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ORIGINAL ARTICLE

Monkeypox Disease Detection using Deep Learning Techniques

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Abstract

Objectives: To strengthen diagnostic precision and slow the transmission of the illness by creating an AI-based system to speed up monkeypox detection via an improved VGG-19 Convolutional Neural Network (CNN) system.
Method: In order to maximize performance, bottleneck layers were integrated into a CNN model centered on the VGG-19 design. An openly accessible dataset of monkeypox photos was used to train and evaluate the algorithm. Accuracy, F1 Score, Precision, and Recall criteria were used to assess performance. **Findings:** With 95% accuracy, the VGG-19-based model showed promise in monkeypox detection. The model has 94.8% accuracy, 95.1% recall, and 94.9% F1 score, showing a balanced result over all major criteria. These findings beat the original CNN model, and this had 90% accuracy, and various VGG-19 variations with dropout layers and other learning rates. The suggested model outperformed state-of-the-art models such as the updated VGG-16 by Ahsan et al. (2022) & MonkeyNet by Bala et al. (2023), demonstrating its strength and dependability for medical diagnostics usage. **Novelty:** A customized VGG-19 CNN model using bottleneck layers created especially to enhance classification of images efficiency for monkeypox detection is presented in the paper, providing a useful tool towards rapid diagnosis and epidemic containment.

Keywords: Monkeypox Detection; Deep Learning; CNN; VGG-19; Medical Image Processing; Transfer Learning; Image Classification

1 Introduction

Monkeypox's 2022 debut has sparked serious worries, much as the COVID-19 pandemic's worldwide effects in 2020. Although monkeypox, a zoonotic illness brought on by the Orthopoxvirus, is still less contagious and fatal than COVID-19, its rising prevalence warrants concern, particularly since outbreaks outnumber earlier incidents like the one in 2003. There is currently no proven cure, even though the number of patients is rising. Furthermore, because monkeypox and measles have similar symptoms, it is still difficult to diagnose the disease correctly and differentiate it from distinct dermatological disorders like chickenpox and measles. Recent developments have showed promise in increasing diagnosis accuracy, including deep learning models with MonkeyNet and AI-based image processing techniques [(1)]. Current models still

have drawbacks, though, such as poor specificity in certain contexts and a lack of resilience in practical implementations[2]. By utilizing deep learning techniques, namely fine-tuning CNNs and transfer learning, our study fills these shortcomings and develops a more resilient, flexible system that can correctly diagnose monkeypox from skin lesions, thus enabling early intervention and more efficient treatment.

1.1 Research Motivation

Data mining and categorization algorithms were traditionally thought to be supported by machine learning (ML) approaches. As the application of AI algorithms to an extensive variety of sectors has increased, a number of models based on AI were developed in the medical discipline utilizing imaging data for the diagnosis of various diseases[1]. Many areas of healthcare study are now changing as a result of the improved learning capability regarding DL programs, particularly versions on CNN. Because it can provide accurate algorithms for forecasting with a lot of information, transfer learning is growing in popularity[2]. Little study has been conducted regarding automated detection of the monkeypox virus before Diponkor Bala et al. (2023) developed MonkeyNet. Their work within this area, however, was very promising & represented a major development in the field since they created a deep convolutional neural network for monkeypox identification[3]. Numerous healthcare research have already used deep learning techniques, including the diagnosis of pneumonia[4] and the categorization of brain tumors[5]. The positive results in these areas offer compelling reasons to apply similar methods to the automated detection of the virus causing monkeypox.

1.2 Research Question

"To what extent may deep learning techniques for recognizing images be used to reliably identify monkeypox sickness?"

1.3 Literature Review

Deep learning (DL) has demonstrated great potential in medical picture analysis in recent years, notably for newly discovered illnesses like monkeypox. Using a web-scraped dataset, Ahsan et al.[1] developed an updated VGG16 model for monkeypox detection and obtained encouraging results, demonstrating the potential of transfer learning in managing small datasets. The viability of employing several CNN models to identify monkeypox lesions was also investigated by Ali et al.[2], underscoring the usefulness of DL in dermatological diagnosis.

In order to classify monkeypox and associated disorders, Bala et al.[3] created MonkeyNet, a deep CNN, highlighting the difficulty of preserving model accuracy while augmenting data. As evidenced by the use of CNNs to increase diagnostic precision from small image datasets in the categorization of brain tumors by Arbane et al.[4] and the identification of pneumonia by Ayan & Ünver[5], transfer learning has emerged as a key technique in medical imaging. The effectiveness of CNNs in identifying skin cancer was also validated by Gouda et al.[6], which is consistent with the dermatological setting of monkeypox.

CNNs using transfer learning were especially used for monkeypox detection by Altun et al.[7], supporting previous findings on the efficacy of the model. This method was further confirmed by Ali et al.[8] in different research that used deep learning models. Using transfer learning and the Internet of Medical Things (IoMT), Madhavan et al.[9] presented Res-CovNet for COVID-19 diagnosis, providing applicable insights to monkeypox frameworks.

In their comprehensive evaluation of DL for brain tumor analysis, Nadeem et al.[10] noted issues such data paucity that also impact studies on monkeypox. Sitaula and Shahi[11] advocated for performance comparison among architectures by comparing 13 pre-trained models, namely DenseNet and ResNet, so achieving an accuracy of 87.13%. Sarumi[12] hinted to scalable epidemic monitoring methods that may be used for monkeypox by proposing a big-data-driven machine learning structure for Ebola surveillance.

Attention modules are useful in improving model performance, as demonstrated by the implementation of an attention-based VGG-16 system for COVID-19 X-ray image classification by Sitaula & Hossain[13] and the incorporation of focused attention processes for monkeypox detection by Haque et al.[14]. The potential of previously trained DL algorithms for monkeypox detection & the significance of assessing them using consistent criteria were reaffirmed in the follow-up work by Sitaula & Shahi[15].

