AlexNet network hyperparameters

Description	Parameters
Rate of learning	Learning rate
Mini batch	Size mini batch
Optimization algorithm (sgdm, rmsprop, adam)	Optimizer
Kernel size in Conv. layer	Kernel Size
Frequency of validation	Validation frequency

3.3.1. Marine predators algorithm

The MPA algorithm is a population-based approach that simulates the steps a marine predator takes to hunt its prey. In the initial phase, the predator remains stationary. In the next stage, it exhibits Brownian motion. Then, in the third stage, it operates according to the Levy strategy. This operation is also applicable to prey, which can be another potential predator. For instance, both sharks and tuna are regarded as marine predators, with tuna often serving as prey for sharks, it acts as a predator for other fish and invertebrates in the marine ecosystem. The steps of MPA algorithm are described as follows:

a) Initialization of the initial population

In population-based algorithms, the initial population (initial solution) constitutes a set of potential solutions to the problem, generated randomly. Here, the initial population consists of a set of initial values for the hyperparameters of the AlexNet network. Each member of the population, referred to as a search agent, represents a potential solution with optimal values for the hyperparameters. As the algorithm iterates, the solution values converge towards optimal values. Therefore, the position of each search agent in the parameter space of AlexNet hyperparameters needs to be optimized. In the MPA algorithm, the primary population is uniformly spread in the search space based on (1).

$$X_0 = X_{min} + rand(X_{max} - X_{min}) \tag{1}$$

where X_{min} and X_{max} are the minimum and maximum limits for the variables, and $rand$ is a vector of uniformly distributed random values in the range of [0,1].

b) Prey and elite matrices

The prey matrix represents the current positions associated with the search agents. In this matrix, each row signifies the current position of the i-th search agent. The matrix of prey is illustrated in (2).

$$Prey = \begin{bmatrix} X_{1,1} & X_{1,2} & \cdots & X_{1,d} \\ X_{2,1} & X_{2,2} & \cdots & X_{2,d} \\ \vdots & \vdots & \cdots & \vdots \\ X_{n,1} & X_{n,1} & \cdots & X_{n,d} \end{bmatrix}_{n \times d} \tag{2}$$

where Xi,j denotes the *j*-th dimension of the *i*-th search agent, n represents the count of search agents, while d indicates the number of dimensions.

According to the theory of "survival of the fittest", elite predators exhibit a higher hunting potential in nature. Therefore, the best solution of each search agent is selected as an elite predator to create the elite matrix.

$$Elite = \begin{bmatrix} X^I_{1,1} & X^I_{1,2} & \cdots & X^I_{1,d} \\ X^I_{2,1} & X^I_{2,2} & \cdots & X^I_{2,d} \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ X^I_{n,1} & X^I_{n,2} & \cdots & X^I_{n,d} \end{bmatrix}_{n \times d} \tag{3}$$

where $\overrightarrow{X^I_{i,j}}$ represents the Elite predator vector of the *i*-th search agent in the *j*-th dimension. Also, n denotes the count of search agents, and *d* denotes the dimensions number.

c) Position update

After creating an initial population and calculating the prey and elite matrices, the search agents' positions need to be updated accordingly. The MPA uses an intelligent approach to balance exploration and exploitation phases. This method utilizes three different movement strategies to update the locations of the search agents. The algorithm consists of three distinct phases to update the locations of the search agents, ensuring a balance between exploration and exploitation operations. These stages are determined in the following:

– The first phase

During the first-third of the search operations (Iteration<1/3*Iteration_max), the agents update their positions using Brownian motion. The new position is calculated using (4):

$$While\ Iter\ < \frac{1}{3} Max\_Iter$$

$$\overrightarrow{stepsize_\iota} = \overrightarrow{R_B} \otimes \left(\overrightarrow{Elite_\iota} - \overrightarrow{R_B} \otimes \overrightarrow{Prey_\iota}\right)\ i = 1, \dots, n \quad (4)$$

$$\overrightarrow{Prey_\iota} = \overrightarrow{Prey_\iota} + P.\vec{R} \otimes \overrightarrow{stepsize_\iota}$$

Here, the vector $\overrightarrow{R_B}$ is composed of random numbers that follow a normal distribution, symbolizing brownian motion. The constant P is assigned a value of 0.5, and vector $\vec{R}$ consists of random numbers that are uniformly distributed within the range of [0,1]. Iter represents the current iteration, and Max_Iter is the maximum number of iterations. Brownian motion assists predators in exploring distinct regions around them, leading to effective exploration in the initial iterations where predators are evenly distributed across the search space, and the distance between them is relatively high.

