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Monkeypox Virus Detection Using Deep Learning Methods

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Abstract— **The fast spread of the recent monkeypox outbreak has become a public health worry in more than 40 nations outside of Africa. Similar to chickenpox and measles, a clinical diagnosis of monkeypox in the early stages might be difficult. A computer-assisted method of detecting monkeypox lesions could be helpful for surveillance and early case identification in areas where confirmatory Polymerase Chain Reaction (PCR) assays are not easily accessible. As long as enough data is available for training, deep-learning techniques help automate the detection of skin lesions. First, we refreshed the "Monkeypox Skin Lesion (MSL) Dataset," which includes photos of monkeypox, other, and normal skin lesions. To enhance the sample size, we enrich the data and set up a 3-fold cross-validation experiment. Following this, multiple pre-trained deep learning models distinguish between monkeypox, normal, and other disorders. These models are ResNet50V2, Xception, and MobileNetV2. An ensemble model consisting of all three is also created. The best overall accuracy is reached by Xception, at 96.19%, followed by ResNet50V2 (93.33%) and the MobileNetV2 model (86.67%). To propose using a typical fine-tuned architecture for different Deep Learning (DL) models for the detection of MonkeyPox virus, and compare the results. To improve the accuracy of the existing research methods.**

Keywords— ***monkeypox; ResNet50V2; MobileNetV2; Xception; virus detection***

I. INTRODUCTION

The skin, the body's largest organ, is composed of water, protein, lipids, and minerals. The skin acts as a barrier against infection and a thermostat for the rest of the body. The skin's nerve endings facilitate the ability to detect temperature [1]. Thinner and more susceptible to harm, the skin ages in tandem with the rest of the body. The diminished capacity of the skin to mend itself with age exacerbates this effect [2]. The two primary issues associated with photoaging are damage to the skin's appearance and an increased risk of skin cancer [2]. A recent multi-country outbreak of monkeypox has prompted worldwide alarm as the world continues its recovery from the COVID-19 epidemic. The World Health Organization (WHO) has stated that the attack poses a moderate risk to global public health but has refrained from designating it as an emergency. World Health Network (WHN) and other healthcare groups have voiced increased alarm [3], [29], [30] and stressed the importance of swift and coordinated international action to combat the disease. The monkeypox virus causes an infectious disease that can spread to humans. This disease is a real possibility from animals to humans and then to other people. After smallpox was eradicated in 1980, it was first recognized as a zoonotic disease in endemic regions. The disease has no discernible clinical characteristics that distinguish it from human smallpox, chickenpox, or warts. The monkeypox virus, unlike other animal pox viruses, can spread rapidly among people [4]. Clinical manifestations of monkeypox include, but are not limited to, a wide range of symptoms (including fever, malaise, weariness, headache, muscular aches, back pain, poor energy, rash, and swollen lymph nodes) and a variety of associated medical problems. The incubation period for the monkeypox virus is 5-21 days, and the fever phase lasts 1-3 days [5].

The monkeypox virus (MPXV) is a member of the orthopoxvirus genus and is responsible for the infectious disease known as monkeypox. The virus was initially found in monkeys in 1959 in a Danish research facility, hence the name Monkeypox virus [6]. In 1970, a child in the Congo exhibiting smallpox-like symptoms was hospitalised, marking the first human case [7]. Human-to-human transmission occurs through contact with infected people or objects [8]. Although it was first noticed in Africa, 3,413 points and one death have since been reported throughout more than 50 countries [9]. There are currently two recognized subtypes of the monkeypox virus: the Central African clade and the West African clade. Fifty people in West and Central Africa got monkeypox in 1990 [10]. However, by 2020, the number of instances had risen to 5,000. Many non-African countries, including Europe and the United States, reported occurrences of monkeypox in 2022 [11], dispelling the myth that the virus solely existed in Africa. The result is an increase in panic and anxiety, with many people taking to the internet to voice their concerns.

PHEIC alerts are the World Health Organization's highest level of warning. The number of cases is increasing in the endemic DRC, and the median age of patients is rising from

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children to young people, as reported in [12], [31]. Due to the worldwide spread of monkeypox, the World Health Organization (WHO) issued a PHEIC [13] on July 23, 2022. WHO received reports of 3413 laboratory-confirmed cases and one death from the beginning of the year through the end of June from five countries/territories across five WHO Regions [13]. In the past, such alerts have been issued in response to the COVID-19 virus, polio, the 2014 Ebola outbreak, and the 2016 Zika virus pandemic [14].

The monkeypox virus currently has no effective treatments available. The only real option is to create a vaccine. Monkeypox is often diagnosed using a polymerase chain reaction (PCR) or a skin lesion test with electron microscopy. PCR, the gold standard for virus confirmation, has also been utilized in recent years for the diagnosis of COVID-19. Additionally, AI-based techniques could aid in detection via virus image processing and analysis. Breast cancer, skin cancer, and diabetic retinopathy have benefited from deep learning using Convolutional Neural Networks (CNNs) for medical image analysis.