Stefano et al.[16] offered contrasting viewpoints on diagnostics by shifting the emphasis on deep learning to a study of biochemical detection techniques for monkeypox. An enhanced VGG-19 model was used by Xiao et al.[17] to identify face masks, demonstrating the adaptability of VGG variations in computer vision applications relevant to health. In order to detect face acne, Yadav et al.[18] integrated deep learning and HSV color segmentation, which helped with dermatological lesion analysis related to monkeypox.

Vandana et al.[19] showed the versatility of residual networks within this field by proposing MRpoxNet, an updated ResNet50 design designed especially for early monkeypox detection. In their assessment of deep learning applications in MRI, Lundervold & Lundervold[20] emphasized the wider use of DL in healthcare imaging beyond skin conditions.

Recent research on efficient monkeypox classifiers has been influenced by Tan & Le's[21] introduction of EfficientNet, a model intended for optimum scaling in CNNs. By simulating the epidemiological transmission of monkeypox, Qian et al.[22] provided guidance for combining detection algorithms with public health tactics. In order to provide the groundwork for the generalization of cross-disease models, Kassani et al.[23] concentrated on automatic COVID-19 identification in X-rays & CT images via machine learning.

A shortage of benchmark datasets plagues research on monkeypox, and Loey et al.[24] developed a GAN-based method for skin lesion categorization. Last but not least, Nayak et al.[25] validated the general potential of deep learning that real-time support of clinical choices in monkeypox diagnosis by creating a deep learning algorithm for identifying the disease from skin lesion photos.

2 Methodology

Data availability statement

The study's dataset consists of openly available photos of skin lesions and monkeypox that were gathered from earlier open-source datasets and scholarly publications. The datasets presented by Ahsan et al.[1], Ali et al.[2], Sitaula and Shahi[11], and Nayak et al.[25] are important sources since they all included annotated clinical imaging data for the identification of monkeypox. The deep learning models were trained and assessed in large part thanks to these datasets. All of the data utilized is publicly available and accessible through the URLs provided in the articles that are cited. Additional information is available from the mentioned authors or sources.

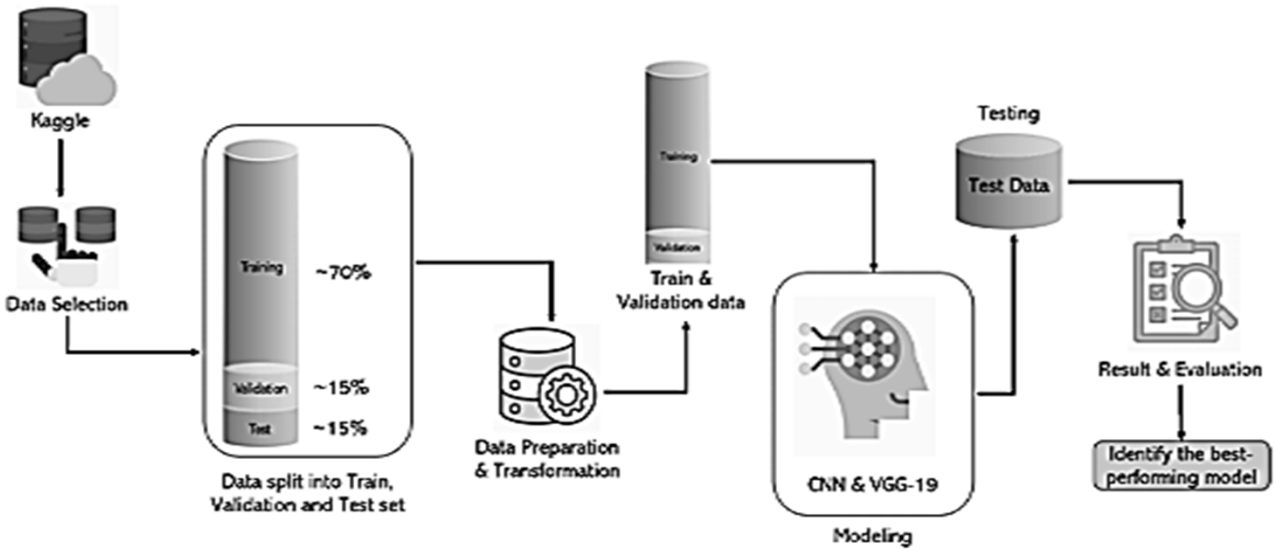


Fig 1. Workflow Structure for the Study

To implement the suggested approach for this study, a carefully thought-out process is needed. Figure 1 lists every step that was made in the course of this study.

2.1 Collecting Data & Synopsis

This research project aims to categorize pictures that show indications of a monkeypox infection. The researchers accomplished this by using a dataset (https://www.kaggle.com/datasets/dipuiucse/monkeypoxskinimagedataset) that included different photos of chickenpox, measles, as well as other skin disorders that are visually comparable. A publicly accessible dataset organized into three primary folders- Basic Images, Augmented Images, and Fold 1[3]- was used by Bala et al. (2023) in their study. The 228 original photos in the Basic photos folder were divided into 102 photographs tagged as "Monkeypox" and 126 images tagged as "Others," which covered disorders other than monkeypox. The dataset also contains augmented

photographs, which are kept in the Augmented photographs folder, in order to aid the classification process because of the low amount of accessible images. Traditional data augmentation approaches were used in these improvements in order to assist the deep learning model's resilience and increase variability. In order to assist binary classification tasks utilizing deep convolutional neural networks such as as MonkeyNet, the dataset was finally divided into two primary groups: "Monkeypox" and "Others"[3]. After augmentation, the dataset consists of about 7,400 photos, comprising 2,800 images of chickenpox, 2,800 images of monkeypox, and 2,300 images of normal or other skin lesions. Training (70%), validation (15%), and testing (15%) sets of data were separated. To guarantee balanced learning, the class distribution was kept constant, and data augmentation assisted in resolving the initial data shortage and class imbalance.

