

A Supervised Learning-Based Classification Technique for Precise Identification of Monkeypox Using Skin Imaging

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Abstract—The monkeypox epidemic has spread to nearly every nation. Governments implement several strict policies, to stop the virus that causes monkeypox. For effective handling and treatment, early identification and diagnosis of monkeypox using digital skin lesion images is critical, and this work employed deep learning architectures to achieve this goal. This article presents a supervised learning-based classification method designed for the precise identification of monkeypox cases. The analysis was conducted using an open-source dataset from Kaggle, consisting of digital images of monkeypox, which were processed using advanced image processing and deep learning techniques. The data was categorized based on findings related and unrelated to monkeypox. A deep neural network with 50 layers and up to 35 folds was utilized to identify regions of interest, which could be indicative of characteristics relevant to computer-assisted medical diagnosis and enable us to solve image processing and natural language processing tasks with high accuracy. In terms of performance, the proposed method achieved an accuracy of 96% during cross-validation classification testing. This outcome demonstrates the potential for computer-assisted diagnosis as a supplementary tool for medical professionals. Amid the monkeypox outbreak, this method offers a technical and objective assessment of patients' skin conditions, thereby simplifying the diagnostic process for specialists.

Keywords—Deep learning; monkeypox; medical image processing; image classification; cross validation

I. INTRODUCTION

The infectious illness known as "mpox," or monkeypox, has spread quickly across the globe and is characterized by fever, muscle pains, and skin lesions that resemble boils. In response, the World Health Organization (WHO) raised the warning level to its maximum in July by classifying it as a public health emergency of international concern (PHEIC) [1]. When a tourist returned from Nigeria, where the disease is widespread, the epidemic began in the UK. However, there have previously been isolated occurrences of this kind, and those outbreaks ended swiftly. This time, the disease began to spread from the first cluster of patients and appeared in various European, Australian, and American nations [2].

Although African epidemiologists have been warning for

several years that patterns of transmission seem to be shifting in endemic nations, scientists are still unsure of the exact reason for the virus's rapid expansion. As of December 19, 110 countries have reported more than 83,000 cases, with 66 fatalities, according to W.H.O. Encouragingly, the weekly total of new cases worldwide has dropped by 49.3%; this past week saw 265 new cases globally, compared to 523 from December 5–11 [1–3]. Currently, the Americas are considered to be at greater risk than Africa. The Americas (90.5%) and Europe (4.9%) accounted for the majority of cases recorded over the previous four weeks [3]. Fig. 1 shows the DNA structure of monkeypox, while Fig. 2 highlights the 10 most affected countries worldwide.

In some regions of the globe, the pandemic may have decreased due to the availability of the currently preventable JYNNEOS monkeypox vaccine, but nations below the poverty line have been left behind. Given that monkeypox may mutate and become harder to manage in the future, experts argue that it is imperative to administer the vaccination in a fair and equitable manner [4].

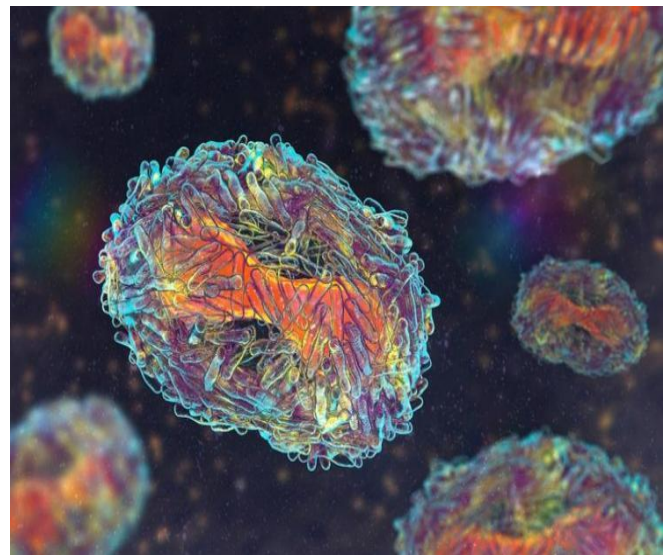


Fig. 1. Monkeypox DNA image [1].

