

PoxTLNet50: Deep Learning-based Approach for Accurate Image Detection of Monkeypox Disease

Anu V Kottath¹, Ranjana P.²

¹Research Scholar, ²Professor, Department of computer science and engineering, Hindustan Institute of Technology and Science, Chennai, India

E-mail: ¹anukottath@gmail.com, ²pranjana@hindustanuniv.ac.in

Abstract

The public's health is seriously threatened by the viral disease known as monkeypox. Accurate and timely diagnosis is essential for successful control and suppression of outbreaks. Deep learning (DL) approaches have produced encouraging results in the classification of medical images in recent years. The proposed PoxTLNet50 model combines ResNet50V2 DL architecture with a transfer learning technique for the classification of monkeypox diseases using the MSID (Monkeypox Skin Image Dataset). The MSID dataset consists of high-resolution skin images collected from patients diagnosed with monkeypox, encompassing a variety of disease stages and severity levels. The PoxTLNet50 model performance was assessed using a variety of performance metrics, and it attained an accuracy of 98.83%. The PoxTLNet50 model helps for early detection and management of monkeypox, aiding healthcare professionals and public health agencies in timely interventions and preventive measures.

Keywords: Monkeypox, ResNet50V2, Deep learning, Transfer Learning, ROC

1. Introduction

The globe recently went through a pandemic, and it is still recuperating from its negative impacts. Unfortunately, new transmissible diseases, including Ebola and monkeypox, have emerged as COVID-19's incidence and prevalence decline. 77 nations had recorded more than one case of the monkeypox disease as of July 2022. According to the World Health Organization (WHO), this outbreak internationally poses a moderate threat to public health,

but it has refrained from stating that it is an emergency in terms of public health [1]. A virus belonging to the Poxviridae family, is the disease-causing agent of monkeypox. Contrary to its name, "monkeypox," this virus is actually of rodent origin. The initial case of human infection with the monkeypox virus was officially documented in 1970. Monkeypox, has been present for several decades in central and west Africa, wherein tropical rainforests are common and unique to this area, has seldom spread to other regions of the world due to animal exports from the region being the primary source of transmission. However, the disease has recently expanded more widely compared in the past and has been identified in a variety of persons from various places. In light of the severe global consequences of the COVID-19 pandemic, there has been a heightened focus on closely monitoring cases of monkeypox. While monkeypox has not yet reached pandemic proportions and is currently exhibiting epidemic characteristics, its surveillance is deemed essential to prevent potential future outbreaks [2]. The major symptoms of Monkeypox diseases are rashes that develop on the skin during a period of 1 to 5 days and the earliest rashes are frequently seen on the face before spreading to different parts of the body. Due to its resemblance to chickenpox rashes, this disease can be mistaken for another. Lesions can appear over the body in hundreds of lumps in some patients, while blisters are less common in other patients. In severe circumstances, the lesions could combine and result in widespread rashes on the surface of skin. The rashes usually resolve completely within a timeframe of 2 to 4 weeks, depending on the disease's severity, and the disease recovers. Figure 1 shows various stages of MPX lesions [3].

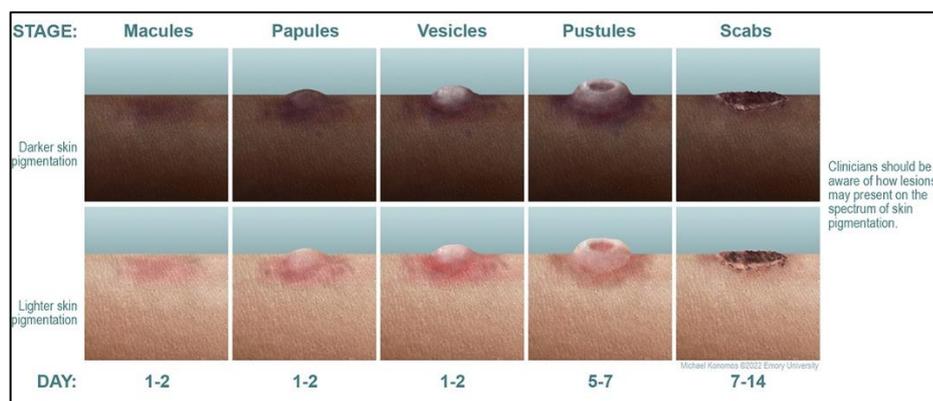


Figure 1. The Several Phases of the Monkeypox Lesion [4]

