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An Overview of Deep Learning Models for Prediction of MPOX Disease

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Abstract: *Infections from pathogenic organisms including bacteria, viruses, and fungus are what cause communicable diseases. Due to the limits of diagnostic techniques and the associated costs, infection diagnoses are frequently delayed or made late. This could lead to the infections spreading and have a negative impact on effective therapies. Another major problem is the dearth and unequal distribution of specialized physicians in urban and rural areas. Contrary to non-communicable illnesses, early detection is essential to halt the spread of communicable illnesses and new threats like Mpox, which otherwise could infect millions of people globally. Artificial intelligence is widely used, particularly in the medical field. Deep learning, a kind of AI, processes health care data incredibly quickly and accurately—even better than doctors. Therefore, establishing a deep learning-based medical diagnostic system for communicable disease prediction can aid in a more accurate diagnosis than current practices. With the use of several deep learning models based on transfer learning, we suggest a communicable disease diagnostic system for anticipating Mpox. The method determines if a person has Mpox or not based on a photograph of their skin lesions.* To *reduce loss and increase accuracy, techniques like data augmentation, transfer learning, and fine-tuning are increasingly used. According to experimental findings, this model offered greater accuracy when compared to other current literature studies. Our approach can aid in the early detection of Mpox infections, stop the disease's spread, and guarantee that treatments can be administered on schedule.*

Keywords: CNN, pre-trained model, Deep learning, Transfer learning, Monkeypox, Disease prediction

I. INTRODUCTION

Many of the infectious diseases affecting humans are zoonoses, means they came from animals. This includes the swine flu from pigs, Ebola virus, which came from primates and the novel corona virus from bats etc. Early warning of new zoonoses is important, to deal with the viral spread and prevent it from becoming a pandemic. The Mpox virus was initially discovered in 1958 after sickening monkeys were transported from Singapore to a Danish research facility. However, the virus was isolated from a child in the Democratic Republic of the Congo who was thought to have smallpox and the first verified human case was published in 1970 [1]. There are two separate clades of Mpox: the West African clade and the Congo Basin clade. Since Smallpox immunization stopped in 1980, there has been a sharp rise in instances of Mpox in Africa. People who have received Smallpox vaccine have a lower chance of getting Mpox. Another reason for increasing cases of Mpox in Africa is the encroachment by people on the areas where virus-carrying animals live [2].

In many regions of the world where the disease is not endemic, incidences of Monkeypox have been reported since 2022. Outside of Africa, person-to-person transmission of Monkeypox has been verified [3]. The epidemic of Monkeypox in 2022 has been deemed a public health emergency of global concern by the World Health Organization (WHO). [1]

Fever, headache, tiredness, myalgia and lymphadenopathy are some of the early signs of Monkeypox [1]. Mucosal lesions appear in the mouth after one to two days, and then skin lesions appear on the face and other places, such as the

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palms and soles. The number of lesions can range from a few to thousands, and the rash may or may not spread to the rest of the body. The lesions progress through macular, papular, vesicular, and pustular phases during the course of the next 2 to 4 weeks [1]. Before crusts form, lesions are in the pustular phase for 5 to 7 days. After all crusts have fallen off, the illness usually clears up within 3 to 4 weeks, and patients are no longer regarded as contagious.

Mpox infection can cause serious health issues, including death, in some individuals, including pregnant women, newborns, kids, and those with underlying immune weaknesses. Close contact with someone who has Mpox rash allows the disease to transmit from one person to another. When a person comes into direct touch with an infected animal, such as an antelope, a terrestrial rodent, or a tree squirrel, they may contract Mpox. If the animals are not properly cooked, the virus can also be contracted by eating them. The method of treatment for viral infections is supportive symptom management. However, there are precautions that can be taken to avoid an outbreak. Until all lesion crusts have peeled off, the infected person should stay in isolation, wear a mask, and keep sores as covered as possible. Contact with wild animals in areas where Mpox is prevalent should be avoided, especially when they are ill or dead (including their meat and blood).

A viral culture isolation test or a PCR test for Monkeypox DNA using patient specimens can also be used to determine Mpox infection [4]. Oral medicines like Tecovirimat and Brincidofovir, used to treat the Smallpox virus, have been approved by the Centres for Disease Control and Prevention (CDC) [5]. For the prevention of Mpox, smallpox vaccinations (MVA-BN and LC16) [5] have also been authorized. Only those at risk are given consideration for vaccination.Recently, there was a multi-nation outbreak of Mpox in South East Asia, the Eastern Mediterranean nations, Europe, the Americas, Africa, and the Western Pacific [3]. The World Health Organization (WHO) has taken this very seriously, issuing clinical and public health recommendations and gathering hundreds of experts and researchers to advance research and development on Monkeypox and create new diagnostics, vaccines, and therapies [1].