Medical professionals can benefit from the use of machine learning techniques for the early diagnosis of skin diseases. Ahsan et al. [10] recently employed web mining to obtain and have expert-verified images of Monk epoxy, chickenpox, measles, and routine photos. In addition, they compared two techniques for transfer learning using the VGG-16 model and found one superior [18]. Comparatively, the first approach investigated splitting pictures of diseased people into either Monkeypox or Chickenpox groups, while the second approach augmented the images. Without any data augmentation, a 97% success rate was seen while classifying monkeypox, but a 78% success rate was found after enriching the data.

Existing works on disease identification using Deep Learning methods for viruses have mainly used the transfer learning approach [19], [20], [15], [16], [17], [27], [28] with well-established pre-trained Deep Learning algorithms. For the most part, Ahsan et al. [18] are the only researchers who have investigated the detection of the monkeypox virus. The early results of their idea seem promising in this area. But there are three major drawbacks to it. To begin, these models are severely restricted by their focus on binary categorization. Two, they don't consider any other pre-trained Deep Learning models for transfer learning, instead focusing solely on VGG-16. To top it all off, their models could be clearer to understand. Because of this, they are establishing credibility among health professionals is challenging during mass screening.

This research proposes a Monkeypox Virus Detection with Deep Learning Methods (MVD-DLM) to retrieve the corresponding dataset. We'd use the Monkeypox Virus (MV) dataset to perfect the proposed technique for training. To compare the efficacy of different Deep Learning models, we'd use their averaged Precision, Recall, F1-score, and Accuracy across five separate trials. Our goal was to improve overall performance by ensembling the most successful models.

- To propose using a typical fine-tuned architecture for different Deed Learning models for MonkeyPox Virus Detection and compare them.
- To improve the accuracy of the existing MVD-DLM.

II. LITERATURE REVIEW

To identify or diagnose skin issues, image processing and computer vision problems must be addressed. Many research projects have examined the feasibility of using AI-based image processing, particularly DL-based image processing, to detect and analyse different types of skin illnesses. Monkeypox was first identified in humans in the Democratic Republic of the Congo (DRC) in 1970, and since then, it has spread throughout the West and Central African tropical rainforests [21].

The monkeypox virus is closely related to the variola virus [21], a member of the Poxviridae family of enveloped, double-stranded DNA viruses. The monkeypox virus's original hosts were squirrels, Gambian pouched rats, dormice, and non-human primates [21]. Several countries worldwide have reported monkeypox cases since the beginning of 2022. There have been 5,135 confirmed cases across 66 countries in the Americas, Europe, Africa, the Eastern Mediterranean, and the Western Pacific regions (as of 30 June 2022) [22]. Following the rapid spread in non-endemic nations with no epidemiological ties to endemic areas, the World Health Organization (WHO) classified the disease as a moderate global health risk [21]. Researchers [23] employed a machine learning technique called a support vector machine (SVM) to identify characteristics in EEG epochs that could distinguish Alzheimer's patients from controls. A processing strategy based on quantitative EEG (qEEG) was developed to automatically differentiate AD patients from healthy controls. The study's accuracy was good, as it considered the various methods used to diagnose each patient.

Viral infection with fever and a rash similar to smallpox can be caused by the monkeypox virus, an orthopox virus that can infect people. Since smallpox was eradicated in 1980, monkeypox has become humans' deadliest orthodox virus infection. Most reported cases have come from remote villages in Central and West African countries, namely in areas bordering on tropical rainforests, where humans may come into touch with infected animals. Direct contact with the respiratory droplets of an infected person, either at home or in a medical setting or with contaminated objects or materials, such as bedding, can result in the development of monkeypox in a susceptible individual. Although these are the most common ways for the virus to spread from person to person, monkeypox outbreaks typically include only a handful of cases and do not spread throughout the population. This is due to the very contagious nature of monkeypox. Quick action in the face of an epidemic makes stopping the disease's spread far easier. Other monkeypox cases have been recorded in different countries due to importation by tourists or domestic animals infected with the virus [24].

Hassan et al. [25] proposed using a convolutional neural network (CNN) and a long short-term memory (LSTM) with pre-trained word vectors taken from IMDB movie reviews to detect polarity. The resulting four-layer convolutional neural network (CNN) classifier featured two convolutional layers, two pooling layers, and two output layers. In the trials, the combined CNN + LSTM model outperformed both the CNN model (accuracy: 87.0%) and the LSTM model (accuracy: 81.8%). Using a novel method that combines CNN and bidirectional LSTM, Shen et al. [26] were able to identify the polarity of movie reviews. Reviews, both positive and negative, were accurately determined using this procedure. The accuracy of the combined CNN and LSTM classifiers is 89.7%, which is significantly higher than that of either model used alone (83.9% and 78.5%, respectively). The resulting four-layer convolutional neural network (CNN) classifier featured two convolutional layers, two pooling layers, and two output layers. Combining the CNN and LSTM models improved accuracy from 81.8% to 88.3% in the trials.