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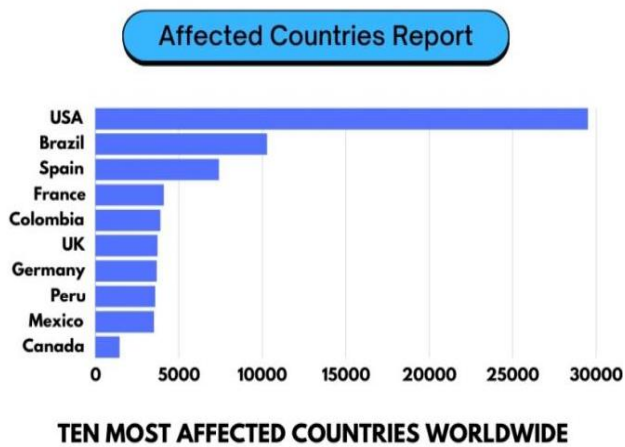


Fig. 2. Affected countries of monkeypox worldwide [1].

Artificial Intelligence (AI) and Deep Learning have demonstrated remarkable results across various domains, transforming the way tasks are approached. In agriculture, AI-powered models have optimized crop management [5,6], disease detection[7], and yield prediction [8,9]. In education, adaptive learning platforms are tailoring educational content to individual needs, enhancing student engagement and success. In finance, AI-based algorithms are improving fraud detection, risk assessment, and investment strategies. In healthcare, AI and Deep Learning have revolutionized diagnostics, treatment plans, and patient management through the precise analysis of complex medical data [10–13].

Specifically in healthcare, AI has significantly enhanced decision-making by enabling more accurate diagnosis and personalized treatments through the interpretation of medical images, patient records, and genetic data [10–13]. This progress can extend to infectious diseases, where a deep learning could be employed for precise identification of Monkeypox using skin imaging. By leveraging AI's ability to analyze and differentiate subtle features in skin lesions, the technique could improve early detection and reduce misdiagnosis. This would facilitate timely interventions, reducing the spread of the disease and enhancing patient outcomes, demonstrating AI's critical role in addressing emerging public health challenges.

In this study, a computer-aided diagnostic (CAD) system using deep learning and artificial intelligence (AI) techniques is proposed for potential pulmonary follow-up due to its accuracy and ability to optimize reaction times. AI has played a significant role in medical diagnosis [14, 15]. Expert interpretation is facilitated by the technique's automated and objective assessment of pulmonary follow-ups, which is enabled by artificial neural network designs. Since artificial neural networks (deep learning) have proven to be successful, AI has also been applied to medical image processing [16, 17]. The development of trustworthy and accurate medical diagnostics has garnered significant attention in recent years. Artificial neurons are layered and interconnected to transfer signals in neural network techniques, with intermediate layers being hidden. These networks, along with more advanced learning processes, form the foundation of deep learning,

which generates categorization approaches that are both optimal and precise [18, 19]. Main aim of the research is to develop a technique which can classify image efficiently without leaving a single skin lesion in images which can help doctors to treat well and detect the disease at its initial stage.

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

- Our suggested technique uses images with $224 \times 224 \times 3$ the RGB spectrum dimensions and those without monkeypox lesions.
- To implement pre-processing steps using Resnet 50 to generate the feature vector($1 \times 1 \times 2048$) then the its subsets are defined using its increase and decrease in fold values which solve image processing and natural language processing tasks with high accuracy.
- To Classify various methods likes SVN, LR, KNN, NB, NC evaluates the accuracy and precision value depending upon various folds

II. RELATED WORK

Monkeypox disease is often mistaken for other illnesses, leading to misdiagnosis and inappropriate treatment. Early diagnosis and treatment of this contagious disease are crucial. Detecting monkeypox typically requires expert interpretation and clinical examination, which can delay the treatment process. AI-based detection can assist in the early identification of this disease. There are limited studies in the literature on this topic, which are discussed in detail below, along with Table I.