Machine learning techniques have been effectively used to analyze and classify medical data. As a huge amount of data is being generated in the medical sector, different Machine learning algorithms have been successfully applied to this huge medical in the past decades. Earlier machine learning techniques used in disease diagnosis include K-nearest neighbours (KNN), support vector machines (SVM), Decision Trees, random forests, Naïve Bayes etc [6]. Traditional machine learning methods, however, required time consuming feature extraction for training models. The effectiveness of such conventional Machine Learning methods will be greatly reduced when used on large datasets thatincorporate images. Additionally, accuracy is a crucial deciding element when adopting such procedures.

The capability of deep learning to analyze images with a remarkable degree of accuracy has led to its use in the field of digital image processing [7]. Its core design is an artificial neural network that is set up in layers. The layers are responsible of converting input data into output and facilitating learning through the features extracted at each layer. Deep learning has emerged as a popular approach for many real-world application domains, including medical image analysis, video/audio/image processing, etc., due to its ability to learn from massive datasets and its predicted accuracy. Data is filtered in deep learning models through the cascading of many layers, and each subsequent layer derives the findings by using the output values from the prior layers.

Deep Neural Networks include Convolutional Neural Networks (CNN) [8]. The CNN excels in the field of image processing because it can extract local characteristics and can reduce parameters. The scope of CNN in the medical field is greater than that of other models since the medical industry generates a large amount of image data.

1.1 Challenges

Conventional methods for diagnosing communicable diseases are expensive, time-consuming, dependent on experts, and occasionally inefficient because they entail a human visual inspection. Human bias is also likely to have an impact on these methods, reducing their accuracy. Studies have looked into the use of Deep Learning algorithms using images, symptoms, etc. to overcome these unreliable methods for disease detection [9], [10].

A viral zoonotic infection called Mpox can transfer from animals to people as well as from one person to another. The Mpox virus, an orthopoxvirus [11] that shares structural similarities with the Smallpox virus, is what causes Mpox. Due to its resemblance to chickenpox and the measles, a clinical diagnosis of Mpox in its early stages can be difficult [12].

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1.2 Motivation

Rapid identification of suspected cases may be possible using computer-assisted detection of Mpox lesions.Given enough training examples, deep learning techniques have proven useful for automatic detection of skin lesion. However, there are currently very few publicly accessible datasets for the Monkeypox virus. As per the available information, some of the studies on AI-based Monkeypox detection are available as preprints [13,] [14], and [15].

Transfer learning [16] on already trained models or building a network from scratch are both used to train image classification models. It takes a lot of work to train a CNN model from scratch since it needs access to huge datasets with millions of images. Using pre-learned weights from a model that has been trained to recognize comparable objects, transfer learning is a strategy. Prior to use, these weights are loaded. In other words, transfer learning refers to using information learned from addressing one problem to solve others that are connected to it. When access to big training datasets is restricted, it is frequently utilized by academics to help enhance the performance of deep learning models. Additionally, transfer learning has been shown to produce improved disease identification accuracy.

In the process of transfer learning, a base network is initially trained on a base dataset, and the features picked up from this task are then transferred to a new network to train on a different dataset and task. If the characteristics are appropriate for both base and target activities, the process will succeed. Pre-trained models have performed well in tasks related to image categorization when used with similar data.

1.3 Objectives and Contributions

In the current study, we make use of the Monkeypox Skin Lesion Dataset from Kaggle [12], [17], and [18], which includes skin lesion images of the diseases measles, chickenpox, smallpox, measles, and Mpox. Our main objective was to study the performance of transfer learning models on prediction of Monkeypox and compare the results with a CNN model which is developed from scratch.

We experimented with nine different types of transfer learning models in prediction of Monkeypox. An 18 layer custom CNN model was also designed. The experiment shows the superiority of transfer learning models in prediction. The experimental results on this small dataset are encouraging, but the predictive power of these models can be improved with a bigger, more diversified dataset.

A mobile or web based application can also be developed using a deep neural network that is trained on images of different classes of disease images. The application can be made to do the binary classification on the input images fed to the application via a laptop or mobile camera. The architecture presented in this work is built on transfer learning and is easily adaptable to the needs of both web and mobile apps.

II. LITERATURE REVIEW

This section discusses about studies that have been conducted in the prediction and diagnosis Monkey pox. M. M. Ahsan [14] et al. introduced a Monkeypox2022" dataset which is accessible to everyone via a shared GitHub repository. A variety of open-source and internet sites with no usage limitations were used to gather the images for the collection. Additionally, they put out a modified VGG16 [19] model that takes into account two different investigations. For Study One, the dataset includes 47 Chickenpox and 43 Monkeypox images, whereas for Study Two, the dataset includes 1167 other diseases samples and 587 augmented Monkeypox samples. Their research shows that the proposed model can correctly identify patients with Monkeypox in Studies One and Two with an accuracy of 97.1% (AUC = 97.2) and 88.0% (AUC = 0.867), respectively. [14]