Evidence from this systematic research by E. M. Bunge et al. [32] suggests that the number of confirmed and suspected cases of monkeypox in Nigeria has increased from 3 in the 1970s to 181 in 2017-2019. Similar to the current outbreak, the increase in patients from the 1990s (n = 511) to the years 2000-2019 (¿28,000) is significant. Eighty percent to ninety-six percent of outbreaks were caused by those who had not gotten the immunization. Unfortunately, only 10.1% of Nigerians were vaccinated in 2016.

III. METHODOLOGY

Such self-learning algorithms are essential to the field of artificial intelligence. Such algorithms are adaptable and evolving as more information is gathered about the project [33]. Technology to address these issues is constantly growing. These mental representations are necessary for self-learning programmes to operate [34]. Artificial neural networks (ANNs) have their nodes (neurons) connected in layers, just as real neural networks. This neural network serves as a data repository, an algorithmic processor (with positive or negative weighting), and a sensory output mechanism. ANNs' multi-tiered structure and sensitivity to minor patterns show great promise. These networks can engage in "deep learning" [35], [36].

A deep transfer learning system is developed in this study to categorise monkeypox viruses. The dataset's class imbalance issue is first addressed, then pre-processing and other augmentation methods are used to generate a wide range of new data. In the second step, characteristics are automatically extracted, and pre-trained models for identifying and classifying monkeypox are used. The proposed process is depicted in a flowchart in Figure 1.

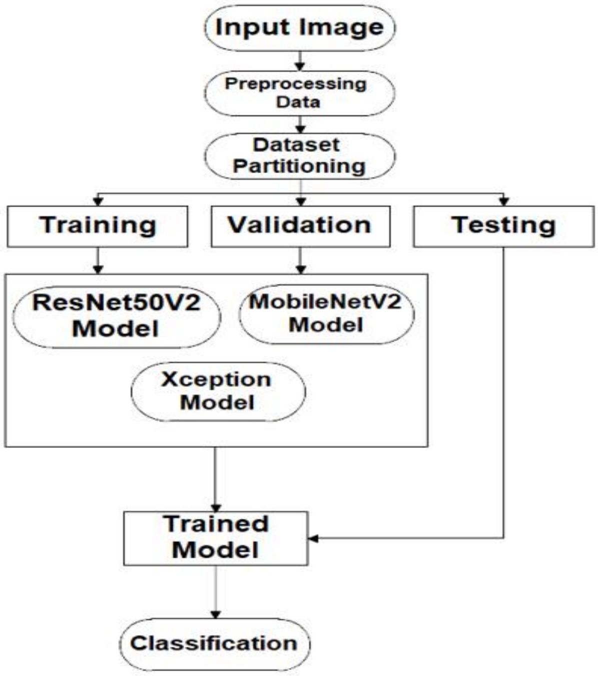

Fig. 1. Proposed method flowchart.

A. DataSet

The success of deep learning strategies depends on having access to a reliable dataset. Specifically, we're using the following dataset to finish this investigation. A. Monkeypox Skin Lesion Dataset 2022 The Monkeypox Skin Lesion (MSL) dataset archive [37] has the most extensive collection of high-quality monkeypox viral photos made available for study. In total, there are 4658 photos in the collection, with 1168 belonging to the Monkeypox class, 1439 to the others class, and 2051 to the Normal class. Different types of these classes are illustrated in Figure 2. The photos belonging to the proper category were chosen at random. Then, methods like rescaling, width shifting, rotation, shear range, horizontal flip, and channel shifting were employed to enhance the data further.

Fig. 2. (a) Monkeypox, (b) Others, and (c) Normal classes of the MSL 2022 dataset.

B. *Image Pre-Processing*

Each image in the MSL dataset is preprocessed to ensure more uniform classification outcomes and superior features. Over-fitting is a risk when training with the CNN method; therefore, having a large image dataset was crucial.

C. *Image Resizing*

The MSL dataset has 6000 × 4000 versions of all images. Dataset dimensions are adjusted to 224 × 224. The model's performance will be drastically lowered, but the processing time will be cut in half.