Dipanjali Kundu et al. [20] presented a secure Federated Learning and deep learning-based framework for monkeypox virus detection using skin lesion images. The framework aims to improve classification performance while maintaining data confidentiality. The CycleGAN generator augments training and test data, and synthetic images are divided into four groups for local techniques. ViT-B32 outperforms other classifiers with an impressive accuracy of 97.90. The approach ensures user data privacy and effectively performs categorization tasks, making it relevant in medical contexts with limited datasets and data privacy concerns. Sitaula et al. [21] evaluated 13 pre-trained deep learning techniques (including VGG-16, InceptionV3, Xception, MobileNet, EfficientNet, etc.) for monkeypox detection using the publicly available Monkeypox virus image dataset. They trained the techniques on the ImageNet dataset. The study included 1,754 images, consisting of 329 chickenpox, 286 measles, 587 monkeypox, and 552 normal images. They developed a technique using the Keras library in Python. The proposed ensemble learning technique outperformed the 13 deep learning techniques, achieving an accuracy of 87.1% (precision: 85.4%, recall: 85.4%, F1-score: 85.4%). Xception was the second-best technique with an accuracy of 86.51%, while precision, recall, and F1-score were 85%. Alakus and Baykara [22] classified monkeypox disease and warts based on their DNA sequences. They employed various DNA mapping techniques and deep learning. The study used 110 genome sequences, consisting of 55 monkeypox virus and 55 human papillomavirus sequences. To address the data imbalance, they used the zero-padding

technique. Five DNA mapping techniques achieved an average classification accuracy of 96.08%, with the integer DNA matching technique achieving the highest accuracy at 99.5%. This demonstrates the successful detection of monkeypox and warts through DNA mapping and classification. Ali et al. [23] addressed the challenge of early clinical diagnosis of monkeypox, similar to chickenpox and measles, through computer-aided detection. They created a dataset of skin lesion images from various sources, consisting of 228 images. Three classification techniques were used: VGG16, ResNet50, and InceptionV3. ResNet50 achieved the highest accuracy (82.96% ± 4.57), VGG16 performed competitively (81.48% ± 6.87), and InceptionV3 had the lowest accuracy (74.07% ± 3.78). A community technique using majority voting outperformed ResNet50 and was integrated into a prototype web application. Haque et al. [24] aimed to classify human monkeypox disease from images using a pre-trained deep learning technique. The study utilized VGG-19, Xception, DenseNet121, MobileNetV2, and EfficientNetB3 deep learning techniques for classification. A uniform approach was applied to customize all pre-trained techniques. To enhance the network's focus on more pertinent feature maps, a convolutional block attention module was incorporated. The initial preparation of the MSLD involved resizing the images to a resolution of 224x224x3 for training purposes. In the research, many hyperparameters were used to maximize the effectiveness of the strategies. The design that included Xception, CBAM, and thick layers performed better than other techniques in the findings, obtaining a validation accuracy of 83.89% in the classification of human monkeypox and other illnesses. Sahin et al. [25] developed a mobile app using deep learning to detect monkeypox from video footage captured on mobile devices.

They used the MSLD dataset and deep transfer learning with Matlab. Transfer learning is a machine learning technique where a model trained on one task is adapted to improve performance on a related but different task, often with fewer data [28]. MobileNetV2 (91.11%) and EfficientNetB0 (91.11%) achieved the best results in 60 epochs. MobileNetV2, with precision (90%), recall (90%), F1-score, and accuracy (91.11%), outperformed other techniques and was integrated into an Android mobile app, allowing easy pre-screening for monkeypox. Ahsan et al. [26] developed an AI-driven decision support system using CNNs. Their study used a dataset of 572 images (monkeypox and normal). They employed twelve different CNN techniques for classification, with MobileNetV2 achieving the highest accuracy (98.25%), precision (96.55%), specificity (100%), and F1-score (98.25%). The study also highlighted that MobileNetV2 is suitable for mobile-based monkeypox testing due to its smaller technique size. Ahsan et al. [27] created a dataset of patient images infected with monkeypox. The researchers aimed to detect monkeypox virus in patients using a modified pre-trained VGG16 technique. The study collected a total of 1,915 images, including monkeypox, chickenpox, measles, and normal images, as well as augmented versions. Two separate studies were conducted, one with a small dataset and the other with a medium-sized dataset. In the first study, using a small dataset, the VGG16 technique achieved training and testing accuracy rates of 97% and 83%, respectively. In the second study, with a medium-sized dataset, the technique achieved accuracy rates of 88% in training and 78% in testing. The proposed technique's predictions were validated through cross-validation by medical professionals. The study suggests that this technique could be used to develop a mobile-based diagnostic tool.

