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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. Similarly 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 MVD-DLM.

Keywords: Monkeypox, ResNet50V2, MobileNetV2, Xception

1. 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 vulnerable to harm, the skin ages alongside the rest of the body. The diminished capacity of the skin to mend itself with age exacerbates this effect [2]. The two main issues related to photoaging are damage to the skin's look 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] 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 identified as a zoonosis in endemic regions. The monkeypox virus has been detected on rare occasions in the rainforests of Central and West Africa, especially the Democratic Republic of the Congo. The disease has no discernible clinical characteristics that set it apart from human smallpox, chicken pox, or warts. Monkeypox virus, in contrast to other animal pox viruses, may spread quickly among people [4]. Clinical manifestations of monkeypox include but are not limited to, a wide variety of symptoms (including but not limited to fever, malaise, weariness, headache, muscular aches, back pain, poor energy, rash, and swollen lymph nodes) and a wide variety of medical problems. The incubation period for the monkeypox virus is 5-21 days, and the fever phase lasts 1-3 days [5].

Monkeypox is considered as an infectious disease that is spread through monkeypox virus (MPXV). This belongs to the genus orthopoxvirus and historically this virus was explored in 1959 in Denmark. [6]. The very first case was identified in human beings in Congo during the 1970's when a small kid was admitted to the hospital with similar symptoms of smallpox. [7]. It spreads through contact with an infected person, animal, or material. [8]. Initially, monkeypox emerged inside the African region, but now it has reached more than 50 countries with total 3,413 confirmed cases and one fatality [9]. At the moment, there exists two varieties of the monkeypox virus; one, the Central Africa varient, and another, the West Africa varient. In 1990, only 50 people in West and Central Africa contracted monkeypox [10]. The number of reported incidents, however, increased to 5,000 by the year 2020. Although it was previously believed that monkeypox only occurred in Africa, numerous non-African countries, including Europe and the United States, reported cases of the virus in 2022 [11]. As a result,

widespread panic and worry are on the rise, with many people airing their concerns on online platforms. The World Health Organization issues its strongest warning, known as a PHEIC. According to [12], the median age of monkeypox victims is increasing from children to young adults, and the number of cases is rising in the endemic DRC. The World Health Organization (WHO) declared a PHEIC [13] because of the global monkeypox outbreak on July 23, 2022. From the beginning of the year through the end of June, five countries/territories across 5 WHO Regions reported 3413 laboratory-confirmed cases and one fatality to WHO [13].

Similar warnings were issued for the covid-19 virus, polio, the 2014 Ebola outbreak, and the 2016 Zika virus spread [14]. There exists no treatment for the monkeypox virus worldwide. The alternate preventative measure includes vaccination. Monkeypox is diagnosed with PCR or Skin Lesion Test and the PCR method is believed to be more authentic. In addition, the Artificial Intelligence (AI)-enabled tools have the capabilities to detect them using virus image processing. Medical image analysis using deep learning with Convolutional Neural Networks (CNN) has been utilized effectively in healthcare to detect breast cancer [14], skin cancer [15], and diabetic retinopathy [16].

Different researchers have used DL models for the detection of COVID-19, Chicken Pox, Herpes, and others. For instance, Sandeep et al. [17] looked into how well deep learning (DL)-based algorithms could identify a variety of diseases such as Psoriasis, Chicken Pox, Vitiligo, Melanoma, Ringworm, Acne, Lupus, and Herpes. For classification, they used the model VGG-16 model to compare their result with the CNN. Further, they constructed eight illness groups to classify the skin lesion [18]. The detection rate using their method was 78%. In [19], they proposed a Convolutional Neural Network (CNN) based virus detection of Herpes Zoster Virus (HZV). When tested on a set of 1,000 images, the ability to detect HZV early resulted in an accuracy of 89.6%. Machine learning methods are helpful in the medical field for the early detection and diagnosis of skin diseases. Ahsan et al. [10] recently used web mining techniques to acquire and have expert-verified photos of Monk epoxy, Chickenpox, Measles, and Normal. They also tested transfer learning using the VGG-16 pretrained model, comparing two methods [20]. The first method was classifying photographs into two disease categories, Monkeypox and Chickenpox, whereas the second method was combnied to the images. A 97% success rate was observed while classifying monkeypox without any augmentation of data, while a 78% success rate was reported after augmenting the data.

