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Monkeypox Diagnosis Using MRMR-Based Feature Selection and Hybrid Deep Learning Models: ResNet50V2, NASNetMobile, and InceptionV3

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Abstract

Monkeypox, like many other epidemics diseases, has been spreading rapidly. Its transmission through both respiratory droplets and physical contact has significantly contributed to its fast dissemination. The emergence of the first major outbreaks in the African region in 2022, followed by the disease spreading at an epidemic level, has raised global concerns. Although this potentially fatal disease can be partially detected through PCR methods, it often exhibits symptoms similar to other skin diseases, making accurate diagnosis challenging. At this point, computer-aided detection systems, particularly those based on image processing techniques, become crucial. The primary aim of this study is to enable the automatic diagnosis of monkeypox using deep learning methods by enhancing classification performance through the selection of the most significant features among multiple models. In this study, a hybrid deep learning approach is proposed that integrates transfer learning models such as ResNet50V2, NASNetMobile, and InceptionV3 with the mRMR (Minimum Redundancy Maximum Relevance) feature selection method. The features extracted from each model were concatenated to form a unified feature vector, from which the 10 most relevant features were selected using the mRMR algorithm. Finally, classification was performed based on these selected features. Experiments were conducted on three different datasets—MSLD, MSCI, and MSID—containing various skin lesion diseases. The proposed approach achieved accuracy rates of 92.00%, 92.50%, and 87.65%, respectively. Among these, the highest accuracy was observed on the MSCI dataset, with a rate of 92.50%. This hybrid approach demonstrated high performance across diverse datasets and significantly contributed to clinical diagnosis processes by enabling the accurate identification of not only monkeypox but also other visually similar skin lesions.

Keywords: "Monkeypox, ResNet50V2, NASNetMobile, InceptionV3, mRMR."

1. Introduction

Skin diseases, which can affect individuals of all ages due to environmental factors, are caused by various viruses [1]. In dermatological conditions, transmission through physical contact is common, and spread via bodily fluids and particles is almost inevitable [2]. Infected individuals significantly increase the risk of transmission in crowded environments such as public transportation, and international travel facilitates the spread of outbreaks across regions [3]. Monkeypox was first identified in humans in 1970 in the Democratic Republic of the Congo and has since become endemic in the dense forest regions of several Central and West African countries [4]. The primary reason for its prevalence in forested areas is that the disease was initially observed in rodent species and monkeys. Since 1970, the number of cases has steadily increased, with a notable surge after 2017, peaking in 2022 [5]. Mpox, a member of the Orthopoxvirus genus from the Poxviridae family, is a zoonotic virus with a broad host range, capable of infecting many mammalian species, including humans, and is characterized by a high rate of animal-to-human transmission [6]. Figure 1 illustrates the replication cycle of the Mpox virus within a host cell following infection, as well as the mechanism of action of antiviral drugs. The virus can enter the cell in two different ways: either by endocytosis (being engulfed with fluid and particles) or through direct fusion with the cell membrane. After entry, the virus sheds its outer layers and releases enzymes into the host cell, targeting the DNA. Unlike many other viruses, Mpox replicates not in the cell nucleus but in specialized areas called "viral factories" [7]. Currently, diagnosis of the disease relies on identifying symptoms such as an incubation period of 7–14 days, fever, headache, fatigue, myalgia (characterized by tenderness, stiffness, and pain), swelling of lymph nodes, and skin lesions in infected patients. However, these symptoms are not sufficient for definitive diagnosis, as similar clinical signs may appear in various other skin diseases. Therefore, accurate diagnosis requires laboratory techniques such as virus isolation, electron microscopy, immunohistochemistry, and PCR (Polymerase Chain Reaction) [8]. Nonetheless, the similarity in clinical manifestations between Monkeypox (Mpox) and other dermatological lesion diseases poses challenges for

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timely and accurate diagnosis using conventional medical approaches. Traditional diagnostic tools and methods often rely on time-consuming laboratory tests and expert interpretation, which can lead to delays in treatment and increase the risk of disease transmission through contact. Recent studies have demonstrated that machine learning (ML) and deep learning (DL) algorithms can effectively analyze images of skin lesions along with clinical data to enable rapid and accurate diagnosis of similar viral and bacterial skin diseases. This highlights the significant potential of applying ML/DL techniques in Mpox diagnosis and their capability to enhance clinical decision support systems.

