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MRpoxNet: An enhanced deep learning approach for early detection of monkeypox using modified ResNet50

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Abstract

Objective: To develop an enhanced deep learning model, MRpoxNet, based on a modified ResNet50 architecture for the early detection of monkeypox from digital skin lesion images, ensuring high diagnostic accuracy and clinical reliability.

Methods: The study utilized the Kaggle MSID dataset, initially comprising 1156 images, augmented to 6116 images across three classes: monkeypox, non-monkeypox, and normal skin. MRpoxNet was developed by extending ResNet50 from 177 to 182 layers, incorporating additional convolutional, ReLU, dropout, and batch normalization layers. Performance was evaluated using metrics such as accuracy, precision, recall, F1 score, sensitivity, and specificity. Comparative analyses were conducted against established models like ResNet50, AlexNet, VGG16, and GoogleNet.

Results: MRpoxNet achieved a diagnostic accuracy of 98.1%, outperforming baseline models in all key metrics. The enhanced architecture demonstrated superior robustness in distinguishing monkeypox lesions from other skin conditions, highlighting its potential for reliable clinical application.

Conclusion: MRpoxNet provides a robust and efficient solution for early monkeypox detection. Its superior performance suggests readiness for integration into diagnostic workflows, with future enhancements aimed at dataset expansion and multimodal adaptability to diverse clinical scenarios.

Keywords

Monkeypox, deep learning, machine learning, CNN, MRpoxNet, image processing, pandemic, multi-classification

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Introduction

One of the viruses that started to create concern in numerous regions after the COVID-19 pandemic is the monkeypox virus, which has recently surfaced. Although formerly well-known and mostly observed in western and central Africa, the virus has recently started to affect other human populations differently. People get the monkeypox virus from infected animals, which is present in the bodies of rats and other animals.[1] Previously, the disease was limited to certain areas, and instances were linked to families because to the limited transmission from wild animals to humans and the necessity for intense and extended contact for human-to-human communication. The virus that causes monkeypox is a member of the Orthopoxvirus genus and family of Poxviridae. The variola virus causes smallpox, the cowpox virus causes

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cowpox, and the vaccine virus is used to make the vaccination against smallpox. Despite the name "monkeypox," the virus that causes the disease. Animals such as rats are where it all starts.[2] The virus was first identified in 1958 following two separate outbreaks of a smallpox-like disease in caged monkey colonies, leading to its name, monkeypox.

Humans can get the monkeypox virus via an infected animal or from an affected individual. The infectious agent that causes monkeypox has an incubation period following exposure, as is the case with many viruses. Symptoms typically appear between five and twenty-one days after infection. Monkeypox most commonly affects children aged six months to one year. Although the symptoms are similar to smallpox, the disease follows a different course. Common symptoms include fever, headaches, back pain, muscle aches, swollen lymph nodes, fatigue, and skin lesions that resemble small, fluid-filled blisters, similar to chickenpox.[3] The rash develops between one and five days following the onset of the first monkeypox symptoms. The face is usually where the first rashes show up. Other bodily parts then get infected with the illness. Some people may also develop lesions in the oral mucosa, eyes, or vagina. The sickness might be confused for chickenpox because of the rashes' resemblance. Eventually, the rash starts to heal and takes on crusty patches. There may be fewer blisters in some people's lesions, or hundreds of blisters dispersed over the body in others. The rashes usually go away and the patient heals in two to four weeks, depending on the severity of the illness. Monkeypox has a death rate of three to six percent.[4] Unfortunately, there is not a specific drug or vaccine to prevent the monkeypox virus. Treatment for monkeypox primarily focuses on managing symptoms and providing supportive care. In some cases, antiviral medications are used for other orthopoxvirus.[5] A test for skin lesions using the polymerase chain reaction, or PCR test, is also a time-consuming method of electron microscopy for a lengthy period to identify pox.[6] The inadequate accessibility of polymerase chain reaction (PCR) test kits and the stringent specifications for laboratory environments in research centers will cause a delay in the precise identification of those under suspicion.[7] Because monkeypox lesions resemble those of otherpox infections, it can be difficult to identify monkeypox lesions and results in incorrect diagnoses. Furthermore, the clinical appearance of monkeypox lesions may be unknown to medical staff, which might further impede appropriate diagnosis. Furthermore, there is a chance that patients and medical personnel may get monkeypox via physical tests used to identify the illness. In accordance with a previous study,[8] a patient suspected of having monkeypox should be placed in isolation. In addition to these, the monkeypox virus is now spreading over a number of nations. Disease detection is therefore crucial. Artificial intelligence (AI) has applications in the diagnosis of illnesses, particularly those that are contagious. Artificial intelligence has made it possible to learn about the illness without visiting a laboratory or hospital.[9] Deep learning (DL) techniques have developed as a potent tool for image analysis and pattern identification and have shown promise for application in the diagnosis of various illnesses. AI in image processing has become a modern technology in recent times. DL is a branch of machine learning (ML) that leverages many layers of artificial neural Networks (ANNs) to identify patterns and generate predictions from images. Convolutional Neural Networks (CNNs) are a type of DL algorithm that have been effectively used in many medical imaging applications, such as lung nodule identification, cancer detection, and skin lesion categorization.[6] Even though medical images offer a thorough perspective, mistakes can still happen when diagnosis takes too long because of the huge images. DL techniques might be used to increase the diagnostic accuracy of monkeypox in order to overcome this problem. It is important to employ investigative and classification techniques, such as DL algorithms, in order to make well-informed judgments and avoid misdiagnosis. Medical image analysis has also made good use of transfer learning, which is the process of starting a new task with a pre-trained technique for a different task. Inference from images is made possible by deep convolutional neural Networks (DCNNs). This process treats a wide range of illnesses. This paper aims to develop a deep CNN that is efficient in detecting monkeypox. DCNN enables inference from images. A lot of disorders are treated with this procedure. The goal of this article is to create an effective deep CNN for the detection of monkeypox.[10] Deep CNNs may be created in a variety of ways which achieve accuracy above 90% but the limitation is the lack of available data and clarity of disease. So, the primary research questions based on the research are as follows:

1. How can we improve deep learning techniques to better detect monkeypox from skin images?
2. What impact does changing the ResNet50 technique have on detecting monkeypox?
3. How does the MRpoxNet technique perform compared to other techniques like VGG16 and AlexNet in detecting monkeypox?
4. How do image preprocessing and data augmentation help in training better techniques for monkeypox detection?
5. How does the size and quality of the dataset affect the success of deep learning techniques in identifying monkeypox?

This paper's primary research contributions can be summed up as follows:

- The proposed technique, "MRpoxNet," is a sequential neural technique comprising convolution layers, batch normalization, dropout, and fully connected layers,

designed to detect monkeypox at an early stage—even with a single lesion in an image.
- Feature extraction in MRpoxNet begins with max-pooling layers to reduce the dimensionality of feature maps, followed by a series of convolutional layers to increase depth and further reduce spatial dimensions.
- A sigmoid activation function is utilized in the final output layer to facilitate efficient multi-class classification in monkeypox detection.
- Extensive pre-processing and data augmentation expanded the dataset to 6116 images, each with dimensions of $224 \times 224 \times 3$, significantly enhancing the model's performance.
- Compared with existing state-of-the-art techniques, the proposed MRpoxNet achieves superior accuracy, precision, recall, and F1-score.

Literature review

A. Akram et al. presented a new classification technique to classify lesions from monkeypox, utilizing data augmentation techniques and a framework named "SkinMarkNet." The skin lesion images that were gathered from the Kaggle data repository for this study's dataset included a range of lesion characteristics and demographics. The lack of labeled data is addressed in this study by employing image data augmentation techniques. The training dataset is enhanced by this augmentation, which raises the technique's effectiveness. Furthermore, the innovative aspect of this research is the use of three well-known techniques—Inception, Xception, and ResNet—for ensemble learning and feature extraction. In recent research studies, SkinMarkNet has demonstrated impressive results, outperforming classic ML and DL methods with an accuracy of 90.615% for monkeypox lesion categorization. Furthermore, a comprehensive comparative study is conducted using modern methodologies and ML techniques to confirm the effectiveness of the suggested technique. Overall, the results highlight how better monkeypox lesion categorization can be achieved by utilizing sophisticated DL architectures and data augmentation techniques. This will help with early diagnosis and intervention in clinical settings as well as public health surveillance initiatives.[11]

M. Velu et al. highlighted the global health threat posed by monkeypox, noting the increasing daily cases reported across numerous countries. This research proposes two ways to increase the precision of monkeypox image classification: Multi-layer neural technique parameter tweaking and reinforcement learning. The proposed methods were based on feature extraction and classification; the machine learning techniques are binary proposed algorithms that improve neural technique parameters; the Q-learning algorithm determines the rate at which an act occurs under a particular condition. The algorithms showed 95% recall, 95% accuracy, and 96% f1 scores for monkeypox sickness using a readily available dataset. The best accuracy (about 0.985) was shown by the machine learning technique in comparison to conventional learning techniques. This idea may be used by physicians to treat cases of monkeypox, and by government agencies to monitor the disease's present state and historical trends. In the future, clinics and hospitals may employ transfer learning techniques, larger datasets, and CNN techniques based on Generative Adversarial Networks (GANs).[12]