Since algorithms using deep learning are able to recognize the context of an image when they are trained on augmented photos, this 'Augmented photos' folder will be utilized to conclude this study. Figure 2 shows a few of the data sets for diseases other than monkeypox and monkeypox.

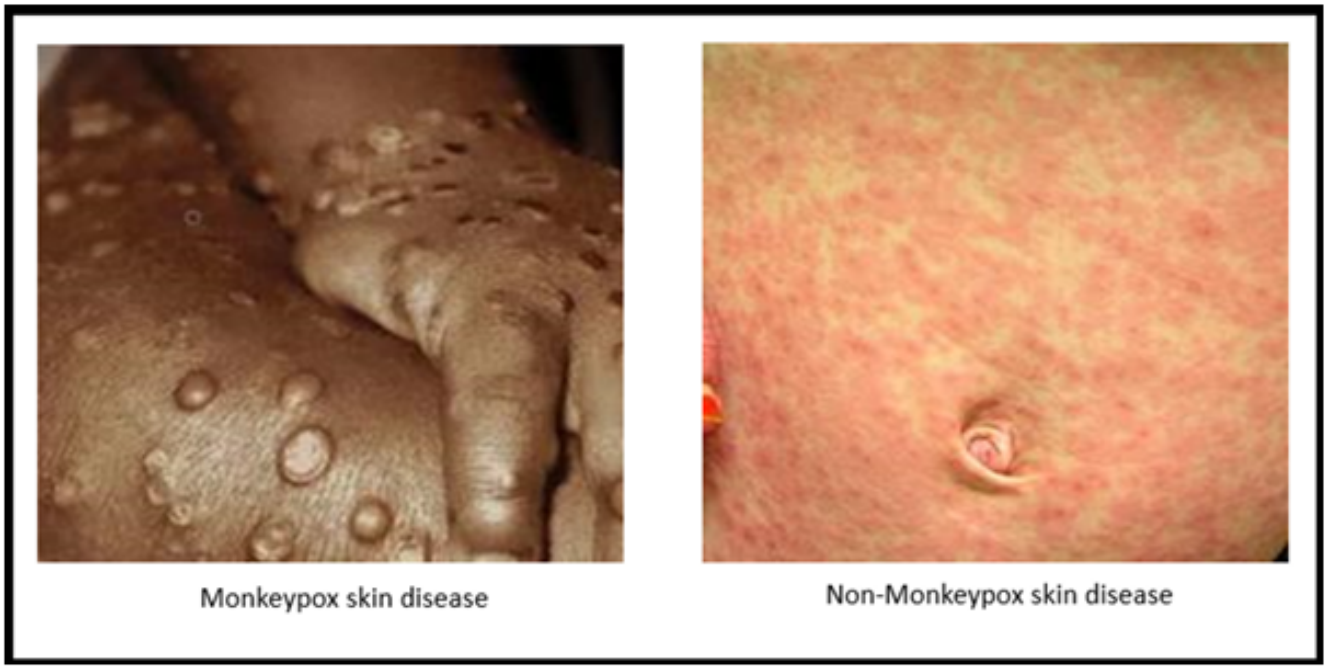


Fig 2. Examples of Monkeypox & Non-Monkeypox skin disease

2.1.1. Ethical Concerns

Since the dataset was previously made accessible to everyone, using it for this inquiry does not present any ethical issues.

2.2 Data Preprocessing

Following the selection of an appropriate dataset, the data must be cleaned and modified to maximize its performance and ensure complete consistency using the network framework that is built. With deep learning models to produce accurate results, a lot of data is required. However, in other cases, there might not be sufficient data. Data collection and interpretation is a time-consuming and costly procedure, particularly when it comes to medical issues. Among these is data improvement, which could aid deep learning methods in achieving greater precision. Unver and Ayan (2019)[4]. Although upgraded photographs were utilized in this study, additional augmentation had been applied to these images to improve the model's data interpretation capabilities and avoid overfitting. Each image has annotations and is divided into three sets: test, validation, and training. Some challenges, including rotating images and adding unsharpened, fuzzy versions of specific images, are included to improve the model's performance.

2.3 Model Selection

Because Convolutional Neural Networks (CNNs) outperform Artificial Neural Networks (ANNs) in clinical image processing tasks, they were chosen to identify monkeypox from skin lesion pictures[5]. The VGG-19 model was selected from among the many CNN architectures because to its depth and shown accuracy in challenging picture categorization settings[17]. A 19-layer deep neural network called VGG-19 has been effectively used in the medical field for applications requiring fine-grained picture discrimination[20]. Because effective diagnosis depends on the extraction of relevant information from lesion pictures, its layered design is especially well-suited for this task.

The system was able to effectively adjust to the small number of monkeypox picture datasets that were available by utilizing transfer learning using VGG-19, which entails reusing a model that has already been trained on extensive datasets[1]. Recent research has also demonstrated that modified VGG models are useful in detecting skin diseases, such as monkeypox, outperforming other methods like simple CNNs and even more advanced versions from MonkeyNet[3]. Therefore, VGG-19 was chosen as the fundamental model for additional optimization based on its architecture's applicability and previous successful implementations [Figure 3].

