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Optimization of Feature Selection Using Greylag Goose Optimization Algorithm for Monkeypox

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Abstract

Monkeypox is an illness like smallpox that began to spread through several countries at a relatively rapid pace. The rash is among monkeypox's most outstanding clinical features; however, a similar rash is evident in measles and chickenpox patients as well. AI and computer vision are well on their way to becoming must-have medical tools. For instance, computer-aided design (CAD) uses visual data to diagnose diseases such as chickenpox and measles at their early stage. Proposing a similar utilization of the AlexNet pre-trained model in extracting the differential features from MSID, the research has recorded an impressive precision rate of 0.932295, a testament to the credibility and precision of our research. We apply feature selection to reduce the extracted features in our proposed binary Greylag Goose Optimization (bGGO) method, a novel approach that we believe has the potential to significantly outperform existing models. It gives a better average fitness of 0.60068 and fixed best fitness as 0.50248. The presented model, with its novel approach, is discussed with several other optimization models, namely, binary waterwheel plant algorithm (bWWPA), Boosted Dipper Throated Optimization (bDTO), binary particle swarm optimizer (bPSO), binary whale optimization algorithm (bWAO), binary gray wolf optimizer (bGWO), and binary firefly algorithm (bFA). For the possibility of a difference between the subjects in the suggested approach and other methods, the results were subjected to the Wilcoxon signed-rank test and Analysis of variance.

Keywords: Monkeypox, Meta-Heuristic Optimization, Feature Selection, Analysis of Variance.
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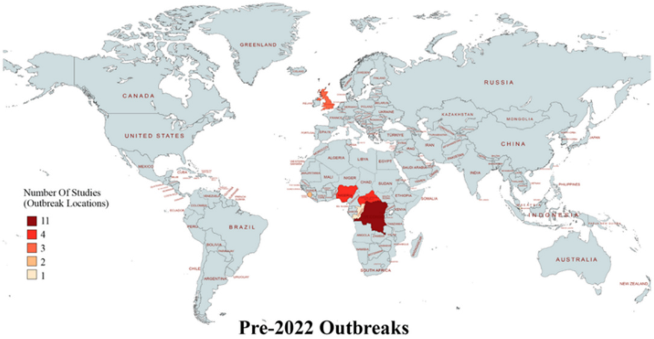
1. Introduction

In 2022, after preventive measures to face the coronavirus to decrease the number of infections and deaths, the World Health Organization (WHO) received many alerts from many European countries and America about a new outbreak of a ghost that threatened the world again, called monkeypox. The orthopoxvirus strain, which causes monkeypox, spreads quickly, as illustrated in Figure 1. Before 2022 and after the spread of a fatal disease like COVID-19, monkeypox first appeared in western Africa in the seventies of the last century. It can spread by animal bites, respiratory droplets, direct physical contact, and mucus from the mouth, nose, or eyes [1]. It was challenging to diagnose the disease because of its similarity to the orthopoxvirus family (smallpox, chickenpox, and measles). They all have similar symptoms, like rashes, fever, fatigue, headache, muscle pain, and a high temperature [2]. The disease's main symptoms are rashes that appear after 3-5 days of infection and then appear all over. The body becomes so painful after 3–4 weeks that the virus's incubation disappears, and the skin returns to its original shape [3]. Although the monkeypox fatality rate is 3% of infected cases, it still presents a headache because of the threat of a new commercial shutdown. Researchers applied numerous tests, including polymerase chain reaction (PCR), CT scans, and clinical examination, to detect monkeypox, but they still need to achieve the desired results [4].

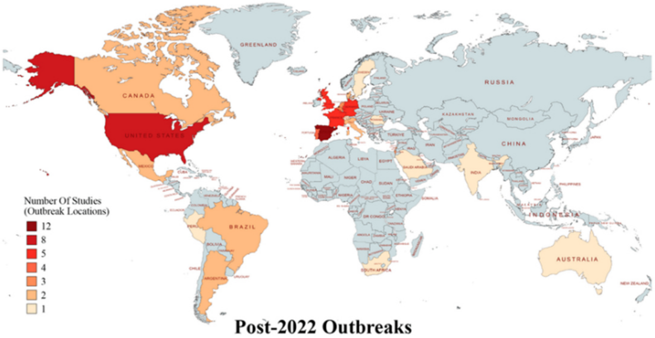
Many remote and impoverished rural locations worldwide now have numerous medical restrictions. Such an infectious virus could spread quickly without insufficient medical personnel and an inadequate healthcare system. Furthermore, there is a chance for accurate and complete sickness reporting and delays in the current medical system. For early diagnosis of COVID-19 to stop the infection and avoid death, it was essential for early detection before spreading all over the lungs [5]. Artificial intelligence (AI) can enhance the efficiency of medical systems. AI can apply feature selection algorithms to eliminate superfluous and insignificant characteristics from the data. Many studies have demonstrated that choosing the most essential characteristics simplifies the learning model and enhances its capacity to generalize in the shortest amount of time [6].

We applied different pre-trained models (GoogleNet, VGG19, AlexNet, and ResNet50) to extract the most extensive features of the disease. In the feature extraction process, AlexNet had the best model performance because it reached an accuracy of 93.22%. Next, we used Greylag Goose Optimization (bGGO) and six other binary algorithms (bWWPA, bDTO, bPSO, bWAO, bGWO, and bFA), along with more binary optimization models, to find the best features for the extracted group. We applied parametric and non-parametric statistical tests, including an analysis of variance (ANOVA) and a Wilcoxon signed rank test, to verify the hypothesis. We can summarize the main contribution as follows:

- The Monkeypox Skin Image Dataset MSID is currently undergoing pre-processing.
- Offer deep-learning techniques for diagnosing monkeypox.
- Extract the most common features from AlexNet.
- We use the Greylag Goose Optimization Algorithm (bGGO) to optimize the extracted features.
- We use the Wilcoxon rank and ANOVA tests to test the bGGO hypothesis.



Pre-2022 Outbreaks



Post-2022 Outbreaks

Figure 1: Monkeypox Outbreak after Several Reports [7]

The following sections form the paper's structure: Section 2 presents related work, followed by a proposed method in Section 3, the outcome of our proposed method in Section 4, and finally, the conclusion and future directions.

2. **Related Works**

The following studies were examined to demonstrate the deep learning rule for early monkeypox identification and containment. The researchers utilized the available image dataset to assess the model's performance. Still, it was too tiny, so they had to employ data augmentation techniques to prevent overfitting and underfitting issues. The color and texture information of the skin are the most crucial characteristics for detecting and identifying skin disorders. The size and shape of each unique lesion are also influenced by the type of sickness and the intensity of the ailment. Choosing which traits to employ in conventional methods is an uphill task. Furthermore, as it affects the classification algorithm's accuracy, it is crucial to determine the attributes pertinent to the issue. However, features may be automatically and effectively learned by evolutionary processes. It separates the picture into areas based on the pixels, the borders, or the regions themselves using one of the many image segmentation methods available [8].