The "Monkeypox Skin Lesion Dataset (MSLD)" was created by Shams Nafisa Ali [13] et al and includes skin lesion photographs of the Measles, Chickenpox, and Monkeypox. The sample size is increased by data augmentation [18]. Monkeypox and other diseases are categorized using pre-trained deep learning models like VGG-16, ResNet50 [20], and InceptionV3 [21]. The three models are also combined into an ensemble. ResNet50 achieves the highest overall accuracy of 82:96(4:57%), followed by the ensemble system and VGG16, which both obtained accuracy of 81:48(6:87%) and 79:26(1:05%). [13]

Mohammad Arafat Hussain [15] et al. explored the viability of classifying distinct types of pox from digital skin images of pox lesions and rashes using AI algorithms. They used a database that includes pictures of the rashes and skin lesions

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caused by five different diseases, including Cowpox, Chickenpox, Smallpox, and Measles, as well as pictures of healthy skin. Seven deep models, namely ResNet50, Inception-V3, SqueezeNet [22], MnasNet-A1 [23], MobileNet-V2 [24], and ShuffleNet-V2 [25], DenseNet121 [26] were examined for their ability to accurately classify diseases. They discovered that deep AI models can detect Monkeypox with an 85% accuracy rate using digitized skin images [15].

An analysis of a Deep Learning-based Technique for Forecasting Monkey Pox from Skin Sores is conducted by BSH Shahyeez Ahamed, R Usha, and G Sreenivasulu [27]. In addition to deploying a pre-trained deep learning model for disease prediction based on symptoms, the research offers a brief investigation into the growth and transmission of Monkeypox throughout the world.

Dipanjali Kundu, Umme Raihan Siddiqi, and Md. Mahbubur Rahman [28] conducted a comparison of machine learning algorithms (K-NN and SVM) and deep learning methods (Vision Transformer, RestNet50). Chicken pox and Monkey pox were separated into separate groups using a layer-based convolutional neural network (CNN) using transfer learning and pre-trained models like RestNet50. The K-NN ML model has the best accuracy, coming in at 84%. The Vision Transformer (ViT), on the other hand, outperforms the other models with a 93% accuracy rate.

Mohamed Torky, Ali Bakheit, Mohamed Bakry, and Aboul Ella Hassanien [29] applied and compared the Dense Net-121model with the convolution neural network (CNN) model for diagnosing Monkeypox using a skin image dataset of MPX and Measles pictures. The Dense Net-121 model's advantage over CNN in diagnosing MPX instances with a testing accuracy of 93% is the most important finding of this research.

Chiranjibi Sitaula [30] et al, in their study compared 13 different pre-trained deep learning models for the MPox virus detection. The experiments was done on a publicly available dataset, which results in average Precision, Recall, F1-score, and Accuracy of 85.44%, 85.47%, 85.40%, and 87.13%, respectively with the help of the proposed ensemble approach.[30]

III. METHODS

This section briefly describes the data collection, technologies-deep learning and transfer learning, the creation of the suggested updated deep transfer learning models, as well as the experimental setup employed in the experiment and finally the implementation.

3.1 Data Collection

The primary goal of this research is to distinguish the "Monkeypox" from diseases that are similar [2]. As a result, we classify images of skin lesions caused by the Chicken pox, Small pox, HFMD, and Measles as belonging to the "Non Monkeypox" class. The datasets is taken from Kaggle [12], [17], [18] and from the Git Hub database. There are a total of 279 Monkeypox skin lesion images, 107 Chicken pox images, 91 Measles images, 150 Small pox images and 200 HFMD skin images.

3.2 Deep Learning

Machine learning, a sub domain of artificial intelligence, and deep learning is a sub domain of Machine learning. Based on the availability of labelled data, there are three main deep learning approaches: supervised learning, where all the training data is labelled; semi-supervised learning, when some of the training data is labelled; and unsupervised learning, where only unlabeled data is offered. Deep learning-based image classification employs supervised training, in which labelled image datasets are utilized to determine the class that most accurately depicts the item in images using activation functions like softmax in the final output layer.

Deep Artificial Neural Networks (ANN) is used in deep learning to discover patterns and make conclusions from input data. A number of artificial neurons are present in ANN, which employs them to recognize and store information, just like the biological neurons found in the brain. Input, output, and one or more hidden layers are all parts of an ANN. In a neural network, a neuron uses mathematical operations known as activation functions. Sigmoid Function, Hyperbolic Tangent Function, and others are a few of this activation function.

Deep Neural Networks include Convolutional Neural Networks (CNN) [8]. Convolution layer, Pooling layer, and Fully Connected layer are the three layers in CNN. The convolutional layer is the foundation of CNN. The convolution layer's job is to extract features from the source image. The convolution layer has numerous convolution kernels.

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Similar to the neurons in a feed-forward neural network, each component of the convolution kernel has a matching weight coefficient and bias value. Convolution kernels are slid onto the image and the elements they relate to are multiplied by and added to the features of the covered image. This procedure can reduce parameters and have the effect of extracting local features. [8].

