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VirLesDetNet: Pre-Trained Hybrid Deep Learning Approaches for Virus-Based Skin Lesion Detection

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ABSTRACT

The monkeypox virus is a DNA virus with a double-stranded structure and belongs to the Orthopoxvirus family. While skin lesions are a major indicator of monkeypox, they are often indistinguishable from early-stage chickenpox and measles lesions, leading to potential misdiagnoses. To address this issue, a new hybrid deep learning model has been developed to classify skin lesions into four categories: normal, monkeypox, chickenpox, and measles, using the publicly available Monkeypox Skin Images Dataset (MSID). The dataset was initially expanded through image preprocessing and data augmentation techniques. Seven pre-trained deep learning models were then trained individually. After evaluating their performance, the top three models were selected, and an ensemble model was created to improve overall accuracy through majority voting based on the probabilistic outputs from these models. The model's effectiveness is validated by accuracy, recall, precision, F1 score, and a confusion matrix. The proposed ensemble model, which combines EfficientB3, ResNet152, and MobileNetV3, achieved a detection accuracy rate of 94.82%.

1. INTRODUCTION

1.1 Background

The monkeypox virus, part of the Orthopoxviridae family, is a highly infectious DNA virus with a double-stranded structure [1-3]. It exhibits clinical symptoms similar to those of chickenpox and measles, and is categorized under the Poxviridae family and Orthopoxvirus genus [1, 4]. Identified initially in a monkey at a research facility in 1959, it was subsequently named monkeypox [5, 6]. The virus's natural hosts include animals such as squirrels, Gambian opossums, and primates [1, 3], while transmission frequently occurs through rats and monkeys, with human-to-human spread also reported [7, 8].

The first recorded human infection of monkeypox occurred in 1970 in the Democratic Republic of Congo, coinciding with the global smallpox eradication campaign [9]. The virus spreads through direct physical contact, respiratory droplets, bites from infected animals, or exposure to contaminated surfaces [10, 11]. Monkeypox has an incubation period of 5 to 21 days, with illness severity influenced by the individual's immune response and viral load [1]. Early symptoms, generally appearing within the first 1-5 days, include fever, swollen lymph nodes, muscle pain, fatigue, and headaches. A rash usually follows, appearing on areas such as the face, hands, and feet, and progresses through five stages: macules, papules, vesicles, pustules, and finally, crusted lesions, over a period of 2-4 weeks [12]. Rising transmission rates of monkeypox have led to increased concern. While only about 50 cases were reported in Western and Central Africa in 1990 [13], by January 2023, cases had surged to 65,353 across 100 countries, spanning the Americas, Europe, Africa, the Eastern Mediterranean, and the Western Pacific regions [4, 8, 14, 15]. The World Health Organization (WHO) has classified monkeypox as a moderate health risk, underscoring the need for swift global response [1]. Despite considerable efforts, the Centers for Disease Control and Prevention (CDC) states that no fully effective treatment currently exists for monkeypox [12]. However, two drugs, Brincidofovir and Tecovirimat, which the CDC initially approved for chickenpox, are also available for treating monkeypox [16]. Though a vaccine is considered the ultimate solution for prevention, a reliable vaccine specifically for monkeypox in humans has not yet been developed, although research continues. Some countries have reportedly utilized varicella virus vaccines for monkeypox treatment [17].

Diagnosis typically starts with a visual examination of skin lesions, followed by a review of exposure history. The virus can be confirmed most accurately through electron microscopy of skin lesions. Polymerase chain reaction (PCR) testing from skin rashes, samples, fluids, crusts, or biopsies is another method used to detect monkeypox [1, 12, 13, 18], although PCR testing is not universally accessible. In certain cases, antigen and antibody detection methods can mistakenly identify monkeypox as the highly contagious varicella virus [18]. Mortality rates for monkeypox are estimated between 3% and 6% [19], making early detection and isolation crucial to controlling the virus's spread. While PCR is the preferred confirmation method, image analysis can be an effective

preliminary diagnostic tool in regions with limited resources, helping to curb outbreaks. Monkeypox poses diagnostic challenges for clinicians due to its rarity and its skin manifestations, which can resemble those of chickenpox, measles, and smallpox [1, 4]. This resemblance has led researchers to focus on developing image-based classification models for skin lesions related to various viral diseases, including monkeypox, chickenpox, and measles.

This study presents a hybrid model aimed at classifying skin lesions from monkeypox, chickenpox, measles, and healthy skin. The structure of the paper is outlined as follows: Section 2 details the dataset used, data augmentation techniques, and the proposed detection framework; Section 3 reports the model's results and compares them with findings from other research, based on performance metrics; Section 4 offers a summary of the key findings and suggests areas for further research.

1.2 Contribution and novelty

Research on detecting virus-related diseases through deep learning (DL) has largely relied on transfer learning, using well-established pre-trained DL models. However, previous studies highlight three main limitations that this research seeks to overcome:

1. Most models are designed for binary classification, typically distinguishing monkeypox from other conditions. However, differentiating monkeypox lesions from chickenpox and measles lesions is essential, given their similar visual characteristics. This study develops a DL model for a four-class classification problem (normal, monkeypox, chickenpox, and measles), addressing these distinctions more comprehensively.
2. Previous studies often employ outdated DL models for predictions through transfer learning. In contrast, this study introduces an ensemble deep neural network framework to improve monkeypox lesion detection accuracy. Seven pre-trained DL models were evaluated, and the top three were combined using majority voting, creating a more robust final prediction output.
3. Limited datasets in prior studies have restricted model accuracy and reliability. This research utilizes the largest publicly available monkeypox dataset, with additional data generated through augmentation techniques to ensure broader and more reliable model training.