Recognizing MPX early can be challenging due to its resemblance to other diseases such as smallpox, roseola, and scarlet fever. Additionally, because polymerase chain reaction (PCR)

testing is not frequently accessible, it might be challenging to make a rapid diagnosis and put the proper measures, such as isolation and therapy, into place.

In addressing this challenge, the integration of automated systems utilizing Machine Learning (ML) and Deep Learning (DL) holds promise, particularly through the use of distinct convolutional neural networks (CNNs). These networks have shown significant success in distinguishing between images representing a range of different diseases, as demonstrated in prior research [5,6]. The development of DL approaches as a valuable tool for pattern detection and analysis of images in recent years has shown potential for use in the early diagnosis of certain diseases. DL is an instance of ML that extracts characteristics from images and makes predictions using numerous layers of ANNs [7]. CNNs, a subset of deep learning algorithms, have proven highly effective in numerous medical imaging applications, that also includes the classification of skin lesions, breast cancer diagnosis, and lung nodule detection [8]. However, the accuracy of medical image diagnosis can be compromised when dealing with large images or time constraints. Deep learning techniques, such as CNNs, offer a potential solution to enhance the precision of medical image diagnosis, facilitating well-informed decisions and reducing the risk of misdiagnosis. Additionally, transfer learning (TL), which utilizes pretrained models for new tasks, has been successfully applied in medical image analysis, further advancing the field. In this research, a new model which is a transfer learning-based technique for the identification of monkeypox is proposed.

2. Related Work

In order to classify monkeypox disease, previous studies were reviewed using DL techniques. With the help of DL, the CNN architecture, and VGG-16 TL, Ariansyah et. al. [9] suggested image classification to distinguish between MPX as well as measles. To classify MPX, pooled several datasets, including those against measles, chickenpox, normal, as well as all diseases. The majority vote had an accuracy of 0.97 for MPX vs. chickenpox, 0.79 for MPX vs. measles, 0.96 for MPX vs. normal, and 0.80 for MPX vs. all. Several CNN-based pretrained models were used, together with majority voting, to get these results. Ali et. al. [10] generated skin lesion images through open-source webpages and used data-augmentation techniques by 3-k-fold cross-validation to expand the dataset in the context of the categorization of MPX lesions of the skin with DL methods. To categorize MPX and other disorders, they put pre-trained models like InceptionV3, ResNet50, and VGG-16 to the test.

The ResNet50 model was chosen since it has the most significant accuracy rate out of all of these. The F1 Score for the ResNet50 is 0.82. The TL approach was modified by Ahsan et al. [11] for the purpose of detecting MPX disease. They gathered the data for the dataset from online resources. They created a modified VGG-16 approach that combined data from two distinct analysis, and they used the VGG16 model to get AUC scores of 0.88 to 0.97. The study's accuracy rate without data augmentation was 88.08%, while its accuracy rate with augmentation was 97.18%. They also highlighted about the model's predictions and the features they were able to extract, which helped describe the beginning of MPX by obtaining significant deep features.

