FMDB *Transactions on Sustainable Health Science Letters*

A Comparative Analysis of CNN-Based Pretrained Models for the Detection and Prediction of Monkeypox

Rejwan Bin Sulaiman[1,*], Sourav Saha[2], Trina Chakraborty[3], Tithi Paul[4]

[1]Department of Computer Science and Technology, Northumbria University, Middlesex Street, London, United Kingdom.
[2,3]Department of Computer Science and Engineering, Shahjalal University of Science and Technology, Kumargaon, Sylhet, Bangladesh.
[4]Department of Computer Science, University of Barishal, Kornokathi, Barishal, Bangladesh.
rejwan.sulaiman@northumbria.ac.uk[1], souravsaha0152@gmail.com[2], trinasustcse41@gmail.com[3], tithi.cse3.bu@gmail.com[4]

Abstract: Following the COVID-19 epidemic, Monkeypox, which is an uncommon illness, elicited concerns from specialists in the medical field. It is a cause for concern because Monkeypox is difficult to diagnose in its early stages, as its symptoms may resemble those of measles and chickenpox. In addition, there is a knowledge gap among healthcare experts regarding this rare ailment. As a consequence, there is a pressing need to develop a new method to combat and predict the disease at the initial stages of viral infection. This research included a variety of pretrained convolutional neural network (CNN) models. The models that were used included VGG-16, VGG-19, Resnet50, Inception-V3, DenseNet, Xception, MobileNetV2, Alexnet, LeNet, and majority Voting. To conduct this study, several different datasets were integrated, including the following: Monkeypox against chickenpox, Monkeypox versus measles, Monkeypox versus normal, and Monkeypox versus all disorders. In the case of Monkeypox versus chickenpox, majority voting scored 97%, while Xception scored 79% for Monkeypox versus measles, MobileNetV2 scored 96% for Monkeypox versus normal, and LeNet scored 80% for Monkeypox versus all.

Keywords: Pretrained Models; Healthcare Professionals; Restnet50 and Inception-V3; DenseNet and Xception; MobileNetV2 Architecture; Alexnet and LeNet; Majority Voting; Monkeypox Disease.

Received on: 02/11/2024, **Revised on:** 11/01/2025, **Accepted on:** 03/03/2025, **Published on:** 07/09/2025

Journal Homepage: https://www.fmdbpub.com/user/journals/details/FTSHSL

DOI: https://doi.org/10.69888/FTSHSL.2025.000499

Cite as: R. B. Sulaiman, S. Saha, T. Chakraborty, and T. Paul, "A Comparative Analysis of CNN-Based Pretrained Models for the Detection and Prediction of Monkeypox," *FMDB Transactions on Sustainable Health Science Letters*, vol. 3, no. 3, pp. 125–134, 2025.

Copyright © 2025 R. B. Sulaiman *et al.*, licensed to Fernando Martins De Bulhão (FMDB) Publishing Company. This is an open access article distributed under CC BY-NC-SA 4.0, which allows unlimited use, distribution, and reproduction in any medium with proper attribution.

1. Introduction

At a time when the globe was still struggling to recover from the devastation caused by COVID-19, the deadly Monkeypox virus emerged. This virus can be transmitted from animals to people. The disease presents with symptoms analogous to those of smallpox but less severe. In 1958, a Danish researcher working in a laboratory in Copenhagen, Denmark, made the first discovery of the Monkeypox virus. In 1970, the Democratic Republic of the Congo was the site of the first human A virus outbreak, which can spread from one person to another through the exchange of bodily fluids, respiratory droplets, and infected

*Corresponding author.

items such as bedding, among other routes [24]. Following the COVID-19 epidemic, the globe is now facing a new danger in the form of Monkeypox. The World Health Organisation (WHO) [26] asserts that the current Monkeypox outbreak is not a pandemic but rather an endemic. When a disease is present only in a specific location, geographic region, or environmental setting, it is referred to as endemic. As of right now, the World Health Organisation (WHO) [26] has identified the following countries as being endemic to Monkeypox: Benin, Cameroon, the Central African Republic, the Democratic Republic of the Congo, Gabon, Ghana (identified only in animals), Côte d'Ivoire, Liberia, Nigeria, the Republic of Congo, and Sierra Leone. According to the WHO, among the endemic regions, the Democratic Republic of Congo has the largest number of deaths and suspected cases, which are 58 and 1284, respectively, at this point, and have been confirmed. WHO has reason to believe that there will be other developments in the case in the coming days. According to our research, the article believes the Monkeypox epidemic is in the early stages of its first wave of transmission, comparable to the early stages of the COVID-19 pandemic. Seven hundred eighty cases of Monkeypox have been reported throughout a total of 27 nations that are identified as nonendemic regions. The United Kingdom and Northern Ireland have the most Monkeypox cases, with 207. This is followed by Spain and Portugal, which have 156 and 138 cases of the disease, respectively (Figure 1).