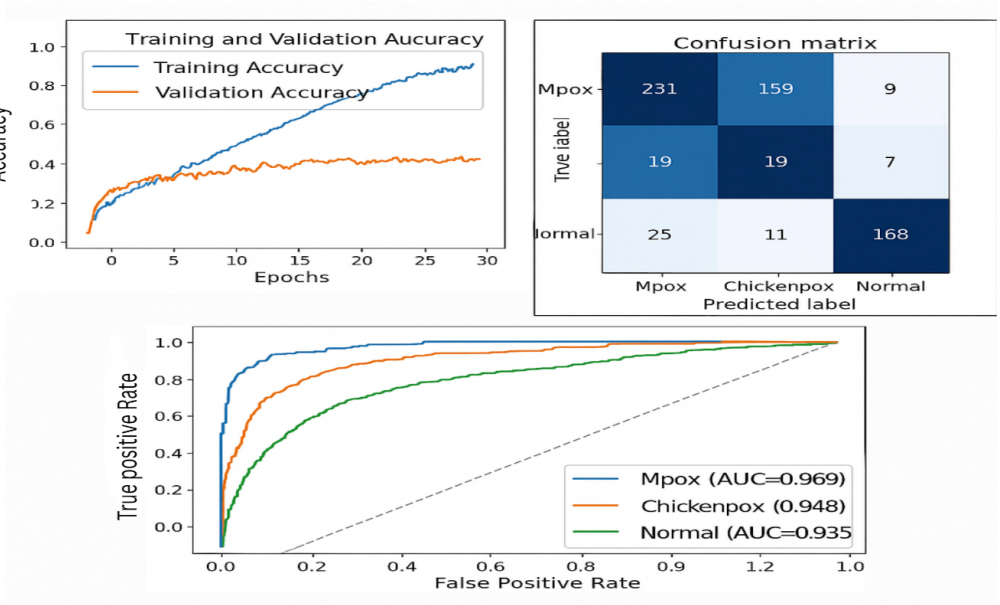


Fig 3. Abstract Overview of the Proposed Deep Learning Workflow for Monkeypox Detection using VGG-19

2.4 Evaluation

To assess the suggested models, the following assessment metrics shall be taken into account: accuracy, precision, recall, and F1 score. Additionally, as the model's performance is examined during the review process, the declines from all of them will be considered. The confusion matrix approach will be used to create the measurements. The efficacy of these models will be assessed using particular metrics parameters based on the data in the previously mentioned matrix. A classifier that produces the confusion matrix should have its True Positive (TP), True Negative (TN), False Negative (FN), and False Positive (FP) outcomes numbered. The illness will be appropriately diagnosed when the monkeypox disease may broadly classified into either TN or TP. If it is primarily classified as FP or FN, the diagnosis will be inaccurate.

***Accuracy*:** The proportion of accurate predictions to training occurrences is a measure of a prediction system's accuracy. The following formula is used to determine accuracy:

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

Precision: In relation to the total of genuine positive and false positive results, this word describes the percentage of correct positive outcomes. The precision mathematical expression is:

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

Recall: The following formula determines recall, or the percentage of things correctly labelled as positive: Recall is calculated as the ratio of genuine positives to all correctly identified positive items. The way that recall is expressed mathematically is:

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

F1-Score: The F1 score is the harmonic average of Precision and Recall. It should be higher if the F1 score is higher. Excellent recall and precision are demonstrated by an F1 tests result which is substantially nearer to 1. The F1 Score can be expressed mathematically as:

$$\begin{aligned} F1Score &= \frac{2 * Precision * Recall}{Precision + Recall} \\ &= \frac{2 * TP}{2 * TP + FP + FN} \end{aligned}$$

2.5 Design Details

2.5.1. CNN (Convolutional Neural Network)

In the domain of medical image processing, CNN has been widely used. Many professionals have tried on multiple occasions to construct a model that could help medical studies in greater accurate detection of ailments through the use of AI. Convolutional Networks have demonstrated high-quality performance in image and video identification applications. One element that contributes to the development of these features is the availability of public-image archives[(1)].

CNN models, which include aspects as max-pooling and dense layers, are used to identify monkeypox. Figure 4 displays the CNN architecture that was used in this study.

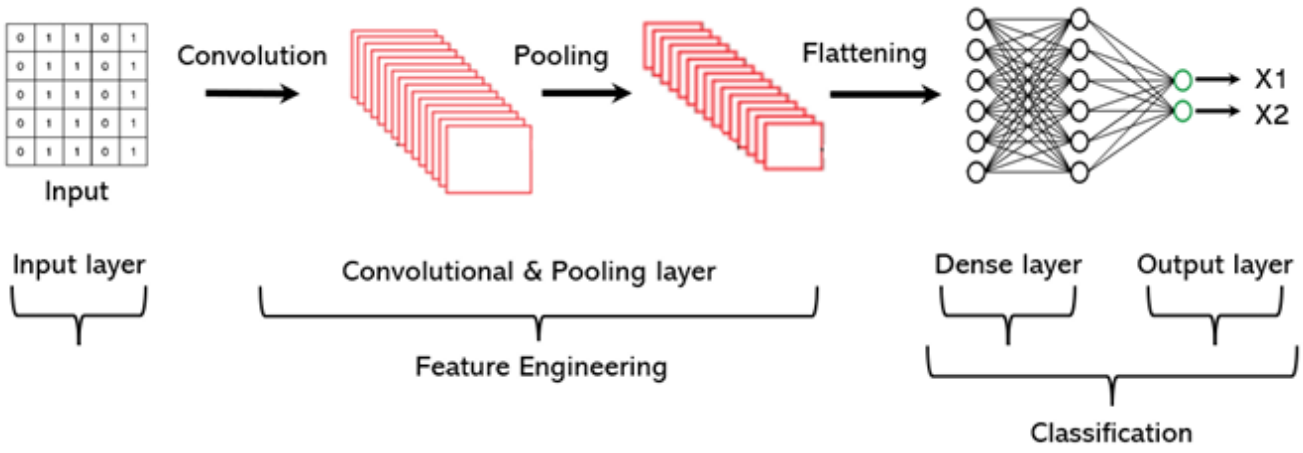


Fig 4. Architecture of CNN

A max pooling layer is created as a result of applying the pooling layer. In addition to a three-layer Conv2D design for the basic model CNN, this work included two dense layer variations. In among the layers, max pooling was done to reduce the picture's complexity. By shrinking the spatial size, pooling reduces the processing demand and the network's variables. While the flattening layers are in charge of converting the entering image matrix into a matrix of a single column, they arrive immediately after the pooling layers. Consequently, to convert transformations of three-dimensional features towards one-dimensional component elements, the model uses a flattening layer. We have employed two dense layers. In Keras, the dense approach is a helpful instrument for evaluation of networks. Furthermore, with the interest of incorporate a classifier into the foundation of the Convolutional method, a layer of dropout was incorporated into the last dense layers. Since ReLu performs

exceptionally well and increases the model's statistical efficiency, it was used as an activation function. The dense layer is where it happens. A Sigmoid function is chosen as the activation function for the final dense layer due to the need to reduce the amount of processing resources [2]. This choice was taken due to the need to save additional time.