A. K. Mandal et al. utilized the core principles of particle swarm optimization (PSO), focusing on exploration and exploitation, to identify images for monkeypox viral detection and prediction. The study employed the International Skin Imaging Collaboration (ISIC) images for testing and analysis. Four pre-trained deep-learning techniques are compared with the proposed technique PSOMPX for detecting viruses that cause monkeypox: VGG16, ResNet50, InceptionV3, and Ensemble. The technique outperforms other techniques because of its numerous features, with a total accuracy of 90.01% (F1-Score: 85.87%). The proposed methods enhance the recognition accuracy of monkeypox cases in images by employing a hidden Markov technique, digital image processing techniques, particle swarm optimization for image segmentation, and GLCM-SVM classifier.[13]

M. H. Ariansyah et al. employed an image classification technique for distinguishing between the illnesses of monkeypox and measles. To simulate the illness, they applied DL with CNN architecture and VGG-16 transfer learning. The VGG-16 technique provides great accuracy, with an epoch 15 accuracy of 83.333%. The voting classifier method might be used in future research to improve the technique's performance. The technique intends to help in health system planning and administration, medicine, and epidemiology research by facilitating the diagnosis, treatment, monitoring, and management of measles and monkeypox illnesses.[14]

R. Pramanik et al. offered an ensemble learning-based method for identifying the monkeypox virus in images of skin lesions. The system assesses InceptionV3, Xception, and DenseNet169, three pre-trained deep learners, and calculates probability from these techniques. The outcomes were incorporated into an ensemble and beta function-based normalizing technique. A five-fold cross-validation setup was used to evaluate the system on a dataset that was available to the general public. The technique gets average scores of 93.3%, 88.9%, 96.7%, and 92.3% for evaluation metrics. Early discovery and treatment were essential for the present monkeypox outbreak, which poses a serious danger to civilization. In order to improve diagnosis, the research attempts to increase the data size utilizing the most recent DL-based techniques and attention-based techniques. This whole solution may be taken into account for deployment in real-time.[15]

H. Iftikhar et al. presented research highlighting the rising number of new cases and fatalities from the mpox virus (MPV) as a major public health concern. To mitigate its impact, a hybrid forecasting system has been developed using the world's daily cumulative confirmed and death series. The system was decomposed into two subseries, a trend component and a stochastic series using the Hodrick-Prescott filter. Comparative analysis with benchmark models like AR, ARMA, NPAR, and ANN was performed. The new hybrid models, HPF-1 and HPF-4, demonstrated superior performance in key performance indicators. The models can be used to forecast other diseases in the future. Governments and stakeholders must ensure strict adherence to standard operating procedures to mitigate the outbreak's impact.[16]

Wilfredo Meza Cuba et al. presented a time-series ensemble technique in this study to analyze and forecast the spread of monkeypox in four highly affected countries. The approach involves processing the first cumulative confirmed case time series, addressing variance stabilization, normalization, stationarity, and a nonlinear secular trend component. The accuracy of the models is evaluated using typical accuracy mean errors, graphical evaluation, and an equal forecasting accuracy statistical test. The approach can be used to forecast other diseases in the future.[17]

H. Iftikhar et al. presented another paper that employed filtering and combination techniques for accurate short-term forecasts of infected monkeypox cases. The method filters

Table 1. Description of dataset.

Class	Description	Image size	Source of data
Monkeypox	279 monkeypox lesion images	224*224*3	Kaggle repository [17]
Non-monkeypox	107 chickenpox and measles images	224*224*3	[17]
Normal skin	770 normal and healthy skin images	224*224*3	[17]

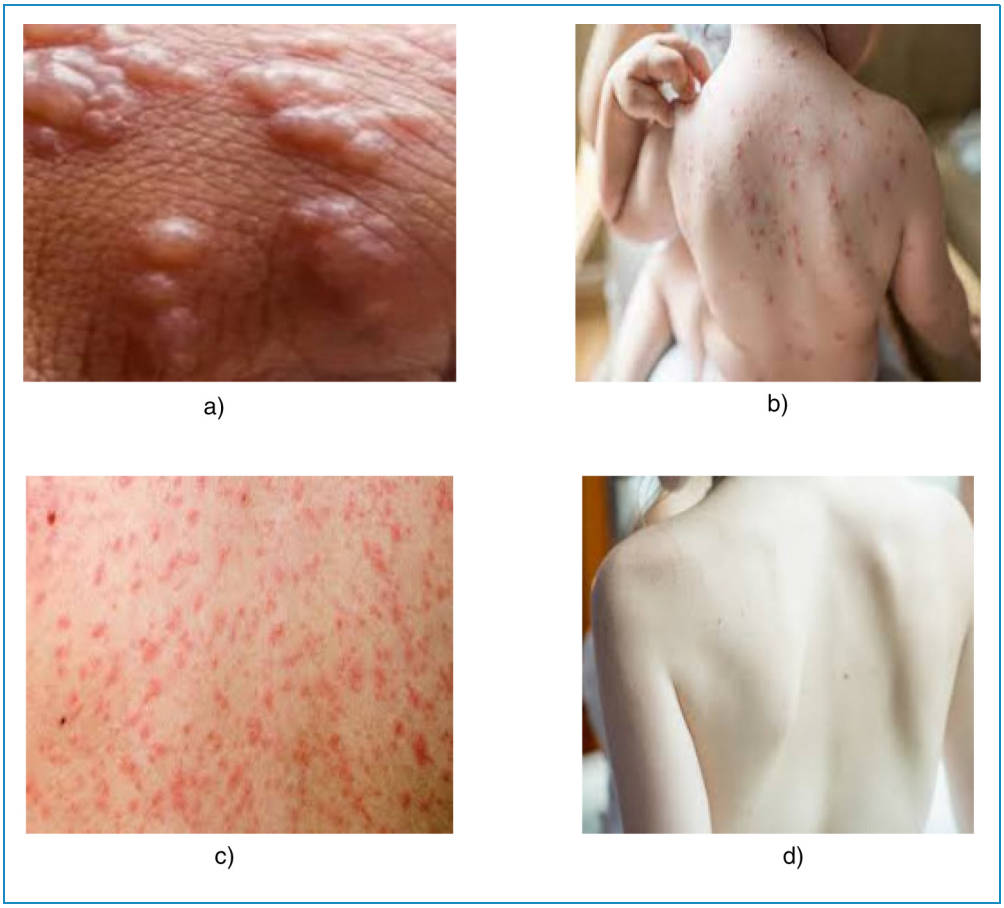

Figure 1. Samples from images of dataset: (a) monkeypox, (b) chickenpox, (c) measles/acne, and (d) normal skin.

the original time series into long-term trends and residual series, and then predicts the filtered subseries using five standard machine learning models and their possible combination models. The method achieves a forecast of 14 days, enabling early detection of the spread and risk, enabling timely and effective treatment. The approach is tested using four different time series and five different machine learning models.[18]

The literature highlights several promising approaches for detecting, classifying, and forecasting monkeypox cases. A. Akram introduced "SkinMarkNet," a framework that leverages data augmentation and ensemble learning using Inception, Xception, and ResNet models to achieve 90.615% accuracy in lesion classification, surpassing traditional methods. M. Velu et al. suggested enhancing monkeypox image classification through multi-layer neural technique optimization and reinforcement learning, achieving 95% recall, 95% accuracy, and a 96% F1 score. A. K. Mandal et al. employed particle swarm optimization (PSO) principles for detecting and predicting monkeypox, with their PSOMPX model demonstrating superior performance due to its feature set. Additionally, H. Iftikhar et al. developed a hybrid model for forecasting daily global cases and deaths, while Wilfredo Meza Cuba et al. proposed a time-series ensemble technique to analyze and predict monkeypox spread in four severely affected countries. Building on this foundation, our research will explore further advancements in classification accuracy, feature extraction, and forecasting capabilities for more effective monkeypox detection and monitoring.

Methodology

This paper uses the Monkeypox dataset together with additional datasets of pox images in an attempt to categorize illnesses using DL architectures. Recently, DL architectures—a subfield of ML—have gained a lot of popularity and are frequently employed. CNN architectures, a subfield of DL, were employed in this investigation. CNN architectures have been compared with the developed technique.[19] The next part looks at the layers, the created method's structure, and the data sets that were employed.

Data collection

The "Monkeypox skin images dataset" (MSID), kaggle repository is a publicly available source from which data for this study were gathered. This research is a computational, experimental study aimed at developing a deep learning-based model for monkeypox detection using digital skin lesion images. The study was conducted remotely at Chitkara University, Punjab, India, over six months (August 2023 to February 2024). Data collection, preprocessing, model development, training, and evaluation were performed entirely on datasets obtained from online open-source repositories. Two classes—Monkeypox and Non-Monkeypox (normal and otherpox)—included in the dataset are utilized for binary classification. Images labeled as monkeypox, non-monkeypox (including chickenpox, measles, and other skin conditions), and normal skin were included to ensure comprehensive representation. Images with sufficient resolution (minimum 224×224 pixels) to enable accurate feature extraction were selected. Only datasets that were publicly available and licensed for research use were included. Images with incomplete metadata or ambiguous labeling were excluded. Low-resolution images ($<224 \times 224$ pixels) and those with significant artifacts or obstructions were removed to maintain data quality. Duplicate images were eliminated to avoid data redundancy and bias during model training. There are skin images of 279 monkeypox lesions in the Monkeypox class. However, there are 877 skin images of non-monkeypox lesions in the Non-Monkeypox class (including normal skin and otherpox images).[20] Table 1 displays a thorough description of the data. A visual depiction of the dataset's image distribution is shown in Figure 1, which also shows the ratio of images with monkeypox lesions to those without them. These data offer important insights into the dataset utilized for training and assessment in the work, as it is essential for comprehending the makeup of the dataset and the relative representation of various lesion types.