Pooling layers aids in dimension reduction. The ultimate classification of the disease is done at the fully connected layer. Convolutional and pooling layer counts are entirely experimental and initially unknowable. We often choose the number of layers that provide the most accuracy. Additionally, an experimental number of epochs are taken. Rotationally, CNN is not invariant. It implies that even if the image is rotated via an angle, CNN will not be able to recognize it. It is not scale invariant either. Therefore, in order to acquire decent results, we must enrich [31], the data with rotated and scaled images of the training dataset before training.

3.3 Pre Trained Deep Models

Many pre-trained models, such as VGG 16, exist.VGG 16, VGG-19 , ResNet50, Resnet152V2, Inception V3, DenseNet 121, Xception [32], NasNetMobile, DenseNet 169 and MobileNetV2 exist that can be directly used by Transfer learning. In this work proposed we use modified ResNet50, ResNet152 V, VGG-16, MobileNet-V2, Inception-V3, Xception, DenseNet121, DenseNet169 and NasNetMobile models to check their feasibility in Monkeypox classification. In these models, the number of trainable parameters varies.

Oxford VGG Model: This has numerous layers and is a typical deep convolutional neural network architecture. Compared to VGG19, which has 16 convolutional layers and 3 fully connected layers, VGG16 has 13 convolutional layers and 3 fully connected layers. A. Zisserman and K. Simonyan from the University of Oxford developed this model. The structure was built only using convolutional layers of size 3x3, max pooling layers of size 2x2 and fully connected layers at the end. The model requires that input image should be of size 224 x 224 (RGB image).

Google Inception model: A convolutional neural network design of 48 layers deep is called Inception-v3. Convolutions, average pooling, max pooling, concatenations, dropouts, and fully linked layers are some of the symmetric and asymmetric building pieces that make up the model. The model makes considerable use of batch normalization, and loss is calculated using Softmax.

Microsoft ResNet Model: Residual Network is abbreviated as ResNet. Due to issues like the degradation problem and the vanishing gradient problem, training deeper neural networks has proven to be challenging. Residual learning makes an effort to address both of these issues. The ResNet model employs ReLU activations. ResNet50 is a 50 layer residual network, and it also comes in ResNet101 and ResNet152 varieties.

The NASNet used reinforcement learning to frame the ideal CNN architecture. Neural Architecture Search, or NAS, was created by Google Brain. The goal of NASNet is to find the optimal set of filter sizes, output channels, strides, and layer counts within the specified search space. The accuracy for the searched architecture on the provided dataset was the reward after each search action. NASNetMobile refers to the scaled-down version.

Google developed the robust convolutional neural network architecture known as MobileNetV2. It works well on mobile platforms. This model was created with the intention of minimizing the number of computations and parameters without sacrificing performance. To boost MobileNets' functionality, MobileNetV2 added inverted residuals and linear bottlenecks. The network can calculate activations and maintain additional information after activation with the aid of inverted residuals.

Each layer in the DenseNet convolutional network architecture is linked to every other layer. By applying a composite function operation that combines the convolution layer, pooling layer, batch normalization layer, and non-linear activation layer, the output of the first layer serves as an input for the second layer. They facilitate feature reuse, strengthen feature propagation, address the vanishing gradient issue, and minimize the number of parameters.

Xception is a 71-layer convolutional neural network design that only uses separable convolution layers based on depth. It is an addition to the Inception Architecture that uses depth-wise Separable Convolutions in place of the regular Inception modules.

These CNN models are assessed based on their accuracy throughout training, validation, and testing. The capacity of a deep learning model to recognize objects across various datasets and circumstances is reported via testing accuracies. Therefore, it is essential to increase testing precision on unobserved data from several datasets. Precision, recall, and

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F1-score are additional measures frequently used to assess the effectiveness of deep learning models. In investigations where datasets include class imbalance, the F1-score measure is crucial.
The experiment was run in a Keras 2.2.4 environment using a Tensorflow 1.13.1 backend. The system used to conduct the experiment runs Windows 10 and has 8GB of RAM. No graphics processing units (GPUs) were utilized during this experiment.

3.4 Implementation

The implementation involves the following stages: Data set preparation→Pre-processing→Create deep learning Model →Train the model→ Prediction as shown in Figure -1 and Figure -2.

3.4.1 Data Set preparation

To differentiate between instances of Monkeypox and cases without Monkeypox is the primary goal of this effort. As a result, we classify images of skin lesions caused by HFMD, Measles, Chickenpox, and Smallpox as belonging to the "Non Monkeypox" category. The dataset was compiled using images from the Kaggle and Git Hub databases and is divided into two categories: Monkeypox images and non-Monkeypox images. There are 824 total photos in the data set, of which 20% are selected for testing.

3.4.2 Data Pre-processing

The input image is scaled down to 224 by 224 for the Transfer learning model. We've set the batch size to 32, which results in 20 steps for each training period. (The number of steps per epoch for training is determined by dividing the total number of training objects by batch size 32.) Since our image dataset is rather small, sample variety is added by randomly applying changes to the training images, like rotation and horizontal flipping. This lessens over fitting and exposes the model to various facets of the training data. Using the Keras image processing toolkit, various augmentation techniques were used, including rotation, flipping, width shift, height shift, and more.