Existing works on disease identification using Deep Learning methods for viruses have mainly used the transfer learning strategy [4], [21] with well known pre-trained DL models. For the most part, Ahsan et al. [20] are the only ones who have researched detecting 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.

The current study would propose a Monkeypox Virus Detection using Deep Learning Methods (MVD-DLM), which would identify the dataset. The proposed method would be trained on the Monkeypox Virus (MV) dataset. We would assess the performance of each DL model using averaged Precision, Recall, F1-score, and Accuracy over five folds cross validation. We would ensemble the best-performing models to improve the overall performance. The main objective of this research is to resolve these issues. The following are the contributions of the present research:

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

2. LITERATURE REVIEW

To identify or diagnose skin issues, image processing and computer vision problems must be solved. 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 as human in the Democratic Republic of the Congo (DRC) in 1970, and since then, it has spread throughout the west and central African tropical rainforests [22].

The monkeypox virus is closely related to the variola virus [22], which is also 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 [22].

Researchers [23] employed a machine learning technique called support vector machine (SVM) to look for characteristics in EEG epochs that could distinguish Alzheimer's patients from controls. A processing strategy based on quantitative EEG (qEEG) was created to distinguish AD patients from healthy controls automatically. The study's accuracy was good since it considered the many 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 to 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 other 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 performed better than either the CNN model (accuracy: 87.0%) or the LSTM model (accuracy: 81.8%). Using a novel method using the combination of CNN and bidirectional LSTM, Shen et al. [26] could identify the polarity of movie reviews. Reviews, both good and negative, were identified accurately using this procedure. The accuracy of the combined CNN and LSTM classifiers is 89.7%, which is significantly greater than 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. The most extensive collection of images of Monkeypox skin was presented in [27] by the researchers themselves. The images of healthy and diseased skin were collected using web scraping to form a comprehensive public picture collection. Images of infected skin ranged from measles to cowpox to chickenpox to smallpox to Monkeypox.

The Monkeypox Skin Lesion Dataset (MSLD) was created by the authors of [28] and features images of skin lesions caused by measles, chickenpox, and Monkeypox. Most images were collected from open-access sources like the internet, news websites, and case reports. We extend our sample size in the first step and set up a three-fold cross-validation experiment. In the next step, various DL models, including VGG-16, ResNet50, and InceptionV3, are used to classify diseases like Monkeypox. The best overall precision is reached by ResNet50. In [10], authors proposed employing a DL model trained on images of monkeypox lesions to identify the disease. The model would be based on a VGG16 image recognition algorithm variant. The dataset was created by compiling images from several open-source and online sources, making it more secure for use and dissemination in the context of the development and deployment of any ML model. Two research used the updated version of the VGG16 model. In both cases, they found that the model successfully identified Monkeypox patients. This model's ability to predict outcomes and extract relevant aspects of the Monkeypox virus aided our understanding of the virus.