– The second phase

In the next one-third of the search operations (1/3*Iteration_max <Iteration<2/3*Iteration_max), half of the population is allocated for exploration using brownian motion, while the other half uses levy flight for exploitation. The new positions for half of the population are calculated based on (5).

$$While\ \frac{1}{3} Max\_Iter < Iter < \frac{2}{3} Max\_Iter$$

For the first half of the population;

$$\overrightarrow{stepsize_\iota} = \overrightarrow{R_L} \otimes \left(\overrightarrow{R_L} \otimes \overrightarrow{Elite_\iota} - \overrightarrow{Prey_\iota}\right)\ i = 1, \dots, n/2 \quad (5)$$
$$\overrightarrow{Prey_\iota} = \overrightarrow{Prey_\iota} + P.\vec{R} \otimes \overrightarrow{stepsize_\iota}$$

Also, for the other half using levy flight,

$$\overrightarrow{stepsize_\iota} = \overrightarrow{R_L} \otimes \left(\overrightarrow{R_L} \otimes \overrightarrow{Elite_\iota} - \overrightarrow{Prey_\iota}\right)\ i = n/2, \dots, n \quad (6)$$
$$\overrightarrow{Prey_\iota} = \overrightarrow{Elite_\iota} + P.CF \otimes \overrightarrow{stepsize_\iota}$$

Here, the vector $\overrightarrow{R_L}$ consists of random numbers that follow a Levy distribution, symbolizing a levy flight. The variable CF represents an adaptive metric for regulating the step size of the levy flight, calculated as (7).

$$\mathrm{CF} = \left(1 - \frac{\mathrm{Iter}}{\mathrm{Max_{Iter}}}\right)^{\left(2\frac{\mathrm{Iter}}{\mathrm{Max_{Iter}}}\right)} \quad (7)$$

– The third phase

During the last stage of optimization (Iteration>2/3*Iteration_max), the entire population is allocated for exploitation.

$$While\ Iter\ > \frac{2}{3} Max\_Iter$$

$$\overrightarrow{stepsize_\iota} = \overrightarrow{R_L} \otimes \left(\overrightarrow{R_L} \otimes \overrightarrow{Elite_\iota} - \overrightarrow{Prey_\iota}\right)\ i = 1,2, \dots, n \quad (8)$$
$$\overrightarrow{Prey_\iota} = \overrightarrow{Elite_\iota} + P.CF \otimes \overrightarrow{stepsize_\iota}$$

In this phase, the predators' transition from brownian motion to levy flight focus on their best local search for enhanced exploitation. The adaptive variable CF significantly aids predators in restricting search ranges in specific neighborhoods for exploitation and preventing wasted efforts due to the long steps of levy flight in inappropriate domains.

d) Update of elite matrix

Once the positions of the search agents have been adjusted, the fitness value for each agent is evaluated. If the fitness value for the current solution of the *i*-th search agent surpasses the previous fitness value, the current position of that agent will be updated in the elite matrix. This comparison is conducted for all search agents in each iteration.

e) Fish aggregating devices effect

Research findings indicate that sharks are observed in the vicinity of fish group activities for more than 80% of their time. For 20% that remains, they perform longer jumps in various dimensions, possibly seeking environments with different prey distributions. Fish aggregation devices (FADs) are perceived as local optimum, and their influence is akin to becoming ensnared at these points within the search space. Considering

the longer jumps during this phase prevents getting trapped in local optimum. Therefore, the FADs effect is determined as (9).