This study's contributions and innovations include the following:

- By including three conditions with visually similar lesions, this study addresses a four-class problem, advancing holistic problem-solving in disease classification.
- Results for all seven pre-trained DL models in monkeypox detection were generated and compared using a refined architecture.
- The three highest-performing pre-trained models were integrated through majority voting to strengthen detection reliability and success rates.
- Results of the proposed ensemble framework are compared with individual pre-trained network architectures, highlighting the advantages of the ensemble method.

1.3 Related works

Research efforts towards early detection of the monkeypox virus have been somewhat limited, leaving room for improvement in the results. The studies in this area revolve around detecting the Monkeypox virus, detailing the datasets used, classification methods employed, and the achieved outcomes.

Nayak et al. [20] leveraged deep learning methods to diagnose monkeypox by analyzing visual features in skin lesion images. To evaluate the effectiveness of their approach, they used a publicly accessible dataset and tested it on five well-established pre-trained neural networks: GoogLeNet, Places365-GoogLeNet, SqueezeNet, AlexNet, and ResNet-18. Each of these models brings unique strengths to feature extraction and image recognition, offering a diverse set of architectural frameworks for comparison. By applying these varied models, Nayak et al. aimed to determine which architecture would best distinguish monkeypox from other conditions based on skin lesion imagery, contributing to a more accurate and efficient diagnostic approach. The optimal parameters were selected using hyperparameter. With an accuracy of 99.49%, ResNet18 achieved the highest rating among the aforementioned models. A distinction was drawn between monkeypox and other diseases, citing Alakus [21]. Images of various illnesses as well as chickenpox were used. In the second phase, data classification was performed using a Siamese deep learning model, achieving an accuracy score of 91.09%. Örenç et al. [22] created EfficientNetB3, ResNet50, and InceptionV3 using picture datasets that they acquired from Kaggle. The best model is resNet50, based on the three models' results. With an accuracy of 94.00%, resNet50 has the greatest accuracy value. Akın et al. [23] explored various deep learning models for classifying monkeypox skin lesions, including ResNet-18, ResNet-50, VGG-16, DenseNet-161, EfficientNet B7, EfficientNet V2, GoogLeNet, MobileNet V2, MobileNet V3, ResNeXt-50, ShuffleNet V2, and ConvNeXt. Among these models, MobileNet V2 demonstrated the highest performance, achieving an accuracy of 98.25%, sensitivity of 96.55%, specificity of 100.00%, and an F1-score of 98.25%, making it the top performer in their analysis. Additionally, Özaltın and Yeniay [24] leveraged MobileNet V2 as a feature extractor, integrating it with a Support Vector Machine (SVM) for classification purposes. By applying the Chi-Square method to select relevant features, they successfully classified 500 features with SVM, reaching an accuracy rate of 99.69%. This approach highlighted the effectiveness of combining deep learning-based feature extraction with traditional machine learning classifiers for improved accuracy in identifying monkeypox lesions.

In a related study, Sathwik et al. [25] explored models such as SVM, CNN, VGG16, VGG19, ResNet50, ResNet101, EfficientNet B0, EfficientNet B1, and EfficientNet B2 for detecting monkeypox lesions using images from the Kaggle open-source monkeypox dataset. Among these models, ResNet and VGG19 reached the highest accuracy, each achieving 92% in identifying the lesions.

A Q-learning approach for multilayer neural network parameter tuning and reinforcement learning for the classification of monkeypox images was created by Velu et al. [26]. For monkeypox, they received 96% f1 scores, 95% recall, and 95% accuracy. Almufareh et al. [27] utilized deep learning models (Inception V3, ResNet50, MobileNet V2, and EfficientNet B4) to classify skin lesions as either MPXV positive or negative. Their methodology was evaluated using both the Monkeypox Skin Image Dataset (MSID) and the Kaggle Monkeypox Skin Lesion Dataset (MSLD), assessing

model performance based on balanced accuracy, sensitivity, and specificity. In related research, Lakshmi and Das [28] employed models such as VGG16, VGG19, ResNet50, ResNet101, DenseNet201, and AlexNet for the detection and classification of monkeypox symptoms, with ResNet101 achieving the highest accuracy at 98.59%. Uysal [29] developed a hybrid AI system for identifying monkeypox from skin images, utilizing a four-class classification scheme (chickenpox, measles, monkeypox, and normal). Models including CSPDarkNet, InceptionV4, MnasNet, MobileNetV3, RepVGG, SE-ResNet, and Xception were tested. To improve classification, the top two models were combined with a long short-term memory (LSTM) network, resulting in a unique hybrid model that achieved 87% test accuracy. Ahsan et al. [13, 30] introduced the "Monkeypox2022" dataset, the first open-access dataset for monkeypox classification, containing 1905 images in four categories: monkeypox, chickenpox, measles, and normal. This dataset, gathered from online sources, was shared on GitHub. By applying their modified VGG16 deep neural network model, Ahsan et al. achieved a 78% accuracy in distinguishing monkeypox lesions in a binary classification problem (monkeypox vs. other). Ali et al. [19] also compiled skin lesion images into four distinct categories—monkeypox, chickenpox, measles, and normal—forming the "Monkeypox Skin Lesion Dataset (MSLD)," which has become a valuable resource for advancing research in this field.