TABLE I. LITERATURE REVIEW OF RELATED WORK

| Reference | Data type | Technique | Accuracy | Research Gap |
|---------------------|---|---|---|--|
| Kundu et al.[20] | a total of 381 images of monkeypox, 102 images of chickenpox, 110 images of measles, and 293 images of normal skin. | federated learning (FL) with Cycle GANS and deep learning-based techniques such as MobileNetV2, Vision Transformer (ViT), and ResNet50 for the classification | Proposed technique accuracy 97.90% | Limited datasets and data privacy |
| Sitaula et al. [21] | Monkeypox virus dataset images (329 chickenpox, 286 measles, 587 monkeypox, and 552 normal images) | 13 pre-trained deep learning techniques (including VGG-16, InceptionV3, Xception, MobileNet, Efficient-Net, etc.) | Proposed technique accuracy 87.13%. | Less accuracy rate |
| Alakus et al.[22] | 55 monkeypox virus and 55 human papilloma virus sequences | DNA mapping techniques | Proposed technique accuracy 99.5%. | Very small Dataset used |
| Ali et al. [23] | 228 images from open source data set | VGG16, ResNet50, and InceptionV3 | ResNet50 accuracy (highest accuracy) (82.96% ± 4.57), VGG16 accuracy (81.48% ± 6.87), InceptionV3 accuracy (lowest accuracy) (74.07% ± 3.78). | Need of improved segmentation technique |
| Haque et al.[24] | MSLD | VGG-19, Xception, DenseNet121, MobileNetV2, and EfficientNetB3 | Accuracy: 83.89% | Less accuracy rate |
| Sahin et al. [25] | MSLD 112 images | MobileNetv2, EfficientNetb0 | MobileNetv2 (91.11%) and EfficientNetb0 (91.11%) achieved the best results in 60 epochs. | Small dataset used and less augmentation used |
| Ahsan et al.[26] | Dataset of 572 images (monkeypox and normal). | AI-driven decision support system using CNNs (MobileNetv2) | MobileNetV2 highest accuracy (98.25%), precision (96.55%), specificity (100%), and F1-score (98.25%) | MobileNetV2 is suitable for mobile-based monkeypox testing due to its smaller technique size |
| Ahsan et al.[27] | Open source Dataset 1915 images | VGG16 | Proposed accuracy 88% | Need to develop a mobile-based diagnostic tool |

III. MATERIAL AND TECHNIQUES

A. Deep Learning Classification Techniques

In this study, CNN-based deep learning techniques, namely VGG16, ResNet50, EfficientNetB3, Xception, and InceptionResNetV2, were used to perform image-based classification of monkeypox disease. Brief descriptions of these techniques are provided below:

VGG16 is a deep learning technique developed at the University of Oxford. VGG stands for Visual Geometry Group, and 16 refers to the number of layers in the technique [20]. VGG16 is a CNN technique commonly used for image classification tasks. Convolutional, fully linked, and pooling layers make up the approach. The pooling layers highlight key characteristics and condense the bulk of the data [20]. Because of its depth, VGG16 is a large approach with a significant number of learnable parameters. Large datasets and more challenging picture classification tasks are often better served by it. VGG16 became well-known, especially when it performed well on the ImageNet dataset. It is known for emphasizing the fundamental structure of convolutional networks and the depth of its layers, which has influenced the development of related techniques that use weighted convolutional layers and depth.

In deep learning, one popular Convolutional Neural Network (CNN) approach is called ResNet50. Microsoft Research first introduced the ResNet (Residual Network) approach in 2015 with the express purpose of resolving issues related to depth in deep networks. ResNet50 is a 50-layer deep network that uses a unique building component known as a residual block. These blocks introduce skip links in the network's transitions, which attempt to mitigate the issue of gradient vanishing that arises in deeper networks. In comparison to earlier techniques, the residual blocks allow information to move across the network more quickly and smoothly [29]. ResNet50 has pooling layers, activation functions, and convolutional layers—basic CNN building blocks. Additionally, it has a global average pooling layer in the center of the network that uses smaller feature maps to summarize data.

A version known as ResNet blends the ResNet and Inception architectures [30]. While the ResNet design makes use of residual connections to solve gradient vanishing in deep networks, the Inception architecture is composed of convolutional layers with filters of varying sizes. ResNet seeks to integrate these two topologies to make training deeper and more complicated networks easier. While the ResNet blocks maintain information flow by using connections to prevent gradient vanishing, the Inception blocks combine convolutional layers with filters of varying sizes to capture a broad variety of characteristics. Extreme Inception, a term that is shortened to "Xception," is a deep learning approach [31]. It is based on the CNN architecture, more precisely on an Inception approach variant. Improving the Inception network's processing efficiency is the primary objective of Xception. It deviates from the conventional CNN technique by optimizing the convolution operations in the Inception blocks to achieve this.