Data preprocessing

This stage is critical to the DL technique because it guarantees that the input data are prepared correctly for technique training, which improves technique accuracy. This stage involves feeding the acquired data into the technique after it has undergone six pre-processing steps. Pre-processing processes include label encoding, data_format setting, rescaling the pixel value, in-place

Table 2. Despription of images.

Class	Types of images	Image size	No of augmented images
Monkeypox	279 monkeypox lesion images	224*224*3	1476
Non-monkeypox	107 chicken pox images	224*224*3	566
Normal skin	770 normal and healthy skin images	224*224*3	4074

augmentation, resizing images to uniform sizes, and data.[21] This section describes each step in the pre-processing process.

Resizing the image. Resizing an image involves either up-sampling or down-sampling it. The dataset's images need to be the same size as the CNN technique.

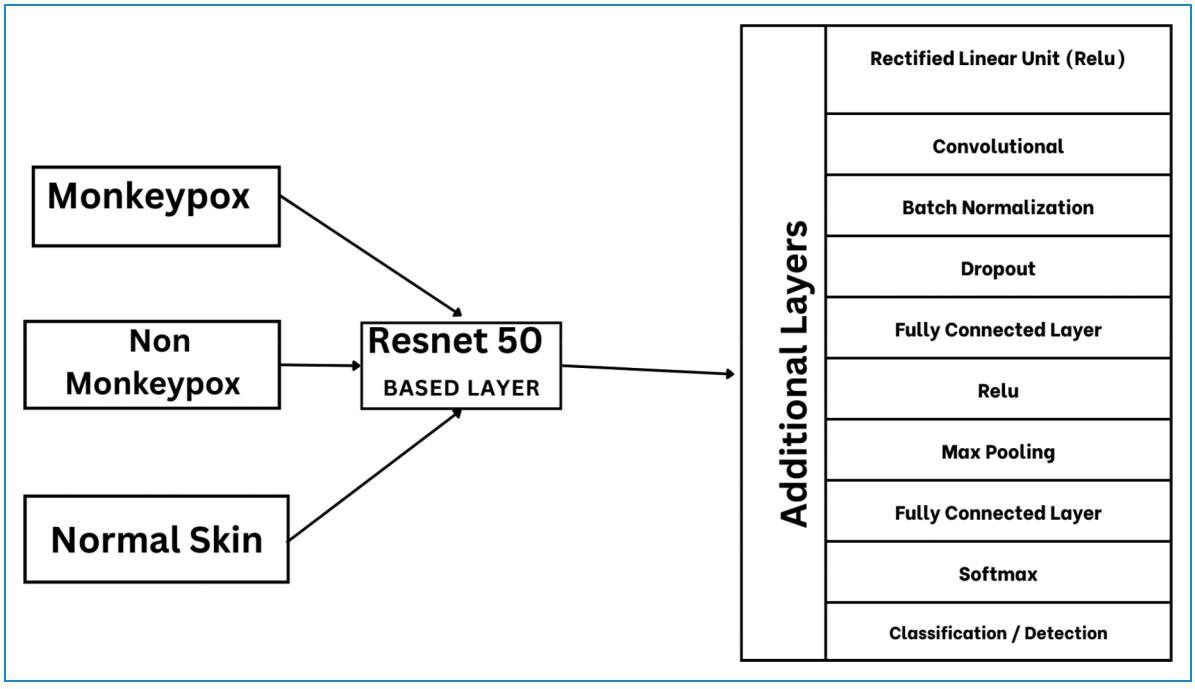

Figure 2. Architecture of the proposed technique.

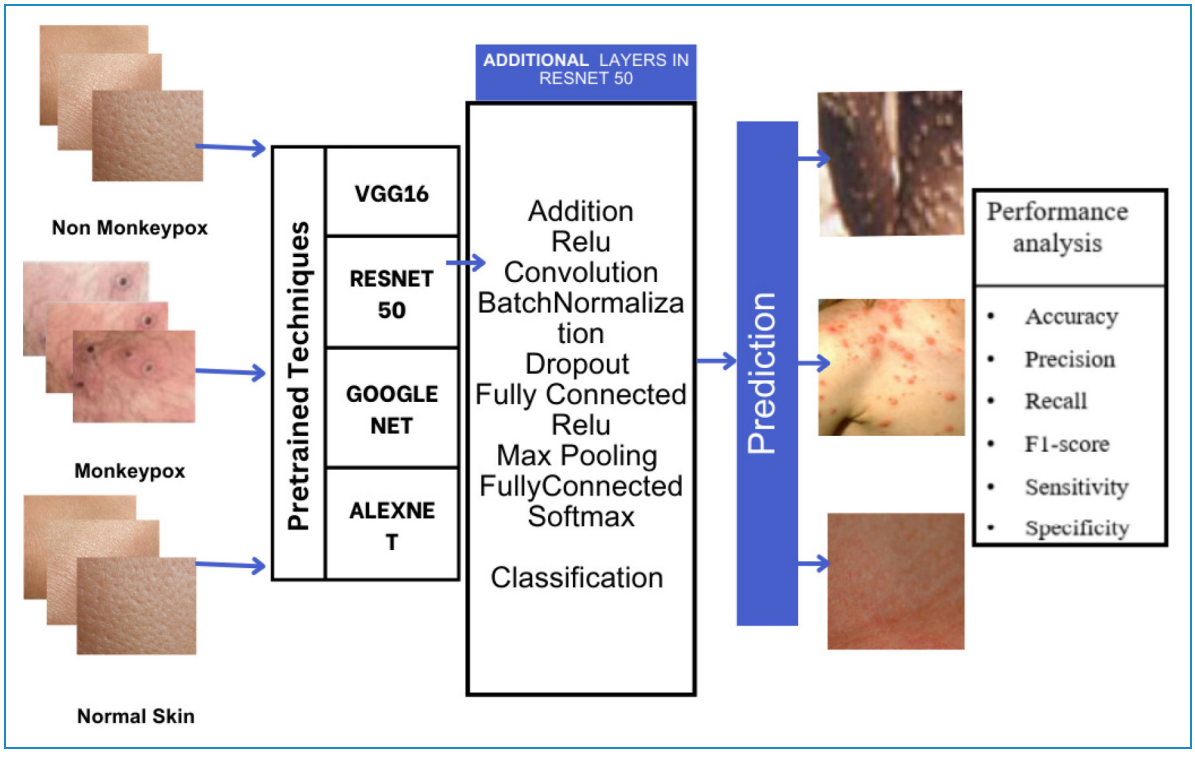

Figure 3. Flow diagram of the proposed technique.

Table 3. Properties of layers used in proposed technique.

	Layers	Type	Dimension
1	Image_input	Input	224 × 224 × 3
2	conv_1	Convolution	112 × 112 × 64
172	additional_16	Addition	7 × 7 × 2048
173	relu	Relu	7 × 7 × 2048
174	convo_2	Convolution	7 × 7 × 32
175	batch	BatchNormalization	7 × 7 × 32
176	d_out	Dropout	7 × 7 × 32
177	fullyc_1	Fully Connected	1 × 1 × 2
178	dimension	Relu	1 × 1 × 2
179	max_pooling	Max Pooling	1 × 1 × 2
180	fullyc_2	FullyConnected	1 × 1 × 2
181	fullyc_softmax	Softmax	1 × 1 × 2
182	output	Classification	-

Table 4. Attributes of proposed technique, i.e., "MRpoxNet."

Attribute	Parameters using Stochastic Gradient Descent with Momentum(SGDM)
Max_Epochs	4
MiniBatchSize	10
Shuffle Validation	every-epoch
Frequency	6
InitialLearnRate	1.000e-04
Total Iteration	172

Therefore, the purpose of these phases is to guarantee that every image has the same size. Additionally, this step is utilized to lessen the computational load of the technique's training. This is made possible with the help of the TensorFlow Keras preprocessing module for Python. In this investigation, the image's size is fixed 224*224*3 was chosen as the image size is that it provides for improved performance, quicker convergence, and more precise training of the technique.[22]

Rescaling. Normalizing the image data to a specified range of 0 to 1 is known as rescaling. The pixel values of images may be changed from the native range of 0 to 255 to the required range of 0 to 1, which is more suited for neural technique techniques, using the ImageDataGenerator class. Pixel values vary across distinct images. The technique only sees certain images if the rescaling process is not used, which causes overfitting. During the training process, this procedure makes sure that every image is given the same weight and value. To execute this procedure, an escale parameter has been applied, which multiplies each pixel by a predetermined ratio in order to obtain the required scaling. In this case, the pixel values are rescaled using a ratio of 1/255, or around 0.0039.[23]

Data format. The study's data format indicates that the input tensor's last dimensions are channels. The image is shown in this style as a 3D tensor that correlates to (height, width, and channels). Within frameworks for DL such as TensorFlow and In Keras, this format serves as the default value. While during training, in assessing the technique, this format guarantees consistency, effective data manipulation, and calculation.[24]

Data augmentation. Random image changes carried out using in-place data augmentation have been implemented in this pre-processing step, meaning that the dataset size does not grow. Augmented data are driven from original data with some minor changes. In the case of image augmentation, we make geometric and color space transformations (flipping, resizing, cropping, brightness, and contrast) to increase the size and diversity of the training set throughout each epoch during training, and each iteration, capturing new patterns and characteristics. ImageDataGenerator is a Keras image preprocessing library that is used to alter the image. The ImageDataGenerator function offers several image modification operations, such as brightness range, zoom range, horizontal flip, and more.[25] In general, evenly split and bias-free datasets yield superior results in implementation of CNN techniques for the detection of monkeypox. To obtain a diverse and extensive dataset for experimental assessment, the Kaggle MSID (Monkeypox Skin Image Dataset), which contains 1,156 images, was used as a benchmark for monkeypox detection. Through data augmentation, the total number of images was increased to 6,116. The number of augmented images increased to 6116. These images were then further divided into three categories i.e., monkeypox, non-monkeypox (contains images from chickenpox, measles, and skin cancer) and normal images that are displayed in Table 2.