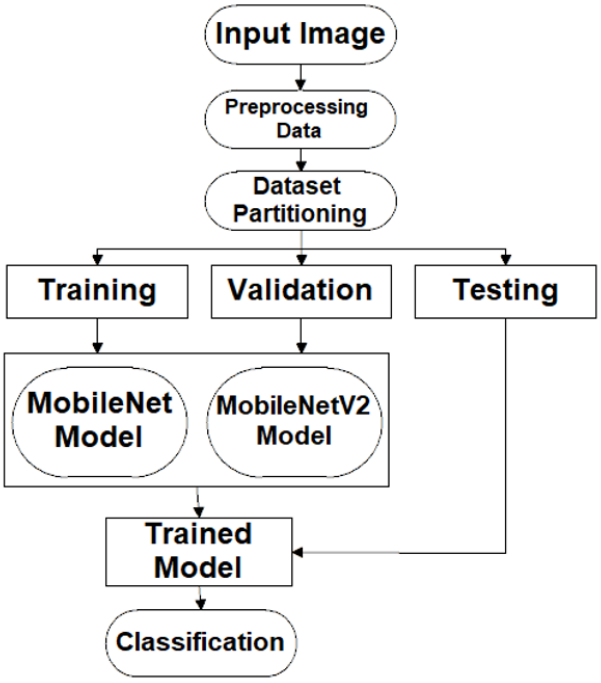

Figure 1. Proposed method flowchart.

3. 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 project [29]. Technology to address these issues is constantly growing. These mental representations are necessary for self-learning programmes to operate [14]. 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" [30], [31].

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.

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.

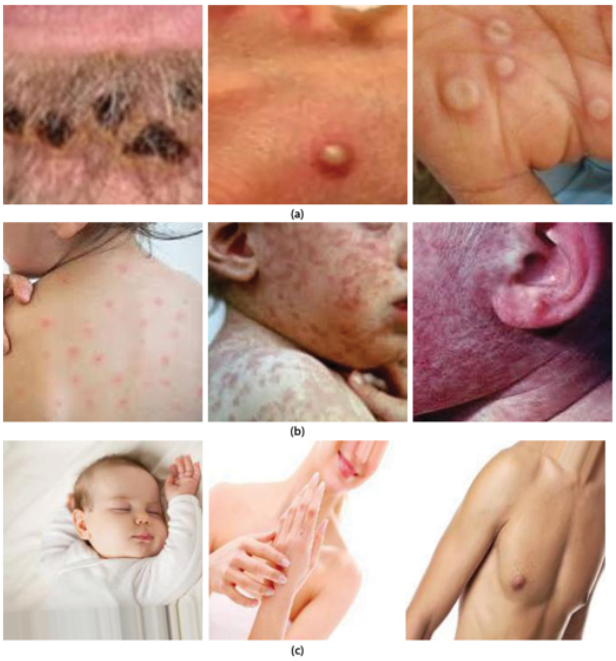

Figure 2. (a) Monkeypox, (b) Others and (c) Normal classes of MSL-2022 dataset.

1) Monkeypox Skin Lesion Dataset 2022

The Monkeypox Skin Lesion(MSL) dataset archive [32] 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.

B. 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.

C. 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 a 75%/15%/10% split for training, validation, and testing. Training, validating, and testing on the MSL dataset required 4658 photos, as shown in Table I. Data categorised as monkeypox, others, and normal classes, accounting for 75% of the total images, were used to train the model in the current work. The last 25% 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**

D. The Proposed Methodology

1) ResNet50V2 Base Model

ResNet is one of the most well-known and successful models in computer vision competitions [33]. There are a plethora of others; InceptionResNetV2 [34], MobileNet [35], and GoogleNet [36] 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.

2) MobileNetV2 Base Model

In this study, we apply the deep transfer learning MobileNetV2 [35] 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 [35]. 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. The small amount of RAM required is a plus, and the fast processing time simplifies tinkering with the settings. To better understand the MobileNetV2 framework, the relationships between the depthwise separable convolution, the linear bottleneck, and the inverted residual are examined.

3) 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 provide a new design for a deep convolutional neural network in which depthwise separable convolutions are used in place of the Inception modules. Our Xception [37] 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 [37] 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.

E. 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.

1) 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.

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

2) 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:

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

3) 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:

$$Recall = \frac{TP}{(TP + FN)} \tag{3}$$

4) F1 Score

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

$$F1Score = \frac{2 * (Precision * Recall)}{(Precision + Recall)} \tag{4}$$

4. RESULTS AND DISCUSSION

We used powerful Graphics Processing Units (GPUs) on a new Google Colab [38] 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 Crossentropy 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.