In [1], the authors proposed the following modifications to the base architectures for monkeypox detection with the intended goal of improving performance; they proposed a VGG19 – MobileNetV2 – Vision Transformer (ViT) model that was initialized to enhance the pre-trained model VGG16 by changing F. C. layer with the 'SoftMax' activation function, and they also trained the weight of the convolution layers properly. The authors used two datasets from Kaggle wherein Kaggle has two classes for binary classification. The first dataset comprises 76 images, including 43 images of monkeypox and 33 standard images; the second dataset comprises 818 images, of which 587 belong to monkeypox and 231 standard images. Data was split by 80:20 for training and testing before, whereas for the second dataset, the accuracy for VGG19 was measured at 93%, corresponding to 94% F1-Score. MobileNetV2 was the best model, achieving 99% accuracy and 94% F1-Score for the second dataset.

An early detection method for monkeypox disease called monkeynet was introduced in [2], which aids doctors in early detection. We then applied the model to a dataset of four classes, totally 770 images 279 monkeypox, 107 chickenpox, 91 measles, and 293 standard cases. However, due to the limited quantity of images, they conducted a pre-processing stage to boost the image count to 8689 across all classes, thereby preventing over-fitting issues. We divided the data into 80:20 train: test ratios. The suggested model (monkeynet) has a convolution, max-pooling, and dense layer. These components comprised the CNN structure, which identified the most common features and simplified the feature selection process when using densenet201. Different machine learning and deep learning models calculated their performance according to accuracy, precision, and 5-fold cross-validation. The proposed model is a modified Dense Net-201 that reaches a level of precision of 93.19, 98.92, Recall of 93.19, 98.91, and an F-1 score of 93.15, 98.91. Test accuracy was 93.19, 98.91, AUC 0.9918, and 0.9997 for the original and augmented datasets. Grad-CAM enabled a good understanding of the model's prediction and created a heat map representing gradient information going into the last convolutional layer.

In [3] applied the hybrid of the particle swarm optimization algorithm and Biruni Earth radius (bPSO-BER) to improve the feature extracted by the Google Deep algorithm and identify the most unique feature within the group of features that GoogLeNet selected. The proposed algorithm in binary form was given and compared with the other six optimization techniques in detail above. In the case of bPSO-BER, the best results were obtained; in particular, the accuracy of the selected feature was equal to 0.938023, the sensitivity got to 0.625, and the specificity was 0.9980039. On the other hand, the best previous results before feature selection yielded an accuracy of 0.9020618; the sensitivity of this test is 0.74 for the magnitude of .625 with a specificity of 0.99315068. They also used statistical tests, analysis of variance (ANOVA), and Wilcoxon signed Rank test to test the hypothesis.

In [4], they adopted the presented here Reinforcement learning algorithms Deep Q-learning Network (DQN), Double Deep Q-learning Network (DDQN), policy Gradient, and Actor-Critic to enhance the diagnosis and classification of monkeypox. They employed the neural network for feature extraction and classification of the data with reinforcement learning and the Adam optimizer. This enhanced the outcomes and precision of the offered model or presumptuous EfficientNet B3. The dataset consists of two classes: The augmented dataset contained 228 images: 102 images of monkeypox and 126 images of other diseases. They split the data into training, validation, and testing (70:10:20) for monkeypox, while the other set consists of 1428 images of monkeypox and 1764 images of other diseases. They used four pre-trained models and calculated their performance: VGG-16 reached the top 5 error rates of 90. 2%

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accurate, while ResNet 50 is 85.12%, Inception v3 91.1%, DenseNet-169 92.75%, while the accuracy of the tested COVID-19 cases was 92.01%. Subsequently, compared with Reinforcement learning, DQN was 96.5%, DDQN was 89.7%, Policy Gradient 78.7%, actor-critical was 80. 7%, and Malneural 97.7%.

researchers [10] enhanced the transfer learning method to raise monkeypox detection rates. They publicly released the image dataset and placed it on the GitHub website. The dataset was formed using the information collected from several online sources. Finally, it is possible to obtain the AUC value, several true positives, true negatives and false values in the vicinity of 0.88 and 0.97 using the VGG16 model; they built a new model based on modifications of this work that included the information of two experiments.

A study by authors of [11] proposed an improvement in feature selection and classification applied to monkeypox. The chosen data encompassed two classes for binary classification, with 770 images Before using the technique, images splitted into training, testing, and validating segments 60:20:20 [9], and after augmentation, there are 2500 images. Features were extracted using GoogLeNet because it emerged as the most discriminant layer for monkeypox. The utilized technique is called Binary Dipper Throated Optimization (bDTO), and the feature selection process takes place by choosing input features with binary values. Features were trained using four models, and a comparison was made between the four model performances: AlexNet, VGG19, ResNet50, and Google Net; the best model was chosen, which was Google Net. The accuracy of this model was 82%. They also suggest that a metaheuristic algorithm (dipper-throated optimization) (DTO) be applied to enhance selecting features. For the outcome detection, they used a decision tree classifier. The method proposed in this paper yielded an accuracy of 94%. This test measures a specificity of 61% with a sensitivity of 95% and a negative predictivity of 35%.

The Mendeley dataset was used in [12] to utilize the monkeypox classification and detection method. It consists of two classes: monkeypox and others that are far more complex and bear seeds of destruction within their core. It contains 228 images: 102 for monkeypox and 126 for others [13]. After augmentation, the number of images in the two classes was twenty-four hundred ninety-six, which after RoI pooling and normalizing resulted in 3192. To avoid the overfitting problem, the data was separated into 80:20 training and testing. CNN was employed to get the most discrete layer, which includes layers that down sample feature maps and fathom the totality of neurons connection. They applied four models: CNN, VGG-19, Inception v3, and Autoencoder. Autoencoder effectively completed the reduction of the input domain space and constructed the output space. An autoencoder is a neural network of multiple layers that can automatically control the number of members. They applied the hyperparameter of the (ADAM) Optimizer for optimal performance with a particular learning rate of 0.001 and the evaluation uses the binary cross entropy loss function on Inception v3, CNN, VGG-19, and Autoencoder architectures. Their scores were 96.56%, 93.43%, 94.06%, and 85.62%, respectively.

A mobile application was introduced in [14] to classify monkeypox from other diseases; two datasets were applied with different images for these classes: the first dataset had 228 images; 102 were monkeypox images, whereas the others were different [10]. The second dataset was in the form of images with 770 images, of which 279 were monkeypox images, and the remaining 491 were other data with division of training set as 60%, validation set as 20%, and testing set as 20% [15]. They employed nine layers and used values in the units where the first layer consisted of 1024, and the last consisted of 4 only. Next, ReLU was added as a parameter of the activation function of this network while making SoftMax one of the parameters of the activation function of the last network layer in the bigger CNN size. The result had an accuracy of 99% and a precision of 99%, recall was 100%, and F-score was 98%.