Table 5. Confusion matrix of the technique.

Class		Predicted class		
		Monkeypox	Otherpox	Normal skin
Actual class	Monkeypox	T	F	F
	Otherpox	F	T	F
	Normal skin	F	F	T

Table 6. Confusion matrix performance value after training for monkeypox detection.

Class	Predicted class		
	Monkeypox	Otherpox	Normal skin
Monkeypox	25	0	1
Otherpox	0	50	0
Normal skin	1	2	29

Table 7. Results of performance metrics for the proposed technique "MRpoxNet."

	Monkeypox	Otherpox	Normal skin
Accuracy (%)	98.1	98.1	96.3
F1 score (%)	96.3	98	93
Precision (%)	98	98	96
Sensitivity (%)	96.3	96.08	96.67
Specificity (%)	98.7	98	96.5

Proposed technique

The ResNet50 design served as the foundation for the proposed technique. The ResNet50 architecture's input layer has been modified to 224 * 224 * 3.[26] Afterwards, the input layer was changed, followed by the convolution layer. In the end, 10 additional layers were added to the ResNet50 design in place of the five previously removed levels. The ResNet50 technique's accuracy rate has grown as a result of the additional layers, because the ResNet50 architecture performs well in biomedical images, it served as the foundation for the proposed technique that was built. The ResNet50 design was chosen because it would result in a more efficient technique once it has been trained, as opposed to starting from scratch. This technique's current body of knowledge has been applied. Following the modifications to ResNet50, the number of layers increased from 177 to 182. The architecture and flow diagram of the proposed technique is shown in Tables 2 and 3.

Here, Figure 2 represents the architecture of the proposed technique where images of monkeypox, non-monkeypox and normal images used pretrained ResNet50; then, five layers of ResNet50 are deleted and 10 additional layers of ReLU are added, which are responsible for transforming the summed weighted input from the node into the activation of the node or output for that input-based layer; the next layer is the convolutional layer which can be generated by stacking the activation maps of every filter along the depth dimension; then, batch normalization is applied which improves the efficiency and reliability of neural techniques by normalizing the inputs of each layer. At the training time, a dropout layer randomly sets some input elements to zero and scales the remaining elements. This changes the technique architecture between iterations, making it harder for units to fix each other's mistakes. Dropout layers can be used with most types of neural techniques, including dense, fully connected, convolutional, and recurrent layers. They can be applied to any or all of the technique's hidden layers, as well as the visible or input layer, but not the output layer. Dropout layers can make a technique more robust by breaking apart circumstances in which technique tiers co-adapt to fix mistakes. Then, again ReLU is added and additional major benefits of ReLUs are sparsity and a reduced likelihood of vanishing the gradient. The first recall of the definition of a ReLU is shown in equation (1):

$$h = \max(0, a), \quad h = \max(0, a)$$

Where,

$$a = Wx + ba = Wx + b. \tag{1}$$

One major benefit is the reduced likelihood of the gradient to vanish. This arises when $a > 0a > 0$. In this regime, the gradient has a constant value. In contrast, the gradient of sigmoids becomes increasingly small as the absolute value of x increases. The constant gradient of ReLUs results in faster learning. The other benefit of ReLUs is sparsity. Sparsity arises when $a \leq 0a \leq 0$. The more such units that exist in a layer the more sparse the resulting representation. Sigmoids on the other hand are always likely to generate some non-zero value resulting in dense representations. Sparse representations seem to be more beneficial than dense representations. Then, max pooling is added In the process of max pooling, only the maximum value within a small window or region is selected as a representative, while discarding other

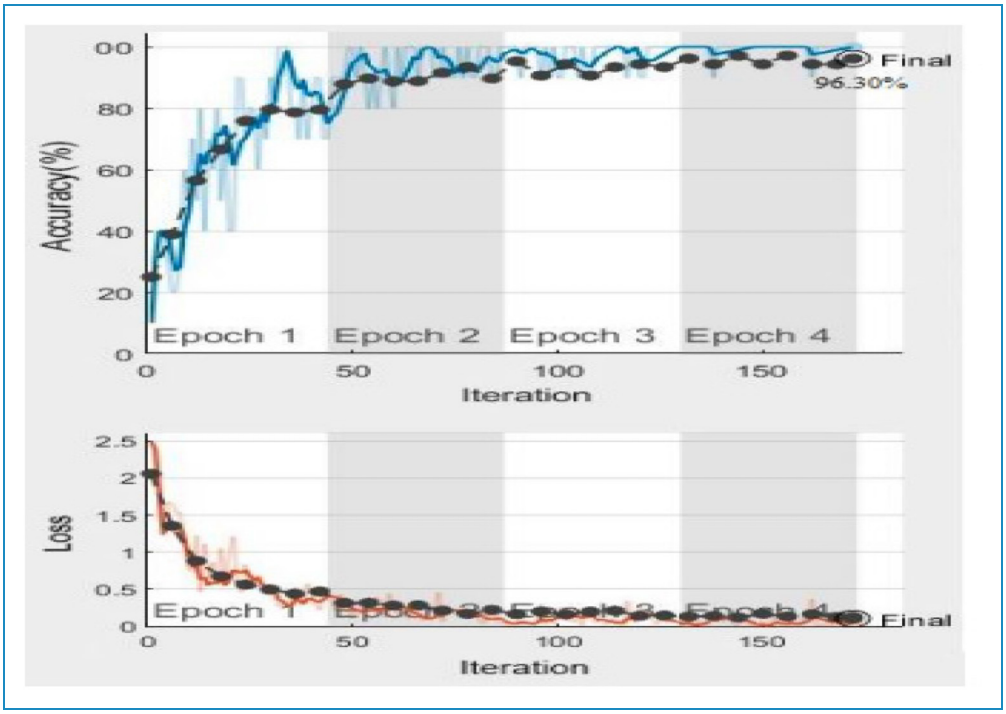

Figure 4. Accuracy and loss graphs for the proposed technique.

Table 8. Performance value of the ResNet.

	Monkeypox	Otherpox	Normal skin
Accuracy	97.1	95.1	92.5
F1 score	94.8	95	86
Precision	97	98	96
Sensitivity	92.3	92.08	92.67
Specificity	96.7	98	96.5

detailed information. This operation leads to partial information loss in the original data and reduces the accuracy of features. The mathematical expression of this method is shown as equation (2).[26,27]

$$\mathrm{Fmax}(x) = \max\{xi\}\ {}^{n}_{i=0} \tag{2}$$

where x is the value of the input image in the pooling region; then, the fully connected layer also contributes to regularization and technique capacity control. The large number of parameters in the fully connected layer enables the technique to learn complex representations, but it also increases the risk of overfitting. To mitigate this, regularization techniques such as dropout or L2 regularization can be applied to the fully connected layer, preventing the technique from relying too heavily on any single connection. Then, the softmax function converts a vector of numbers (an array of K values (z)) into a vector of probabilities, where the probabilities of each value are proportional to the relative scale of each value in the vector. It is thus a function that turns several numbers into quantities that can be perhaps interpreted as probabilities shown in equation (3):

$$f = \frac{e^{zk}}{\sum_{k=1}^{K} e^{zk}} \tag{3}$$

It is often used in the final, output layer of a neural technique, especially with classification problems. The last layer added is the classification layer and the detection layer that computes the cross-entropy loss for classification and weighted classification tasks with mutually exclusive classes. This layer infers the number of classes from the output size of the previous layer. Basically, in this process of analyzing an image and predicting its class or category, the model extracts features from the image to determine the most likely label from a set of predefined classes. The aim is to create a technique that can accurately recognize and classify scares of skin diseases in an image. Figure 3 presents the flow diagram of the proposed technique. The same additional layers are employed with pre-trained techniques like VGG16, Basic ResNet50, GoogleNet, AlexNet by using the same dataset images; then, by predicting its class, the performance is analyzed by calculating evaluation metrics like Accuracy, Precision, Recall, F1 score, sensitivity, and specificity. The results are then compared with those of the proposed technique.