D. *Data Augmentation*

Overfitting has been mitigated, and the dataset's diversity has been increased by using the image data generator function of the Keras library in Python to supplement the original data in the training set. The computational burden was lessened by using a scale transformation, which made use of reduced pixel values within the same range. Each pixel's value was 0–1 thanks to the parameter value (1. /255). This is why a 25∘ rotation change was applied to the images. Images can be rotated or flipped horizontally or vertically by any amount using the width shift range transformation with a width shift value of 0.1. We could vertically move the training images by adjusting the height shift range parameter to 0.1. With a shear angle of 0.2, the image was extended along the other axis while keeping the original orientation along one. Images were enlarged if the zoom range argument was more significant than 1.0 and shrunk if it was less than 1.0. Therefore, a 0.2x zoom was used to increase the size of the image by 0.4 times. Flip allowed for the horizontal inversion of the image. We selected a zoom range of 0.5 to 1.0 because our brightness transformation used a scale where 0.0 was wholly dark and 1.0 was utterly brilliant. Channel values are randomly shifted by a value determined from the provided range, and Table 8 shows that a channel shift transformation with a 0.05 channel shift range produced the closest fill mode.

E. *Training, Validation, and Testing*

Training, validation, and testing sets were generated from the complete MSL dataset. Using a labelled dataset, the proposed Monkeypox Virus Detection using Deep Learning Method (MVD-DLM) successfully predicted labels for all photos. Using the training dataset, the MVD DLM model was trained; the validation and test sets were then used to evaluate the model's performance. Therefore, we divided our datasets into an 84%, 13%, and 3% split for training, validation, and testing, respectively. Training, validating, and testing on the MSL dataset required 4,658 photos, as shown in Table I. The data categorized as monkeypox, others, and normal classes, which accounted for 84% of the total images, were used to train the model in the current work. The last 16% of photos were split between validation and testing using the MSL dataset.

TABLE I. SUMMARY OF THE MSL-2022 DATASET

Split	**Classes**	**Label Samples**	**Total Samples**
Training	Monkeypox	980	3952
	Others	1162	
	Normal	1810	
Validation	Monkeypox	168	601
	Others	252	
	Normal	181	
Testing	Monkeypox	20	105
	Others	25	
	Normal	60	
Total			**4658**

F. *The Proposed Methodology*

1) *ResNet50V2 Base Model*

ResNet is one of the most well-known and successful models in computer vision competitions [38]. There are a plethora of others; InceptionResNetV2 [39], MobileNet [40], and GoogleNet [41] are just a few examples. These models are educated on information from numerous diverse image datasets. Using these model weights that have already been trained, transfer learning methods can quickly and effectively address a wide variety of computer vision problems without having to train new models from scratch. Photos of several plant species were fed into the ResNet50 model with pre-trained weights to perform transfer learning. In subsequent paragraphs, I will describe the internal workings of the ResNet50 model and its extensive library of pre-trained weights. ResNet50 is a 50-layer convolutional neural network model. Figure 3 depicts the ResNet50 model's architecture, which includes the ResNet50 fine-tuning setup.

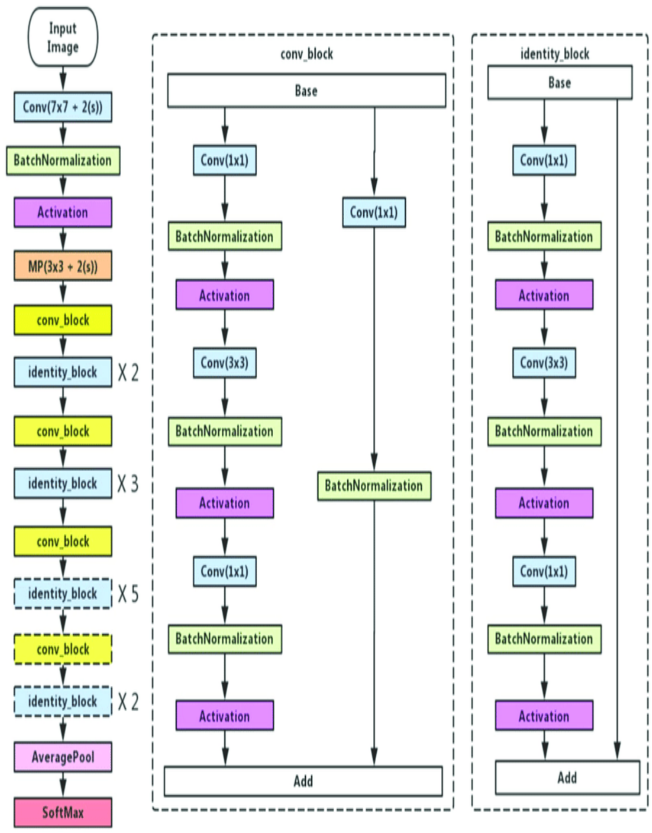

Fig. 3. ResNet50V2 Base Model Architecture.