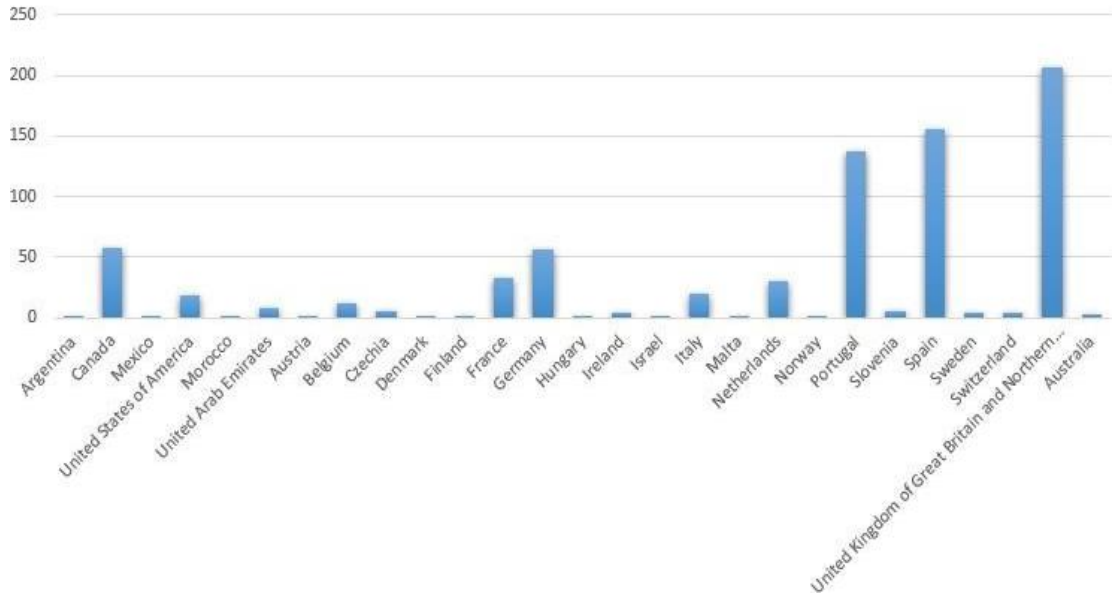

Figure 1: Monkeypox confirmed cases

Although Monkeypox is not as infectious as COVID-19, its incidence is still rising. In West and Central Africa, there were just 50 confirmed cases of the illness in 1990. However, by 2022, thousands of cases of the disease had been reported. In the past, it was thought that the disease had never appeared outside Africa. But in 2022, those infected with the virus were tracked down and identified in several nations across the United States and Europe. People's anxiety and stress levels are rising as a direct result of the rising number of reported incidents [17]. As a result, it is witnessing widespread panic across both social and traditional media. What is the current treatment? Another factor that contributes to people's anxiety is the lack of any remedies that have been developed up until this point. At this time, there is no treatment available for those infected with the virus that causes Monkeypox. The Centres for Disease Control and Prevention (CDC) [5] reports that several medicinal treatments, also known as countermeasures, are available for this disease. These include medicines specifically developed for the treatment of smallpox. Medicines such as Tecovirimat, Cidofovir, Vaccinia Immune Globulin Intravenous (VIGIV), and Brincidofovir are used to treat Monkeypox.

These medicines are also widely used to treat smallpox. Researchers are now developing an EAIND to support the development of Brincidofovir as a therapy for Monkeypox. Although many successful vaccines have been developed for illnesses like Monkeypox, and researchers are currently using them to treat it, there are also limitations. What are the current limitations? One of the disease's most apparent downsides is that there is now no known treatment for it. In addition to this disadvantage, another constraint is the difficulty in making an early diagnosis. This infectious disease is said to be contagious until the scabs that have formed on the skin have peeled off, according to the Rare and Imported Pathogens Laboratory (RIPL). Because the disease appears to be smallpox in the images (a-e) above, a pathology diagnosis is required. As a potential solution to this problem, our team is exploring machine learning to diagnose the disease at its early stages. To leverage machine learning, the paper needs sufficient data to train the model. In the case of Monkeypox, one limitation is the lack of a readily accessible public

dataset for modelling Monkeypox diagnosis. How have deep learning and machine learning models been used over the years in medical imaging? (Figure 2).