Depth-wise separable convolution is the method used to accomplish this improvement. Two steps of convolution operations are carried out by depth-wise separable convolution. A point-wise convolution layer is used in the first stage to capture relationships between several channels and modify the input data's dimension. The second step is a depth-wise convolution layer, which improves computing efficiency by processing each input data channel independently. The CNN technique known as EfficientNetB3 is used in deep learning [32]. It belongs to the family of EfficientNets, and EfficientNetB3 is a scalable and effective technique. Compound scaling is a technique that EfficientNet uses to automatically scale deep learning approaches to different sizes. The purpose of EfficientNetB3 is to be applied to larger and more intricate datasets. The method improves efficiency on smaller datasets by combining depth features with scalability. To handle input images, EfficientNetB3 uses a variety of convolutional layers, activation functions, and pooling layers [32, 33].

B. Data Set

The study used a dataset that included skin lesion images classified into two groups: those with monkeypox and those without (chickenpox and measles). The University of Dhaka research team in Bangladesh [33] contributed to the dataset, which was augmented to contain approximately 3,192 images with dimensions of $224 \times 224 \times 3$ in RGB. There were 228 images in the original dataset, of which 102 belonged to the monkeypox class and 126 to the other class. This dataset has a comparatively modest amount of images, especially when considering the deep learning environment. The only restriction was that more images were obtained by using image enhancement. Through picture augmentation, the dataset was increased by a factor of fourteen. After augmentation, there were 1,428 images in the monkeypox class and 1,764 images in the 'others' class. An unequal distribution of images was observed between the 'others' and monkeypox classes. To address this imbalance, data augmentation techniques were applied to create more samples for the monkeypox class. By adding these extra examples, the dataset's classes were distributed more evenly, as shown in Fig. 3, which displays 1,764 images in each class.

To further enhance the dataset's durability, the researchers used stratified sampling to divide it into seven folds. This technique ensured that the monkeypox class and the other classes were represented proportionally in each fold. The stratified split of the dataset into folds allowed for a more accurate evaluation and validation of the technique's effectiveness by taking into account any variances in the distribution of classes within the dataset. The technique's ability to generalize was assessed by applying cross-validation on multiple data subsets and evaluating its performance on each fold. This experiment used two subsets of the dataset, namely the training set and the testing set. The testing set, consisting of 252 images, provided a more thorough insight into the technique's ability to categorize monkeypox images. The training set consisted of 1,512 enhanced images used for training the classification system. To develop a reliable and efficient classification technique, it is essential to carefully analyze the segmentation of this dataset [34, 35].

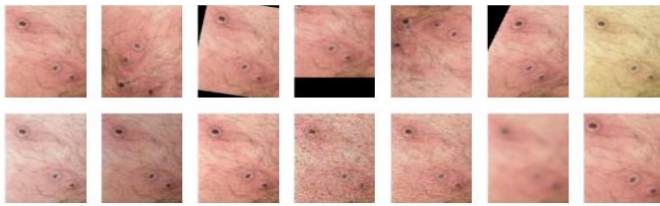


Fig. 3. Sample augmented monkeypox images from dataset.

IV. PROPOSED TECHNIQUES

The approach is based on the categorization of the images in Fig. 4; the technique diagram is comprehensive and includes the dataset. High reliability is achieved by identifying the optimal settings for executing the procedure. Python, an open-source programming language, was used to develop the method. The approach is divided into many steps; however, the preprocessing step is crucial for successful classification. In particular, the first phase focuses on the initial analysis, as the experiment was conducted using the dataset to enable the CNN to extract features from the images related to the identification of monkeypox.

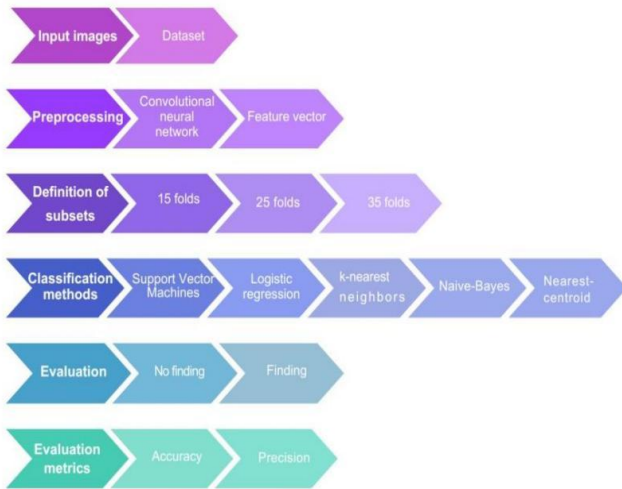


Fig. 4. Technique of the proposed technique.