They employed VGG-16, ResNet50, and InceptionV3 deep neural network architectures for lesion class detection, with ResNet50 achieving 92.96% accuracy, VGG-16 reaching 81.48% accuracy, and their ensemble model achieving 79.26% accuracy. They also developed a web application for online image detection, emphasizing the need for a larger dataset to account for demographic differences. Sitaula and Shahi [31] used thirteen pre-trained deep neural network architectures on the Monkeypox2022 dataset (three lesion variants and one normal class). The highest performing Xception and DenseNet169 DL models were combined using the majority vote approach to create an ensemble model with 87.13% accuracy. Islam et al. [32, 33] addressed data limitations by web scraping, curating the Monkeypox Skin Image Dataset 2022. Their analysis of skin images in six categories resulted in ShuffleNet-V2 achieving the highest success with 79% accuracy. They further improved predictions with an ensemble model, reaching 83% accuracy.

Alakus and Baykara [34] examined the similarity between monkey flower visuals and some types of sigils that could cause confusion during diagnosis. Ali et al. [19] designed a deep neural network to detect monkeypox by analyzing DNA sequences of HPV and MPV, reaching an average accuracy of 96.08% and an F1 score of 99.83% in classifying DNA maps. Eid et al. [35] introduced a parameter-optimized LSTM deep network for monkeypox detection, achieving a predictive success rate of $R^2 = 0.73$ through hyperparameter tuning using the BER optimization algorithm. Abdelhamid et al. [36] enhanced monkeypox image classification by employing AlexNet, VGG-19, GoogleNet, and ResNet-50 models with transfer learning for feature extraction, reaching a 93.80% classification accuracy with GoogleNet and a hybrid feature selection method on the Monkeypox Skin Images Dataset (MSID).

Sahin et al. [37] created an Android app for detecting monkeypox, leveraging pre-trained models such as ResNet18, GoogleNet, EfficientNetb0, NasnetMobile, ShuffleNet, and MobileNetv2, which were specifically optimized for monkeypox detection using MATLAB. MobileNetv2 demonstrated the highest accuracy, reaching 91.11%, and was subsequently converted to a TensorFlow Lite model for integration into the Android platform. On three different mobile devices, average processing times for image extraction were recorded as 197 ms, 91 ms, and 138 ms. Miran et al. [38] employed an LSTM model to predict chickenpox cases using data from the CDC and web sources, achieving a correlation coefficient of 0.97114 and a sum of squared errors of 341.01547, outperforming linear regression methods. Haque [39] applied five deep neural network models—VGG19, Xception, DenseNet121, EfficientNetB3, and MobileNetV2—enhanced with a convolutional block attention module (CBAM) for monkeypox detection. The Xception-CBAM-Dense architecture yielded the best results, with an accuracy of 83.89%.

Kumar [40] worked on classifying monkeypox lesions using the Monkeypox-Skin-Lesion-Dataset. He extracted features with AlexNet, GoogleNet, and VGG16Net and utilized classifiers such as SVM, KNN, Naïve Bayes, Decision Tree, and Random Forest. The highest classification accuracy, 91.11%, was obtained by combining the Naïve Bayes classifier with features from VGG16Net. Dwivedi et al. [41] compared three deep neural network models for monkeypox lesion detection. Their study on the Monkeypox2022 data set resulted in detection accuracies of 84%, 87%, and 77% for the ResNet50, EfficientNetB3, and EfficientNetB7 models, respectively. Ozsahin et al. [8] curated a data set with two classes (monkeypox and chickenpox) using images from two open-source datasets. They developed a CNN model with four convolutional layers to identify and categorize monkeypox and chickenpox lesions. Comparing their model with five well-known DL models (VGG16, VGG19, ResNet50, AlexNet, InceptionV3), their suggested technique significantly outperformed the others, achieving a test accuracy of 95%. A novel diagnostic approach was proposed by Almutairi [4] to divide patient cases into two categories as pox (monkeypox, chickenpox, and measles) and normal). They used five DL models that have already been trained (Xception, MobileNet, MobileNetV2, VGG19, VGG16, and MobileNet) for diagnostic framework. The hyperparameters of these models have been determined with a metaheuristic algorithm to provide high performance. In addition, seven machine learning models were utilized to classify the extracted features in this study. The effectiveness of the proposed framework was evaluated on two publicly accessible datasets, MSID and MPID, with results presented accordingly. The VGG16 model combined with maximum voting (k=7) yielded the highest performance within the diagnostic framework, achieving accuracy, sensitivity, specificity, precision, and F1 score values of 97.44%, 94.81%, 97.67%, 94.72%, and 94.67%, respectively. Gairola [42] employed the Monkeypox Skin Lesion Dataset (MSLD) for a two-class classification task, using feature extraction with three deep learning models and a fusion approach involving six different machine learning models (DT, SVM, KNN, LR, NB, RF). Their approach achieved the highest performance using the AlexNet+VGGNet+NB combination, with an accuracy of 95.55%.

Irmak et al. [43] trained and tested their classification approach for monkeypox lesions using the Monkeypox Skin Image Dataset, comparing the performances of three pre-trained models—MobileNetV2, VGG16, and VGG19. Their findings indicated that MobileNetV2 had the highest

predictive accuracy, reaching 91.38%, with precision at 90.5%, recall at 86.75%, and an F1 score of 88.25%. Agrawal et al. [44] used ResNet50, EfficientNet-B3, VGG16, and InceptionNetV3 on an image dataset from Kaggle, with EfficientNet-B3 demonstrating the highest accuracy at 93%. Haque et al. [45] enhanced monkeypox detection through deep transfer learning combined with a convolutional block attention module (CBAM). They applied channel and spatial attention mechanisms to five models (VGG19, Xception, DenseNet121, EfficientNetB3, and MobileNetV2), achieving an accuracy of 83.89% with an Xception-CBAM-Dense-based architecture for distinguishing monkeypox from other conditions.