In another work, Sahin et al. [12] created an Android application that employs DL for the classification of images into positive or negative categories. This classification is achieved by submitting the image to a DCNN- deep convolutional neural network directly on the mobile device, utilizing the Camera2 API of the Android platform . They also created a prototype website for evaluating MPX. The network was evaluated on six pretrained algorithms and trained using publicly available data (MSLD), with MobileNetV2 attaining the maximum performance with an accuracy of 91.11%. In this instance, categorization was done utilizing mobile Android applications using transfer learning techniques on image data. The MobileNetv2 model was not improved by the authors in any way. Using skin image analysis, Kumar et al. [13] used a variety of CNN-based algorithms and ML techniques to identify MPX disease. Three models based on CNN and classification algorithms, AlexNet, GoogleNet, and VGG16, and as well as classifiers with different ML techniques, including DT, Naive Bayes (NB), KNN, SVM and Random Forest, were utilized to extract features from the images. According to their research, the naive Bayes algorithm with VGG16Net provided an overall accuracy level of 91.11%.

Haque et al. [14] has done a work on deep TL with CBAM- convolutional block attention module. For precise categorization, the CBAM is designed to concentrate on the feature map's most pertinent regions. A neuro-fuzzy-based model was developed by Tom and Anebo [15] to identify monkeypox viral variations in various pox families. 18 symptoms associated with monkeypox were considered by the authors along with indicators from the Nigeria Centre for Disease Control and other sources regarding MPX diagnosis. The disadvantage of the suggested system is that it cannot use the 18 inputs that were theoretically examined during research. The dataset for the study was also kept a secret. The system performs only passably. Additionally, not all of the symptoms of monkeypox are visible in the input group.

3. Materials and Methods

Images from MSID are used as input for the suggested MPX classification model. The acquired images are then pre-processed utilizing techniques such as rescaling and normalization. Then next is image data augmentation. The basic DL model, known as ResNet50V2, served as the foundation for the PoxTLNet50 model. Then these ResNet50V2 TL models are subjected to training and evaluation. Last but not least, MPX images are fed into the suggested model, which uses binary classification to determine whether the outcome will be Normal or Monkeypox. The Figure 3 shows PoxTLNet50 model framework.

3.1 Dataset

The MSID dataset has four unique groups: chickenpox, monkeypox, measles and category representing normal cases; nevertheless, all of these are combined into one class to ensure consistency of the problem. The full dataset was produced by Islamic University's Department of Computer Science and Engineering in Kushtia-7003, Bangladesh. The dataset is loaded and read using Keras and the TensorFlow DL package. Figure 2 displays the proposed model's image count.