2) *Xception Base Model*

To connect the depth-separable convolution process with the regular convolution used in convolutional neural networks, scientists have developed inception modules (a depthwise convolution followed by a pointwise convolution). A depthwise separable convolution can be thought of in this setting as an Inception module where the maximum height is fixed. Based on these results, we propose a new design for a deep convolutional neural network, where depthwise separable convolutions are employed in place of the Inception modules. Our Xception [42] design outperforms Inception V3 on a larger, more diverse image classification dataset consisting of 350 million images and 17,000 classes. On the ImageNet dataset, however, Xception [42] outperforms Inception V3 by a small margin (for which Inception V3 was built). The performance improvements of the Xception architecture are not due to an increase in capacity but rather to more efficient use of model parameters.

To accomplish complex tasks, the Xception neural network design employs depth-separable convolutions. Google's research staff developed it. Inception modules, used in convolutional neural networks, are a "middle ground" between traditional convolution and the depth-wise separable convolution method, as explained by Google (a depthwise convolution followed by a pointwise convolution). From this perspective, it becomes clear that a depth-wise separable convolution is comparable to an infinitely tall Inception module. To make use of this finding, they suggest a novel Inception-like architecture for deep convolutional neural networks that use depthwise separable convolutions in place of Inception modules.

3) *MobileNetV2 Architecture*

In this study, we apply the deep transfer learning MobileNetV2 [40] architecture to the problem of face mask classification. Many factors led to the selection of the MobileNetV2 architecture. MobileNetV2 is a framework that optimises execution speed and memory utilisation while reducing the cost of failures [40]. MobileNetV2 relies mainly on the framework created by MobileNetV1. As the dataset used to train the model was very small, using a compact but expressive framework like MobileNetV2 helped mitigate the possibility of over-fitting. To better understand the MobileNetV2 framework, the relationships between the depthwise separable convolution, the linear bottleneck, and the inverted residual are examined. The architecture of the mobileResNetV2 model is shown in Figure 4.

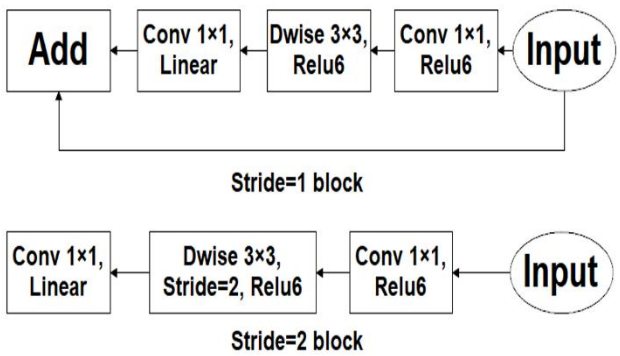

Fig. 4. MobileNetV2 Base Model Architecture.

G. *Evaluation Measures*

The proposed method was evaluated on the testing dataset after the training phase. Accuracy, F1 score, precision, and recall were used to verify the architecture's performance. In the following sections, we'll investigate the performance measurements used in this study. True positives (TP), true negatives (TN), false negatives (FN), and false positives (FP) are defined and represented mathematically in the following.

a) *Classification Accuracy*

The accuracy of a classification system can be evaluated by determining what percentage of its predictions were correct and what percentage were incorrect.

$$\text{Accuracy} = (TP+TN) / (TP + TN + FP + FN)$$

b) *Precision*

When analysing the effectiveness of a model, classification accuracy may not always be the most appropriate metric to employ. For instance, this is one of the scenarios where there is a considerable gap in socioeconomic status. It's a safe bet to assume that each sample is of the highest possible quality. If the model isn't picking up any new information, it would be irrational to infer that all components belong to the best class. Therefore, when we talk about accuracy, we refer to the fluctuation in findings you receive while measuring the same object several times with the same tools. The term "precision" refers to one of these statistics and can be defined as follows:

$$\text{Precision} = TP / (TP + FP)$$

c) *Recall*

Another critical parameter is called recall, and it refers to the percentage of input samples that are of a type that the model can accurately predict. The formula for the recall is as follows:

$$\text{Recall} = TP / (TP + FN)$$

d) *F1 Score*

The f1 score is a statistic utilised to contrast recall and precision.

$$\text{F1Score} = 2 * (\text{Precision} * \text{Recall}) / (\text{Precision} + \text{Recall})$$

IV. RESULTS AND DISCUSSION

We used powerful Graphics Processing Units (GPUs) on a new Google Colab [43] Pro account for training and testing. We used transfer deep learning models for this task. All experiments were performed with the Adam optimizer and a learning rate of 0.0001 to train the proposed MVD DLM using Sparse Categorical Cross-entropy loss functions. The optimal val_loss models were kept throughout the training phase, which consisted of 10 iterations with an initial batch size of 8. These settings were suggested by the ResNet50V2, Xception, and MobileNetV2 models: 8 batches, 5 epochs, early stopping, and model saving depending on val_loss.