$$\overrightarrow{Prey_i} = \begin{cases} \overrightarrow{Prey_i} + CF\left[\overrightarrow{X_{min}} + \vec{R} \otimes \left(\overrightarrow{X_{max}} - \overrightarrow{X_{min}}\right)\right] \otimes \vec{U} \; if \; r \leq FADs \\ \overrightarrow{Prey_i} + [FADs(1-r) + r]\left(\overrightarrow{Prey_{r1}} - \overrightarrow{Prey_{r2}}\right) \; if \; r > FADs \end{cases} \quad (9)$$

The symbol $FADs$ denotes the likelihood of FADs exerting an impact on the operational procedure, set to 0.2. Also, $\vec{U}$ represents a binary vector with arrays containing zero and one, generated randomly. Additionally, the variable r represents a random number uniformly distributed in the range of 0 and 1. The variables $r1$ and $r2$ correspond to random indexes of the Prey matrix.

f) Memory and elite matrix update

Given the outlined considerations, marine predators derive advantages from a robust memory that enhances their success in hunting. This ability is emulated through memory preservation in the MPA. Upon updating the prey and incorporating the FADs effect, the fitness of each solution in the current iteration is juxtaposed with its equivalent from the preceding iteration. If the current solution's fitness value is higher, it replaces the preceding solution. The pseudocode outlining the MPA algorithm for optimizing the parameters of the AlexNet neural network is illustrated in Pseudocode 1.

Pseudocode 1. The MPA algorithm pseudocode

```
Input: Maximum Iteration Number, initial value of Parameters that must be optimized
(Learning Rate, Mini-Batch Size, Optimizer function, Kernel Size and Validation Frequency),
Permissible range of variables.
Output: Optimized Value of Learning Rate, Mini-Batch Size, Optimizer function, Kernel Size
and Validation Frequency
Initialize search agents' population
While (maximum iteration number reach)
Calculate the fitness value and generate the Elite matrix.
If Iteration<Max_Iteration/3
Update prey-matrix according to Eq. 4
Else if max_ Iteration /3< Iteration <2*max_ Iteration /3
for first half part of population (i=1,…,n/2)
update prey-matrix according to Eq. 5
for the second part of the population (i=n/2,…,n)
update prey-matrix according to Eq. 6
Else if Iteration >2*max_ Iteration /3
update prey-matrix according to Eq. 8
End (if)
Updates Elite-matrix according to current fitness and previous fitness that saved in memory
Applying fads effect and update prey-matrix according to Eq. 9
End while
```

4. THE EXPERIMENTAL RESULTS

In this stage, we provide the simulation outcomes of the suggested model for the diagnosis of skin cancer. Initially, evaluation criteria are introduced. Subsequently, the findings of the presented method are analyzed and a comparison with other techniques is performed. It should be noted that simulations are conducted using Google Colab. Additionally, data are divided into training and test datasets. In this process, 70% data is considered for training and 30% for test and evaluation.

4.1. Dataset

In this study, the HAM-10000 dataset is utilized for skin cancer detection. The HAM10000 database containing 10,015 dermatoscopy images depicting various skin lesions. The dataset was gathered from patients in Australia and Austria. The images have dimensions of 600*450 pixels and are centered crops. This database consists of 7 classes, each representing a specific disease. These classes are reported in Table 2. Some examples of the database images are illustrated in Figure 3.

Table 2. HAM-10000 database classes

Class No.	Disease type
0	Actinic keratoses and intraepithelial carcinoma/bowen disease
1	Basal cell carcinoma
2	Benign lesions of the keratosis
3	Dermatofibroma
4	Melanoma
5	Melanocytic nevi
6	Vascular lesions