1) 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.
2) When compared to its predecessors, the proposed MVD-DLM shows significant improvement in terms of accuracy.
3) 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 3. As observed in Figure 3, 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.

When applied to all classes in the test set, the ResNet50V2 base model produced an average accuracy of 93.33%; however, ResNet50V2 achieved a precision of 89%, recall of 85%, and 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.

We could visually evaluate the categorization accuracy of different models using a confusion matrix. Predictions

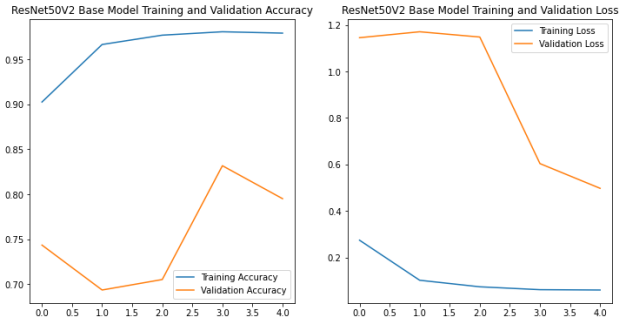

Figure 3. The ResNet50V2 Base Model of Accuracy and Loss Graph.

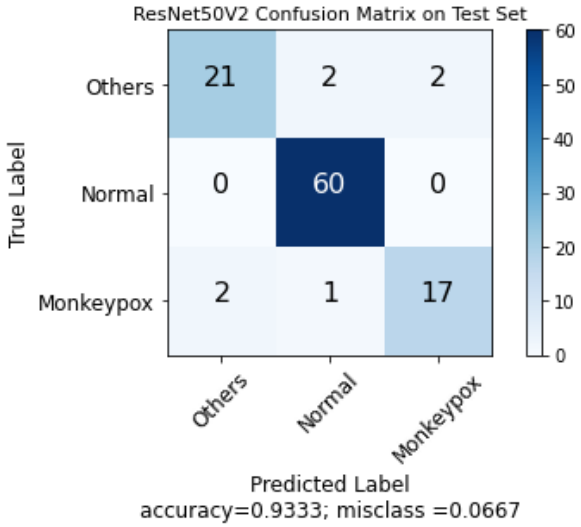

Figure 4. The ResNet50V2 Base Model Confusion Matrix on Test Set.

that turned out to be inaccurate are represented by rows in the confusion matrix that is not on the diagonal. Darker colours indicated higher classification accuracy in the matching ResNet50V2 base model for each class, while lighter colours showed misclassified data. Confusion matrices from the test set will be used to measure ResNet50V2's overall effectiveness (shown in Figure 4). Predictions made by the ResNet50V2 baseline model were 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 demonstrate that the ResNet50V2 basic model performs wonderfully.

2) The Performance of Xception Base Model

On the MSL-2022 data set, the efficiency of the Xception 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. The training accuracy is

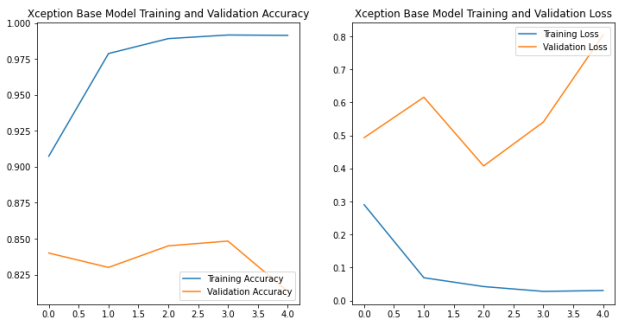

Figure 5. The Xception Base Model of Accuracy and Loss Graph.

shown to rise from 90% after the first epoch to a final value of 99.14% in Figure 5. Figure 5 displays the remarkable reduction in validation 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.