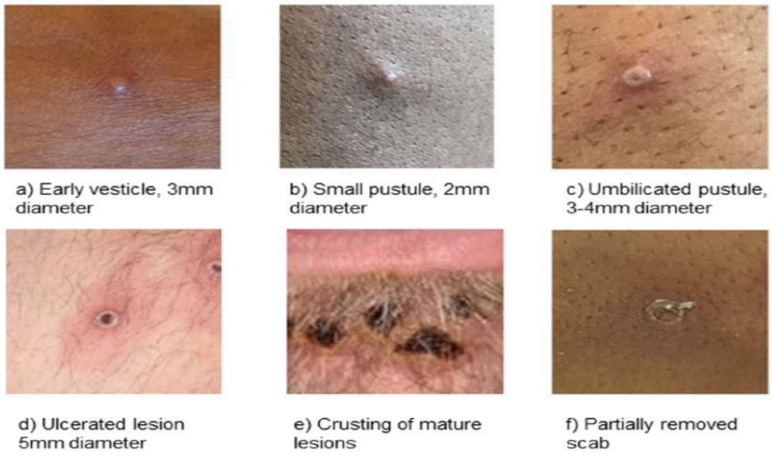

Figure 2: Different stages of Monkeypox

Identifying medical conditions is just one of the many fields in which machine learning has been applied for a long time [25]; [15]. For instance, early diagnosis of bone disorders, Newborn Brain Maturity, Network Abnormality Detection, Pneumonia Detection, Credit Card Fraud Detection, and Diabetic Prediction, among many others [20]; [18]. Researchers are working hard, despite these restrictions, to build machine learning algorithms that could recognise illnesses such as Monkeypox. Machine learning can provide medical professionals with accurate and rapid may imaging solutions [1].

Scope and Motivation: Image processing is inherently challenging. Working with a small dataset adds another layer of complexity to the issue at hand. Because Monkeypox is an uncommon illness and the current epidemic is in its early stages, there is a compelling need for an innovative strategy to detect and prevent Monkeypox at the earliest stages of individual infection. As part of this research paper, a variety of machine learning algorithms, including DL, CNN, and ANN, will be considered to develop an innovative prediction model with increased precision. The following problem statements will be attempted to be answered in this paper:

- Does over-sampling improve the accuracy/of medical image classification (other benchmarks)?
- Does the pre-trained CNN architecture predict better than the other models?
- What are the methods that can be used to tackle a limited dataset in the Monkeypox case to detect the virus at the early stage of its lifecycle?

2. Related Work

The development of AI models across several fields, including emotion analysis, fruit image analysis, and chest x-ray images, has led to the development of medical image analysis AI models for diagnosing various virus-related diseases [23]. For instance, Sandeep et al. [22] studied the use of deep learning (DL)-based techniques to identify a variety of skin conditions, including psoriasis, chickenpox, vitiligo, melanoma, ringworm, acne, lupus, and herpes. They used the VGG-16 pre-trained model to evaluate their convolutional neural network (CNN) classification of skin lesions into eight distinct disease categories [14]. Their technique offered a 78% detection accuracy. Transfer learning (TL) is the process of applying a model trained on one machine learning task to another using a dataset that has already been used to train the model. Transfer learning for computer vision is widely used across several applications. Pre-trained models with the highest popularity and recognition include VGG, ResNet, InceptionNet, and others [2].

By enabling models to be trained with very little data, pretraining has significantly shifted the field of artificial intelligence. When employing TL, there are two key benefits [9]. First, it excels in both large and small datasets. Second, when a pre-trained model is used, it is easy to reduce overfitting by using a larger dataset [9]. To assess the key variables for controlling a smallpox outbreak in a major city with a population of 2 million, a stochastic model has been developed to simulate the progression of an epidemic managed by ring vaccination and case isolation [12]. Numerous organisms, including bacteria (Yersinia pestis, Bacillus anthracis), fungi, protozoa, and viruses (Ebola, Influenza, and Variola), are listed by the World Health Organisation as having the potential to be used as biological weapons. Secondary occurrences in the event of a chemical or toxic attack, a toxic attack, or an attack by an agent like Bacillus anthracis, for which human-to-human transmission is unusual, would be

unlikely. However, serial human-to-human transmission is more likely in the event of an attack by infectious organisms such as smallpox [12]. According to earlier research on predictive measures, several patterns can be extracted from medical tracings and medical imaging, including the diagnosis of diabetic retinopathy, the detection of malignant cells in dermatology, and the identification of brain tumours in MRI scans [6]. These are just a few examples [11]. Classification algorithms that consider prior medical cases may hasten prediction and even identify potential illness onset, allowing treatment before harmful symptoms develop [6].

Artificial neural networks (ANNs) have previously improved the performance of potentially outdated and ungeneralizable indices or heuristics still used in the healthcare industry [6], helping doctors make better-informed diagnoses. Machine learning is, therefore, a crucial technique for addressing the information gaps in these tests and improving the reliability and accuracy of the forecast. Successful implementation of such an ANN will also reduce the risk of the disease worsening and the associated financial impacts [21]. The main result that approaches ultimately achieve is overall patient satisfaction [6]. In the healthcare industry, especially when it comes to rare diseases or abnormalities, the challenge of class imbalance within the data collection, or when classes are considerably over- or over-/underrepresented, commonly occurs. Think about a scenario in which smallpox has reappeared, and doctors need to quickly distinguish between spots symptomatic of chickenpox and those of smallpox to hasten eradication.