2. MATERIAL AND METHOD

The current study utilized the Monkeypox Skin Images Dataset (MSID) [46], the largest publicly available dataset for monkeypox classification, accessible at this link. (https://www.kaggle.com/datasets/dipuiucse/monkeypoxskinimagedataset). The dataset is divided into four categories: (1) normal/healthy, (2) chickenpox, (3) measles, and (4) monkeypox. All images were sourced from internet-based health websites. The dataset was developed by Diponkor Bala and Md. Shamim Hossain, affiliated with the Department of Computer Science and Engineering at Islamic University, Bangladesh, and the School of Computer Science and Technology at the University of Science and Technology of China (USTC), respectively.

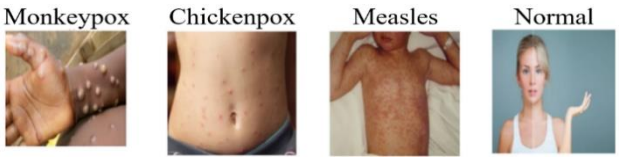


Figure 1. Sample image from the datasets

Table 1. Features of MSID dataset

Class Name	Account of Image	Size of Image
Class-1: Chickenpox	107	
Class-2: Measles	91	
Class-3: Monkeypox	279	224×224
Class-4: Normal	293	
Total	770	

Table 1 displays the distribution of images across the different classes in the dataset, along with details about image sizes. Figure 1 provides a sample image from each class within the dataset.

2.1 Image pre-processing

In order to increase success in classification studies, two basic pre-treatments are generally applied to the data set. The first of these processes is image enhancement and the second is data set duplication. Poor camera quality and environmental conditions cause digital image degradation. Image purification gives good results to increase classification success. Therefore, within the scope of this study, image contrast enhancement was applied to the data set in order to better see the details of the region of interest in the image. In this study, histogram equalization was applied to improve image quality by enhancing contrast and emphasizing pixel differences. This process involved creating a histogram based on pixel intensity values and transforming it to achieve a more evenly distributed contrast. Given the limited size of the dataset, data replication techniques were also employed to enhance classification accuracy within the deep neural network architecture. Table 2 summarizes the data augmentation techniques and associated rates/parameters used in this research. Various transformations based on position, color, and zoom were applied to generate image variations while maintaining dataset integrity. The parameters for these techniques were selected based on insights from prior studies and similar research in the field. These augmentation methods not only improve the model's ability to generalize and predict accurately but also help to prevent overfitting by introducing diversity and flexibility to the training data [33].

Table 2. Data augmentation methods used in this study

Augmentation Method	Range
Shear	0.2
Zoom	0.2
Rotation	0.2
Height weighting	0.2
Channel ship	0.2
Width shift	0.2
Horizontal flip	True
Vertical flip	True

In this study, various data augmentation methods have been utilized. 'Shear' is used to introduce deformation by shifting the image at a certain angle. 'Zoom' creates different perspectives by zooming in or out the image. 'Rotation' adds diverse viewpoints by rotating the image at a certain angle. Additionally, 'Height weighting' enables obtaining samples of different sizes by altering the height dimension of the image. 'Channel shift' introduces color variations by shifting the color channels. 'Width shift' generates samples of different sizes by altering the width dimension of the image. 'Horizontal flip' mirrors the image along the horizontal axis, while 'Vertical flip' mirrors it along the vertical axis, offering different perspectives of the original image and increasing data diversity. Combined with other transformations like rotation, scaling, brightness adjustment, and zoom, these methods improve the model's ability to recognize new, unseen images. These techniques help the model learn from a broader data range, preventing overfitting and enabling stronger classification performance.

2.2 Proposed pre-trained hybrid deep learning model (VirLesDetNet)

In this study, a new diagnostic framework has been proposed to classify cases under four classes: normal, measles, chickenpox and monkeypox. The primary goal of the proposed diagnostic framework is to enhance the prediction success by combining the three best-performing out of the 9 pre-trained CNN architectures. Figure 2 illustrates a graphical representation of the proposed method. First, mesh weights pre-trained using the ImageNet dataset were used as starting weights in monkeypox network training. Table 3 summarizes the layer structure of the proposed framework.

The pre-trained model, called the base model, is followed by the dropout, flattening, dense and drop-dense, and output layers, respectively. There are7 pre-trained CNN models used

in this study. These models are DenseNet 121, DenseNet 169, DenseNet 201, EfficientNetB3, EfficientNetB7, EfficientNetB5, MobileNetV3, ResNet152. Each model's predictions were assessed using five performance metrics, and the three best-performing models were then combined through a majority voting approach to enhance overall accuracy. In this system, each classifier casts a vote for a specific class, and the class that receives the majority of votes becomes the final prediction.