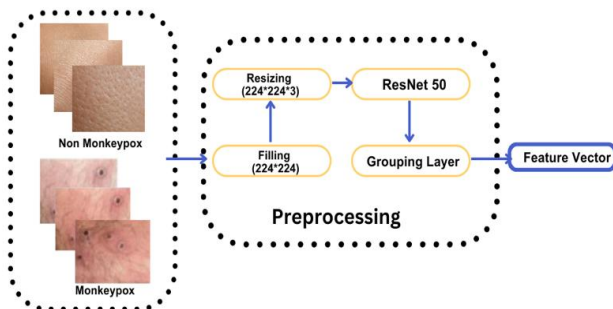


Fig. 5. An illustration of the first phase and the pre-processing steps to generate the feature vector.

The schematic diagram of the first and second phases is shown in Fig. 5. The residual neural network ResNet50, which was used, contains 50 hidden layers [36]. This artificial neural

network consists of three layers of artificial neurons: one input, fifty intermediate (hidden), and one output. The process of creating a matrix from the feature vectors is based on residual learning. By putting neural networks through performance tests with partial and random changes to their connections, residual learning increases the technique's accuracy and enhances its ability to solve complex problems with greater reliability.

Here is a list of the four preliminary processing phases shown in Fig. 4: All input images are scaled to 224×224 pixels, and if the appropriate dimensions are not met, zeros are added to the perimeter of the original image. The pixel values in each layer are adjusted from 0 to 255. A new matrix with dimensions of $224 \times 224 \times 3$ is then created by converting the images to three layers (the RGB spectrum). In the case of single-layer image graphs, the same layer is repeated in each channel. After completing these procedures, the images are fed into the ResNet50 network. The convolution process and the network's fundamental architecture are illustrated in Fig. 4. Up until the middle pooling layer is reached, the input image is subjected to successive convolution and sampling processes. The grouping layer features are extracted as a vector with dimensions of $1 \times 1 \times 2048$ in this layer. This vector, generated for each image in the dataset, contains general attributes of the images retrieved by the approach, such as saturation, brightness, and intensity.

The final step in producing the feature vector is carried out using machine learning techniques; in other words, classifier techniques are applied to categorize the dataset. The ResNet50 neural network acts as an image feature extractor; by utilizing the convolutional base of this network, the most significant and distinctive features of the images are obtained. This is achieved not through machine learning, but rather through deep learning, using artificial networks that extract the most relevant features to enable optimal classification.

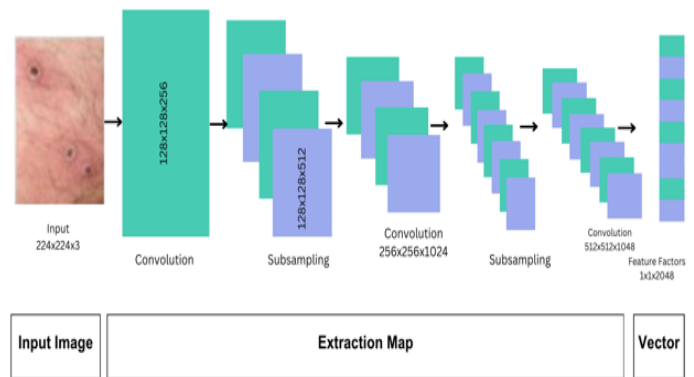


Fig. 6. The convolutional technique and the ResNet50 network's easy layout.

Even though a single CNN [37] may be used for both feature extraction and classification, there are several advantages to utilizing different techniques for each task. As a result, the automated classification approach used consisted of three stages: pre-processing, feature extraction (via CNN), and the classification system as shown in above Fig. 6.