3.4.3 Create the deep learning model

Start by launching the pre-trained model with weights loaded from ImageNet. The include top=False option allows us to load a network without the classification layers at the top, which is the best configuration for feature extraction. The convolutional basis is frozen and a classifier is added on top of it in the following stage. The base layer weights cannot be adjusted while training because the convolutional base is frozen. The model must be assembled before the network is trained. This requires defining parameters for the optimizer, loss function, and metrics that will be computed during the training. Adaptive momentum estimation (Adam), an optimizer that frequently exhibits exceptional performance in binary image classification, is used for this model. Categorical-Cross Entropy is the loss function used to determine the loss for this model.A custom deep CNN model is also set up with 18 layers having similar parameters

3.4.4 Training the model

The top layers of a neural network that is being trained learn by back propagation since they are not frozen, in contrast to the other layers that are. The weights will need to be adjusted during the training process to go from generic feature maps to features particular to the dataset. The pre-trained model's top layers should have their weights adjusted, together with the classifier's extra training, to improve performance. The base model is unfreeze, and the lower layers are made un-trainable. Recompile the model and retrain it after that.

3.4.5 Prediction

The classifier is used as a reference in the test stage after training the train data to build the model. The test data will be categorized in the last stage by predicting the class to which the provided test data belongs. As a result of classification, a patient with Monkeypox is identified by the label "0," while a patient with non-Monkeypox is identified by the label “1”.

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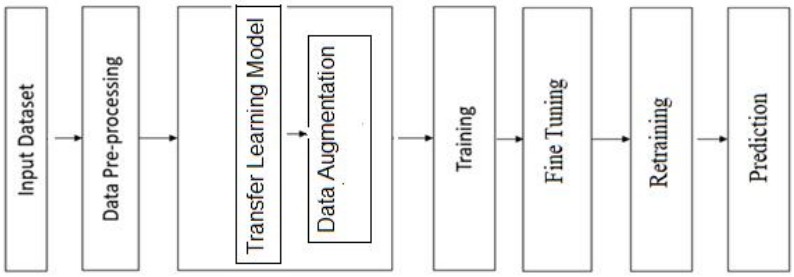

Figure 1: Proposed Transfer Learning Model

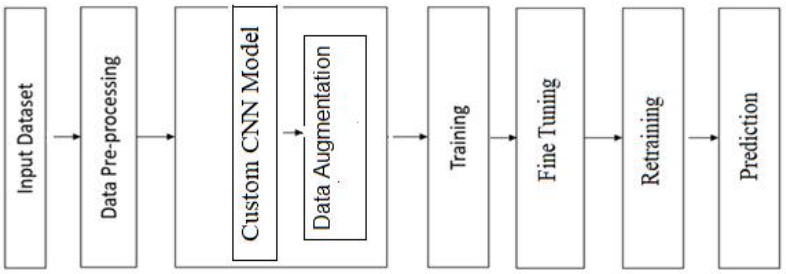

Figure 2: Proposed Custom Model

IV. RESULTS

Once the model is built, it is to be evaluated to make an assessment of how good our predictions are. The results of the experiment are quantified and presented using common statistical techniques like accuracy, precision, recall, and F1-score.The percentage of correctly classified data instances over all data instances is called accuracy:

$$\text{Accuracy} = \frac{TP+TN}{TP+FP+TN+FN}$$

The proportion of accurately predicted positive observations to all of the predicted positive observations is known as precision.

$$\text{Precision} = \frac{TP}{TP+FP}$$

Recall is the percentage of accurately predicted positive observations to all of the actual class observations.

$$\text{Recall} = \frac{TP}{TP+FN}$$

F1 score - The weighted average of Precision and Recall is the F1 Score. Consequently, this score considers both false positives and false negatives.

$$\text{F1 score} = 2 \times \frac{Precision \times Recall}{Precision+Recall}$$

Where
TP: True Positive (cases of Monkeypox accurately predicted).
TN: True Negative (cases of Non Monkeypox accurately predicted).
FN: False Negative (wrong Non Monkeypox prediction),
FP: False Positive (wrong Monkeypox prediction).