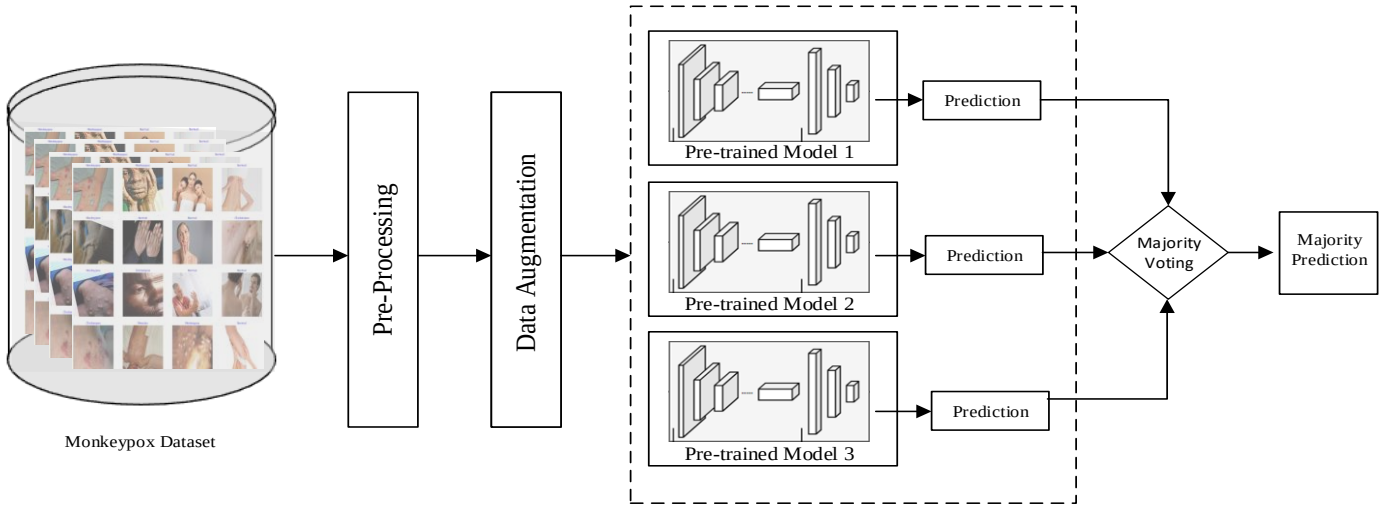


Figure 2. Proposed ensemble deep learning based model (VirLesDetNet)

Table 3. Proposed frame with modified architecture

Layer Type	Specifications
Image_RGB	Dimensions: 224×224×3
DenseNet121, DenseNet201, EfficientNetB3, EfficientNetB7, EfficientNetB5, MobileNetV3, ResNet152	Pre-trained base models
Dropout	Dropout Rate: 0.5
Flatten	Applied after Dropout Layer 1
Dense	Units: 256, Activation: ReLU
Dropout	Dropout Rate: 0.5
Dense	Units: 128, Activation: ReLU
Dense	Units: 4, Activation: Sigmoid

2.3 Model hyperparameters optimization

In DL models, the most basic elements that determine the structure of the network and affect the performance / success of the network are the unique variables (hyperparameters) of the network. In order for the model prediction success to be high, it is extremely important to choose the optimal hyperparameters, that is, to optimize the parameters. Since the transfer learning method was adopted in the current study, pre-trained models' hyperparameters were transferred without changing them directly. The primary goal of the proposed diagnostic framework is to ensure consistency and reliability by initially maintaining fixed hyperparameters across the model configuration. However, to achieve the highest possible performance, the hyperparameters of the pre-trained model were carefully fine-tuned using a grid search approach. This process involved testing a range of batch sizes, from 10 to 100, and experimenting with different epoch values between 50 and 100 to find the most effective combination. Additionally, the influence of seven distinct optimizers was examined to identify the one that would yield the most stable and accurate results for this application. The grid search also explored varying learning rates within the range of [0.001, 0.3] and momentum values from [0.0, 0.9], allowing for an in-depth understanding of how these parameters impact the model's ability to converge and avoid overfitting. Following extensive testing, the optimal configuration was identified as a batch size of 32, 100 epochs, the Stochastic Gradient Descent (SGD) optimizer, a learning rate of 0.001, and a momentum value of 0.0, yielding the best overall performance.

2.4 Performance evaluation metrics

To assess the effectiveness of the proposed framework for monkeypox detection, five primary performance metrics were calculated: accuracy, precision, recall, F1 score, and specificity [47]. These metrics provide a comprehensive evaluation of the model's classification performance, balancing both accuracy and the model's ability to correctly identify positive and negative cases. In these formulas, TP denotes the count of true positives, representing correctly identified positive cases. FN stands for false negatives, indicating instances where positive samples were mistakenly classified as negative. TN refers to true negatives, representing the correctly identified negative cases, while FP represents false positives, where negative samples were incorrectly classified as positive.

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \quad (1)$$

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \quad (2)$$

$$\text{Recall} = \text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}} \quad (3)$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}} \quad (4)$$

$$\text{F1-Score} = \frac{2 \times \text{Precision} \times \text{Sensitivity}}{(\text{Recall+Precision})} \quad (5)$$

3. RESULT AND DISCUSSION

Within the scope of this study, all image preprocessing, data replication, model creation, model training and calculation of performance metrics were developed using Keras package and Python programming language. The generated ensemble diagnostic method model was created utilizing architectures on the Kaggle platform and was accelerated using the platform's GPU capability. Table 4 shows the distribution of train, validation and test datasets for both cases. In this distribution, the ratio of 80:20:10 was adopted and the selection was made randomly. Data augmentation was applied solely to the training and validation sets, keeping the test set unchanged. This approach enhances test reliability by evaluating model performance on original data.