- We used the MSL-2022 dataset to assess the efficacy of the given ResNet50V2, Xception, and MobileNetV2 models, enhancing the datasets with various forms of augmentation.

- When compared to its predecessors, the proposed MVD-DLM shows significant improvement in terms of accuracy.
- The results were compared with state-of-the-art techniques.

A. THE Performance Analysis of the Proposed Monkeypox Virus Detection using Deep Learning Methods (MVD-DLM)

1) ResNet50V2 Proposed Model Performance on MSL-2022 Dataset

We evaluated and analysed the performance of the ResNet50V2 base model on the MSL dataset. Validation accuracy for the model increased from 74.33% at the end of the first epoch to 79.50% after the most recent epoch. Training accuracy improves from 90.26% after the first epoch to 97.93% after the last epoch in Figure 5. As ob served in Figure 5, ResNet50V2 validation loss substantially decreased from 78% to 49.75%. Furthermore, identical to the initial loss, the training loss was 27.45% after the first period and 6.06% after the concluding training.

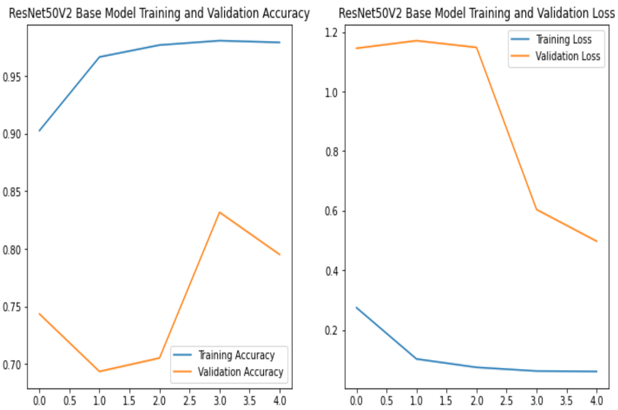

Fig. 5. The ResNet50V2 Base Model of Accuracy and Loss Graph.

Table II details how well the ResNet50V2 base model did on an unseen test set. When applied to all classes in the test set, the model produced an average accuracy of 93.33%; however, ResNet50V2 achieved a precision of 89%, a recall of 85%, and an F1-score of 87% on the Monkeypox class. For the Normal class, the f1 score, precision, and recall averaged 95%, 100%, and 98%, respectively. The Others class is impressive, with a 91% accuracy, 84% recall, and 87% F1 score.

TABLE II. PRECISION, RECALL, F1 SCORE, AND ACCURACY OF THE RESNET50V2BASEMODEL.

Performance Measures	Precision	Recall	F1 Score	Accuracy
Monkeypox	89%	85%	87%	85%
Others	91%	84%	87%	84%
Normal	95%	100%	98%	100%
Average Accuracy				**93.33%**

We could visually evaluate the categorization accuracy of different models using a confusion matrix. Predictions that turned out to be inaccurate are represented by rows in the confusion matrix that are not on the diagonal. Darker colours indicated higher classification accuracy in the matching ResNet50V2 base model for each class, while cesfromthetestsetwillbeusedtomeasureResNet50V2's overall effectiveness (shown in Figure 6). Predictions made by theResNet50V2baselinemodelwere accurate across all image categories, as indicated by the confusion matrix. Using the default parameters for the ResNet50V2 model, the confusion matrix shows that 93.33%of the data were classified correctly, with only 6.67% incorrect classifications. Comparing the confusion matrices for the Monkeypox, Others, and Normal samples demonstrates that the ResNet50V2 basic model performs wonderfully.

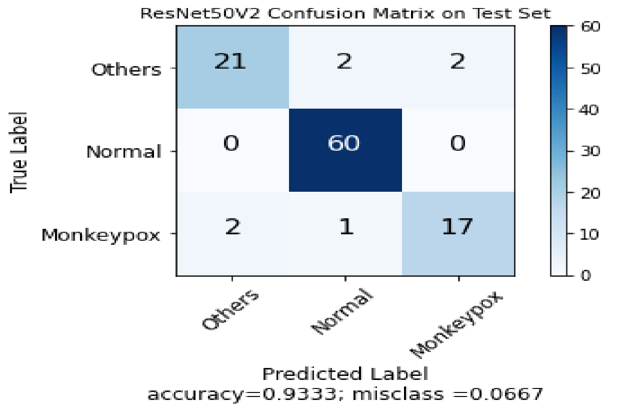

Fig. 6. ResNet50V2 Base Model Confusion Matrix Set.