For differential diagnosis, the following diseases should be considered due to their similarity in clinical signs [8]:

- Measles,
- Bacterial skin diseases,
- Scabies,
- Drug allergies,
- Syphilis,
- Rickettsial pox,
- Smallpox,
- Chickenpox.

Considering that many of the above-mentioned skin diseases share similar characteristics, the use of machine learning (ML) and deep learning (DL) algorithms significantly accelerates the diagnosis process and plays a crucial role in preventing diagnostic errors by physicians [1].

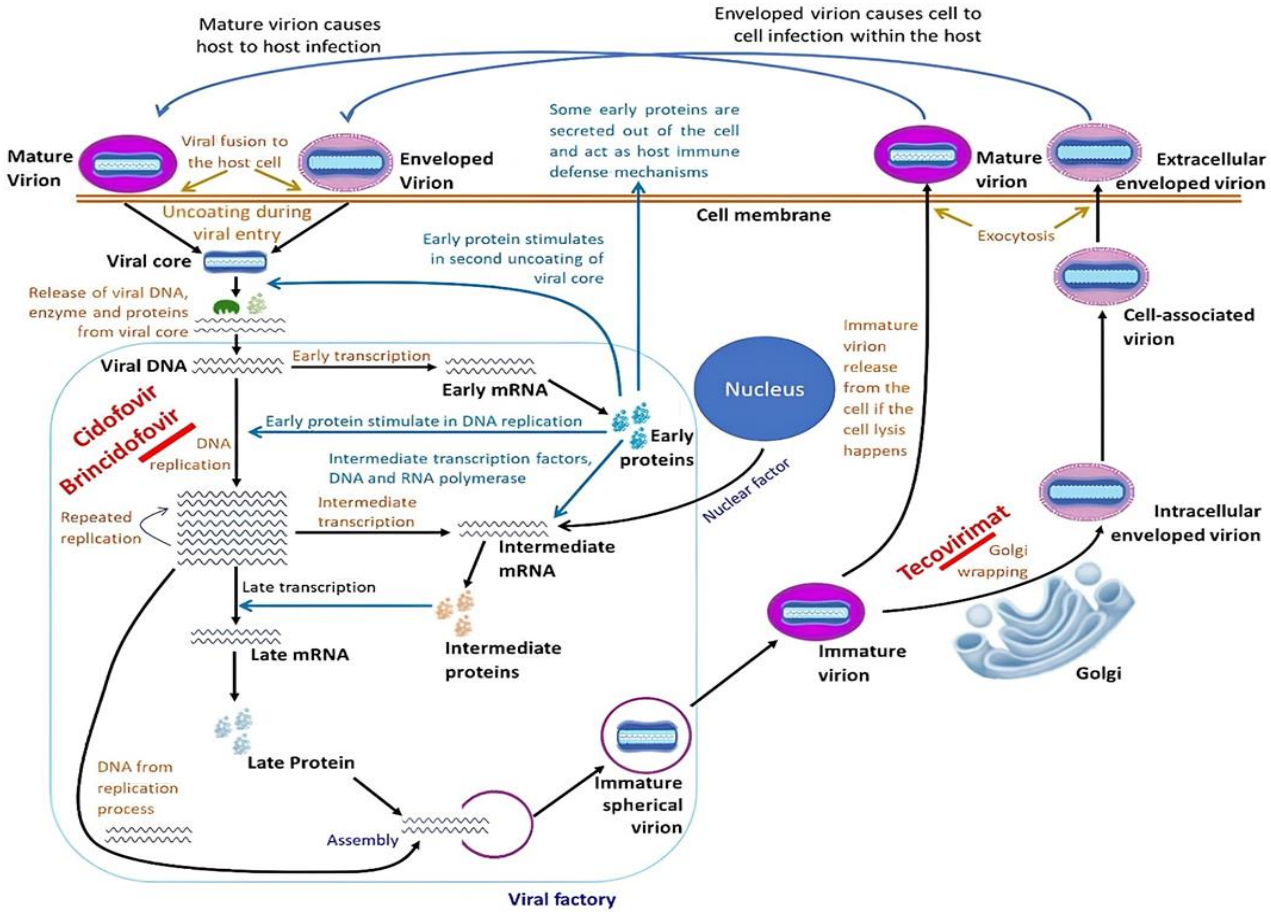


Fig. 1. The effect of Mpox virus on cells after transmission [7]

In recent years, research on deep learning-based diagnostic systems has gained remarkable momentum, especially for identifying monkeypox and other dermatological conditions. One noteworthy contribution in this domain is by Altun et al., who developed a hybrid model based on transfer learning using the MobileNetV3-s architecture. In this study, features were extracted using Convolutional Neural Networks (CNNs), yielding impressive results: an F1-score of 97.8%, AUC of 99%, and an overall accuracy of 96.8% [17]. The MonDiaL-CAD framework, proposed by Omneya Attallah, evaluated eight different CNN architectures, identifying the combination of Xception, ResNet-101, and ResNet-50 as the top performer. This hybrid architecture achieved an accuracy of 97.1% on the MSID dataset and 98.7% on the MSLD dataset [18]. Similarly, Khan et al. introduced the DNLR-NET model by combining DenseNet201 with Logistic Regression. This approach achieved a classification