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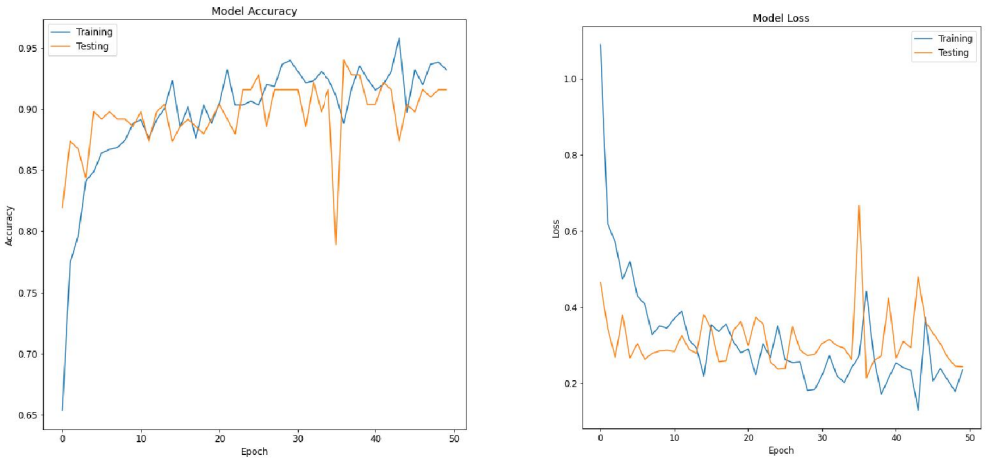
We compare the deep learning models' mean precision, mean recall, mean F1 score, and accuracy as indicated in the Table 1.

TABLE 1: Performance As Measured By Mean Accuracy, Mean F1 Score, Mean Precision, and Mean Recall.

Algorithms	Class	Mean precision	Mean recall	Mean F1 Score	Accuracy
Inception-V3	Monkeypox	.85	.91	.88	.93
	Non Monkeypox	.95	.92	.94	
Densenet121	Monkeypox	.93	.77	.84	.95
	Non Monkeypox	.89	.97	.93	
Resnet50	Monkeypox	.41	.61	.54	.65
	Non Monkeypox	.80	.54	.54	
MobilenetV2	Monkeypox	.88	.79	.83	.96
	Non Monkeypox	.90	.95	.92	
Xception	Monkeypox	.98	.77	.86	.95
	Non Monkeypox	.89	.99	.94	
NasNetMobile	Monkeypox	.92	.64	.76	.94
	Non Monkeypox	.84	.97	.90	
Resnet152V	Monkeypox	.70	.12	.21	.66
	Non Monkeypox	.69	.97	.80	
VGG16	Monkeypox	.84	.68	.75	.86
	Non Monkeypox	.85	.94	.89	
DenseNet169	Monkeypox	.94	.79	.85	.95
	Non Monkeypox	.90	.97	.93	
Custom CNN	Monkeypox	.55	.80	.65	.71
	Non Monkeypox	.87	.66	.75	

4.1 Accuracy and Loss

The accuracy and loss of the model with respect to each epoch count are plotted on a graph. Following figure displays the results of some models using training and testing data.



InceptionV3

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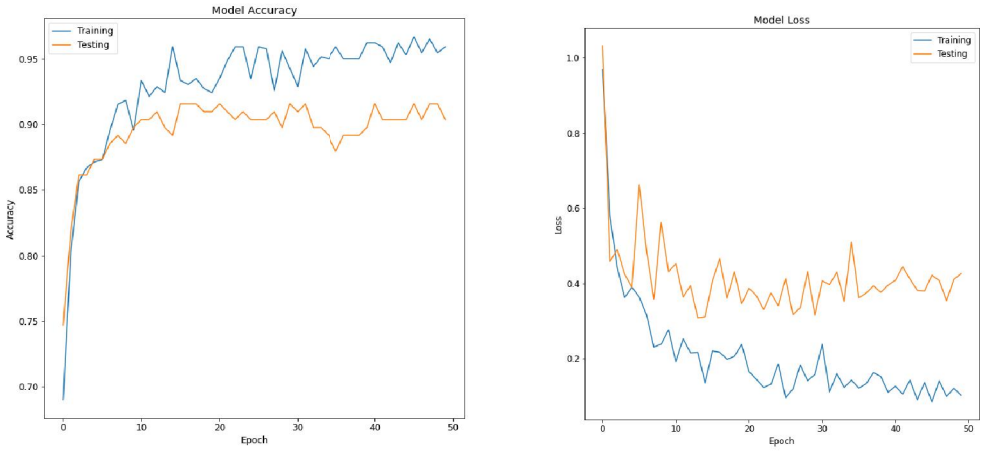
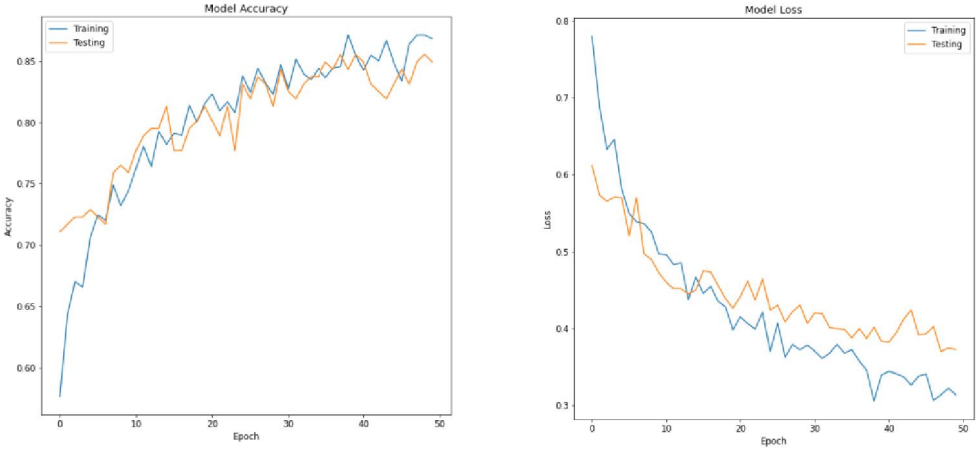