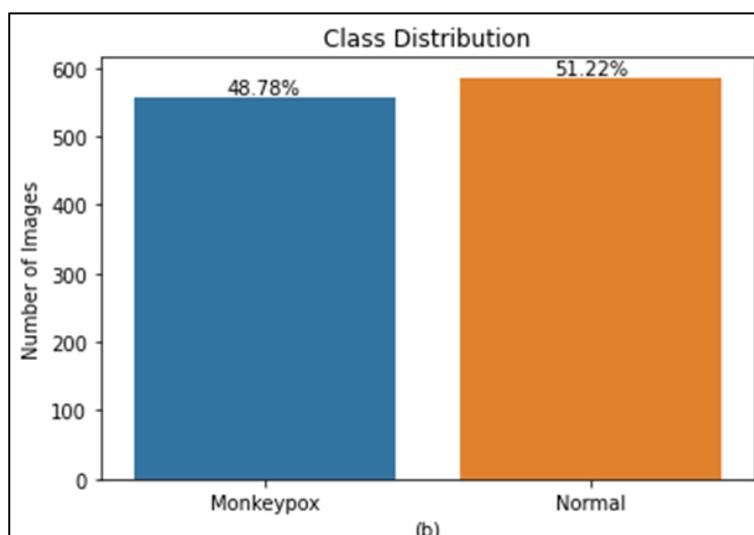


Figure 2. Image Count

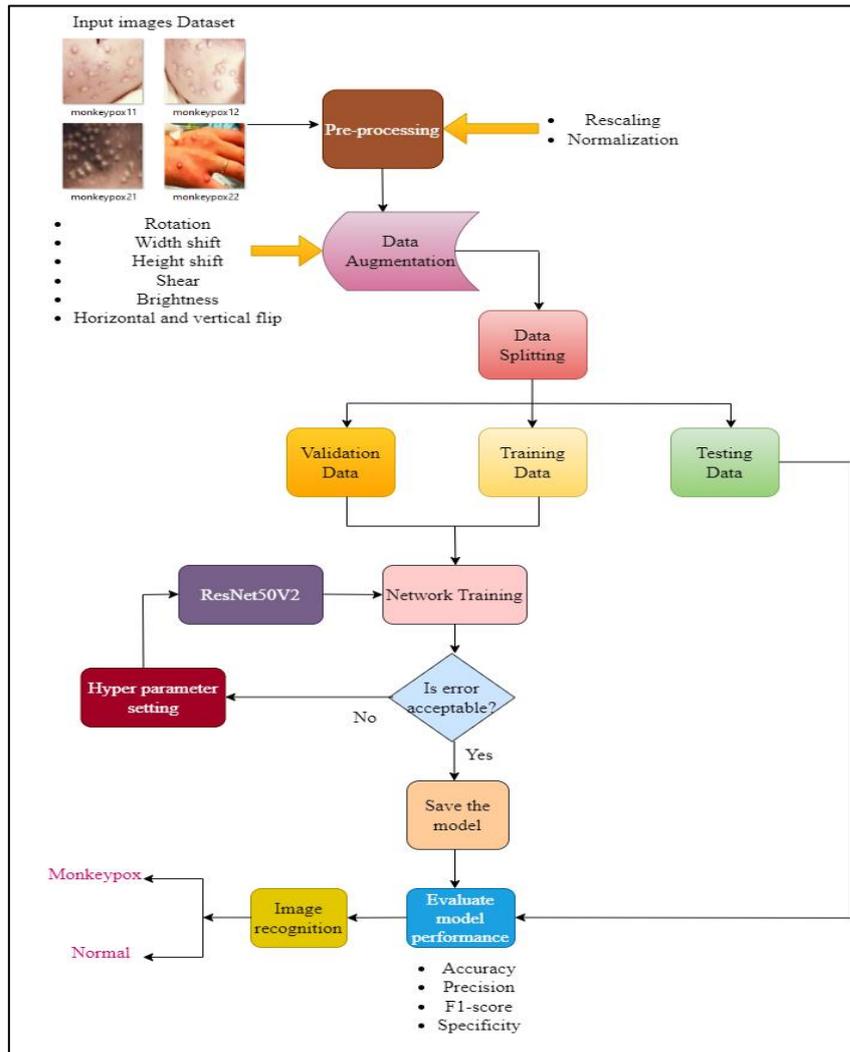


Figure 3. PoxTLNet50 Framework

3.2 Data Pre-processing

3.2.1 Rescaling

Prior to inputting images into the PoxTLNet50 model some pre-processing techniques, including resizing and normalization, were employed to enhance the collected images with varying original sizes. Utilizing OpenCV, all the images were uniformly reduced to 224x224 pixels to adhere to the input requirements of ImageNet pre-trained models, aiming to optimize training efficiency. The process ensured a correct height-to-width ratio during cropping of monkeypox images, with Figure 4 showcasing both the original and cropped images for comprehensive analysis.