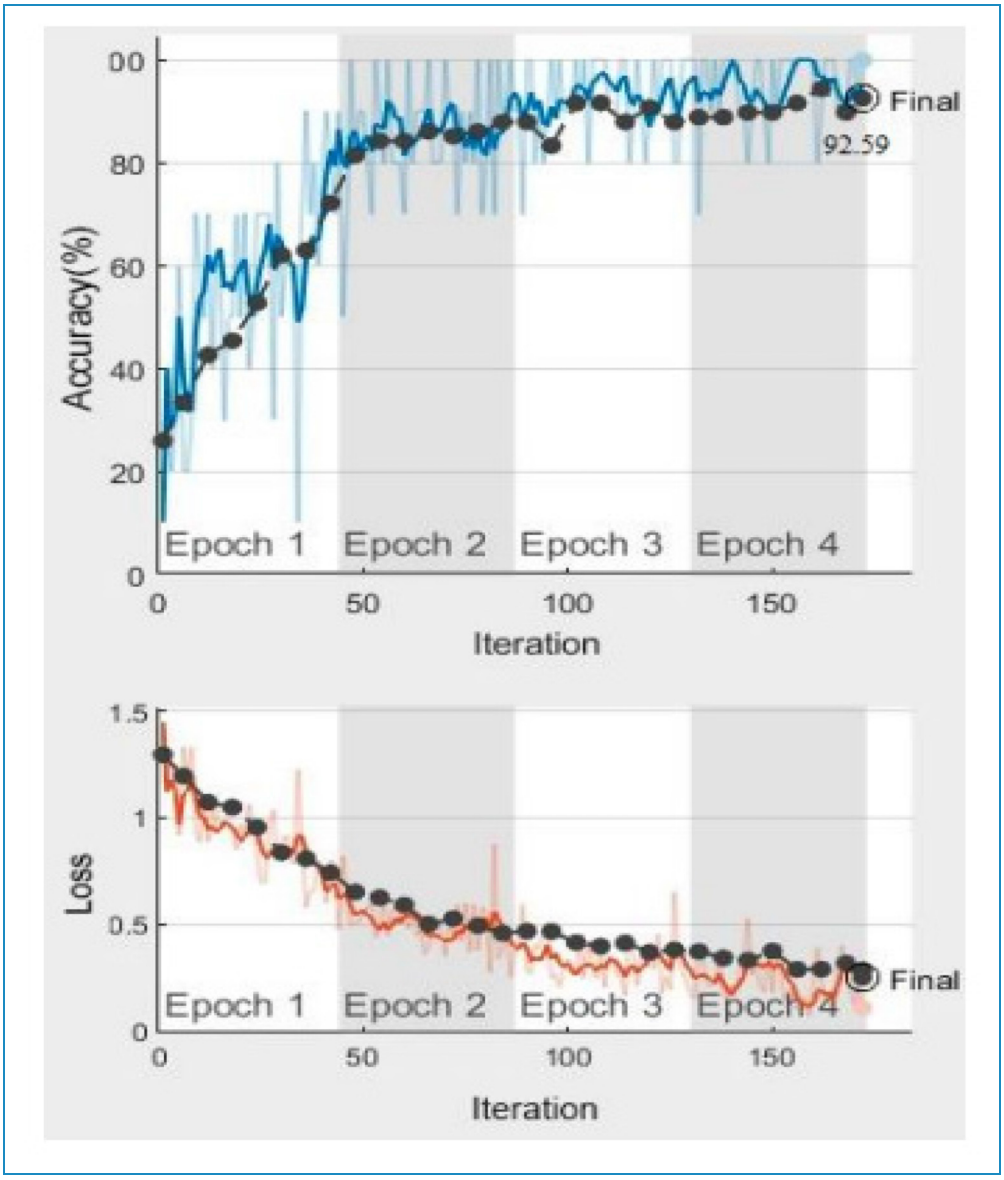

Figure 5. Accuracy and loss graphs for ResNet.

Table 9. Performance value of the GoogleNet.

	Monkeypox	Otherpox	Normal skin
Accuracy	98	92.1	90.5
F1 score	96.4	92	94
Precision	98	92	90
Sensitivity	93.3	85.08	90
Specificity	93	85	88.3

Table 3 depicts the layers with their types and also the dimensions of images at every layer.

Input layer. The generated proposed technique and other techniques start with this layer. The 224*224*3-sized input layer is where the images are first read from.[28] The proposed technique's and other techniques' input sizes are utilized in the application.

Convolutional layer. The input image is shrunk in this layer so that it fits inside the filter's size. In this layer, NxN size

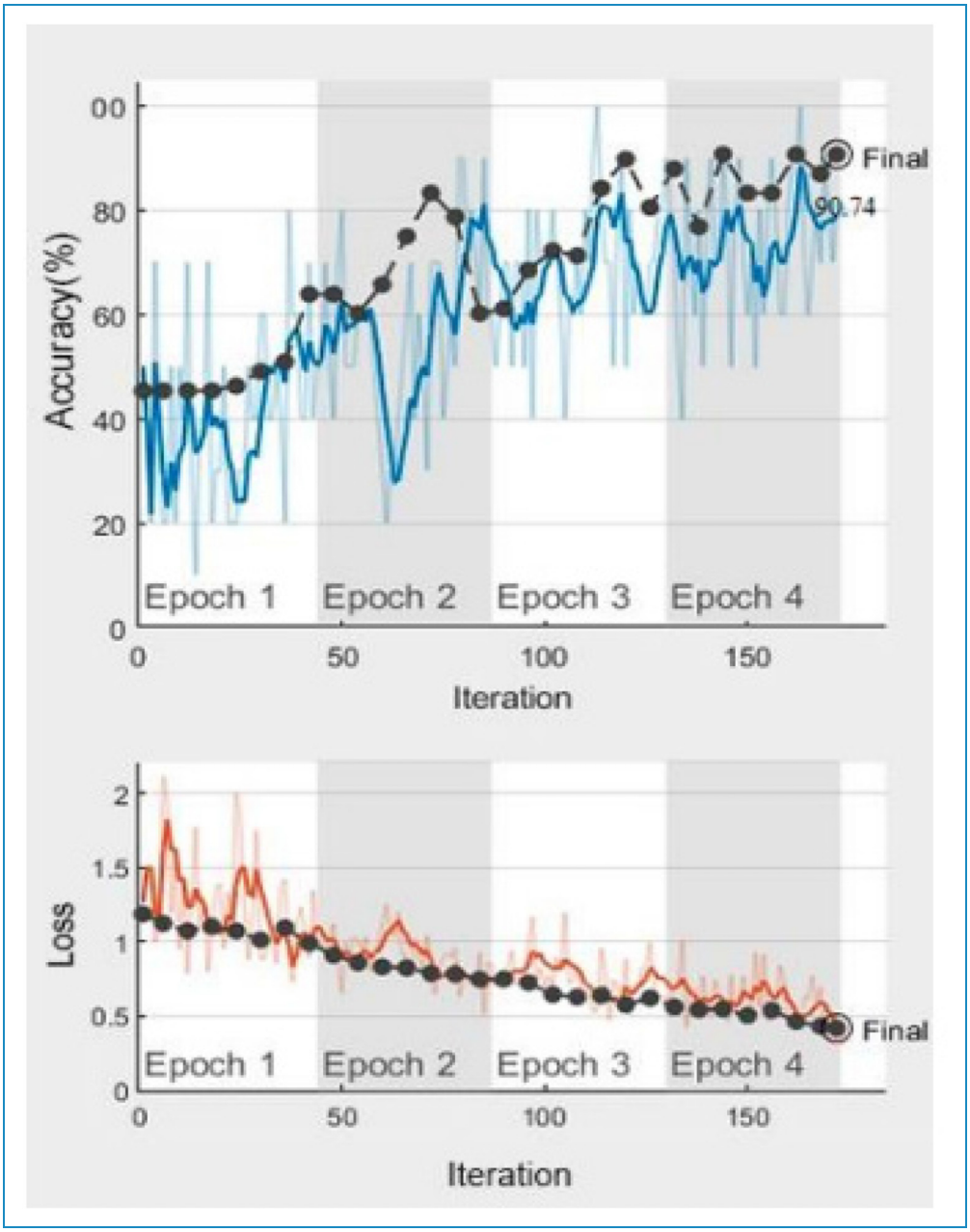

Figure 6. Accuracy and loss graph for GoogleNet.

Table 10. Performance value of the AlexNet.

	Monkeypox	Otherpox	Normal skin
Accuracy	95	93.1	92.5
F1 score	91.8	93.2	78
Precision	95	93	92
Sensitivity	84.3	88.8	95
Specificity	1	97.08	87.67

filters may be selected. Creating feature maps is a succinct way to describe this layer's goal.[29]

Dimension layer. In artificial neural techniques, activation functions are frequently chosen for nonlinear transformation operations. Numerous activation functions have been established in scholarly works. The most favored activation functions among them are Tanh, Sigmoid, and Relu. In the proposed technique created, Relu was given preference.[30] The usage of activation functions is common in DL techniques.