Densent121



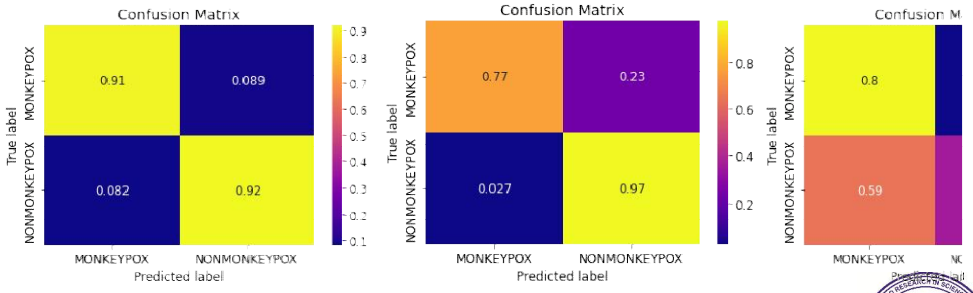
VGG16

Figure 2: Accuracy and Loss plot for the proposed models

It has been found that MobileNetV2 is marginally more accurate than the other.

4.2 Confusion matrix

A table known as a confusion matrix is frequently used to explain how well a classification model performs on a set of test data for which the true values are known. It is a tabular overview of how many predictions a classifier made correctly and incorrectly. The performance of the suggested model in terms of the confusion matrix is shown in the figure below:



InceptionV3 Densent121 Resnet50

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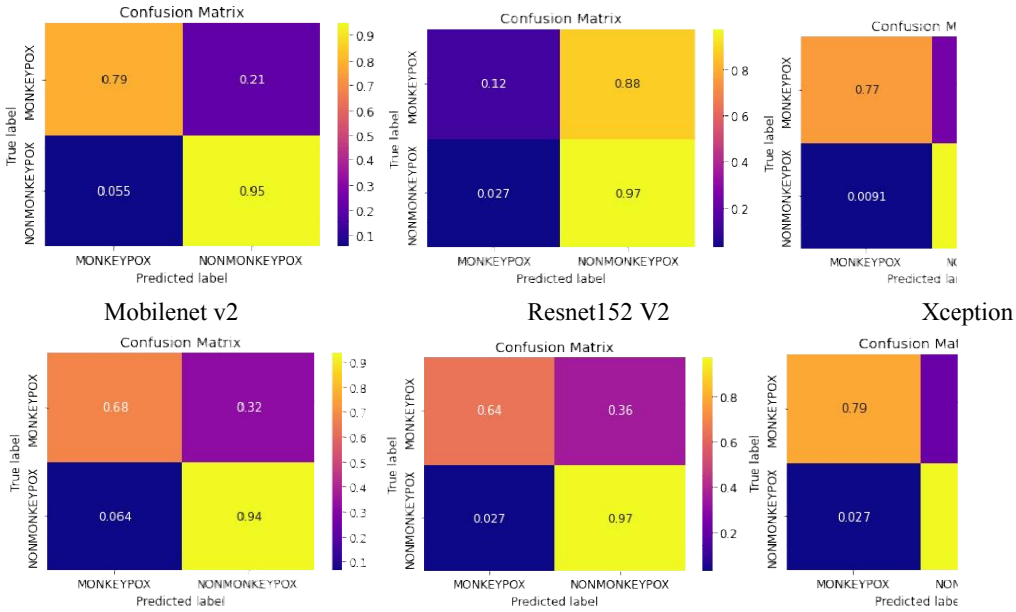