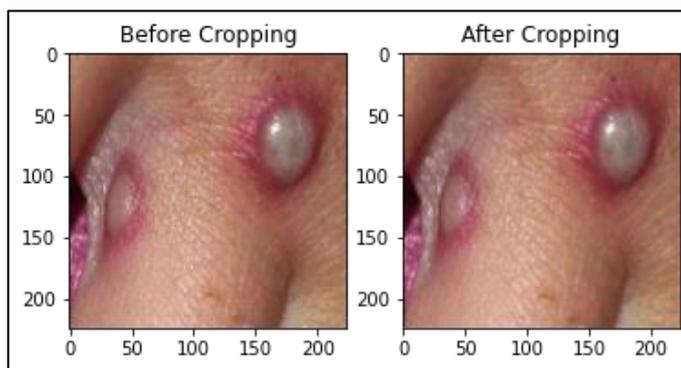


Figure 4. Original and Cropped Image

3.2.2 Normalization

In the preprocessing phase, images and annotations are initially imported into separate datasets for feature scaling, and subsequently, converted into NumPy arrays for further processing. The normalization process, involving feature scaling, ensures the standardization of input data by adjusting independent variables, specifically scaling image values to the range [0,1] through multiplication by the optimal size [255].

3.3 Data Augmentation

By using the data augmentation method random changes were made to the initial data, to augment the size of datasets. The Image Data Generator module of the Keras image processing framework was used to expand the dataset. The Image Data Generator feature offers a number of choices, including flipping, width and height altering, and rotation. Figure 5 and Table 1, illustrates the application of data augmentation, to enhance the dimensions of the dataset and prevent overfitting.

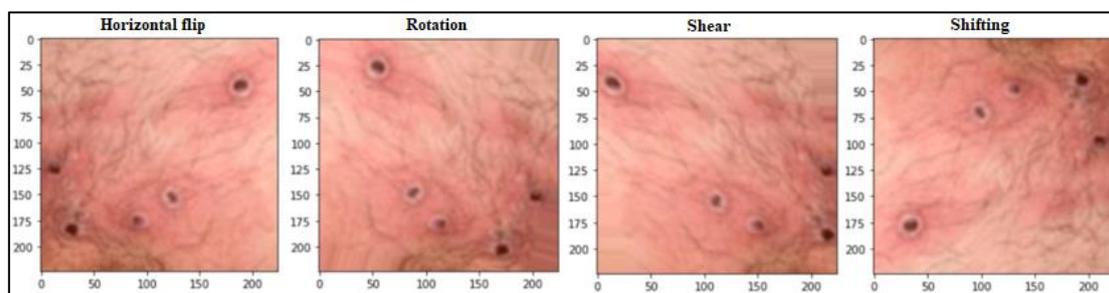


Figure 5. Data Augmentation Methods [17]

Table 1. Data Augmentation Description

Augmentation Method	Value
Rotation range	10
Width shift range	0.1
Height shift range	0.1
Shear range	0.1
Brightness range	[0.3,1]
Horizontal flip	True
Vertical flip	True
Fill mode	nearest

3.4 Splitting of the Dataset

All of the images in the dataset are shrunk into the range (224,224) as a consequence of the feature rescaling, where the width and height of the image are both 224 pixels. Total data divided into a ratio of 70:15:10, (Train, Test, Validation).

3.5 Proposed Methodology

The PoxTLNet50 model backbone structure is built using the ResNet50V2 model. ResNet50V2 is an enhanced variant of ResNet-50 that performs better on the ImageNet datasets than ResNet50 and ResNet101. The ResNet50V2 model begins with batch normalization as the initial step, followed by an activation function, and weight updates after that. Then the weights were optimized using the activation function. The pathway between the input to the output as a means of an identity connection is made possible by ResNet50v2's development, which eliminates nonlinearity [16].

The framework takes the pre-processed dataset of images as input in the form of (224, 224, 3) pixels and outputs a features map at the very final feature extractor layer. The flatten layer serves the function of transforming data from the layer directly above it into a 1-D array, that is then provided as input to the layer above. To create a single feature vector, the result of the previous convolutional layer was transformed into a flattened format. Figure 6 displays ResNet50v2-based architecture for the proposed model and Figure 7 displays the PoxTLNet50 model's optimized structure diagram. Using previously taught ImageNet weights, the PoxTLNet50 model's backbone is trained. The base architecture has been frozen and its weights