3. Methodology

The paper divided the dataset into train, validation, and test to conduct the experiments. It used images from different classes as input and obtained binary predictions indicating whether each image depicts a patient with Monkeypox. The framework is shown in Figure 3, and it briefly describes the stages of the experiment below:

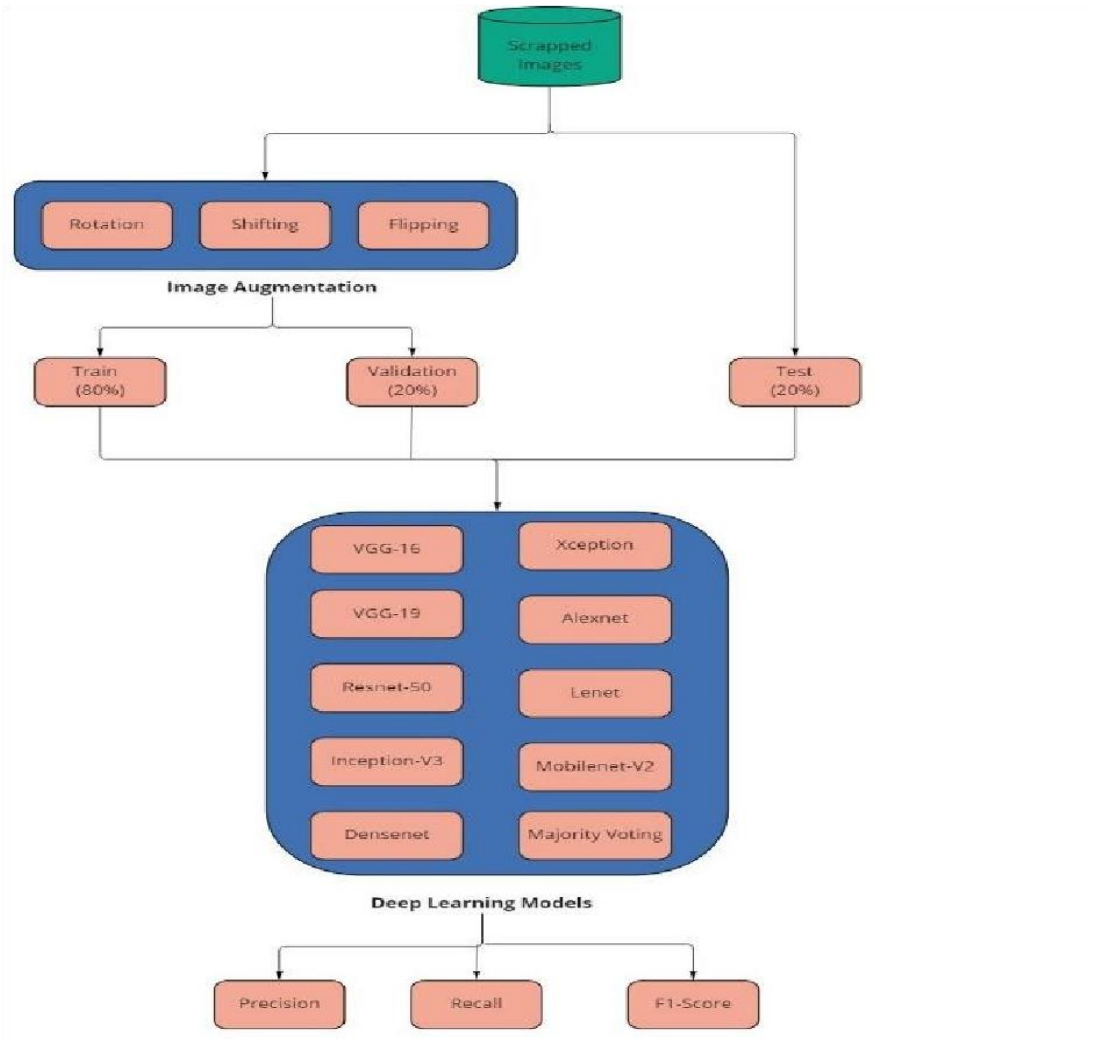

Figure 3: Workflow of detecting Monkeypox

3.1. Data Acquisition and Augmentation

The article adopted the Monkeypox dataset, which contains both real and augmented images of Monkeypox, chickenpox, measles, and the normal class [16]. The images were collected by surfing the internet with relevant search results. They augmented the images using Keras ImageDataGenerator. Various augmentation techniques, such as rotation, shifting width and height, and flipping, were used to augment the images. The final composition of the dataset statistics is presented in Table 1.