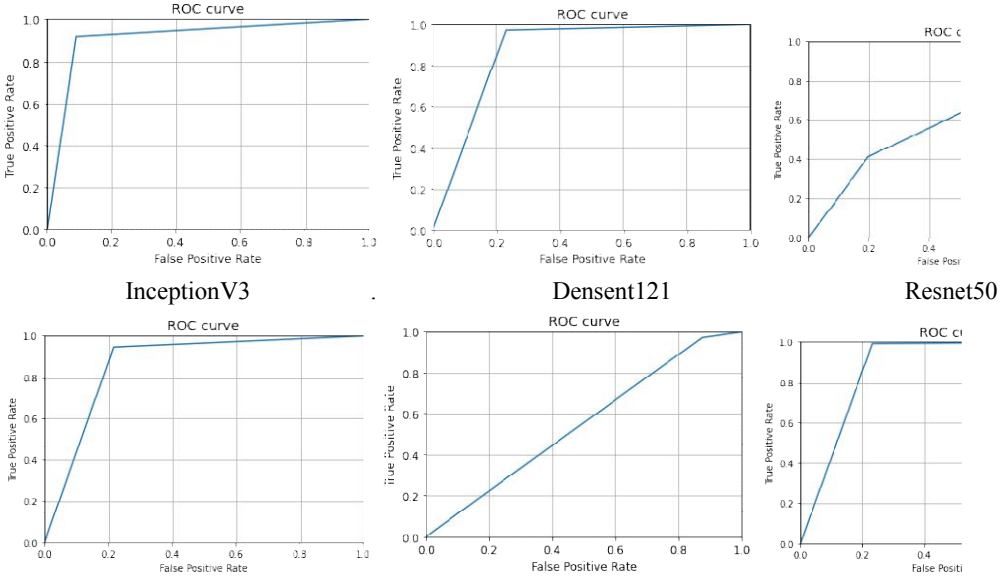
Mobilenet v2 Resnet152 V2 Xception

VGG16 NASNetMobile DenseNet169

Figure 3: Confusion matrices for the proposed models

4.3 The receiver's operating characteristics (ROC)

The true positive rate (TPR) and false positive rate (FPR) are plotted on the X and Y axes, respectively, of the ROC curve. The probability of misclassification is represented by the false positive rate whereas the true positive rate is the recall. The proposed models' ROC curves are displayed in Figure below.Be aware that an AUC score of less than 0.5 suggests that the model is doing poorly, while a number of closer to 1 indicates that the model is performing at its best.



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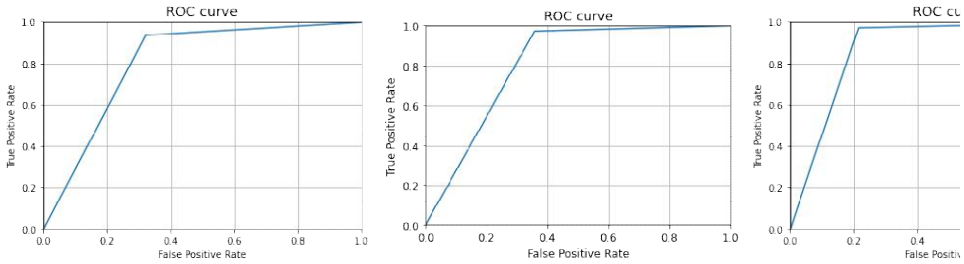

VGG16 NASNetMobile DenseNet169

Figure 4: ROC Curves for the proposed models

V. DISCUSSION

In order to examine the prediction of Monkeypox, various deep learning models were applied. For prediction, we used 9 distinct deep learning models. The primary goals of the proposed effort are to diagnose the presence of Mpox disease and determine if a patient is ill. 160 test photos and 660 training images are available. They are all clearly marked. With data augmentation and fine tuning, the deep transfer learning models were able to classify with an accuracy of up to 96%. Custom CNN model accuracy is only less (71%) as the model is trained with the small data set available.Using pre-trained CNN models and training on a large volume of images can improve accuracy.

5.1 Limitations

For training our models, we used the dataset made accessible by the GitHub and Kaggle repositories. Before the models can be applied in real-world settings, the validity of the Mpox and Non Mpox datasets must be confirmed with the assistance of knowledgeable physicians. Due to time constraints, this verification was not done when we were constructing our models.

Moreover, datasets made public by hospitals may be leveraged to produce better and more trustworthy outcomes. Obtaining such statistics from hospitals was challenging due to the rarity of Mpox cases in the surrounding districts.

VI. CONCLUSION AND FUTURE WORK

The goal of the research was to create a deep learning model that can determine whether a patient has Mpox or not. The capacity of modified CNN transfer learning models to distinguish between individuals with and without Mpox disease is tested. Our research indicates that the updated models that have been developed may discriminatepatients
with Mpox symptoms from others with an accuracy of up to 96% when applying transfer learning techniques. The study shows the effectiveness of the transfer learning strategy on small datasets because the proposed models produced high accuracy results on a limited datasetwhen compared with custom CNN model. We can use different deep learning techniques to try to create a classifier that is more effective in order to enhance this model. Only the Mpox disease is included in the dataset utilized here. Additionally, we may train the model to recognize several communicable disease types and include various variants. The experiment used transfer learning, data augmentation, and fine tuning to identify the condition with up to 96% accuracy.

Patients with Mpox can be diagnosed using our suggested model. Due to time restrictions, the dataset only contains a small number of samples, which has an impact on the model's accuracy. Instead of using one particular hospital or healthcare facility, the data are generally gathered from the range of sources that are now available. Using more authentic datasets can increase reliability. Users on providing an image of their skin lesions can receive a preliminary assessment for Mpox using the models, which can also be made available as a mobile or web application.

Conflict of interest

Manuscript Title: Deep learning models for prediction of Mpox disease.

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