are not altered further before training a full backbone model. The Adam optimizer technique is used to modify the learning rate and weight based on loss backpropagation. A few of the setting options for Adam are alpha, beta1, beta2, and epsilon. Alpha is the learning rate. Beta 1 as well as Beta 2 are hyperparameters that control the decay rates for the first and second moments of the gradients, respectively. A typical value for β_1 is 0.9, indicating that the current estimate is 90% influenced by the previous estimate. β_2 is usually set to 0.999, emphasizing a long-term memory of the gradients' variances. Epsilon (ϵ) is a small constant added to the denominator of the ADAM update rule to ensure numerical stability. Cross-entropy is computed in order to determine the loss in the suggested binary model. Every model has undergone training for various epochs. The accuracy and loss of each model are continuously tracked. Table 2 given below displays the designed architecture's output shape along with a brief model summary.

Table 2. Summary of the Designed Model

Layer (type)	Output Shape	Parameters
resnet50v2 (Functional)	(None, 7, 7, 2048)	23564800
dropout (Dropout)	(None, 7, 7, 2048)	0
flatten (Flatten)	(None, 100352)	0
dropout_1 (Dropout)	(None, 100352)	0
dense (Dense)	(None, 1)	100353
Total parameters: 23,665,153		
Trainable parameters: 100,353		
Non-trainable parameters: 23,564,800		

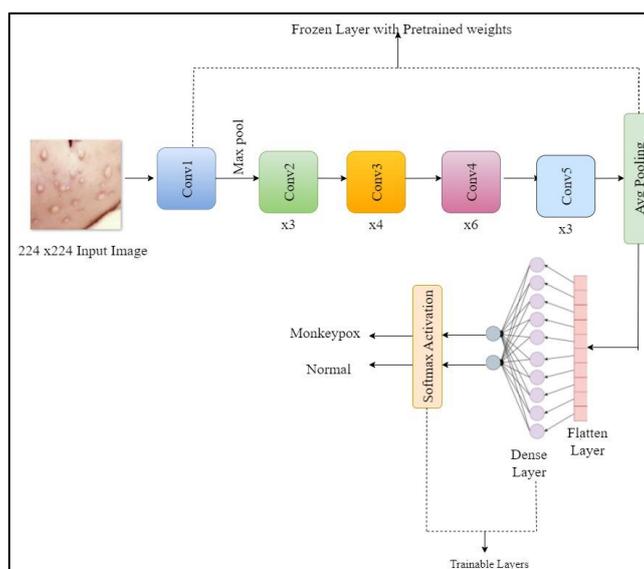


Figure 6. ResNet50v2-based Architecture for Proposed Model

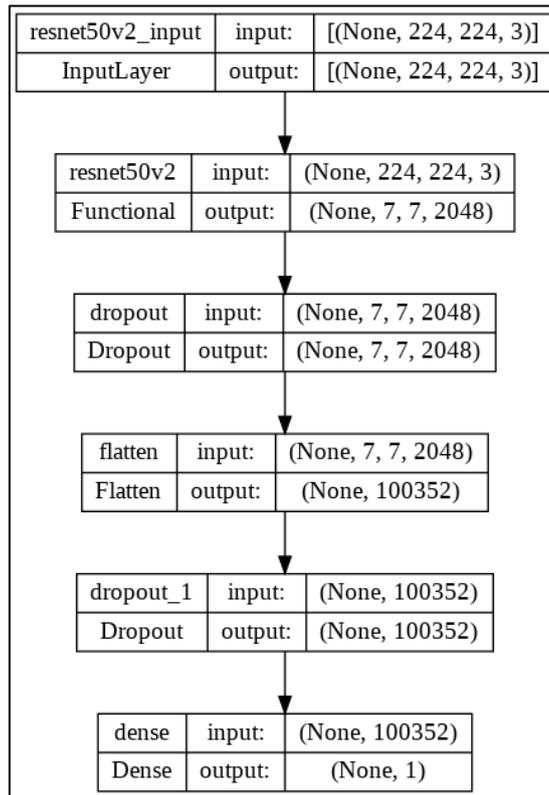


Figure 7. Architecture of PoxTLNet50

3.6 Model Optimization and Hyper-Parameter

The hyperparameters for the deep neural network are determined empirically and has a significant impact on learning. Finally, a wide variety of variables were tested in order to identify the best classification performance, The hyperparameters used are listed in Table 3.