As depicted in [15], the presented web scraping allows any user to find and use a detailed database of images of skin conditions and healthy skin. Pictures of contaminated skin include six similar diseases: infectious disease, like the classic symptoms of monkeypox and caused by the orthopoxvirus. They collected images of skin lesions from chickenpox, monkeypox, Smallpox, Cowpox, normal, and measles [23]. They obtained most of these images from social networks, websites, news galleries, and cases. The first things to try were the data augmentation to dataset to increase number of samples to the databases after collecting more.

In [16], the authors introduced an intelligent healthcare monitoring system to detect monkeypox based on an image dataset from GitHub. To prevent overfitting, the system augmented only two classes of 1905 images, yielding 587 images of monkeypox and 838 other images divided into training and testing at 70% and 30% [17]. Through various parameters related to infected person registration authority, intelligent contracts, decision-making, and interplanetary file systems, the system assisted physicians in monitoring and controlling the spread of the disease. Among the models applied are Xception, VGG16, and VGG19.

The proposed model, a refined version of ResNet50, features 50 hidden layers, including convolution, average, maxpooling, and fully connected layers, to create a fully connected network with the most distinctive features of monkeypox. It compares results based on accuracy and F1-score. The proposed system had an accuracy of 98.80% and an F1-score of 98.81%.

The authors of [18] introduced an Accurate Monkeypox Diagnosing Strategy (AMDS). Two different datasets were used (MPX_Data and MPPD Data); MPPD data was maintained from twenty-five thousand with numerous symptoms, classified into two classes: infected and not infected. Results showed about sixteen thousand cases had monkeypox, while nine thousand were normal [19]. MPX_Data was collected from five hundred people and separated into 350 for training and 150 for testing [20]. At the preprocessing stage, AMDS was divided into two phases (preprocessing and classification) to select the most compelling features and symptoms. Then, in the next stage (classification phase), they used Ensemble classification, a collection of different (two or three) pre-trained models. Different machine and deep learning classifiers were applied to the long Short-Term Memory (LSTM) model because it provides accurate results compared to other classifiers used for MPX data. The Binary Tiki-Taka Algorithm (BTTA) had the highest accuracy of 98.77%. They compared these results to AMDS according to datasets. MPX_Data had the highest accuracy at 98.99%, whereas MPPD_Data had the highest accuracy at 97.09%.

In [21], the authors employed the DL algorithm in different research to classify DNA sequences of monkeypox and the HPV responsible for it. With the help of F1 scores, two DNA mapping methods were evaluated, relying on characteristics such as accuracy, precision and recall. The performance evaluation depicts an F1 score of 99.83 with an average accuracy of 96. 08%. They developed and employed a computerized skin dataset that included pictures of rashes and skin infections from various diseases: incidentally, not only measles, chickenpox, and smallpox, but cowpox and monkeypox are also contained in this. These findings suggest that deep implementations have a high potential to accurately categorize monkeypox from scanners' skin images at 85%.

In the studies by the author [22], They developed and employed a computerized skin dataset that included pictures of rashes and skin infections from various diseases: Measles, Chickenpox, Smallpox, Cowpox as well as Monkeypox. Based on their study, they conclude that deep implementations have a high potential to achieve (85% accuracy) in distinguishing monkeypox from skin images. However, for the more robust detection capacity of those deep models, many training samples need to be trained in the models. We concentrated on categorizing the monkeypox virus to achieve the research objectives using Deep CNN. The result of it is presented in Table 1 below.

Table 1: Related Works Summary

Ref	Methods	Dataset	Accuracy	Tool	Contribution	Type
[1]	Modified Versions of The VGG19 And Mobilenetv2	Kaggle	93% 99%	LIME	classification	2-Class Method
[2]	Monkeynet	[9]	98.91%	Grad-CAM		4-class Method
[4]	Reinforcement Learning (Malneural)	[10]	97.7%	—	Features selection optimization	2-Class Method
[11]	Fine-Tuning The Decision Tree	[9]	94.35%	—	Features selection optimization	2-Class Method
[12]	Inception V3	[13]	96.56%	LSTM	classification	4-Class Method
[14]	MobileNet v2	[10,15]	99%	__	classification	4-Class Method
[15]	Different Augmentation methods	[23]		__	Dataset enhancement	6-class diseases
[16]	Fine-Tuned Resnet50	[17]	98.80%	__	detection	2-class Method
[18]	Fuzzified Voting Scheme (Fvs)	[19,20]	98.77 97.09%	LSTM	Classification detection	2-class Method

3. The proposed method

The five main phases of the proposed method are the collection of the appropriate dataset, preprocessing of the data, feature extraction, optimum feature selection, model training, and statistical assessment. Collecting monkeypox photos involves using a publicly accessible dataset on Kaggle. The selected dataset lacks raw data, so we use data preprocessing methods to enhance the size and quantity of fresh pictures during the augmentation stage. Four popular models, AlexNet, VGG19, ResNet50, and GoogleNet, were trained, tested, and evaluated to determine which deep learning model provides the most fantastic accuracy in identifying monkeypox instances. We input the preprocessed images into the selected models during training and adjust the model's parameters to increase accuracy. The features from the input photos are then extracted using the model that performs most effectively. bGGO subsequently selects the optimal collection of features by processing the retrieved features using the suggested feature selection technique. At this stage, we test the model using accuracy, precision, recall, and F1-score metrics to assess its effectiveness. The procedures and stages that make up the proposed model are depicted in Figure 2.