Using the test data, the Xception base 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 got an F1-score of 91% with 100% accuracy, 84% recall, and 100% recall.

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 colours indicated higher classification accuracy, whereas lighter colours told misclassified data. The test set's confusion matrix will be used to assess Xception's overall effectiveness (shown in Figure 6). As can be 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, Others and Normal samples.

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 from 85.96% after the first epoch to 97.52% after the last epoch, as shown in Figure 7.

The MobileNetV2 base model's overall accuracy across all classes in the test set was 86.67%, with MobileNetV2

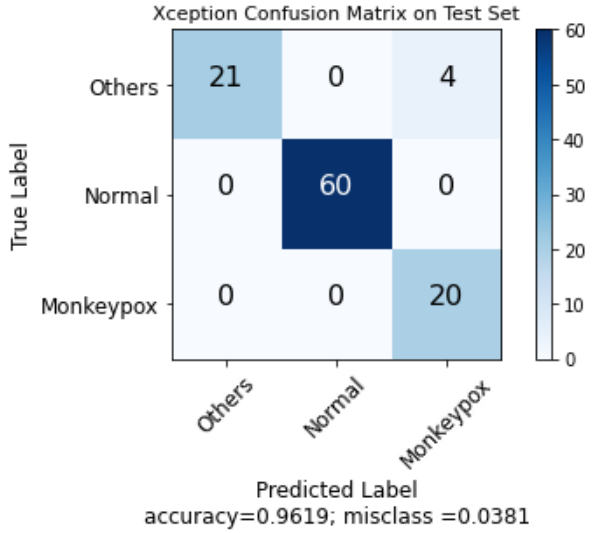

Figure 6. The Xception Base Model Confusion Matrix on Test Set.

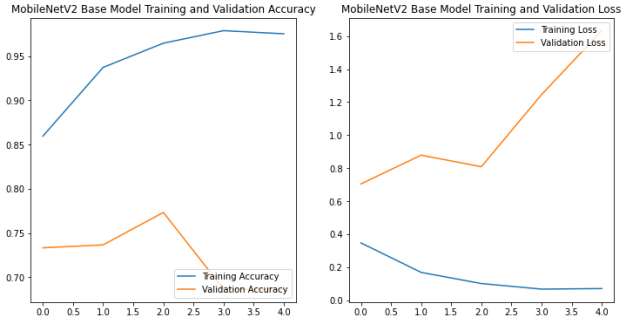

Figure 7. The MobileNetV2 Base Model of Accuracy and Loss Graph.

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%.

To compare the accuracy of different models' classifications, we can use a confusion matrix (like the one displayed in Figure 8. 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,

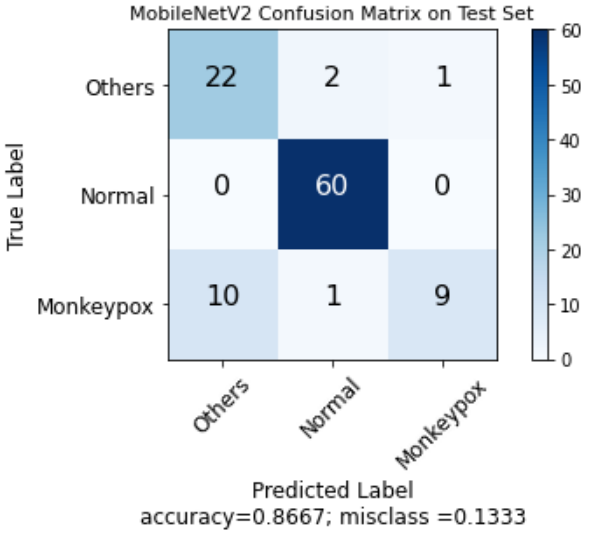

Figure 8. The MobileNetV2 Base Model Confusion Matrix on Test Set.

we can see that the MobileNetV2 basic model performs quite well.

5. 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%).

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