3.2. Transfer Learning with Pre-Trained Models

The article used the first layer of the architecture for transfer learning with pre-trained models, a handy machine learning technique that improves performance by learning from a different task than the intended one. The models have been pretrained on the ImageNet dataset [10]. The researchers removed the final fully connected dense layer and trained on the Monkeypox dataset. The transfer learning model is shown in Figure 3. The researchers applied nine pre-trained models and tested them in the transfer-learning layer to determine which performs better for classification. The models are VGG-16, VGG-19, Resnet-50, InceptionV3, DenseNet, Xception, MobilenetV2, AlexNet and LeNet. The pretrained models have been trained on millions of images, predicting over 100 classes, and allow leveraging features learned from large pretrained models on the small dataset:

- **VGG16:** VGG-16 is a 16-layer deep convolutional neural network. The pretrained version of the network is trained on over a million images from the ImageNet database. The pre-trained network can classify images into 1000 object categories. Therefore, the network has learned rich feature representations for a vast range of image objects. The network has an image input size of 224*224.
- **VGG19:** VGG-19 is a variant of VGG-16 with a 19-layer deep convolutional network. It has also been trained on ImageNet with millions of images, providing strong transfer learning results with an input size of 224*244.
- **ResNet50:** In the ResNet paper, the authors introduce a residual learning framework that is easier to optimise and achieves higher accuracy at increasingly deeper depths. ResNet50 is a variant of this residual network with 50 layers, pre-trained on the ImageNet dataset with an input size of 224*224*3.
- **InceptionV3:** In the inception V3 paper, the authors formulate a way to scale up a network to facilitate added computations as efficiently as possible, and by suitably factorising computations and aggressive regularisation. The input image size for this model is 299*299. However, to maintain ubiquity, the 224×224 image size was also used.
- **DenseNet:** Each layer in DenseNet connects to every other layer in a feedforward manner. The distinct feature of the DenseNet is that it provides several advantages, such as strengthening feature propagation, encouraging feature reuse, significantly reducing the number of parameters, and solving the vanishing gradient problem. The default input size for DenseNet is 224*224.
- **Xception:** A slight variation of the Inception module with the same number of parameters, but because it uses the model architecture more efficiently, it slightly outperforms the Inception model. Here, the Inception module has been replaced with depth-wise separable convolutions. The default input size for Xception is 224x224.
- **MobileNetV2:** The MobileNetV2 architecture is designed based on an inverted residual structure. Here, the input and output of the residual block are thin bottleneck layers, unlike expanded representations in the input of traditional residual models. MobileNetV2, on the other hand, uses lightweight depth-wise convolutions to filter features in the intermediate expansion layer. These measures significantly increase performance. The default input size of Xception is 299*299.
- **AlexNet:** a deep convolutional neural network with 60 million parameters and 650,000 neurons. It consists of five convolutional layers, some of which are followed by max-pooling layers. It also has three fully connected layers, followed by a final 1000-way softmax. The input size of the AlexNet is 256×256.
- **LeNet-5** is one of the early convolutional neural networks, consisting of 5 convolutional layers. The image input size is 32*32.

3.3. Model Loading and Compiling

Researchers have imported all the necessary libraries for compiling the architectures and for loading the layers used to build the network. Researchers have loaded a pre-trained CNN architecture trained on a large dataset. To avoid overfitting, researchers have not trained the entire network. Researchers have frozen some layers and trained only the classifier. Researchers have flattened the lower-layer output and added a dense layer with an activation function. After that, the Researchers compiled the model by defining the optimiser, loss function, and metrics.

3.4. Image Pre-processing

Researchers have loaded our dataset into suitable paths. Researchers have processed the dataset by resizing the images according to the respective models and appending the images to their paths. Researchers have also normalised the dataset [27]; [14].

3.5. Fit the Model

Every pre-trained model has a different number of convolutional, pooling, activation, and dropout layers, among others. To build those architectures, researchers can use TensorFlow and the Keras library in Python. So, the Researchers can import all the necessary Python libraries to build the neural network architecture. Once the model is compiled, the Researchers can fit it using training and validation data, and the variable records the metrics. When fitting the model to the data, it shows the model's accuracy and loss:

- **Predict Model:** With the recorded variable, the Researchers can predict test data and evaluate the model using built-in Python functions. It shows the test data's accuracy and helps us assess the model's performance.

3.6. Determine Confusion Matrix

Researchers can present the predicted values in a confusion matrix, which allows us to determine the precision, recall, and F1 score for the compiled model. A confusion matrix is a format used to evaluate the performance of a classification algorithm. It visualises and summarises the performance of a classification algorithm. So, researchers are using it to look up our model performances:

- **Loss and accuracy plot:** Finally, researchers have plotted the loss and accuracy of bPython's P and y functions as a function of v. By examining the plots, researchers can gain a clear understanding of the model’s performance.