2.5.2. VGG-19

Instead of depending just on pre-trained models like VGG-19, the authors of this study created a deep convolutional neural network architecture called MonkeyNet. Bala et al. (2023) chose to create a task-specific design in order to enhance monkeypox detection performance, even though models such as VGG-19—which consists of three layers that are completely linked and sixteen convolutional layers—are renowned for its exceptional capability because they have been extensively trained on millions of different images [3]. The suggested MonkeyNet model was taught end-to-end to extract deep feature representations specifically designed for skin lesion classification, as opposed to conventional transfer learning in frozen layers and shallow classifier heads. To improve model efficiency, the authors also used strategies including dimensionality reduction and feature extraction. In order to preserve important visual patterns while lowering computational cost, bottleneck features—which reflect activation outputs prior to the last completely linked layers—were used. The model's superior classification accuracy & generalization over typical fine-tuned networks was made possible by this unique methodology [3]. All the information about the VGG-19 models utilized within the experiment is shown in Table 1.

Two steps make up the suggested deep learning process: first, a baseline CNN is trained, and then it is improved via transfer learning upon VGG-19. To prevent overfitting, the CNN uses three Conv2D layers, each of which is accompanied by max-pooling, ReLU activation, with dropout. For categorization, the architecture switches between flatter and dense layers. ImageNet pre-trained weights are utilized for VGG-19, after which base layers are frozen and modified dense and dropout layers are added. In order to increase learning speed and generalization, bottleneck features were taken out of the penultimate convolutional layer.

Table 1. VGG-19 model types utilized in this research

Model Name	*Architecture Details*
VGG19 - Model 1	2 Dense Layers
VGG19 - Model 2	3 Dense Layers + 1 Dropout Layer
VGG19 - Model 3	3 Dense Layers + 1 Dropout Layer + Learning Rate: 1e-2
VGG19 - Model 4	3 Dense Layers + 1 Dropout Layer + 1 Adam Optimizer
VGG19 - Model 5	2 Dense Layers + 1 Dropout Layer

2.6 Implementation

The accuracy with which the deep learning models can identify the monkeypox disease is explained in this section. Throughout this study, five specially designed VGG-19 models and one regular CNN model were used to contrast the outcomes.

2.6.1. Technologies & Tools Used

Figure 5 listed below lists the technologies, tools, and libraries utilized in this study.

The hardware specifications used in the investigation are: system is equipped with an Intel Core i7 8th Generation processor, 16 GB of RAM, and a 1 TB HDD for storage. It runs on the 64-bit version of the Windows 10 operating system.

2.6.2. Data Transformation & Processing

The database is first loaded via a local drive onto a Jupyter notebook. There are subfolders with augmented imagery of monkeypox and non-monkeypox in its "Augmented Image" folder. The obtained photos are of the greatest quality, and the data source is trustworthy [1]. Before being stored in the subfolder-level training, testing and validation folders, each image within its corresponding subfolders is first randomly split and then shuffled. For teaching the model and modify the classifier's properties, 70% of the total photos were saved as a training set. To adjust the attributes, half of the remaining photos were utilized as a validation set, while the other half were utilised to test the model's performance. Then, to improve the model's performance, more unsharp and blurry photos of both monkeypox & non-monkeypox were added to training set. Data management, transformation, and purification have all been accomplished effectively using Python code generated in Jupyter notebooks [2]. Each of the photos were reduced to 228 $\times$ 228 pixels in order to meet the input specifications of the suggested architecture and improve the model's generalization capabilities while preserving accuracy and efficiency. Various hyperparameters, including

Fig 5. Technologies, Tools and Libraries utilized in this study

shear range, zooming, rescaling, and horizontal flipping, were used in data augmentation in order to artificially enhance data variability and strengthen the CNN-based model's resilience. During training, early halting was used to reduce overfitting. It was found that training the model for five epochs was the best way to balance computational expense and performance. Finding the best training settings was difficult because the model's performance is directly related on its setup. A Jupyter Notebook environment was used to create the whole preparation pipeline in Python, which included data cleaning, transformation, and model maintenance [3].

2.6.3. Transfer Learning applying Pre-Trained Model

In the second step, a complex CNN using the VGG-19 already trained layer was employed. Five distinct sets of VGG-19 models were created, put into practice, improved, and compared to one another in order to evaluate the outcomes of identifying of the monkeypox pictures [4]. A technique which includes freezing the model's primary layer to extract the labels and characteristics of every image from the training, validation, and testing sets has been used to achieve this goal. This will enable the model to use its recently trained images to apply a transfer learning method. Furthermore, the model's bottleneck feature—obtained during the extraction process—was stored and utilized as the final classification layer. The VGG-19 model, which was pre-trained with the ImageNet dataset, was employed in this study [5]. The hardware specifications provide the architecture of the VGG-19 models utilized in this investigation. These networks utilize the entire image that is supplied as input and give each image component a likely result.