Table 4. Assignment of dataset split to train, validation and test

Train Set	Validation Set	Test Set
22176	4928	77

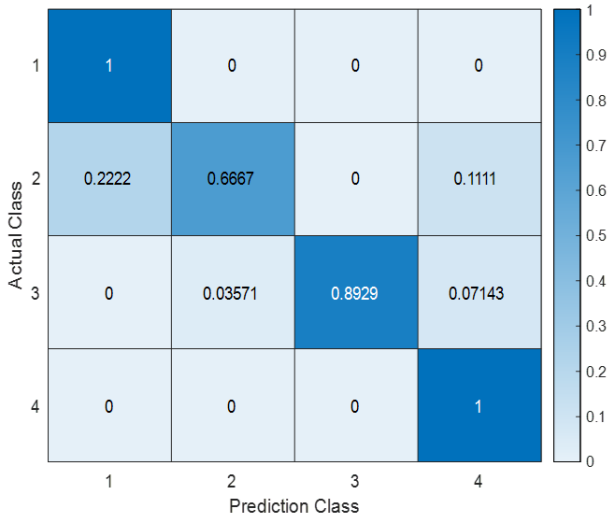
Figure 3 and Table 5 present a performance comparison chart of seven pre-trained DL models and the proposed ensemble diagnostic framework approach. In addition, the matrices of the confusion matrices showing how many of the models predicted to belong to the true class and how many to the false class from the 77 test image data are presented in Figure 3.

Accuracy alone does not adequately capture the models' performance. Thus, the proposed models were further assessed using precision, recall, and F1 score, offering a more comprehensive evaluation. Table 5 summarizes obtained results. When the data are reviewed, it is clear that the ResNet152 design had the best success rate (94%), while the DenseNet121 architecture had the lowest success rate (75%). The Proposed Ensemble model outperforms the best pre-trained model by 2% in classification success. The confusion matrices of five models are shown in Figure 3.

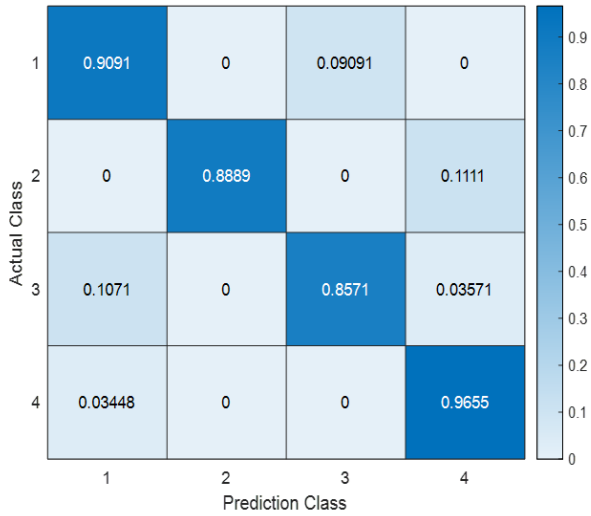
Table 5. Performance results of models for test dataset

Base-Model	Class No	Precision	Recall	F1-Score	AUC	Accuracy
DenseNet 121	1	0.40	0.18	0.25		0.75
	2	0.50	0.56	0.53		
	3	0.81	0.89	0.85		
	4	0.84	0.90	0.87		
DenseNet 201	1	0.75	0.27	0.40		0.78
	2	0.32	0.56	0.59		
	3	0.84	0.93	0.88		
	4	0.76	0.90	0.83		
EfficientNetB3	1	0.85	1.00	0.92		0.92
	2	0.86	0.67	0.75		
	3	1.00	0.89	0.94		
	4	0.91	1.00	0.95		
EfficientNetB7	1	0.64	0.82	0.72		0.86
	2	0.75	0.67	0.71		
	3	0.96	0.82	0.88		
	4	0.90	0.97	0.93		
EfficientNetB5	1	0.62	0.73	0.67		0.83
	2	0.89	0.78	0.78		
	3	0.88	0.75	0.81		
	4	0.90	0.97	0.93		
MobileNetV3	1	0.71	0.91	0.80		0.91
	2	1.00	0.89	0.94		
	3	0.96	0.86	0.91		
	4	0.93	0.97	0.95		
ResNet152	1	0.91	0.91	0.91		0.92
	2	1.00	0.78	0.88		
	3	0.96	0.89	0.93		
	4	0.88	1.00	0.94		
Ensemble Model (EfficientB3+ResNet152+MobileNetV3)	1	0.91	0.91	0.91		0.94
	2	1.00	0.89	0.94		
	3	0.96	0.89	0.93		
	4	0.91	1.00	0.95		