2) Xception Proposed Model Performance on MSL-2022 Dataset

On the MSL-2022 dataset, the efficiency of the Xcetion baseline model was evaluated. Model validation accuracy increased from 84% at the end of the first epoch to 86.01% after the most recent epoch. Training accuracy is shown to rise from 90% after the first epoch to a final value of 99.14% in Figure 7. Figure 7 displays the remarkable reduction in invalidation loss experienced by Xception from an initial value of 80.43% to just 49.33%. The training loss was 29.03% after the first period and 3.05% after finishing training, mirroring the initial loss exactly.

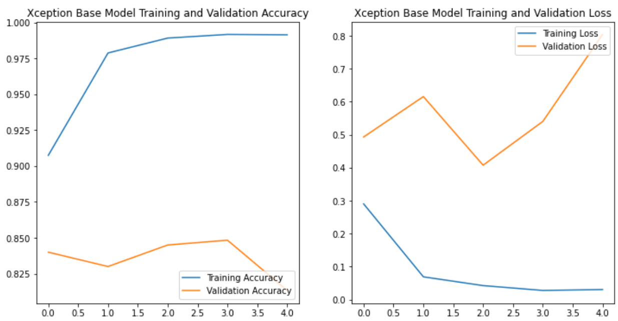

Fig. 7. The Xception Base Model of Accuracy and Loss Graph.

Examining how the Xception base model fared on a naive test set is the focus of Table III below. Using the test data, the model could correctly predict 96.19% of instances across all classes; however, Xception performed even better on the Monkeypox class, achieving 83% precision, 100% recall, and 91% F1-score. The Normal class had an average overall F1 score, precision, and recall of 100%. In the Others class, Xception achieves an F1-score of 91% with 100% accuracy, 84% recall, and 100% recall.

TABLE III. PRECISION, RECALL, F1 SCORE, AND ACCURACY OF THE XCEPTION BASE MODEL.

Performance Measures	Precision	Recall	F1 Score	Accuracy
Monkeypox	83%	100%	91%	100%
Others	100%	84%	91%	84%
Normal	100%	100%	100%	100%
Average Accuracy				**96.13%**

Classification accuracy across multiple models was visually compared using a confusion matrix. Predictions that turned out to be incorrect are represented by rows in the confusion matrix that is not on the diagonal. The corresponding Xception base model for each class showed that darker colors indicated higher classification accuracy, whereas lighter colors misclassified data. The test set's confusion matrix will be used to assess Xception's overall effectiveness (shown in Figure 1). As seen in the confusion matrix, when the Xception model's default settings are used, 96.19%of the data are correctly classified, leaving only 3.81% unaccounted for. Based on the confusion matrix, it was clear that the Xception base model accurately classified Monkeypox and Normal samples.

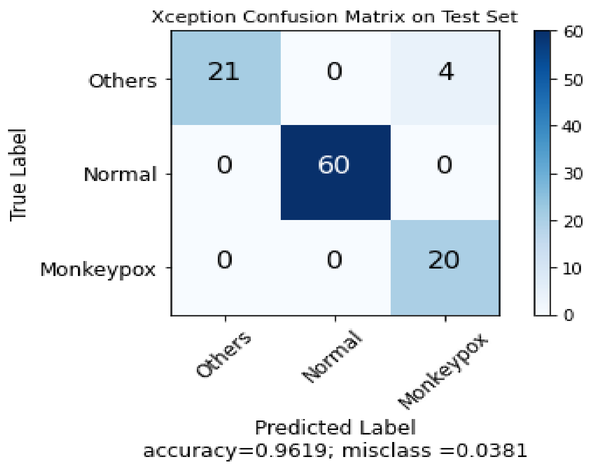

Fig. 8. The Xception Base Model Confusion Matrix on Test Set.

3) MobileNetV2 Proposed Model Performance on MSL-2022 Dataset

We analysed and rated MobileNetV2's performance as the foundational model on the MSL dataset. The validation accuracy of the model rises with each epoch, from 77.33% at the end of the first epoch to 78.67% after the most recent epoch. Training accuracy steadily improves from85.96% to 97.52% after the last epoch, as shown in Figure 9.

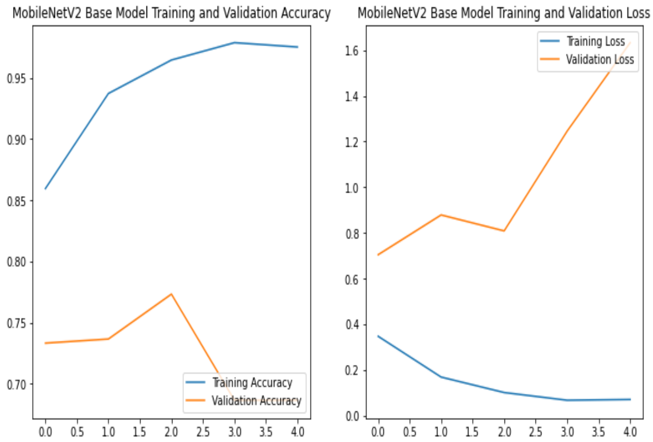

Fig. 9. The MobileNetV2 Base Model of Accuracy and Loss Graph.