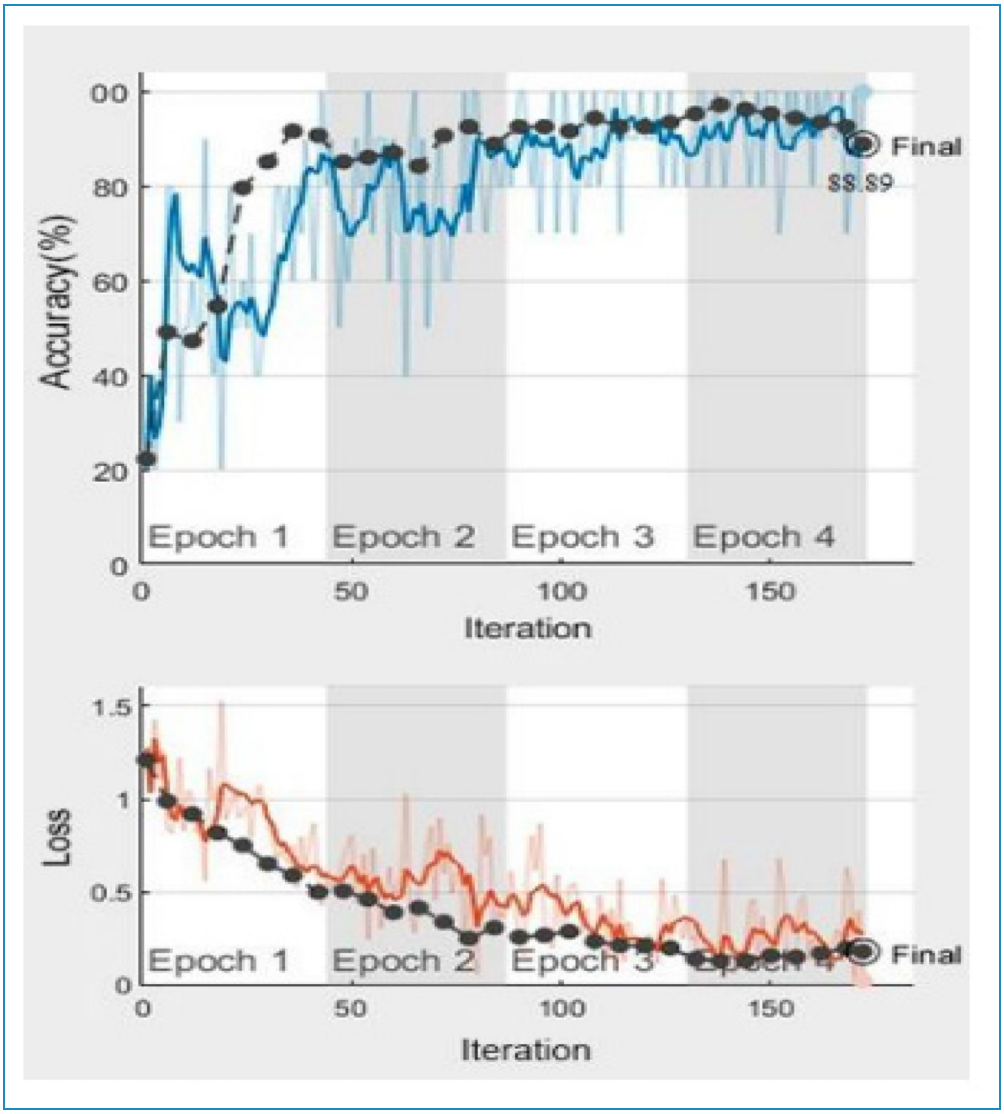

Figure 7. Accuracy and loss graph for AlexNet.

Table 11. Performance value of the VGG16.

	Monkeypox	Otherpox	Normal skin
Accuracy	96.1	94	92.2
F1 score	92.5	93.4	88.5
Precision	96	94	92
Sensitivity	92.5	1	96.2
Specificity	97	90	90.6

Batch normalization. The convolution and fully connected layers' output value should be normalized by this layer. The output of this layer is momentarily normalized.[31] The technique completes the learning process faster and has a shorter training period as a result.

Dropout. The technique is kept from remembering by the implementation of the dropout layer. The technique can over-learn and remember training data. The technique can no longer learn new things if it enters an excessive learning process. Certain nodes in the technique are arbitrarily deactivated by the dropout process.[32] The technique is therefore kept from remembering. Steps for testing and confirmation cannot employ the dropout process.

Fully connected. The incoming data are reduced to a one-dimensional matrix representation by the fully linked layer. Different completely bonded layers are employed in each architectural.[32] There are three classes in this study:

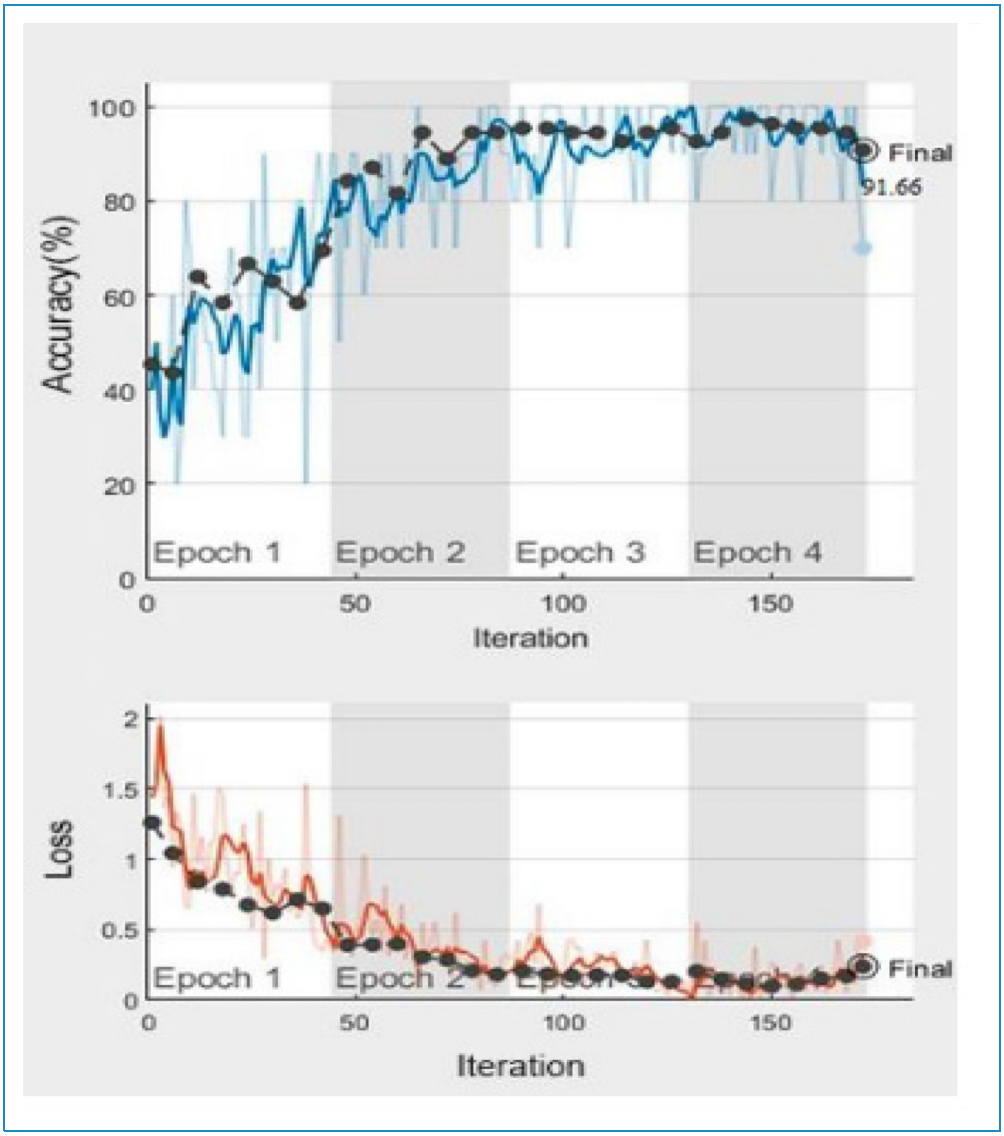

Figure 8. Accuracy and loss graph for VGG16.

Normal, Otherpox, and Monkeypox. The completely linked layer 3 output value of the proposed technique is entered as a result.

Max pooling. The convolution layer is the desired layer before this one. The convolution layer's information is made simpler by the pooling procedure. Average pooling and maximal pooling are the two commonly used pooling techniques. The technique does not learn anything when it pools. For the pooling operation, NxN-sized filters are recommended.[31] The proposed technique that has been built uses maximum pooling.

Softmax. The SoftMax classification layer is reached before it.[32] It delivers a value for every class after carrying out the probabilistic computation built on the technique.

Classification/detection. The architecture's last layer, which generates output value, is this one.[32]

Stochastic Gradient Descent with Momentum (SGDM) is one of the optimizers which is used to improve the performance of the neural technique. CNN architectures and training data used in the developed technique are given in Table 4.

Results analysis

Images of skin lesions from monkeypox, non-monkeypox, and normal skin were mixed for this research. The confusion matrix is one of the most crucial factors in CNN architectures. The confusion matrix is used in the calculation of values such as accuracy, sensitivity, specificity, and F1 score.[33] To sum up,

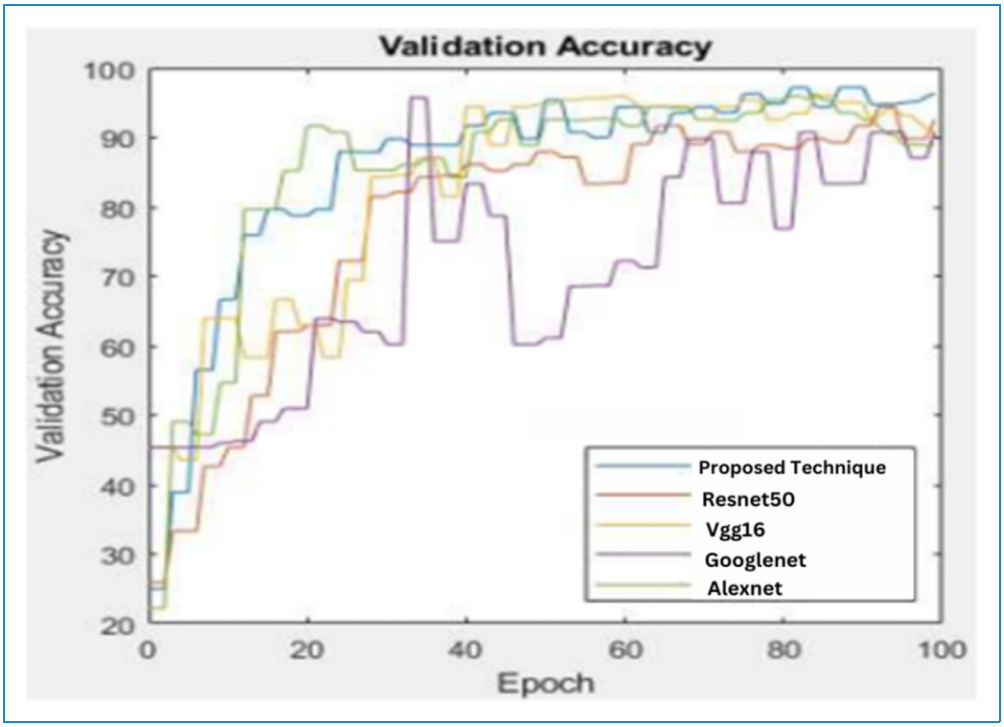

Figure 9. Combined accuracy curves for state-of-art employed techniques and the proposed technique.

the trained technique's image may be compared to the confusion matrix.