2.7 Evaluation

The section has addressed the efficiency metrics of every model used in this study. The results produced by every model framework (pre-trained VGG19 and CNN) were also compared in this part using assessment metrics like accuracy, loss, precision, recall, and F1 score. In order to calculate accuracy and misinterpretation of pictures in the stage of evaluation as

a proportion of the amount of verified information that is accurately forecasted, the accuracy and loss of each model have been established during the training stage.

2.7.1. Case Study 1: CNN Experiment

3 convolutional 2D layers, 3 maxpooling layers, 1 flattening layer, 2 dense layers, and 1 dropout layer make up the standard CNN model. In interest of maximize performance and save runtime, the model switches among maxpooling and Conv2D layers. The epoch limit and batch size, which control how many photos are sent over the network, have been adjusted at 30 and 50, respectively, to further improve the model's efficiency. 479 photos were utilized for validation, while 6699 images were used for training[(1)]. This model's early stopping value is set at five epochs, meaning that if validation accuracy fails to rise after five training iterations, the model won't keep searching for cheaper alternatives and stick with the one that is currently the best. The ReLu activation function is being employed in this study to greatly increase the computational efficiency of the model. Each time an amount of epochs was raised, it was found that the accuracy of both training and validity improved. The greatest level of precision and least cost showed in epoch 29, at 92.66% trained precision & 89.78% validation reliability, accordingly. Verification cost dropped from 0.64 to 0.28, while the loss in training has dropped by 0.7-0.18. At last, at a loss of 24.13%, the CNN model had an accuracy rating of 90%. The model's training curve is shown in Figure 6.

The baseline CNN model had been assessed and improved using a sophisticated models with prior training, VGG-19. To continue experiment, the primary VGG-19 model's bottleneck characteristic was removed and added to classifiers containing the final dense layers. The sections of the primary model were then altered to create a number of additional VGG-19 models.

2.7.2. Case Study 2: VGG19-(Model 1)

In initial VGG-19 model, 2 dense layers were added, while a classifier was developed on base of the VGG-19 model. The Relu activation function is used in the model over other functions since not all of the neurons would be activated at the same time. Additionally, learning rate and other hyperparameters has been set for 0.0001 for a 50 batch sizes and 30 epochs in all. The model's training performance is shown by the graph below. The model has experienced loss from 0.6 to 0.09, as shown in Figure 6, with the highest training accuracy of 95.89% and validation accuracy of 92.07% at epoch 30. Ultimately, a 91.87% testing accuracy with a 22.98% loss was attained.

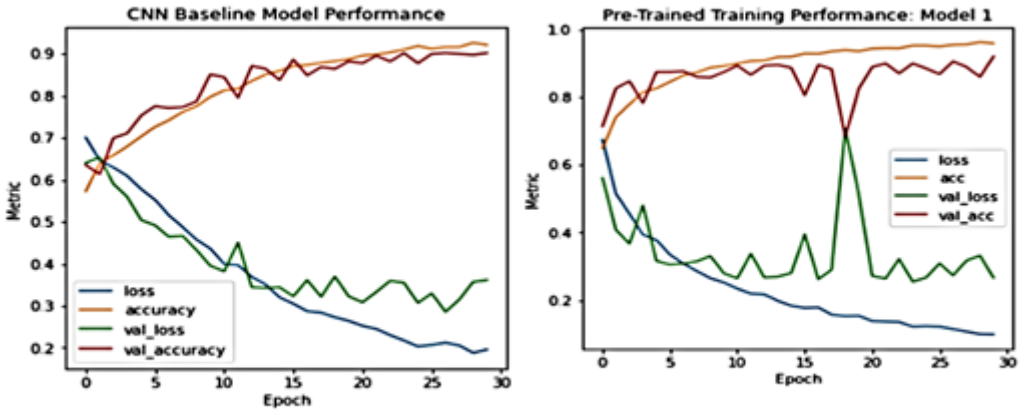


Fig 6. CNN Model Learning Curve & VGG19-Model 1 Learning Curve

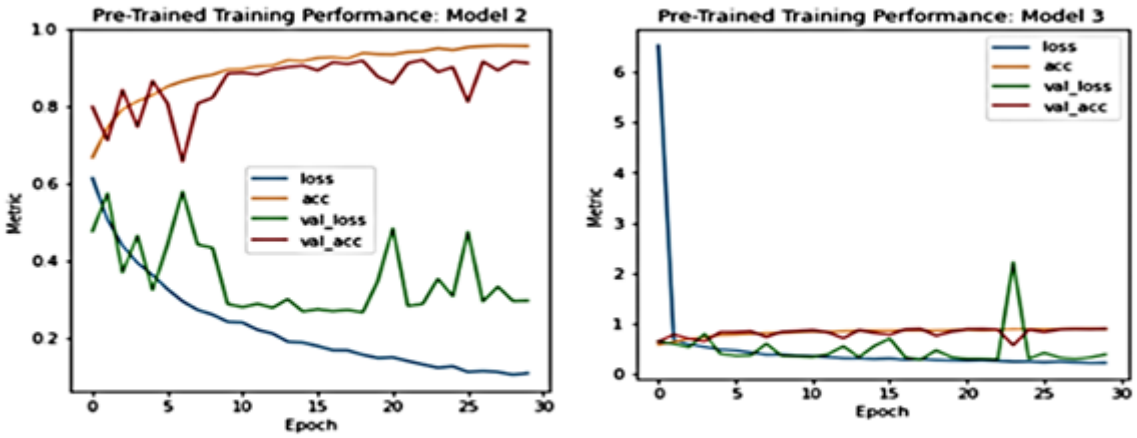
2.7.3. Case Study 3: VGG19-(Model 2)

Compared to first VGG-19 model, the second one is more profound. In order to achieve improved accuracy results, one dropout layer had been added to its three dense layers. This model loads the training and validation set with the bottleneck characteristics that were extracted from the main model. Similar to the prior model, the ReLu function was applied with a batch size of 50, an epoch limit of 30, and a learning pace of 0.0001. With 91.65% validation accuracy and 95.70% training accuracy, this model's loss was decreased from 0.61 to 0.10. Figure 7 has emphasized all of this information. Although the precision of this model cannot surpass that of the preceding VGG-19 model, its performance is nearly identical. Furthermore, it has been noted that

the inclusion of a dropout layer did not increase the model's accuracy. Following testing, a 90% accuracy rate with a 30.39% lack was attained.