V. CONFIGURING THE EXPERIMENT

The cross-validation classification scenario served as the foundation for the suggested technique [38]. There were 57 homogeneous and symmetric images with and without evidence of monkeypox; 114 images were divided using a cross-validation technique. When there are insufficient images in the collection, this type of categorization is suitable [39]. Fig. 3 depicts the cross-validation scenario using automated categorization algorithms. Due to their effectiveness in binary classification—where a set's components are divided into two categories according to a classification rule—the classification techniques used are well-established in the field [40]. Support Vector Machines (SVM) provides an optimal separation that reduces classification risk and increases the margin while also reducing error [41,42]. Logistic regression (LR) is used to predict the probability that a categorical dependent variable will be dichotomous, or divided into two groups [43]. Nearest Neighbors (KNN) uses discrete sample classification to forecast and estimate future values based on proximity, identifying similar data points. Additionally, Naive-Bayes' (NB) success is due to feature independence, which allows the determination of the likelihood that a test case has a particular feature value. Finally, the Centroid-based classifier (NC), derived from distances from the center, takes into account similarity with each class's centroid. The centroid is a vector representing the average frequencies of all terms among the members of a specific class.

The validation was carried out in three sections, with divisions of 15, 25, and 35 folds. Accuracy (A) and Precision (P), two evaluation measures, were used to assess the technique's performance with the dataset. These measures are based on the four elements listed below [44]:

- True Positive (TP): occurs when there is a match between the predicted class of the technique and the actual class of the dataset (finding).
- True Negative (TN): occurs when there is a match between the dataset's actual class (no finding) and the one predicted by the technique (no finding).
- False Positive (FP): occurs when there is a mismatch between the dataset's actual class (no finding) and the one predicted by the algorithm (finding).
- False Negative (FN): occurs when there is a mismatch between the dataset's actual class (a finding) and the one predicted by the technique (no finding).

Accuracy refers to the percentage of all predictions that were made correctly. Precision, on the other hand, indicates the accuracy of the positive predictions, i.e., the proportion of true positive values to all predicted positive values [45].

Metrics are calculated as follows [44]:

$$Accuracy = \frac{TP+TN}{TP+FP+FN+TN} \quad (1)$$

$$Precision = \frac{TP}{TP+FP} \quad (2)$$

VI. RESULTS

Four different classifier techniques were used as the learning strategy in the cross-validation classification scenario. The dataset was split into three studies, as previously mentioned: 15 folds, 25 folds, and 35 folds. The dataset was randomly divided into $K = 15, 25,$ and 35 segments as shown above. $K - 1$ segments were used for training the technique, while the remaining portion was used for performance evaluation. After dividing the dataset into K parts at random, this process was repeated K times to obtain K procedures and assessment outcomes. The final average performance was determined once all evaluations were completed.

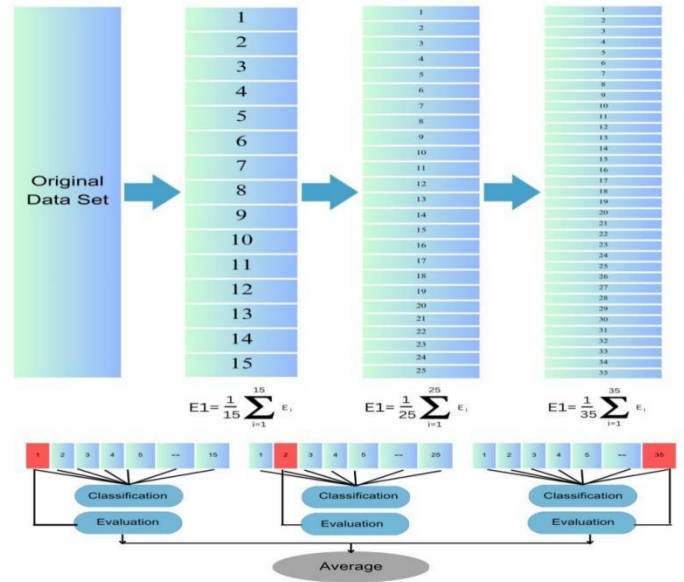


Fig. 7. The K-folds cross-validation strategy uses a single classifier with K values of 15, 25, and 35.

The technique was then retrained for the subsequent divisions. The technique's performance (E) is assessed as follows:

$$E = \frac{1}{k} \sum_{i=1}^k E_i \quad (3)$$

The process for 15 divisions, as well as the divisions of the folds in the dataset, is shown in Fig. 7. The 25 and 35 categories follow the same procedure to determine the performance (E). To compare the outcomes of several predictive classification processes—that is, the five learning strategies used to categorize the images—cross-validation was applied. The results of the various classification techniques are shown in Table II, along with a comparison of the divisional processes and evaluation criteria, which make it possible to identify the most accurate classifier. It is evident that as the number of folds increases, the KNN classifier (nearest neighbors) produces the highest values in the accuracy measure [46].