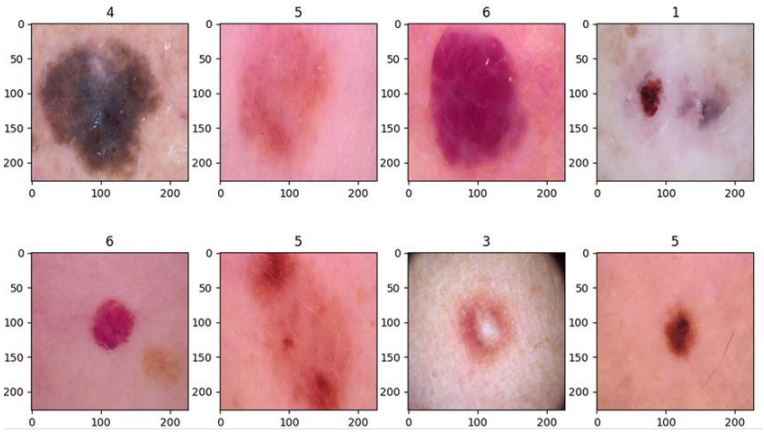

Figure 3. Dataset image examples

4.2. Evaluation metric

In our work, precision, accuracy, recall and F-measure are employed to evaluate the effectiveness of the presented model. The equations for these metrics are presented as follows:

$$Accuracy = \frac{(TP+TN)}{(TP+FP+TN+FN)} \quad (10)$$

$$Precision = \frac{TP}{(TP+FP)} \quad (11)$$

$$Recall = \frac{TP}{(TP+FN)} \quad (12)$$

$$F1\ score = \frac{2*(Recall*Precision)}{(Recall+Precision)} \quad (13)$$

Here, TP represents true positive rate (TPR) of detection, TN denotes true negative rate of detection, FP signifies false positive rate (FPR) of detection, and FN indicates false negative rate of detection.

4.3. Evaluating training process

Figure 4 illustrates the learning curve in terms of the loss function on the training set for 1000 epochs. The loss, also referred to as the cost, quantifies the model's error. The objective of the model is to minimize the loss, which is achieved through techniques such as gradient descent. Hence, as the learning progresses, a smaller loss indicates improved model performance. To quantify the loss, a loss or cost function is evaluated. In Figure 4, the expected evolution of the learning process is observed. It is evident that the loss curve consistently decreases over the course of training. As the learning curve demonstrates, the network loss has increased from 0.5 per 400 epochs to 0.15 per thousand epochs. This means that the learning process in the proposed model has occurred correctly.

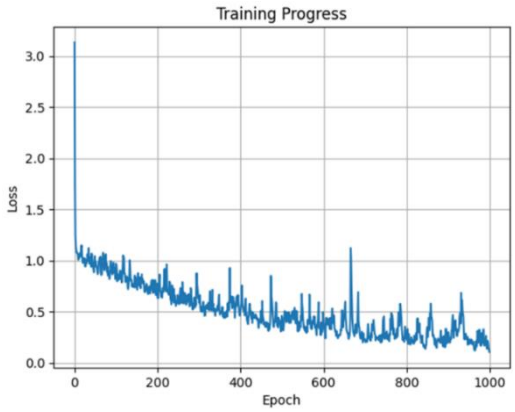

Figure 4. Learning curve

4.4. Result evaluation and discussion

As was mentioned, precision, accuracy, recall, and F1 measure metrics are employed to assess the effectiveness of the presented approach. The numerical findings of the evaluation metrics obtained from simulations for training and test data are presented in Table 3. As can be seen, the parameters of accuracy, precision, F1-score and recall for the training data are 99.11, 99.13, 99.11, and 99.11, respectively. Also, the value of these metrics for the test data is 98.47, 98.51, 98.47, and 98.47, respectively. It is obvious that these parameters achieved higher values for training data than for test data. Since the network has seen this data in the training process.

Table 3. Evaluation metric results for train and test data

Metric	Results for training data	Results for test data
Accuracy	99.11	98.47
Precision	99.13	98.51
Recall	99.11	98.47
F-score	99.11	98.47

Using a range of thresholds, TPR is plotted against the FPR to observe the trade-off between these two measures is observed. A highly accurate classifier tends to be positioned towards the upper left corner of the receiver operating characteristic (ROC) curve, exhibiting a high TPR and a low FPR. Conversely, a poorly performing classifier is typically situated towards the lower right corner of the ROC curve, characterized by a low TPR and a high FPR. Additionally, a random classifier lies along the diagonal line of the ROC curve, indicating an equal TPR/FPR ratio. The ROC curve of the proposed model is depicted in Figure 5. As illustrated, this curve demonstrates a high TPR and a low FPR, positioned near the upper left corner. Consequently, it can be concluded that the presented method has produced accurate results in the skin cancer classification. Figure 5 presents the ROC curve.