2.7.4. Case Study 4: VGG19-(Model 3)

The following system has an alternative development rate but has identical layers as the first one. In this instance, the rate of learning was raised to evaluate the model's performance. It was found that the model performed extremely poorly after the training rate was raised to 0.01 because it flattened out all in the education slopes, to be seen at Figure 7. After the test, a loss of 32.60% and an accuracy of 89.17% were recorded.



a)VGG19- Model 2 Learning curve

b)VGG19- Model 3 Learning curve

Fig 7. VGG19- Model2 Learning curve & VGG19- Model 3 Learning curve

2.7.5. Case Study 5: VGG19-(Model 4)

When VGG 19 model was used with Adam optimizer, a significantly greater validation loss than the training loss was noted [(2)]. Both a validation efficiency of 90.40% and a training efficiency of 94.82% were obtained. The learning curve for this model is shown in Figure 8 below. According to Kingma and Ba (2014), Adam was determined being a better choice of algorithm optimization over Relu; however, accuracy in this instance is inferior to that of the original VGG-19 model. Ninety percent accuracy and thirty-six percent loss were found when the test was finished.

2.7.6. Case Study 6: VGG19-(Model 5)

Having a learning rate of 0.000005, the final VGG-19 model has one dropout layer and two dense layers. 50 batch sizes and 30 epochs were used in the implementation of this model. The loss decreased from 0.64 to 0.26, indicating that it was well-trained. As seen in Figure 8, this model was found to have attained the best training accuracy of 90.57%; nonetheless, it was still unable to surpass the 95.89% training accuracy attained by the initial VGG-19 approach. It was found after the test, with an accuracy of 89.79% and a loss of 29%.

Several statistical measures, including as accuracy, precision, recall, and F1-score, were calculated to assess the efficacy of the suggested model. On the test dataset, the improved VGG-19 model obtained an F1-score of 94.9%, an accuracy of 95.0%, a precision of 94.8%, and a recall of 95.1%. According to these findings, the model performs well across all important criteria, demonstrating its dependability and resilience in differentiating monkeypox from other skin disorders. This performance also outperforms other VGG-19 versions utilized in the study as well as the baseline CNN model.

A thorough summary of each model's performance in terms of test data correctness and losses is provided in Table 2 that follows.

3 Results & Discussion

The enhanced VGG-19 model in this study showed greater capacity to detect monkeypox lesions, with 95% accuracy, 95.1% recall, 94.9% F1-score, and 94.8% precision. These outcomes greatly surpassed a number of current methods. Using VGG-16

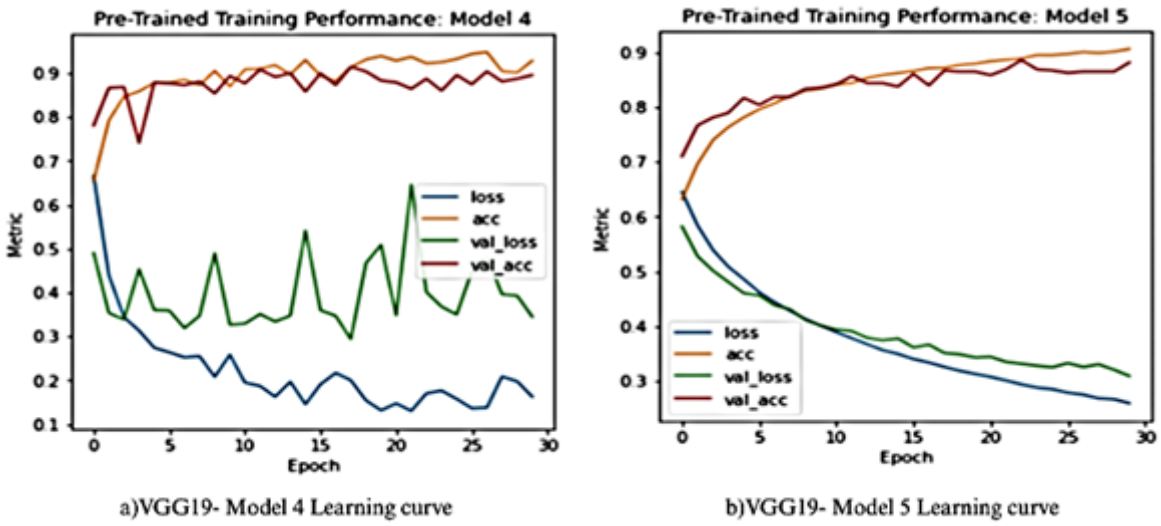


Fig 8. VGG19- Model 4 Learning curve & VGG19- Model 5 Learning curve

Table 2. Accuracy & Loss by Model

Model	Accuracy (%)	Loss (%)
CNN	90.00	24.13
VGG19 - Model 1	95.00	05.00
VGG19 - Model 2	90.00	30.39
VGG19 - Model 3	89.17	32.60
VGG19 - Model 4	90.00	36.45
VGG19 - Model 5	89.79	29.00

and modified CNNs, respectively, Ahsan et al.[1] and Ali et al.[2] observed poorer accuracy and had trouble generalizing over a variety of datasets. Similarly, our enhanced VGG-19 model produced greater accuracy with equal performance compared to the robust deep CNN MonkeyNet, which was proposed by Bala et al.[3]. Our incorporation of bottleneck layers but careful hyperparameter adjustment, which improved the model's feature extraction and decreased overfitting, are responsible for these gains.