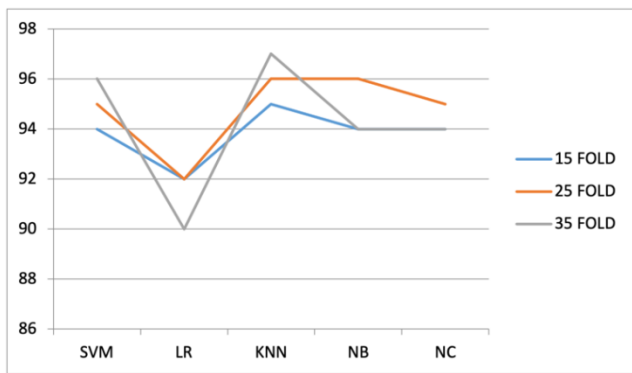


Fig. 8. The precision assessment metric's learning techniques in the three division experiments.

TABLE II. OUTCOMES OF A CROSS-VALIDATION CLASSIFICATION SCENARIO

| Fold | 15 | | 25 | | 35 | |
|------|----------|-----------|----------|-----------|----------|-----------|
| | Accuracy | Precision | Accuracy | Precision | Accuracy | Precision |
| SVM | 92.7 | 94.2 | 93.3 | 95.2 | 93.8 | 95.8 |
| LR | 90.3 | 92.5 | 90.1 | 92.6 | 89.4 | 90.4 |
| KNN | 94.2 | 95.4 | 95.5 | 96.4 | 95.2 | 97.7 |
| NB | 93.0 | 94.7 | 93.7 | 96.2 | 93.7 | 94.9 |
| NC | 92.7 | 94.2 | 93.2 | 95.7 | 93.7 | 94.9 |

VII. DISCUSSION

This shows that the categorization percentage is 94% in 15 divisions, 95% in 25 divisions, and 96% in 35 divisions. The accuracy indicates the proportion of the positive class predicted by the approach and the actual positive class in the dataset, as well as the quality of the classification scenario. In small datasets, the classifier with the best values often performs optimally. Similarly, the accuracy provides a 94% confidence level in the KNN classifier's quality compared to other learning techniques, provided the classes of the variables in the dataset are balanced. The accuracy measure and various folds used in the learning techniques are shown in Fig. 7. According to the suggested approach, the KNN classifier, the reported metrics, and the cross-validation classification scenario with 15, 25, and 35 folds together represent the best automated classification technique for the dataset, including discoveries related to monkeypox. The characteristic vectors of the images are extracted using the ResNet50 networks, and when paired with the approach, the results yield values that are competitive with the state of the art. As demonstrated, this strategy enables us to identify regions of interest within the images. While the current study focused on binary classification, it has been shown that the system can be expanded to categorize different diseases. The deep neural network's feature extraction technique includes the extraction of regions of interest (ROI) as shown in Fig. 8. Once combined, these characteristics are sent to the final classification technique, which utilizes them to provide a prediction.

VIII. CONCLUSION

This article's approach, which utilizes a dataset of patients with monkeypox, has demonstrated success. It gives the binary

labels of finding lesions with monkeypox and non-monkeypox findings. Classification results with 96% precision were achieved using 35 divisions of folds using KNN classification, which improves the image processing quality by identifying even small lesions in skin images. The accuracy of these results not only reflects the quality of the classification scenario and the percentage of the positive class predicted by the technique compared to the actual positive class in the dataset but also improves as the dataset is split into several parts, indicating an increase in the technique's performance. The ResNet50 technique of CNN is a crucial component of the technique, as it enables comparison of the features of images with and without lesions by applying deep learning to identify monkeypox findings. This is accomplished through classifiers that are assessed using metrics that measure how effectively the technique functions. Based on the conclusions acquired, this article can now report on categorizing medical images from a dataset related to monkeypox. The technique provides an automatic and objective estimation of the classification of monkeypox findings, facilitating expert interpretation during the pandemic. This makes the values obtained from the scenario and binary classifier in the quantitative analysis of the imaging study more reliable, leading to a more accurate diagnosis. In future, ascertaining 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. As a result of these findings, the categorization approach serves as a supplementary tool in medical diagnostics.

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