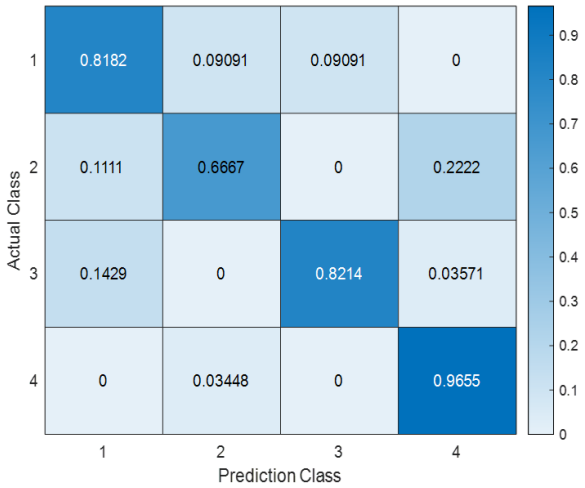
EfficientNetB3



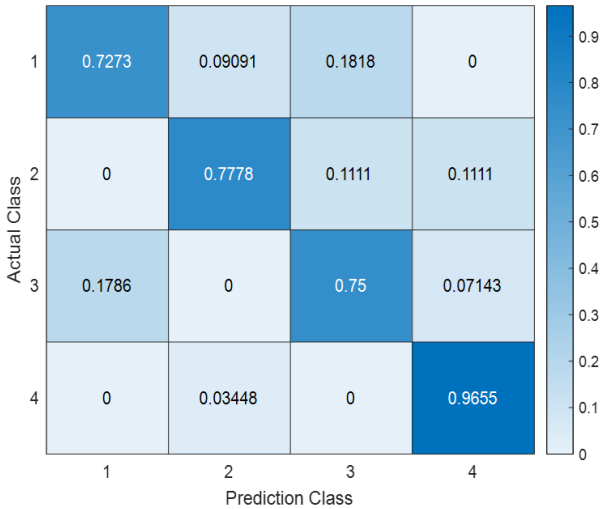
MobileNetV3



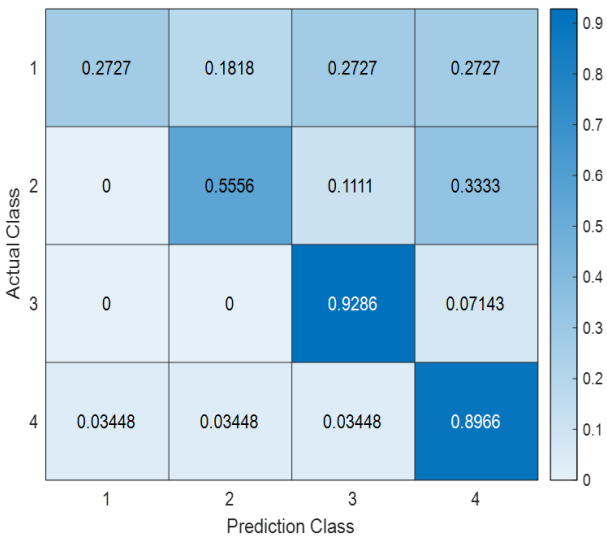
EfficienrNetB7



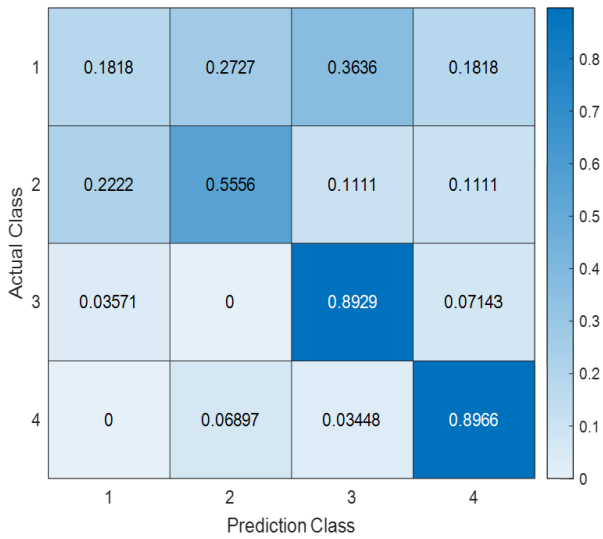
EfficientNetB5



DenseNet201



DenseNet121



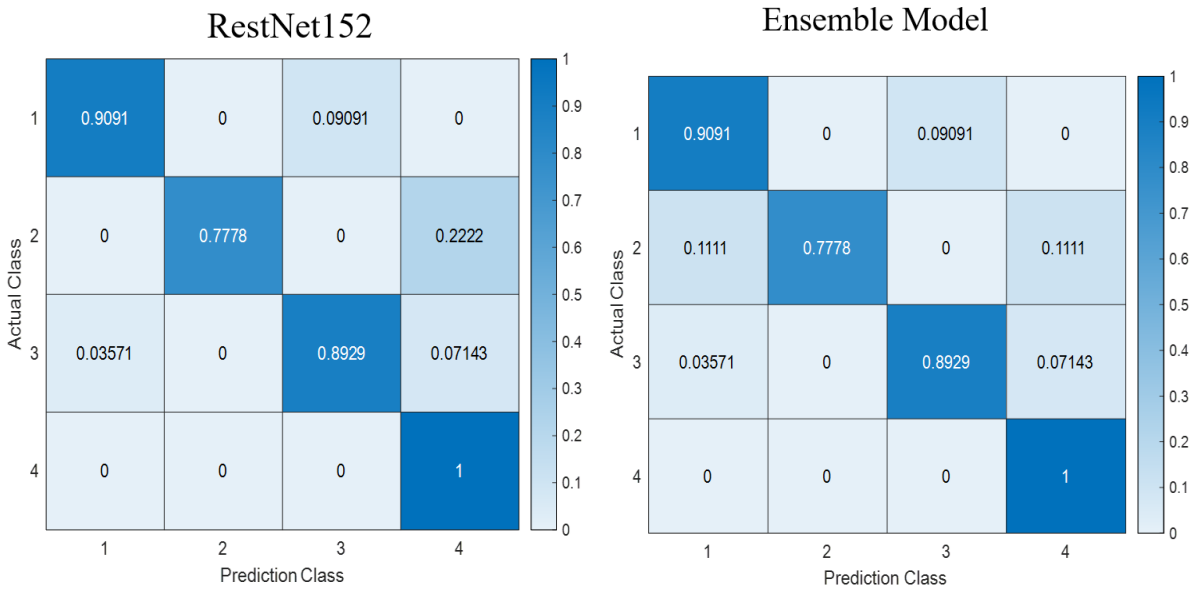


Figure 3. Confusion matrix of used all model for test dataset

Table 6. Comparison of the results obtained with the literature

Ref.	Class	Method	Accuracy
Ali et al. [19]	2 (Monkeypox or other)	VGG16 / ResNet50 /InceptionV3 Ensemble approach	81.48 /82.96 /74.07 79.26
Nahak et al. [20]	2 (Monkeypox or other)	ResNet18	99.49
Alakus [21]	2 (Monkeypox or other)	Siamese deep learning	91.09
Örenç et al. [22]	2 (Monkeypox or other)	ResNet50	94.00
Akın et al. [23]	2 (Monkeypox or other)	ResNet18	98.25
Özaltın and Yeniay [24]	2 (Monkeypox or other)	MpbilNet +K2 and SVM	99.69
Sathwik et al. [25]	2 (Monkeypox or other)	VGG19 +ResNet	92.00
Velu et al. [26]	2 (Monkeypox or other)	Q Öğrenme	96.01
Almufareh et al. [27]	2 (Monkeypox or other)	Inception V3	93.33
Lakshmi and Das [28]	2 (Monkeypox or other)	ResNet101	98.59
Uysal [29]	4 (Monkeypox, Chickenpox, Measle, Normal)	LSTM	87.00
Abdelhamid et al. [36]	2 (Monkeypox or other)	GoogleLeNet+ Sober feature extraction method	93.80
Şahin et al. [37]	2 (Monkeypox or other)	ResNet18 /GoogleNet /EfficientNetb0 NasnetMobile /ShuffleNet /MobileNetv2	73.33 /77.78 /91.11 86.67 / 80.00 /91.11
Haque [39]	2 (Monkeypox or other)	VGG19-CBAM / Xception- CBAM DenseNet121-CBAM /MobileNetV2-CBAM /EfficientNetB3-CBAM	71.86 /83.89/78.27 74.07 /81.43
Kumar [40]	2 (Monkeypox or other)	VGG16Net +SVM /VGG16Net +Naïve Byes/ VGG16Net +KNN /VGG16Net +DT/ VGG16Net +RF	75.55 /91.11 /84.44 84.44 /91.11
Ozsahin et al. [8]	2 (Chickenpox or Monkeypox)	Proposed CNN Model	95.00
Almutairi [4]	2 (Normal or pox)	VGG19 and majority voting	97.44
Gairola [42]	2 (Monkeypox or other)	AlexNet+VGGNet+NB	95.50
Irmak et al. [43]	4 (Monkeypox, Chickenpox, Measle, Normal	MobilNetV2 / VGG16 /VGG19	91.37 /83.62/77.58
Agrawal et al. [44]	2 (Monkeypox or other)	EfficientNetB3	93.00
Haque et al. [45]	2 (Monkeypox or other)	Xception-CBAM-Dense	83.89
In current study	4 (Monkeypox, Chickenpox, Measle, Normal)	(EfficientB3+ResNet152+MobileNetV3)	94.82

Although there are few research studies on Monkeypox lesion categorization in the literature, we believed that comparing the findings of the approach we developed with existing literature would be informative. Table 6 provides a summary of studies that have used the Monkeypox Skin Lesion Dataset (MSLD) along with the results of the current investigation. Upon analyzing previous studies, we could not find any other study that analyzed the same dataset using four categories, except for Uysal [29] and Irmak et al. [43]. Irmak et al. [43] employed MobileNet architectures