- TP (True-Positive): The monkeypox virus was appropriately classified and anticipated.
- FP (False-Positive): The monkeypox diagnosis was incorrectly classified as non-monkeypox.
- FN (False-negative): The data are not monkeypox, but the non-monkeypox is assessed to be monkeypox.
- TN (True-Negative): The data are not monkeypox, and the non-monkeypox is estimated to be non-monkeypox.

Accuracy (A) is defined as the ratio of the entire amount of data utilized to the number of precisely estimated data.[33] Equation (4) provides the formula used to determine the accuracy value.

$$A = \frac{TP + TN}{TP + TN + FP + FN} \tag{4}$$

Equations (5) and (6) provide the Sensitivity (TPR) and Specificity (TNR) value derived from the confusion matrix.

$$TPR = \frac{TP}{TP + FN} \tag{5}$$

$$TNR = \frac{TN}{TN + FP} \tag{6}$$

The formula for calculating the F1 Score value is given in equations (7)–(9), along with formulas for Precision (P) calculation and Recall (R) value computation.

$$F1\ Score = \frac{2{*}P{*}R}{P + R} \tag{7}$$

$$P = \frac{TP}{TP+FP} \tag{8}$$

$$R = \frac{TP}{TP + FN} \tag{9}$$

Table 5 presents the confusion matrix for the technique and Table 6 provides the proposed technique's performance values after it has been trained. Sensitivity, Specificity, F1 Measure, and Accuracy values were calculated by multiplying the total by 100 in all structures. These figures were determined individually for monkeypox, otherpox diseases, and normal image classes. The results of performance metrics for the proposed technique "MRpoxNet" are shown in Table 7 (Figure 4).

After training the proposed technique, the performance metrics are summarized in Tables 8 to 11. These tables illustrate the state-of-the-art results for various pre-trained techniques, including ResNet, GoogleNet, AlexNet, and VGG16, with their accuracy and loss curves shown in Figures 5 to 8. Additionally, the combined accuracy curves of all techniques are displayed in Figure 9, while Figure 10 shows the combined loss curves.

Finally, Figure 9 shows the combined accuracy curves for all techniques, while Figure 10 illustrates their loss curves.

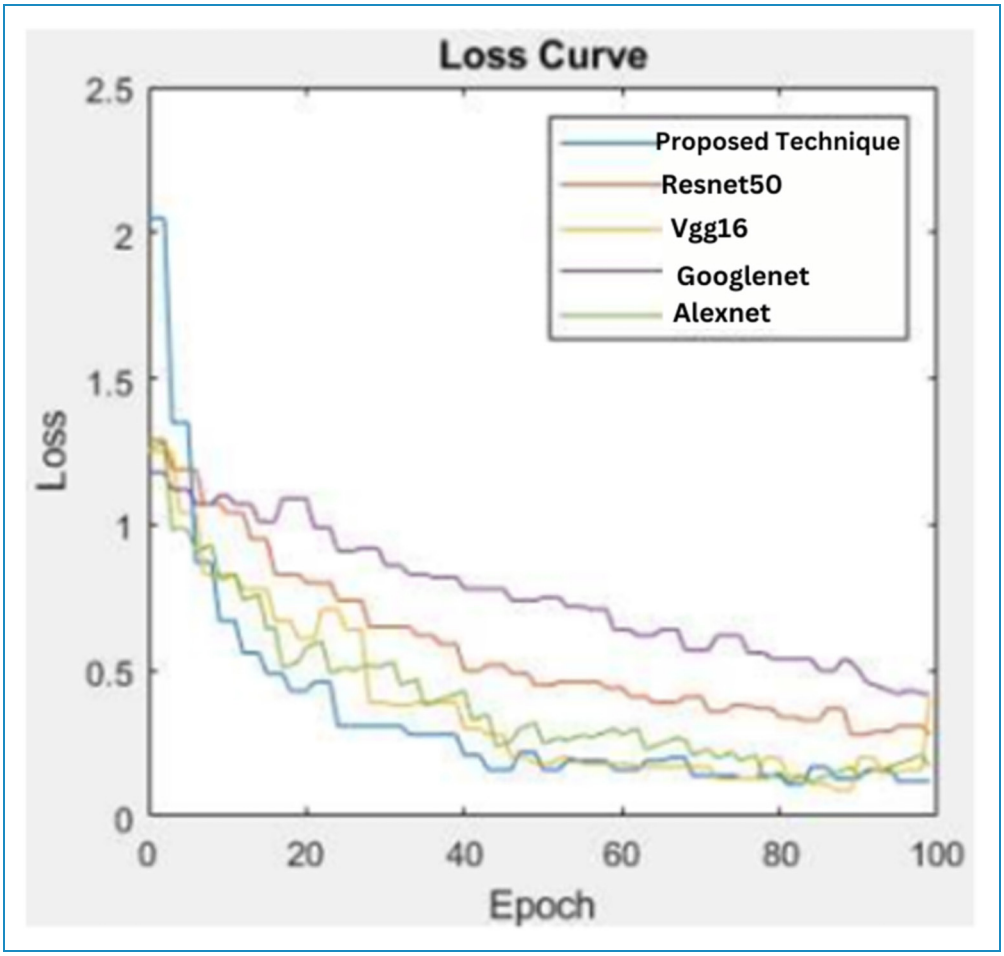

Figure 10. Loss curve for state-of-art employed techniques and the proposed technique.

Table 12. Comparison of the proposed technique with existing state-of-art techniques based on accuracy performance value.

Technique	Accuracy
Proposed technique "MRpoxNet"	98.1
ResNet	97.1
AlexNet	95
GoogleNet	98
VGG16	96.1

So, Table 12 clearly depicts that the proposed technique, i.e., MRpoxnet, achieves the highest accuracy compared to other techniques applied to the same dataset. The following Table 13 depicts that the proposed technique, i.e., MRpoxnet is compared with other pre-trained techniques with related papers.

Table 13. Comparison of the proposed technique with related papers based on accuracy performance value.

	Technique	Dataset	Accuracy
34	ResNet18	MSID	80%
35	ResNet50	Total 117 images. (56 images monkeypox, 74 images normal skin)	94%
36	ResNet50	HAM images 1000	84.42%
	Proposed technique "MRpoxNet"	**279 monkeypox lesion images, 107 chickenpox and measles images, 770 normal and healthy skin images**	**98.1%**

In summary, the work uses deep learning techniques to specifically focus on the image-based categorization of monkeypox sickness. There is always a space for

improvement in the work, especially with regard to dataset growth. However, the study's practical importance remains unaltered. The proposed technique makes a significant contribution to the research community by adding a pre-trained ResNet50 layer to produce better outcomes with a lower loss rate. This shows how DL may help discover serious medical issues, which is a significant advancement in the field of healthcare.

Discussion

Limitation of study

First, there isn't enough open-source data available to train AI techniques. Due to the scarcity of large-scale public datasets for monkeypox, data-hungry DL methods cannot be used. High data volumes are necessary for AI applications to prevent bias and overfitting. Thus, in order to support research, monkeypox data collecting needs to be promoted and made available to the public. A meaningful comparison of the performance of the created techniques will also be possible thanks to their training on popular open-source datasets.

Second, data filtering is required to guarantee data input fidelity into AI techniques and exclude incorrect monkeypox information.

Third, sharing could compromise privacy, particularly when it comes to sensitive raw data. Thus, it is essential to safeguard sensitive data from hackers and malevolent users. For technique training to be effective, data must be properly formatted. Despite the abundance of data, it is challenging to extract meaningful information because the majority of web data is unstructured.

Additionally prone to false negative and incorrect findings are DL algorithms. Thus, it is possible to mix DL algorithms with other ML methods like reinforcement learning and unsupervised learning. It is evident from the aforementioned studies that the majority of researchers diagnosed mpox using skin lesion images. It is important to investigate alternative modalities, such as laboratory indicators and blood testing. The outcomes are often more trustworthy when several modalities are employed. Certain viral strains undergo further mutations after a predetermined period of time. As a result, testing the techniques on data including different mutations is also necessary. Additionally, a variety of datasets from diverse geographic regions must be used to evaluate the techniques.