Table 3. Hyperparameter Specifications

Parameters	Value
Image size	224*224
Validation split	0.18
Weights	ImageNet
Learning rate	0.01
Batch size	64
Number of epochs	50
Optimizer	Adam
Dropout	0.3, 0.5

Activation function of the last classifier layer	Sigmoid
loss	Binary Cross entropy

3.7 Experimental Setup and Implementation

The PoxTLNet50 model were trained using the Python programming language, the Keras package, and the TensorFlow backend, which are commonly employed tools for this purpose . A simple-to-use, open-source library called Keras is designed specifically for neural network models that can use Tensorflow. All simulations performed on the Google Colab Platform utilizing Colab notebooks equipped with Tensorflow, a GPU, 12.75 GB of RAM, 68.50 GB of disk space, and a 64-bit version of Windows 10.

4. Results and Discussion

The effectiveness of the PoxTLNet50 model in classifying monkeypox was evaluated after it was trained on MSID. The experimental results showed that the PoxTLNet50 framework, which relies on the ResNet50V2, obtained a maximum accuracy of 98.83%. Figure 8 summarizes the model's training process over several epochs with a train and validation loss demonstration. The graph indicates a positive correlation between increased epoch counts and improved accuracy. The framework was successfully trained, proving that monkeypox sickness could be classified. The loss also decreased with the epochs, reaching its lowest value at the end of training.

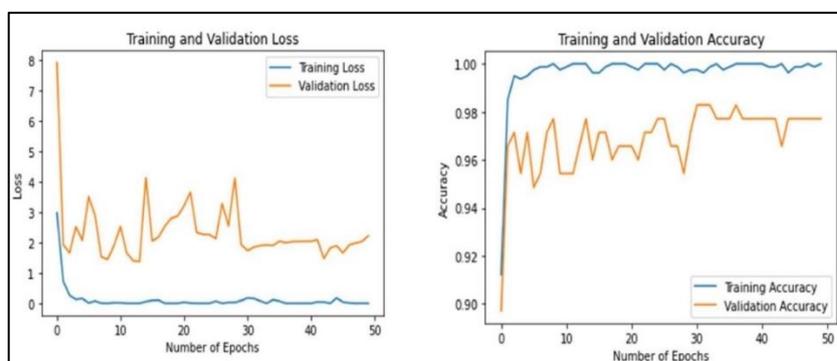


Figure 8. Accuracy Loss Curves with Validation and Training Data

The confusion matrix in Figure 9 shows the number of images classified by the model properly and erroneously. Both the test dataset and the validation dataset were used to produce the confusion matrix. The actual and the predicted outputs are compared in the confusion matrix.