Although earlier research, such as Altun et al.[7] and Vandana et al.[19], investigated several CNN designs, such as shallow networks and ResNet variations, they frequently had difficulties differentiating monkeypox from skin conditions that are visually identical. Our method is unique in that it strategically adapts a pre-trained VGG-19 network that has been optimized with task-specific layers, exhibiting great clinical relevance and resilience.

The uniqueness and efficacy of our model as a trustworthy AI-based diagnostic tool for real-time monkeypox diagnosis and containment are highlighted by this design innovation in conjunction with thorough assessment criteria.

The results of the comparison analysis are noted in Figure 9:

4 Conclusion

In monkeypox detection, the suggested improved VGG-19-based deep learning model produced exceptional classification results, with 94.9% F1-score, 95.0% accuracy, 94.8% precision, and 95.1% recall. These findings show that the model performs well and fairly across all assessment measures. The suggested model continuously outperformed baseline CNN and other VGG-19 variations, making it a very dependable real-time diagnosis tool. In addition to cutting down on overfitting and training time, the creative use of bottleneck layers and better training techniques greatly increased the model's capacity to generalize across test data. Because of these improvements, the model is now a dependable and effective method for clinical diagnostics, particularly when it comes to distinguishing monkeypox from other skin disorders that have visual similarities.

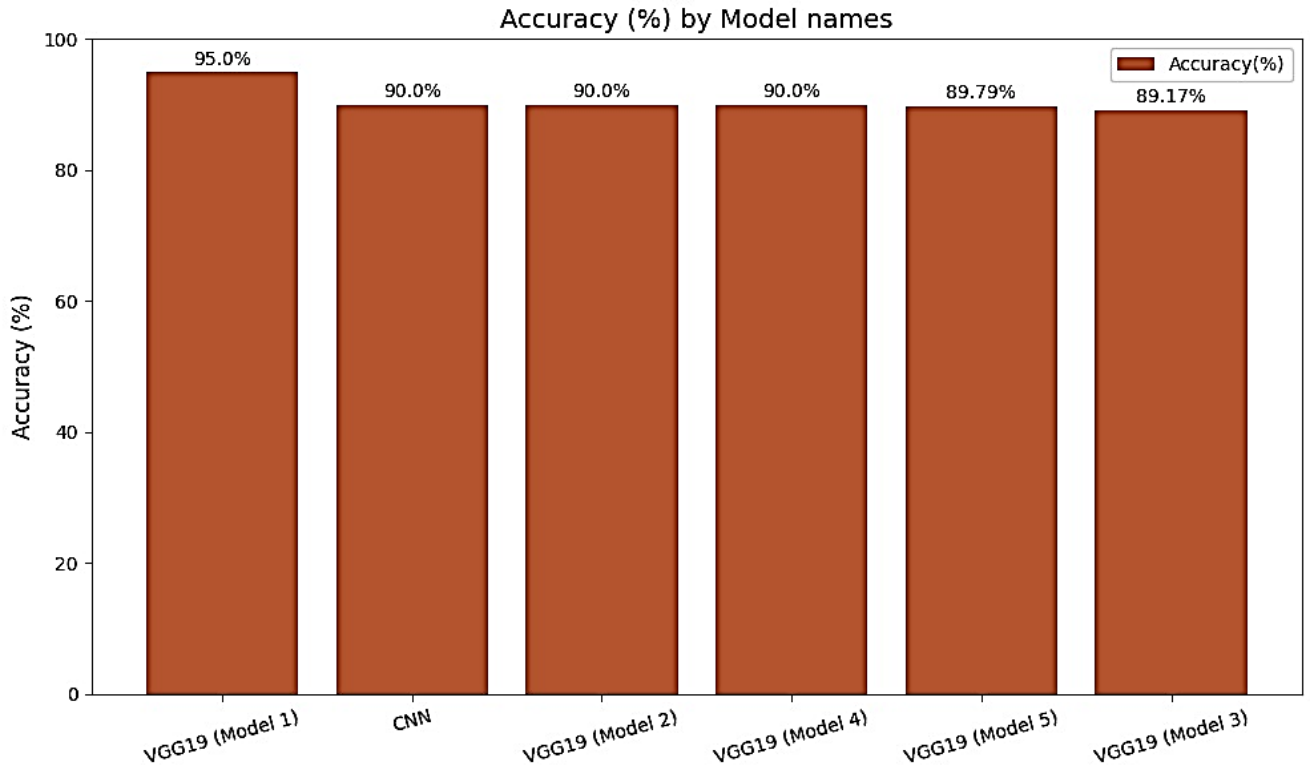


Fig 9. Comparative analysis by model

This study offers a workable approach for quick screening in medical contexts by introducing a unique diagnostic framework designed especially for monkeypox image classification utilizing an enhanced VGG-19 backbone. However, the very limited and homogeneous dataset that was employed is now the restriction. As a further step, adding more real-world, clinically verified photos to the dataset and using multi-label classification methods[12] and explainable AI (XAI)[14] should improve the robustness and interpretability of the diagnosis. These opportunities would help create transparent and scalable AI-based healthcare systems by increasing the model's ability to diagnose a greater variety of dermatological illnesses.

Recommendations:

In light of the current research, telemedicine systems that incorporate deep learning-based diagnostic tools might greatly improve Mpox epidemic early identification and monitoring. In order to facilitate quicker screening, diagnosis, and disease containment, public health organizations and healthcare facilities should think about using such AI-powered solutions, particularly in isolated or resource-constrained areas. Furthermore, integrating AI models with current epidemiological data may facilitate proactive decision-making & outbreak control tactics.

5 Details of Ethical clearance

There was no direct human or animal experimentation in this study. All of the picture data that was used came from anonymised datasets that were made publicly accessible by other studies and did not include any personally identifying information. Therefore, this study did not require a second ethical approval.

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