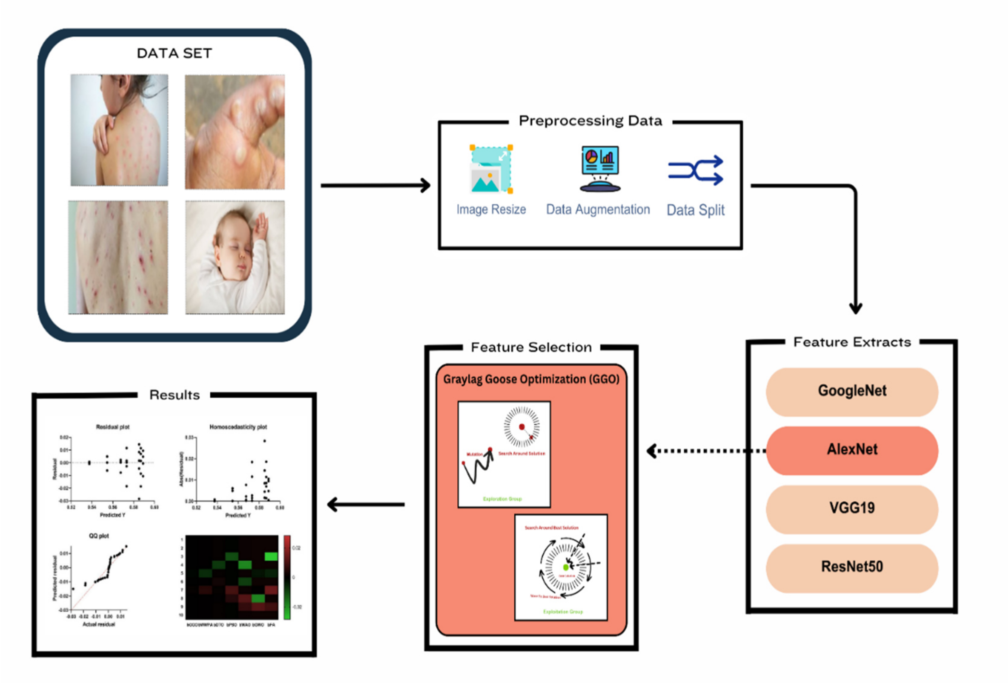

Figure 2: The Overall Framework of the Proposed Model

3.1. Data Preprocessing

The five main stages of the assumed technique are, gather data, data preparation, training, evaluate, and the new method. The first action requires collecting the photos of people infected with Pox. Collection of Data Some of the working people around the globe think that artificial intelligence is necessary in our lives and mostly in the health sector. There are several fast and easy ways for such data collection when it is necessary to access the sites and platforms in various study fields and having an approval for it. However, a hundred years ago, the sole source of information was newspapers and journalists while these days information might require the arrival of lower quality or even wrong information at a faster pace. Our research uses one of the most popular and reliable datasets from the reliable and honest Kaggle platform. The Monkeypox Skin Image Dataset (MSID) consists of 770 RGB images, as shown in Figure 3. Due to data scarcity, more photos were created using data augmentation techniques. Data augmentation techniques were applied to the photos to prevent overfitting and growing the dataset [11].

This increase in the data set increased the accuracy and dependability of the model. Numerous data augmentation methods have been put forward to overcome these two challenges. Data-augmentation approaches may gradually increase the size of the dataset. These methods include, but are not limited to, flipping, rotating (0–360 degrees), shearing, and shifting. With these techniques, which enable the creation of new pictures with just a few modifications to the original photos, a vast and more diverse dataset may be produced for training the deep learning model. The suggested data augmentation techniques seek to improve the model's capacity for generalization by augmenting the dataset with more information [10]. The gathered photos undergo scaling, normalization, and data augmentation in this data preprocessing step. This is a critical step in optimizing the model's performance. Four popular models

(GoogleNet, VGG19, AlexNet, and ResNet50) were chosen and contrasted to increase the model's accuracy for monkeypox virus identification. We use preprocessed photos to train the selected models at this stage of the model training process. The model is fed pictures during the training phase, and its parameters are changed to maximize output. The model is assessed at the last step using accuracy, precision, recall, and F1-score measures. The ultimate model is chosen based on whatever model performs the best. Consequently, the suggested approach must use deep learning techniques to evaluate monkeypox patient photos and correctly categorize and diagnose the illness based on visual traits [24].

Figure 3: Sample Of MSID Dataset

3.2. Convolution Neural Networks

One type of deep neural network often utilized for image classification issues is the convolutional neural network (CNN). Because CNNs are so good at identifying abnormal patterns in skin pictures, MRIs, CT scans, X-rays, and other medical imaging methods, they have been employed widely in the medical industry. The three primary layers of CNN's architecture are convolutional, pooling, and fully linked. Other layers, like dropout layers and batch normalization, may be introduced to aid in regularization and normalization. Convolutional layers employ filters to gather crucial characteristics from pictures by executing a convolution process between a filter and the input obtained from the preceding layer. The last result of the layer is often formed by applying a non-linear activation function, such as ReLU, to the convolution process product. Pooling layers are employed to reduce feature map size and boost CNN performance. Local and global pooling layers are two different types of pooling layers. There are techniques like max pooling and average pooling under each layer group. The final classification is obtained by fully linked layers using the input characteristics taken from the earlier levels [25].

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3.3. Pre-trained model

We developed and utilized CNN as a type of neural network. We used pre-trained models in our classification process due to their capacity to process many images quickly. All images were adjusted to fit the initial size of the model by the image resize process because not all models had the same initial size. Among these different models, we used four to extract the most distinguishing features that make detecting monkeypox much easier. We then filter the extracted feature set to include specific features that determine whether the infected individual continues to have the disease or not. Given the variety of similar skin diseases, each model incorporates a combination of multiple layers. Among the pre-trained CNNs, we used GoogleNet, VGG19, AlexNet, and ResNet50 [26-29]. The picture scaling was done to a standardized goal size of 224 × 224 pixels, which aligns with the input dimension of the selected CNN architectures: GoogleNet, VGG19, AlexNet, and ResNet50. This is due to the wide range of sizes of the photos in the expanded monkeypox image dataset. In addition, during the training phase, we used an image augmentation strategy to prevent over-fitting, which often occurs when using pre-trained advanced CNN models and little information [30].

3.4. Feature Engineering

Feature engineering plays an important role, not just in machine learning methods. With the help of these approaches, the characteristics that machine-learning processes demand are selected. An example of a standard usage case is the symmetry of the feature extraction step and the feature selection step. Thus, feature extraction tries to transform the original data to achieve more variables that could improve the efficiency of the selected machine-learning algorithm. This is not so with feature selection, where the objective is to find and identify the respective features in the data set that are most beneficial for the classification jobs based on specific criteria such as meaningfulness, consistency, and distinctiveness. In implementing the feature selection procedure, we restrain the search space to binary values 0 and 1.

It also means to change the continuous value-based meta-heuristic optimizers to manage the binary outputs respective to the selected features [3]. The most critical process in feature engineering is feature selection, which sets out which features will be used for speed optimization. In the case of the n-feature set, each feature within it has a possible outcome of 1 or 0, depending on the results of the feature selection job. Often, it is initialized with several vectors with randomly chosen features, and then explorations and exploitations are performed to reach the best set of features. A brief introduction of the deep neural network, adapted to perform feature extraction with the help of transfer learning, is stated below: The deep network adopted for feature extraction was AlexNet. However, the other deep networks are introduced without much detail since they are only employed to conduct comparative analysis [30].