4. Experimental Setup

4.1. Train-Test-Val Set Selection

To prevent overfitting and measure the model's performance without bias, the researchers split the data into test and validation sets. The researchers used a stratified split to split the dataset into 70:15:15 (Train: Val: Test). The researchers used the validation set to adjust the early stopping criteria so that the model stops training when validation accuracy drops for two consecutive epochs. On the other hand, the test set was used to evaluate the model's performance after training.

4.2. Model Selection

As there is little to no research on Monkeypox detection, researchers decided to use standard pre-trained architectures for image classification [13]; [4]. The researchers selected the following models: VGG (VGG-16 and VGG-19), Resnet50, InceptionV3, DenseNet, Xception, MobilenetV2, AlexNet, and LeNet. The models were trained on the ImageNet dataset [7]; [8]. As these models have different architectures, our goal was to obtain performance measurements across different situations [3]; [19].

4.3. Training Setup

As the images in the dataset varied in shape and size, the researchers resized all images to a*b*n (where a and b represent the image height and width determined by the model input, and n represents the number of channels). The researchers converted all image types to PNG to maintain symmetry during modelling. The pixel intensities were normalised by dividing each image by 255. The researchers used the Adam optimiser, a batch size of 32, and the 'sparse_categorical_crossentropy’ loss function for all the models. The researchers ran all models for 10 epochs and used an early-stopping metric on the validation set to prevent overfitting.

4.4. Evaluation Metric

As the dataset is small and imbalanced, the Researchers decided to use Precision (P), Recall (R), and the weighted F1 score as our evaluation metrics better to reflect the dataset's composition: results and Analysis.

5. Results and Analysis

Researchers report the results of our models in Table 1.

Table 1: Results of binary classification of Monkeypox detection using different pre-trained models. Here, P, R, and F1 account for precision, recall, and weighted F1 scores

Models																										
	Monkeypox vs Chickenpox						Monkeypox vs Measles						Monkeypox vs Normal						Monkeypox vs All					
	Colour			GrayScale			Colour			GrayScale			Colour			GrayScale			Colour			GrayScale		
	P	R	F1	P	R	F1	P	R	F1	P	R	F1	P	R	F1	P	R	F1	P	R	F1	P	R	F1
VGG-16	95	94	94	94	93	94	61	62	61	83	71	75	97	97	97	93	93	93	56	49	52	36	35	33
VGG-19	94	93	93	94	93	93	66	66	66	73	63	67	97	97	97	89	88	88	43	44	43	95	65	76
Resnet50	96	67	76	76	74	73	57	54	53	87	50	55	77	68	70	77	65	67	50	43	42	99	67	80
Inception-V3	94	94	94	94	93	93	68	64	66	60	61	60	95	95	95	95	95	95	52	48	50	49	47	48
DenseNet	95	41	54	78	59	61	100	66	80	83	63	71	93	93	93	84	82	83	41	43	42	95	66	78
Xception	80	64	65	90	90	90	98	69	79	100	66	80	87	70	73	88	67	71	44	43	44	100	67	81
MobileNetV2	96	96	96	96	96	96	66	66	66	70	67	68	96	96	96	96	96	96	51	47	49	36	38	37
AlexNet	99	39	55	66	66	66	74	64	68	63	58	60	100	51	67	60	58	58	75	62	67	100	33	49
LeNet	70	70	70	74	68	68	84	34	45	92	63	75	100	51	67	76	73	74	99	67	80	100	33	49
Majority Voting	97	97	97	96	96	96	65	66	65	63	66	61	95	95	95	94	94	94	45	48	47	44	59	50

There are four classifications in the dataset: Monkeypox, Chickenpox, Measles, and Normal. There are 161 curated photos in total. After the augmentation, the dataset grows to 1,764 augmented photos, for a total of 1,915 images. This distribution shows the significant augmentation performed to increase the dataset size and balance it for analysis (Table 2).

Table 2: Numerical description of the dataset in terms of the number of images, the number of augmented images, and the total number of images

Class Type	Curated Images	Augmented Image	Total Image
Monkeypox	43	587	630
Chickenpox	47	329	376
Measles	17	286	303
Normal	54	552	606
Total	161	1764	1915

5.1. Comparison Among Different Disease Clusters

The results are significantly good despite the lack of original images. The binary classification shows how well the models can separate images of the Monkeypox class from those of other classes based on disease features. Researchers find that all models can detect Monkeypox with relative ease, even in coloured and grayscale images, compared to chickenpox. The DenseNet even achieved a near-perfect F1 score of 99%. Measles detection is relatively poor due to a lack of original measles data for training. A significant observation is that models also achieve excellent Monkeypox classification results for people without any diseases, with VGG-16 yielding the best F1 score of 95. The researchers also reported results for Monkeypox and all other classes, yielding the highest F1 score of 78.