Future scope

The focus will be on two major goals: developing an easy-to-use web app for monkeypox detection and expanding current algorithms to include new forms of skin problems. The primary goal of this research is to develop a technique that will work for all forms of monkeypox, not just specific forms. This will be accomplished by utilizing many data sources and innovative algorithms in order to obtain a thorough understanding of monkeypox, hence assisting healthcare professionals with diagnosis. By integrating multidisciplinary methodologies and capitalizing on technological developments, we hope to contribute toward a future in which the early and precise identification of graphical interface problems is not only possible but is also the standard for protecting human health and well-being. Cloud deployment is possible for patient data, wearable data, smartphone data, and AI techniques. Physicians have access to them through cloud infrastructure, including skin lesion images uploaded for diagnosis of monkeypox remotely. Incorporating clinical, laboratory, epidemiological, demographic, and other characteristics enables systems-wide analysis for the purpose of allocating healthcare resources. It is also possible to incorporate teleconsultation using remote video conferencing into the system in order to stop the infection from spreading, and in mild situations, suitable symptomatic therapy may be administered remotely. The majority of academics use datasets from a single source or geographic area, and such a system is scalable. A cloud system makes it possible to collect and analyze data from several places in order to identify patterns for high-level strategic planning.

Conclusions

A viral zoonotic disease, monkeypox, may spread from animal to human and between people and the environment. CNN architectures were employed for the early detection of monkeypox using skin images. In this study, the proposed technique for early detection of monkeypox was developed. Data augmentation was performed to minimize bias in the performance results. The technique is built on CNN architecture, specifically ResNet50, modified by removing five of its original layers and adding ten additional layers. This enhanced model achieved an average accuracy of 96.55%. Comparative results were also obtained using other architectures, including AlexNet, ResNet50, VGG16, and GoogleNet. The highest accuracy, 98.1%, was achieved with the improved proposed technique. Future research could further enhance this approach. To ascertain the viability and use of AI-based monkeypox detection systems in clinical settings, researchers can conduct empirical assessments of these systems. It will take patients and healthcare professionals working together to assemble large datasets. Moreover, other designs might be studied to tackle the difficulty mentioned before. Researchers can increase the precision of AI-based monkeypox diagnosis by including other data sources, such as clinical symptoms, laboratory test findings, and patient history.

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Availability of data and materials: The dataset used in this study is publicly available from Kaggle at [https://www.kaggle.com/dsv/3971903] under a Creative Commons Attribution 4.0 International License (CC BY 4.0).

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References

1. Yang H, Zheng J, Wang W, et al. Zr-MOF carrier-enhanced dual-mode biosensing platforms for rapid and sensitive diagnosis of Mpox. *Adv Sci* 2024; 11: 2405848.
2. Tarín-Vicente EJ, Alemany A, Agud-Dios M, et al. Clinical presentation and virological assessment of confirmed human Monkeypox virus cases in Spain: a prospective observational cohort study. *Lancet* 2022; 400: 661–669.
3. Vandana CK. Monkeypox and other skin conditions detection utilizing CNN with VGG16 transfered language. In: 2023 6th international conference on contemporary computing and informatics (IC3I), 2023, pp.931–938. IEEE, Vol. 6.
4. Alshanbari HM, Iftikhar H, Khan F, et al. On the implementation of the artificial neural technique approach for forecasting different healthcare events. *Diagnostics* 2023; 13: 1310.
5. Alakunle E, Moens U, Nchinda G, et al. Monkeypox virus in Nigeria: infection biology," epidemiology, and evolution. *Viruses* 2020; 12: 1257.
6. Shafaati M and Zandi M. Monkeypox virus neurological manifestations in comparison to other orthopoxviruses. *Travel Med Infect Dis* 2022; 49: 102414.
7. Bhattacharya M, Dhama K and Chakraborty C. Recently spreading human Monkeypox virus infection and its transmission during COVID-19 pandemic period: a travelers' prospective. *Travel Med Infect* 2022; 49: 102398.
8. "Monkeypox"- 09-May-2024 [Online], https://www.who.int/health-topics/monkeypox#tab=tab_2 (accessed 5 July 2024).
9. He B, Lu Q, Lang J, et al. A new method for CTC images recognition based on machine learning. *Front Bioeng Biotechnol* 2020; 8: 897.
10. Fu Y, Chen X, Song W, et al. Light-switch electrochemiluminescence-driven microfluidic sensor for rapid and sensitive detection of Mpox virus. *Chem Eng J* 2024; 498: 154930.
11. Akram A, Jamjoom A, Innab N, et al. Skinmarknet: an automated approach for prediction of monkeyPox using image data augmentation with deep ensemble learning models. *Multimed Tools Appl* 2024; 2024: 1–17.
12. Lakshmi M and Das R. Classification of monkeypox images using LIME-enabled investigation of deep convolutional neural technique. *Diagnostics* 2023; 13: 1639.
13. Velu M, Dhanaraj RK, Balusamy B, et al. Human pathogenic monkeypox disease recognition using Q-learning approach. *Diagnostics* 2023; 13: 1491.
14. Mandal AK. Usage of particle swarm optimization in digital images selection for Monkeypox virus prediction and diagnosis. 2022.
15. Kundu D, Siddiqi UR and Rahman MM. Vision transformer based deep learning model for monkeypox detection. In: 2022 25th International Conference on Computer and Information Technology (ICCIT), pp.1021–1026, 2022. IEEE.
16. Iftikhar H, Daniyal M, Qureshi M, et al. A hybrid forecasting technique for infection and death from the mpox virus. *Digital Health* 2023; 9: 20552076231204748.
17. Cuba WM, Huaman Alfaro JC, Iftikhar H, et al. Modeling and analysis of monkeypox outbreak using a new time series ensemble technique. *Axioms* 2024; 13: 554.
18. Iftikhar H, Khan M, Khan MS, et al. Short-term forecasting of monkeypox cases using a novel filtering and combining technique. *Diagnostics* 2023; 13: 1923.
19. Taye MM. Theoretical understanding of convolutional neural technique: concepts, architectures, applications, future directions. *Computation* 2023; 11: 52.
20. Bala D. Monkeypox skin images dataset (msid), [Online], https://www.kaggle.com/dsv/3971903 (2022).
21. Jain R, Kukreja V, Chattopadhyay S, et al. Radial basis function integrated with support vector machine model for breast cancer detection. In: 2024 2nd International Conference on Artificial Intelligence and Machine Learning Applications Theme: Healthcare and Internet of Things (AIMLA), March 2024, pp.1–5. IEEE.
22. Jaradat AS, Al Mamlook RE, Almakayeel N, et al. Automated monkeypox skin lesion detection using deep learning and transfer learning techniques. *Int J Environ Res Public Health* 2023; 20: 4422.
23. Haque ME, Ahmed MR, Nila RS, et al. Human monkeypox disease detection using deep learning and attention mechanisms. In: 2022 25th International conference on computer and information technology (ICCIT), 2022, pp.1069–1073. IEEE.
24. Hossain SI, de Herve JDG, Hassan MS, et al. Exploring convolutional neural techniques with transfer learning for diagnosing Lyme disease from skin lesion images. *Comput Methods Programs Biomed* 2022; 215: 106624.
25. Bala D. Monkeypox skin images dataset (MSID), https://www.kaggle.com/datasets/dipuiucse/monkeypoxskinimagedataset (2022, accessed 6 July 2024).
26. Bala D, Hossain MS, Hossain MA, et al. Monkeynet: a robust deep convolutional neural technique for monkeypox disease detection and classification. *Neural Techniques* 2023; 161: 757–775.
27. Choe J, Lee SM, Do KH, et al. Deep learning–based image conversion of CT reconstruction kernels improves radiomics reproducibility for pulmonary nodules or masses. *Radiology* 2019; 292: 365–373.
28. Goodfellow I, Bengio Y and Courville A. *Deep learning*. Cambridge, London, England: MIT press, 2016.
29. Mittal S. Image classification of satellite using VGG16 model. In: 2024 2nd International Conference on Disruptive Technologies (ICDT), 2024, pp.401–404. IEEE.

30. Shourie P, Anand V and Gupta S. A smart device employs vgg-16 to identify brain stroke using CT scan images. In: 2023 International conference on computing, communication, and intelligent systems (ICCCIS), 2023, pp.232–236. IEEE.
31. Yeh ST. Using trapezoidal rule for the area under a curve calculation. In: Proceedings of the 27th annual SAS® user group international (SUGI'02), 2002, pp.1–5.
32. Vandana CK. Analysis of the Monkeypox outbreak using CNN model: a systematic review. In: 2023 4th IEEE Global Conference for Advancement in Technology (GCAT), 2023, pp.1–6. IEEE.
33. Hasnain M, Pasha MF, Ghani I, et al. Evaluating trust prediction and confusion matrix measures for web services ranking. *IEEE Access* 2020; 8: 90847–90861.
34. Uysal F. Detection of monkeypox disease from human skin images with a hybrid deep learning model. *Diagnostics* 2023; 3(10): 1772.
35. Jaradat AS, Al Mamlook RE, Almakayeel N, et al. (2023). Automated monkeypox skin lesion detection using deep learning and transfer learning techniques. *International Journal of Environmental Research and Public Health* 2023; 20: 4422.
36. Tang D, Chen J, Ren L, et al. Reviewing CAM-Based deep explainable methods in healthcare. *Applied Sciences* 2024; 14: 4124.