3.5. Binary Greylag Goose Optimization (BGGO)

Recently, feature selection has been one of the most critical steps in data analysis. This is a result of feature selection, which removes redundant or unimportant characteristics to lower the high dimensionality of the data. This feature selection optimization technique aims to identify relevant characteristics that minimize classification errors, a goal that has led to its application across diverse fields. Mathematically, feature selection is a minimal optimization problem. Should feature selection issues arise, the GGO algorithm's outcomes will be strictly binary, consisting of either 0 or 1. The series of values of the suggested GGO approach will be transformed to binary values [0, 1] as shown in the stages of Algorithm 1 to facilitate selecting features from the dataset. The sigmoid function is the foundation for the following equation [31].

$$x_d^{t+1} = \begin{cases} 1 \text{ if } Sigmoid(m) \geq 0.5 \\ \quad 0 \text{ otherwise} \end{cases}, \tag{1}$$

$$Sigmoid(m) = \frac{1}{1+e^{-10(m-0.5)}} \tag{2}$$

where x_d^{t+1}E Represents the binary solution at iteration t and dimension d. The Sigmoid function can be used to make the resultant solutions binary. If. It will stay at 0, as shown in Figure 4. The m parameter reflects the characteristics selected by algorithm 1. The binary GGO method is described in detail in

Algorithm 1. Studying the GGO method reveals that the computing complexity is $O(t_{max} \times n)$and will be $O(t_{max} \times n \times d)$Or the d dimension.

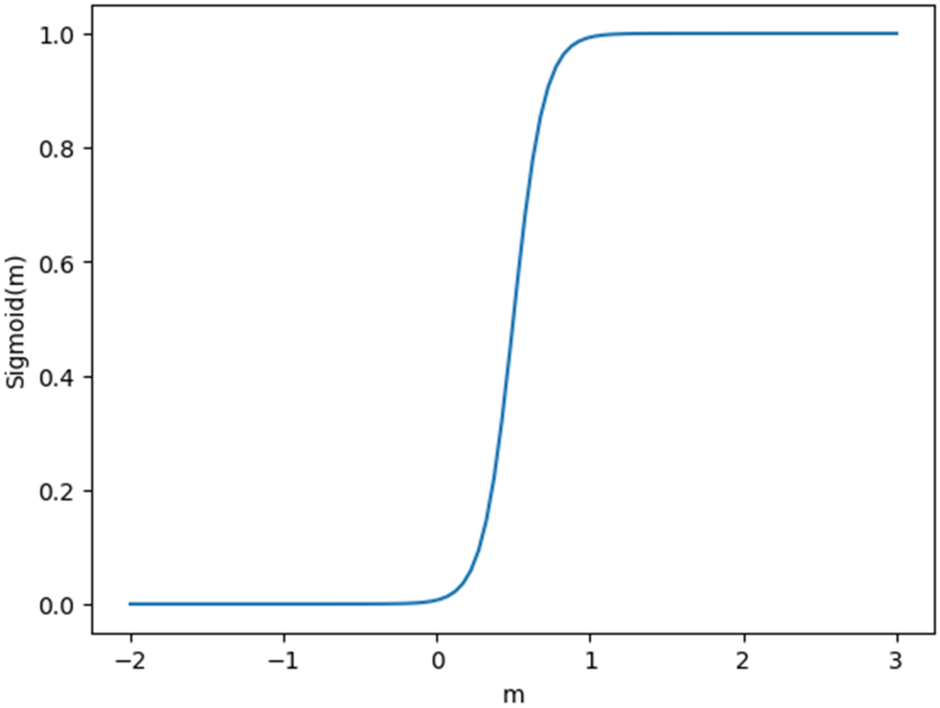

Figure 4: Sigmoid Function

The binary GGO method uses the objective equation. F_n to evaluate a solution's quality. F_n represents the percentage of errors in classification algorithm 1 in the following equation: Error is a selection of features. s and a collection of absent characteristics S.

$$F_n = \alpha Err + \beta s \vee \frac{}{s\vee} \tag{3}$$

Where:

- $\alpha \in [0,1]$ and $\beta = 1 - \alpha$

Indicate the trait's population importance, k-nearest neighbor (k-NN) is a well-liked, basic classification technique. It is considered successful if the method produces a subset of characteristics with a low classification error rate. To ensure the validity of the chosen features, this technique uses the k-NN as a classifier. This experiment does not employ a K-nearest neighbor model; the only criterion for classifier selection is the smallest distance between the query and training examples.