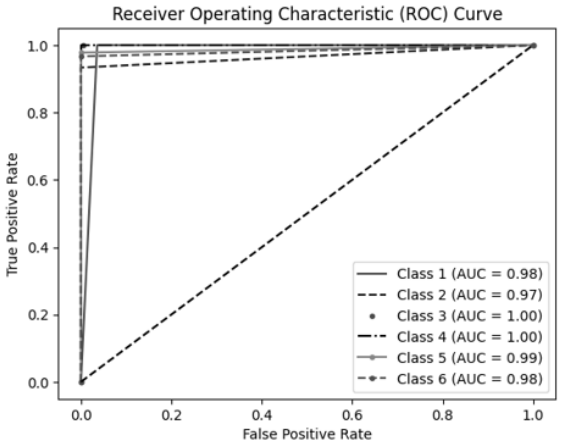

Figure 5. The ROC curves

Here, we delve into the examination and comparison of the outcomes achieved from the presented system with other approaches. Table 4 illustrates the comparison of outcomes based on accuracy, recall, F1 score, and precision metrics. As the tables presents, the presented method is superior to other methods in terms of all criteria. For example, the suggested approach achieved 98% accuracy, while the highest accuracy after the presented approach is related to the SVM with a value of 97%. Our study suggests that higher recall is not associated with poor performance in precision. The proposed method may benefit from recall without adversely impacting precision. In addition, we found that the recall and precision measures were correlated with the F-score measure. The proposed method in this study tends to have an extremely high ratio of Fscore compared to other previous studies. The superiority compared to other techniques is also observed in other criteria which are given in Table 4. The reason lies in the precise and optimal tuning of the AlexNet parameters using the MPA.

It is worth mentioning that this research has investigated simultaneously all the criteria of accuracy, precision, recall, F-measure, ROC curve, and learning curve. While previous studies have not investigated the

simultaneous effect of all these criteria, and previous studies have investigated some of these criteria. In addition, in this paper a comprehensive study in automatic transfer learning based skin cancer diagnosis using fine-tuned AlexNet by MPA algorithm explored. However, further and in-depth studies may be needed to confirm its efficient on more patient. In this study shown that swarm intelligence-based optimization algorithms such as MPA algorithm are more efficient than traditional methods for fine-tuning deep neural network hyper parameters. Future studies may investigate more up-to-date meta-heuristic algorithms for tuning hyper parameters of deep neural networks. Recent observations in the studies of automatic detection of skin cancer show that deep learning-based methods can provide a good performance in diagnosing this disease with high accuracy. Our findings provide conclusive evidence that fine-tuning hyper parameters of pre-trained deep neural network using optimization algorithms based on meta-heuristic methods can lead to better performance of the skin cancer diagnosis model. The results obtained in this work confirm this issue.

Table 4. Results comparison based on accuracy, precision, recall, and F1 score

Method	F-Score	Recall	Precision	Accuracy
KNN [29]	94.71	95.14	95.14	95
DT [29]	95.14	95.57	95.71	95
SVM [29]	97.43	97.57	97.71	97
RF [30]	83	89	91	92
CNN [30]	92	89	91	93
DesNet [30]	83	84	93	95
The proposed method (MPA-AlexNet)	98.47	98.47	98.51	98

5. CONCLUSION

This paper introduces the improved AlexNet neural network with MPA to detect skin cancer. Early diagnosis of this disease will drastically reduce mortality rates and save lives. In recent years, technologies based on artificial intelligence such as neural networks have achieved promising results in this field. Our proposed method involves optimizing the AlexNet network parameters by the MPA algorithm. The results of the simulations show the superiority of the presented approach based on the evaluation parameters used in the experiments. AlexNet neural network is powerful in the field of recognizing and classifying patterns from images. Due to its parallel search capability, the MPA algorithm has a good convergence speed and does not get trapped in local optima. Therefore, the integration of the AlexNet neural network and the MPA algorithm in the proposed method has contributed significantly to its outperformance in comparison with other state-of-the-art methods.

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