The outcomes of an unseen test set utilising the MobileNetV2 baseline model are summarised in Table IV. The overall accuracy across all classes in the test set was 86.67%, with MobileNetV2 achieving 90% accuracy, 45% recall, and 60% F1-score on the Monkeypox class. The Normal class had an average F1 score, precision, and recall of 98%, 95%, and 100%. The Others group excels in every way imaginable. Their F1 score is 77%, their recall is 88%, and their precision is 69%.

TABLE IV. PRECISION, RECALL, F1 SCORE, AND ACCURACY OF THE MOBILENETV2 BASE MODEL.

Performance Measures	Precision	Recall	F1 Score	Accuracy
Monkeypox	90%	45%	60%	76%
Others	69%	88%	78%	88%
Normal	95%	100%	98%	100%
Average Accuracy				**86.67%**

To compare the accuracy of different models' classifications, we can use a confusion matrix (like the one displayed in Figure 10. In a confusion matrix, non-diagonal rows stand for forecasts that didn't pan out. For each class, more accuracy in the MobileNetV2 basic model was represented by darker colours, while lighter colours showed lower accuracy. Confusion matrices from the test set will be used to assess MobileNetV2's overall performance. The predictions of the MobileNetV2 baseline model are completely accurate across the board of image types, as shown by the confusion matrix. If we look at the confusion matrix, we can see that when the MobileNetV2 model was trained with the default settings, 86.67% of the data were identified correctly, and just 13.33% were misclassified. By comparing the confusion matrices for the Monkeypox, Others, and Normal samples, we can see that the MobileNetV2 basic model performs quite well.

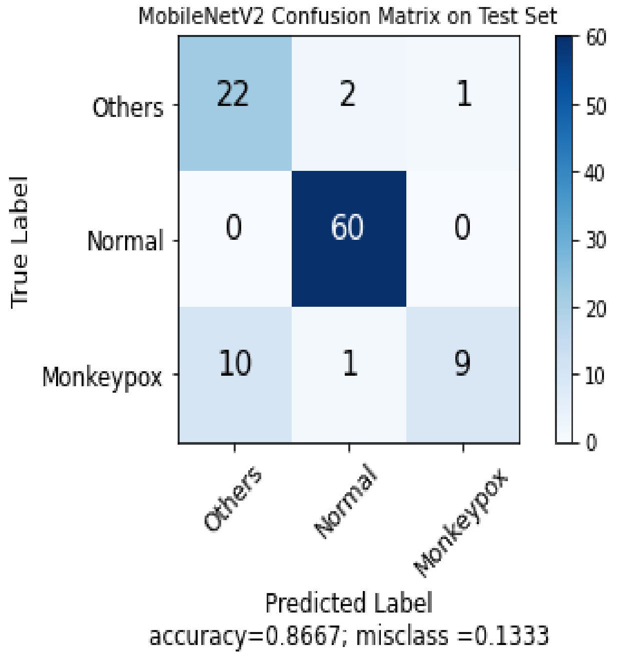

Fig. 10. The MobileNetV2 Base Model Confusion Matrix on Test Set.

TABLE V. CLASSIFICATION ACCURACY OF PROPOSED MODELS ON TEST SET.

Model Name	**Accuracy**
ResNet50V2 Base Model	93.33%
Xception Base Model	96.19%
MobileNetV2 Base Model	86.67%

V. CONCLUSION

Using the publicly available "Monkeypox Skin Lesion (MSL) Dataset," we conducted a preliminary feasibility study using state-of-the-art deep learning architectures (ResNet50V2, Xception, MobileNetV2), leveraging the transfer learning approach. We successfully detected monkeypox from skin lesions in many test cases. Despite the limited size of the dataset, encouraging results from 3-fold cross-validation suggest that AI-assisted early identification of this condition may be feasible. The "Monkeypox Skin Lesion (MSL) Dataset," which has images of monkeypox, other, and normal skin lesions, was first updated. We increased the data size and designed a three-fold cross-validation study. After that, several deep-learning models with prior training can tell the difference between monkeypox and other conditions. ResNet50V2, Xception, and MobileNetV2 are the models in question. Additionally, all three are combined into one comprehensive model. With an accuracy of 96.19%, Xception outperforms ResNet50V2 (93.33%) and MobileNetV2 (86.67%).

Our work has two significant restrictions. To begin, there is room for improvement, given the limited size of the dataset. Second, we may need help deploying our AI solution in a memory-constrained environment because it relies on pre-trained DL models. Therefore, it may be worthwhile to build unique lightweight DL models to enable them to function on constrained hardware.

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