Algorithm 1: bGGO Algorithm

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Initialize GGO population, objective function, and GGO parameters
Convert solution to binary [0 or 1]
Calculate the objective function for each agent and get the best agent position
Update Solutions in the exploration group and exploitation group
while $t \leq t_{max}$ do
   for ($i = 1 : i < n_1 + 1$) do
      if ($t\%2 == 0$) then
         if ($r_3 < 0.5$) then
            if ($|A| < 1$) then
               Update the position of the current search agent in the exploration group
            else
               Update the position of the current search agent based on three random search agents
            end if
         else
            Update the position of the current search agent
            end if
         else
            Update individual positions
         end if
   end for
   for ($i = 1 : i < n2 + 1$) do
     if ($t\%2 == 0$) then
        Update the position of the current search agent in the exploitation group
     else
        Update the position of the current search agent
      end if
   end for
   Convert updated solution to binary
   Calculate the objective function
   Update parameters
   Adjust beyond the search space solutions
   Update Solutions in the exploration group and exploitation group
end while
Return best agent
```

4. Results

4.1. Feature extraction results

the deep neural network uses transfer learning to collect features. Among these deep networks are ResNet50, VGG19, GoogleNet, and AlexNet. The deep network used for feature extraction was AlexNet, which gave the best performance; its accuracy reached 0.932295, the sensitivity level was 0.700635, the specificity was 0.938730, and the F1 score was 0.403016.

4.2. Feature selection results

Further information about feature selection result is described in Table 3. However, as they were meant to be compared, this section provides a quick overview of the other deep networks. Descending feature selection techniques limit the acquired features. To evaluate the chosen and included features, we have used many differently calculated fitness measurement values, such as best fitness, worst fitness, average error, average fitness, average select size and standard deviation fitness, presented in Table 2. The term “best fitness” refers to a fitness value that is the greatest that has ever been attained in the best feature subset that has been optimized.

This statistic must be defined since the maximum possible classification effectiveness is achievable using the specified feature subset. On the other hand, the smallest fitness value achieved during the optimization for the selected feature subset is the poorest fitness. This value is fundamental as it concerns the lowest performance level that the distinct feature subset can point to. The instances of mistakes in the subsequent classifications concerning the subset’s inclusion are termed the ‘average error’ This statistic shows how good the classification model is when used on this subset of features selected.

Table 2: Criteria for Evaluating Feature Selection Results

Metric	Formula
Best Fitness	$min_{i=1}^{M} S_i$
Worst Fitness	$max_{i=1}^{M} S_i$
Average Error	$\frac{1}{M}\sum_{j=1}^{M}\frac{1}{N}\sum_{i=1}^{N} mse\left(\grave{V}_i - V_i\right)$
Average Fitness	$\frac{1}{M}\sum_{i=1}^{M} S_i$
Average fitness size	$\frac{1}{M}\sum_{i=1}^{M}\left(S_i\ \right)$
Standard deviation	$\sqrt{\frac{1}{M-1}\sum_{i=1}^{M}\left(S_i\ -\ \text{Mean}\ \right)^2}$

Metrics like best fitness, worst fitness, average error, average fitness, average select size, and standard deviation fitness can be used to analyze feature selection results and provide important information about the performance of the classification model. They can also be used to judge the selected feature subset's quality, complexity, stability, and robustness. Seven optimization techniques were employed in this investigation. Table 3 displays the results of the assessment criterion using the suggested feature selection approach, along with a comparison to other methods, namely Binary Greylag Goose Optimization (bGGO), Binary Waterwheel Plant Algorithm (bWWPA), Boosted Dipper Throated Optimization (bDTO), and Binary Particle Swarm Optimizer (bPSO) are among the algorithms.

(bFA) is the binary firefly algorithm, (bWAO) is the binary whale optimization algorithm, and (bGWO) is the binary gray wolf optimizer. Features provide an overview of the results from various feature selection methods. After analyzing the table, it is evident that the results of the suggested feature selection (bGGO) technique outperform those of other feature selection techniques. The findings demonstrate the superiority and efficacy of the suggested strategy in identifying the critical set of criteria required for categorizing monkeypox patients. compared with (bGGO), it gives an average error of 0.53748 which is smallest value among different model, also for other the terms show in Table 3, (bGGO) has the lowest value.

Table 3: Comparison of bGGO to Different Optimization Algorithms for Evaluating Selected Features.

	bGGO	bWWPA	bDTO	bPSO	bWAO	bGWO	bFA
Average error	0.53748	0.55468	0.56828	0.58848	0.58828	0.57478	0.58688
Average Select size	0.49028	0.69028	0.63268	0.69028	0.85368	0.61308	0.72478
Average Fitness	0.60068	0.61688	0.62828	0.61528	0.62308	0.62298	0.66718

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Best Fitness	0.50248	0.53718	0.53158	0.59558	0.58718	0.60078	0.58588
Worst Fitness	0.60098	0.60408	0.64668	0.66328	0.66328	0.67698	0.68348
Standard deviation Fitness	0.42298	0.42768	0.42928	0.42708	0.42928	0.42828	0.46388

Table 4 shows a statistical study of the outcomes obtained with bGGO compared to alternative optimization techniques, which are analyzed statistically. The data in this table show that the suggested optimization strategy outperforms the different approaches in yielding superior outcomes. For a more informative understanding. The result of statical analysis is obtained by applying 10 values, the outcome terms (Minimum, 25% Percentile, Median, 75% Percentile, Maximum) which can be easily understood from the following figure.

Table 4: Statistical Analysis of the Results Achieved by the Optimized Selected Features.

	bGGO	bWWP	bDTO	bPSO	bWAO	bGWO	bFA
Number of values	10	10	10	10	10	10	10
Minimum	0.5366	0.5485	0.5598	0.5785	0.5683	0.5548	0.5569
25% Percentile	0.5375	0.5547	0.5682	0.5885	0.5858	0.5727	0.5853
Median	0.5375	0.5547	0.5683	0.5885	0.5883	0.5748	0.5869
75% Percentile	0.5375	0.5547	0.5683	0.5898	0.5897	0.5748	0.5886
Maximum	0.5381	0.5595	0.5698	0.5985	0.5983	0.5848	0.5997
Range	0.0015	0.011	0.01	0.02	0.03	0.03	0.0428
Mean	0.5375	0.5545	0.5675	0.589	0.5868	0.5732	0.5852
Std. Deviation	0.00035	0.00261	0.00276	0.00501	0.00823	0.00742	0.0111
Std. Error of Mean	0.00011	0.000825	0.000873	0.001584	0.002603	0.002347	0.00353