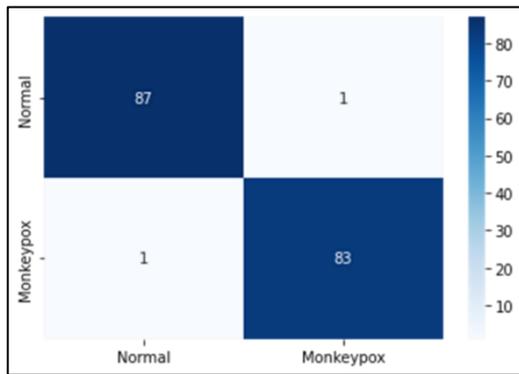


Figure 9. Confusion Matrix

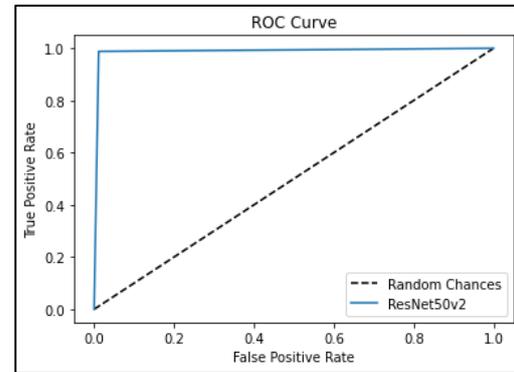


Figure 10. ROC Curve

The ROC (Receiver Operating Characteristic) curve plotted helps in visualizing the performance of the ResNet50V2 in monkeypox classification, as depicted in Figure 10. The curve will determine the model's performance of the model at several classification thresholds, and the corresponding FPR and TPR, demonstrating how well it classifies between monkeypox and normal cases. It is a visual depiction of the efficiency of a classification model. The PoxTLNet50 model achieved an accuracy of 98.8372%, with a precision, recall, and F1-score of 98.8095% and the ROC AUC score was 98.8366%.

Figure 16 depicts the randomly selected sample of 10 test images along with their predicted labels and actual truth labels. If the predicted labels match the true labels, the title of the subplot is displayed in green, indicating that the model has correctly classified the image. On the other hand, if the predicted labels do not match the true labels, the title of the subplot is displayed in red, indicating that the model has made an incorrect prediction. This colour distinction helps visually identify correct and incorrect predictions.

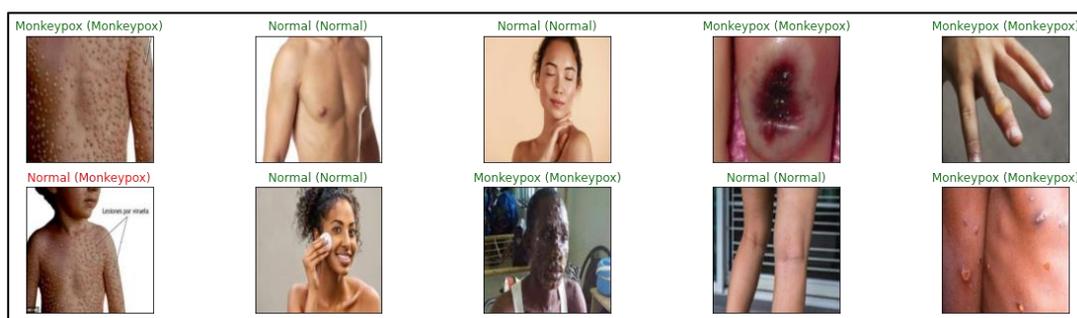


Figure 11. Random Sampling of Test Images: Comparison of Ground Truth and Predicted Labels

5. Conclusion

Monkeypox is a viral disease that has the potential to infect both animals and humans. Accurate and timely diagnosis of the disease is essential for effective control and prevention. This work, employed a new model named PoxTLNet50 for the classification of monkeypox cases, utilizing the MSID dataset. The dataset was systematically partitioned into distinct sets for training, validation, and testing, facilitating comprehensive analysis and model evaluation. The framework was evaluated on the validation set, and the hyperparameters were adjusted to achieve the best performance. Precision, accuracy, recall, and f1 score were used as the four metrics for measuring the model's performance. PoxTLNet50 model achieved an impressive accuracy rate of 98.83%, demonstrating its high level of precision at classifying images of monkeypox. This research emphasizes deep learning models' potential, specifically PoxTLNet50, as a valuable tool in the field of infectious disease detection and classification. Further research and validation are warranted to assess the model's efficiency across diverse datasets as well as real-world scenarios, ultimately paving the way for enhanced monkeypox detection and control strategies.

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