5.2. Majority Voting

Most models showed similar performance in detecting Monkeypox. The researchers examined whether majority voting across the models could improve results or reveal major characteristics. The researchers got mixed results. While chickenpox vs Monkeypox (MvC) and chickenpox vs normal (MvN) got almost top-notch results, Monkeypox vs Measles (MvM) and Monkeypox vs all (MvA) seem to provide an average result.

6. Conclusion and Future Work

This study assessed various deep learning models to ascertain their efficacy in identifying Monkeypox across diverse binary and multiclass classification contexts. The results showed that performance varied a lot depending on the comparison category and the quantity of the dataset. Majority voting turned out to be the best way to classify Monkeypox and chickenpox, with an accuracy rate of 97%. This means that combining predictions from many models can help make the whole system more stable by making up for the flaws of each model. The Xception model, on the other hand, was only 79% accurate in telling the difference between Monkeypox and measles. This shows that there is a lot of overlap between these two illnesses and that it is hard to tell the difference between skin manifestations that look identical. MobileNetV2 did a great job of telling the difference between Monkeypox and normal skin, getting 96% right. This shows that it works well when the variations between classes are more obvious. But the LeNet model only got 80% accuracy in the hard Monkeypox vs. all category, where the dataset was quite unbalanced. This highlights a significant finding from the study: imbalanced datasets diminish model performance by skewing predictions towards the majority class, thereby restricting generalisation capacity. Despite these difficulties, the overall results show that pre-trained models can still find Monkeypox with a high level of accuracy, even with short datasets. The study also stresses that adding more photos, especially from classes that aren't well represented, can make detection far more reliable. This work provides useful insights for creating accurate, accessible, and fast primary screening methods for Monkeypox by using majority voting and looking at how models behave in different situations.

Acknowledgement: The authors extend their profound appreciation to Northumbria University, Shahjalal University of Science and Technology, and the University of Barishal for their indispensable institutional support and intellectual enrichment, which substantially facilitated the fruition of this scholarly endeavour.

Data Availability Statement: Data underlying this study are available from the corresponding author upon reasonable request and in accordance with applicable ethical and institutional regulations.

Funding Statement: This research and manuscript were undertaken without any external financial assistance, institutional grants, or sponsorship of any form.

Conflicts of Interest Statement: The authors affirm that no financial, personal, or academic conflicts of interest influenced the conception, execution, or reporting of this study.

Ethics and Consent Statement: This study adhered strictly to established ethical frameworks and received approval from the competent institutional review board, with informed consent duly obtained from all participants prior to their engagement.