Sum	5.375	5.545	5.675	5.89	5.868	5.732	5.852

Figure 5 shows the average error when employing the proposed feature selection techniques in addition to the other approaches to give a clearer view of the performance of the proposed feature selection method based on result of Table 3, Table 4. This figure shows that, out of all the approaches used in the experiment, the proposed feature selection method performs the best, achieving the lowest average error.

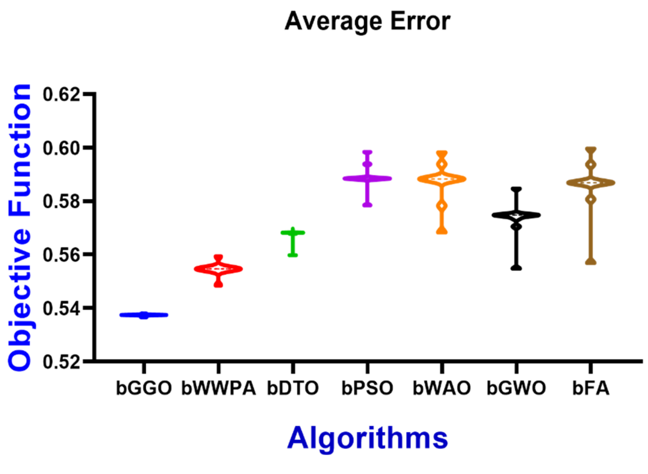

Figure 5: Average Error Plot for Proposed Optimization Algorithm with Different Other Algorithms

Another experiment was carried out to investigate the statistical characteristics of the suggested approach. The statistical distinction between the proposed methodology and alternative approaches to the other six optimization algorithms was the focus of this investigation. The analysis of variance (ANOVA) test and the statistical analysis were used to conduct the statistical analysis in Table 5. The outcomes for the Wilcoxon signed rank test are shown in Table 6. These findings demonstrate the statistical distinction between the suggested categorization and other methods. Using the statistical parameters for the proposed model shown in Table 5, the ANOVA test findings in Table 5 demonstrate how the recommended bGGO feature selection algorithm varies considerably from the other six feature selection techniques. Treatment (between columns) With a tremendous F Value of 88.94 and a p-value of less than 0.0001 compared to the significance level (usually α = 0.05), which shows statistical significance, the Residual (within columns) clearly illustrates this. They are considering that there is just a 0.002584 residual variance.

Table 5: Results of the Analysis of Variance (ANOVA) Test**.**

ANOVA table	SS	DF	MS	F (DFn, DFd)	P value
Treatment (between columns)	0.02189	6	0.003648	F (6, 63) = 88.94	P<0.0001
Residual (within columns)	0.002584	63	4.1E-05		
Total	0.02447	69			

An analysis of two groups from the original population may be done using a non-parametric method known as the Wilcoxon signed-rank test. The outcomes of this test are shown in Table 6. This test indicates if there is a substantial difference between the medians of two related features. The evaluation aimed to compare the efficacy of the recommended bGGO feature selection algorithm to other methods. The results showed that bGGO performed better than the other strategies since its actual median was more significant than the median of all the other techniques. There were 55 signed rankings across all approaches, indicating a wide variation in the outcomes for the different feature selection techniques. Obtaining these findings by coincidence is implausible, as the p-value is less than 0.05. Since the population size was sufficiently small, an exact test was conducted rather than an approximation. The lowest difference between the theoretical and actual medians among all approaches indicated bGGO's better results. All these results suggest that bGGO is a promising feature selection method that operates better than most existing methods.

Table 6: The Wilcoxon Signed-Rank Test for the Proposed Feature Selection Algorithm (bGGO) with other Alternative Approaches.

	bGGO	bWWPA	bDTO	bPSO	bWAO	bGWO	bFA
Theoretical median	0	0	0	0	0	0	0
Actual median	0.5375	0.5547	0.5683	0.5885	0.5883	0.5748	0.5869
Number of values	10	10	10	10	10	10	10
Wilcoxon Signed Rank Test							
The sum of signed ranks (W)	55	55	55	55	55	55	55
The sum of positive ranks	55	55	55	55	55	55	55
The sum of hostile ranks	0	0	0	0	0	0	0
P value (two-tailed)	0.002	0.002	0.002	0.002	0.002	0.002	0.002
Is it exact or an estimate?	Exact	Exact	Exact	Exact	Exact	Exact	Exact
P value summary	**	**	**	**	**	**	**
Significant (alpha=0.05)?	Yes	Yes	Yes	Yes	Yes	Yes	Yes
How significant is the discrepancy?							
Discrepancy	0.5375	0.5547	0.5683	0.5885	0.5883	0.5748	0.5869

Furthermore, the graphs in Figure 6 exhibit the suggested feature selection strategy results. The quartile-quartile (Q.Q.), residual plots, heatmap plot, and homoscedasticity are utilized in this figure to demonstrate the efficacy and stability of the proposed approach. The strength of the chosen criteria in categorizing the cases of monkeypox is shown in the numbers displayed in the Q.Q. Plot, which roughly fits a straight line. These conclusions are further supported by the data shown in the residual, homoscedasticity plot refers to the assumption of the residuals are normally distributed across all levels of the predictor variables. Residual plots are useful for graphically assessing the accuracy of the models in

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relation to different feature selection algorithms. A perfect distribution of residuals would exhibit no noticeable patterns and be evenly spread throughout a horizontal axis showed at zero. Furthermore, the heatmap validates the dominance of bGGO, as it outperformed bWWPA, bDTO, bPSO, bWAO, bGWO, and bFA bGA feature selection algorithms, yielding the most favorable outcomes.

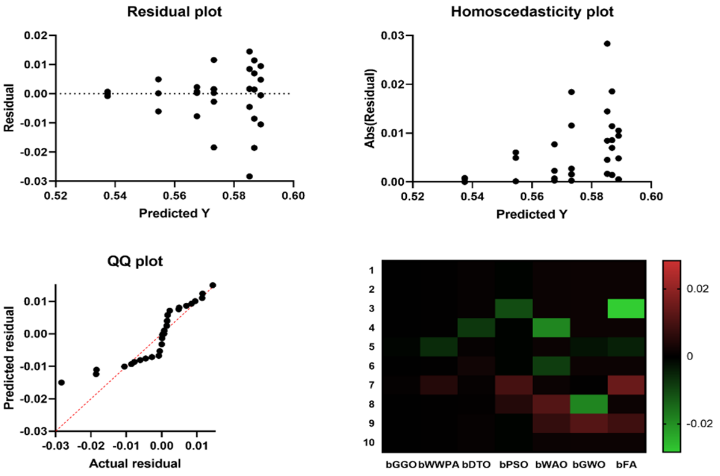

Figure 6: Analysis plots of the outcomes obtained using bGGO

5. Conclusion

This work introduced the optimization of selected features in binary form to improve the classification of monkeypox using the public dataset (MSID). The feature in question determines whether the sample is infected or not. Deep learning and a transfer learning technique were utilized to obtain the dedicated set of characteristics. The AlexNet network, a deep learning system with an accuracy of 0.932295, completes this assignment. Six optimization procedures were used to compare the performance of our proposed method (bGGO) for these properties. The distinguished feature is selected using bGGO, which has an average choose size of 0.49028 and an average error of 0.53748. Statistical analysis included ANOVA and the Wilcoxon signed-rank test to evaluate the recommended strategy's validity and effectiveness.

Furthermore, a set of graphical representations of the results was generated to confirm the robustness and effectiveness of the proposed method. The results demonstrated the superiority of bGGO over other deep-learning models and optimization techniques. In the future, we hope to generalize our proposed method by applying it to a variety of datasets to assess model performance. Additionally, we plan to conduct a comparison using a novel metaheuristic optimization algorithm, the Puma Optimizer (po), and compare its performance with our proposed method.

References

[1] Ahsan, M. M., Ali, M. S., Hassan, M. M., Abdullah, T. A., Gupta, K. D., Bagci, U., ... & Soliman, N. F. (2023). Monkeypox diagnosis with interpretable deep learning. IEEE Access. 10.1109/ACCESS.2023.3300793