and achieved a 91% accuracy rate, while Uysal [29] attained an 87% accuracy rate with LSTM. In the current study, we present the performance of a network architecture developed for four categories, anticipating a lower classification success compared to the two-category problem. However, it is evident that the proposed method demonstrates classification performance even higher than the majority of two-category monkeypox classification problems found in the literature.

We developed an ensemble model by synthesizing the estimation results of the MobiNetV3, ResNet152, and EfficientNetB3 architectures with the hybrid diagnostic framework approach we proposed. We successfully increased the estimation success rate by 3% for multiclass with this approach. However, as seen in the Current Study, the combination of multiple models and the classification of multiple diseases can enhance classification performance.

4. CONCLUSION AND FUTURE WORKS

Monkeypox lesions are challenging to detect at an early stage, as they exhibit similarities to chickenpox and measles. Therefore, there is a need for computer-aided software to detect monkeypox lesions with high accuracy and reliability. In the current study, an ensemble approach is proposed to obtain the final result by combining the prediction results of the three highest-performing CNN models for this problem.

This study utilized the Monkeypox Skin Image Dataset for both training and testing. Four key metrics—accuracy, precision, recall, and F1 score—were calculated to assess the proposed approach. The Ensemble model achieved 94% accuracy, 94% precision, 92.25% recall, and an F1 score of 93.25%. The majority voting method improved accuracy by 3% over the top-performing individual deep learning model. Accurate and rapid disease classification is crucial for tracking its spread and supporting the timely implementation of public health measures. Given the highly contagious nature of the virus, an early and precise diagnosis enables patient isolation, helping to prevent further transmission within the community. This will enable patients to access appropriate treatment early, thereby increasing their chances of recovery.

Finding adequate datasets in this field was extremely difficult, which made achieving acceptable performance and reliability very challenging. The plan for future studies is (1) to create generalizable results across diverse demographics, the dataset should be expanded, and worldwide relationships in data gathering and sharing should be developed; (2) to widen the research by trying different ensemble algorithms; (3) to utilize metaheuristic optimization techniques to optimize hyperparameters, and (4) to develop lightweight deep neural network models that can run on embedded system boards.

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