References

1. A. Kareem, H. Liu, and P. Sant, "Review on pneumonia image detection: A machine learning approach," *Human-Centric Intell. Syst.*, vol. 2, no. 5, pp. 1–13, 2022.
2. A. Krizhevsky, I. Sutskever, and G. E. Hinton, "ImageNet classification with deep convolutional neural networks," *Advances in Neural Information Processing Systems*, vol. 25, no. 6, pp. 84-90, 2012.
3. C. Sitaula, A. Basnet, A. Mainali, and T. B. Shahi, "Deep learning-based methods for sentiment analysis on Nepali COVID-19-related tweets," *Comput. Intell. Neurosci.*, vol. 2021, no. 1, pp. 1-11, 2021.
4. C. Szegedy, V. Vanhoucke, S. Ioffe, J. Shlens, and Z. Wojna, "Rethinking the inception architecture for computer vision," in *Proc. IEEE Conf. Comput. Vis. Pattern Recognit.*, Las Vegas, Nevada, United States of America, 2016.
5. Centers for Disease Control and Prevention (CDC), "Monkeypox in the U.S.," *CDC*, 2022. Available: https://www.cdc.gov/poxvirus/monkeypox/if-sick/treatment.html. [Accessed by 29/09/2024].
6. E. I. Zacharaki, S. Wang, S. Chawla, D. S. Yoo, R. Wolf, E. R. Melhem, and C. Davatzikos, "Classification of brain tumor type and grade using MRI texture and shape in a machine learning scheme," *Magn. Reson. Med.*, vol. 62, no. 6, pp. 1609–1618, 2009.
7. F. Chollet, "Xception: Deep learning with depthwise separable convolutions," in *Proc. IEEE Conf. Comput. Vis. Pattern Recognit. (CVPR)*, Honolulu, Hawaii, United States of America, 2017.
8. G. Huang, Z. Liu, L. van der Maaten, and K. Q. Weinberger, "Densely connected convolutional networks," in *Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition (CVPR)*, Honolulu, Hawaii, United States of America, 2017.
9. H. Lee, S. Eum, and H. Kwon, "Is Pretraining Necessary for hyperspectral image classification?" *IGARSS 2019 - 2019 IEEE International Geoscience and Remote Sensing Symposium*, Yokohama, Japan, 2019.
10. J. Deng, W. Dong, R. Socher, L. -J. Li, K. Li, and L. Fei-Fei, "ImageNet: A large-scale hierarchical image database," *2009 IEEE Conference on Computer Vision and Pattern Recognition*, Miami, Florida, United States of America, 2009.
11. J. Huang and C. X. Ling, "Using AUC and accuracy in evaluating learning algorithms," *IEEE Trans. Knowl. Data Eng.*, vol. 17, no. 3, pp. 299–310, 2005.
12. J. Legrand, C. Viboud, P. -Y. Boelle, A. -J. Valleron, and A. Flahault, "Modelling responses to a smallpox epidemic taking into account uncertainty," *Epidemiology and Infection*, vol. 132, no. 1, pp. 19–25, 2004.
13. K. He, X. Zhang, S. Ren, and J. Sun, "Deep residual learning for image recognition," in *Proc. IEEE Conf. Comput. Vis. Pattern Recognit.*, Las Vegas, Nevada, United States of America, 2016.
14. K. Simonyan and A. Zisserman, "Very deep convolutional networks for large-scale image recognition," *arXiv preprint*, 2014. Available: https://arxiv.org/abs/1409.1556 [Accessed by 14/09/2024].
15. L. Jakaite, V. Schetinin, and C. Maple, "Bayesian assessment of newborn brain maturity from two-channel sleep electroencephalograms," *Comput. Math. Methods Med.*, vol. 2012, no. 1, p. 123456, 2012.
16. M. Ahsan, M. R. Uddin, and S. A. Luna, "Monkeypox image data collection," *arXiv preprint*, 2022. Available: https://arxiv.org/abs/2206.01774 [Accessed by 23/09/2024].
17. M. Ahsan, M. R. Uddin, M. Farjana, A. N. Sakib, K. A. Momin, and S. A. Luna, "Image data collection and implementation of deep learning-based model in detecting monkeypox disease using modified VGG16," *arXiv preprint*, 2022. Available: https://arxiv.org/abs/2206.01862 [Accessed by 10/09/2024].
18. M. M. Hassan, M. A. Mamun Billah, M. M. Rahman, S. Zaman, M. M. Hasan Shakil, and J. H. Angon, "Early Predictive Analytics in Healthcare for Diabetes Prediction Using Machine Learning Approach," *2021 12th International Conference on Computing Communication and Networking Technologies (ICCCNT)*, Kharagpur, India, 2021.
19. M. Sandler, A. Howard, M. Zhu, A. Zhmoginov, and L. -C. Chen, "MobileNetV2: Inverted Residuals and Linear Bottlenecks," *2018 IEEE/CVF Conference on Computer Vision and Pattern Recognition*, Salt Lake City, Utah, United States of America, 2018.
20. N. Nyah, L. Jakaite, V. Schetinin, P. Sant, and A. Aggoun, "Evolving polynomial neural networks for detecting abnormal patterns," *2016 IEEE 8th International Conference on Intelligent Systems (IS)*, Sofia, Bulgaria, 2016.
21. R. Saha, A. Roy Chowdhury, and S. Banerjee, "Diabetic retinopathy related lesions detection and classification using machine learning technology," in *Proceedings of the International Conference on Artificial Intelligence and Soft Computing*, Zakopane, Poland, 2016.

22. R. Sandeep, K. P. Vishal, M. S. Shamanth, and K. Chethan, “Diagnosis of visible diseases using CNNs,” in *Proc. Int. Conf. Commun. Artif. Intell.*, Singapore, 2022.
23. T. B. Shah, C. Cataula, A. Nepean, and W. Goo, “Fruit classification using attention-based MobileNetV2 for industrial applications,” *PLoS ONE*, vol. 17, no. 2, p. e0264586, 2022.
24. UK Health Security Agency, “Monkeypox: Background Information,” GOV.UK, 2018. Available: https://www.gov.uk/guidance/monkeypox [Accessed by 18/09/2024].
25. V. Schetinin, L. Jakaite, and W. Krzanowski, “Bayesian learning of models for estimating uncertainty in alert systems: Application to air traffic conflict avoidance,” *Integr. Comput.-Aided Eng.*, vol. 25, no. 3, pp. 229–245, 2018.
26. World Health Organization, “Public health response to biological and chemical weapons: WHO guidance,” *World Health Organization*, Geneva, Switzerland, 2004. Available: https://www.who.int/publications/i/item/public-health-response-to-biological-and-chemical-weapons-who-guidance-(2004) [Accessed by 09/09/2024].
27. Y. LeCun, L. Bottou, Y. Bengio, and P. Haffner, “Gradient-based learning applied to document recognition,” *Proc. IEEE*, vol. 86, no. 11, pp. 2278–2324, 1998.