[2] Bala, D., Hossain, M. S., Hossain, M. A., Abdullah, M. I., Rahman, M. M., Manavalan, B., ... & Huang, Z. (2023). MonkeyNet: A robust deep convolutional neural network for monkeypox disease detection and classification. Neural Networks, 161, 757-775. https://doi.org/10.1016/j.neunet.2023.02.022

[3] Abdelhamid, A. A., El-Kenawy, E. S. M., Khodadadi, N., Mirjalili, S., Khafaga, D. S., Alharbi, A. H., ... & Saber, M. (2022). Classification of monkeypox images based on transfer learning and the Al-Biruni Earth Radius Optimization algorithm. Mathematics, 10(19), 3614. https://doi.org/10.3390/math10193614

[4] Velu, M., Dhanaraj, R. K., Balusamy, B., Kadry, S., Yu, Y., Nadeem, A., & Rauf, H. T. (2023). Human Pathogenic Monkeypox Disease Recognition Using Q-Learning Approach. Diagnostics, 13(8), 1491. https://doi.org/10.3390/diagnostics13081491

[5] Towfek, S. K., Khodadadi, N., Abualigah, L., & Rizk, F. H. (2024). AI in Higher Education: Insights from Student Surveys and Predictive Analytics using PSO-Guided WOA and Linear

Regression. Journal of Artificial Intelligence in Engineering Practice, 1(1), 1–17. https://doi.org/10.21608/jaiep.2024.354003

[6] Kandel, M. A., Rizk, F. H., Hongou, L., Zaki, A. M., Khan, H., & El-Kenawy, E.-S. M. (2023). Evaluating the Efficacy of Deep Learning Architectures in Predicting Traffic Patterns for Smart City Development. Full-Length Article, Volume 6(Issue 2), 26–35. https://doi.org/10.54216/JAIM.060203

[7] Hatami, H., Jamshidi, P., Arbabi, M., Safavi-Naini, S. A. A., Farokh, P., Izadi-Jorshari, G., ... & Sechi, L. A. (2023). Demographic, epidemiologic, and clinical characteristics of human monkeypox disease pre-and post-2022 outbreaks: a systematic review and meta-analysis. *Biomedicines*, *11*(3), 957. https://doi.org/10.3390/biomedicines11030957

[8] Narayanan, S. J., Jaiswal, P. R., Chowdhury, A., Joseph, A. M., & Ambar, S. (2021). A Computational Intelligence Approach for Skin Disease Identification Using Machine/Deep Learning Algorithms. Computational Intelligence and Healthcare Informatics, 269-295.

[9] Bala, D., & Hossain, M. S. (2022). Monkeypox skin images dataset (MSID) https://www.kaggle.com/datasets/dipuiucse/monkeypoxskinimagedataset.

[10] Ahsan, M. M., Uddin, M. R., Farjana, M., Sakib, A. N., Momin, K. A., & Luna, S. A. (2022). Image Data collection and implementation of the deep learning-based model in detecting Monkeypox disease using modified VGG16. arXiv preprint arXiv:2206.01862.

[11] Alharbi, A. H., Towfek, S. K., Abdelhamid, A. A., Ibrahim, A., Eid, M. M., Khafaga, D. S., ... & Saber, M. (2023). Diagnosis of monkeypox disease using transfer learning and binary advanced dipper throated optimization algorithm. Biomimetics, 8(3), 313. https://doi.org/10.3390/biomimetics8030313.

[12] Pal, M., Mahal, A., Mohapatra, R. K., Obaidullah, A. J., Sahoo, R. N., Pattnaik, G., ... & Rabaan, A. A. (2023). Deep and transfer learning approaches for automated early detection of monkeypox (Mpox) alongside other similar skin lesions and their classification. ACS omega, 8(35), 31747-31757. https://doi.org/10.1021/acsomega.3c02784

[13] Bala, D., & Hossain, M. S. (2022). Monkeypox skin images dataset (msid). Mendeley Data, 6, 2023. (https://data.mendeley.com/datasets/r9bfpnvyxr).

[14] Alhasson, H. F., Almozainy, E., Alharbi, M., Almansour, N., Alharbi, S. S., & Khan, R. U. (2023). A Deep Learning-Based Mobile Application for Monkeypox Detection. Applied Sciences, 13(23), 12589. https://doi.org/10.3390/app132312589

[15] Islam, T., Hussain, M. A., Chowdhury, F. U. H., & Riazul Islam, B. M. (2022). A web-scraped skin image database of monkeypox, chickenpox, smallpox, cowpox, and measles. biorxiv, 2022-08. doi: https://doi.org/10.1101/2022.08.01.502199

[16] Gupta, A., Bhagat, M., & Jain, V. (2023). Blockchain-enabled healthcare monitoring system for early Monkeypox detection. The Journal of Supercomputing, 79(14), 15675-15699. https://doi.org/10.1007/s11227-023-05288-y

[17] https://github.com/mahsan2/Monkeypoxdataset-2022." (Accessed 01.09.2022).

[18] Rabie, A. H., & Saleh, A. I. (2023). Monkeypox diagnosis using ensemble classification. Artificial Intelligence in Medicine, 143, 102618. https://doi.org/10.1016/j.artmed.2023.102618

[19] https://www.kaggle.com/datasets/nafin59/monkeypox-skin-lesion-dataset

[20] http://covid19.nilehi.edu.eg/Available_datasets.php

[21] Alakus, T. B., & Baykara, M. (2022). Comparison of monkeypox and wart DNA sequences with deep learning model. Applied Sciences, 12(20), 10216. https://doi.org/10.3390/app122010216

[22] Hussain, M. A., Islam, T., Chowdhury, F. U. H., & Islam, B. R. (2022). Can artificial intelligence detect Monkeypox from digital skin images?. BioRxiv, 2022-08. https://doi.org/10.1101/2022.08.08.503193

[23] https://www.kaggle.com/datasets/arafathussain/monkeypox-skin-image-dataset-2022.

[24] Jaradat, A. S., Al Mamlook, R. E., Almakayeel, N., Alharbe, N., Almuflih, A. S., Nasayreh, A., ... & Bzizi, H. (2023). Automated monkeypox skin lesion detection using deep learning and transfer learning techniques. International Journal of Environmental Research and Public Health, 20(5), 4422. https://doi.org/10.3390/ijerph20054422

[25] Thorat, R., & Gupta, A. (2024). Transfer learning-enabled skin disease classification: the case of monkeypox detection. Multimedia Tools and Applications, 1-19. https://doi.org/10.1007/s11042-024-18750-7

[26] Nayak, T., Chadaga, K., Sampathila, N., Mayrose, H., Gokulkrishnan, N., Prabhu, S., & Umakanth, S. (2023). Deep learning based detection of monkeypox virus using skin lesion

Doi: https://doi.org/10.21608/jaiep.2024.300937.1002
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images. Medicine in Novel Technology and Devices, 18, 100243. https://doi.org/10.1016/j.medntd.2023.100243

[27] Gairola, A. K., & Kumar, V. (2022, December). Monkeypox disease diagnosis using machine learning approach. In 2022 8th International Conference on Signal Processing and Communication (ICSC) (pp. 423-427). IEEE. 10.1109/ICSC56524.2022.10009135

[28] Luong, H. H., Khang, N. H., Le, N. Q., Canh, D. M., & Ha, P. S. (2023). A proposed approach for monkeypox classification. International Journal of Advanced Computer Science and Applications, 14(8). DOI:10.14569/IJACSA.2023.0140871

[29] Sorayaie Azar, A., Naemi, A., Babaei Rikan, S., Bagherzadeh Mohasefi, J., Pirnejad, H., & Wiil, U. K. (2023). Monkeypox detection using deep neural networks. BMC Infectious Diseases, 23(1), 438. https://doi.org/10.1186/s12879-023-08408-4

[30] Lakshmi, M., & Das, R. (2023). Classification of monkeypox images using LIME-enabled investigation of deep convolutional neural network. Diagnostics, 13(9), 1639. https://doi.org/10.3390/diagnostics13091639

[31] El-Kenawy, E. S. M., Khodadadi, N., Mirjalili, S., Abdelhamid, A. A., Eid, M. M., & Ibrahim, A. (2024). Greylag goose optimization: nature-inspired optimization algorithm. Expert Systems with Applications, 238, 122147. https://doi.org/10.1016/j.eswa.2023.122147