accuracy of 97.60%, outperforming Random Forest and Support Vector Machine (SVM) models tested on the same data [19]. Asif et al. also adopted an ensemble strategy by merging DenseNet201, MobileNet, and DenseNet169 architectures. Their method achieved an accuracy of 97.78% [20]. Likewise, Sitaula and Shahi evaluated 13 pretrained deep learning models on the Monkeypox2022 dataset, achieving 87.13% accuracy using a combination of Xception and DenseNet169 validated through five-fold cross-validation [21]. Another effective hybrid approach was proposed by Luong et al., who integrated MobileNet with Logistic Regression. Their system demonstrated 97% accuracy, highlighting the strength of combining deep learning with machine learning techniques for disease classification [22]. Gülmez designed the MonkeypoxHybridNet model by combining ResNet50, VGG19, and InceptionV3 architectures. The model achieved 84.2% accuracy, outperforming the individual networks. The addition of a dropout layer helped reduce overfitting and enhanced robustness [23]. Rampogu carried out a comprehensive study evaluating both deep learning and machine learning models using public datasets like ISIC. CNN models such as ResNet50, VGG19, EfficientNetB3, DenseNet121, MobileNetV2, and Xception were examined. Among them, ResNet18 achieved the highest accuracy at 99.49% [24]. Saleh and Rabie proposed a hybrid framework combining Weighted Naive Bayes, Weighted KNN, and LSTM models. Their approach incorporated Few-Shot Learning (FSL) and Weakly Supervised Learning (WSL) layers, enhanced with a Confusion-Based Voting mechanism. On an imbalanced dataset with 500 samples, their model achieved a classification accuracy of 98.48% [25]. Fatih Uysal presented an innovative hybrid model that combined RepVGG and MnasNet with an LSTM layer to capture temporal dependencies, achieving an accuracy of 87% [26]. In a separate study, Tasci used the HAM10000 and Kaggle datasets to compare various CNN models. In his hybrid model, supported by the ReliefF feature selection algorithm, AlexNet and ResNet50 achieved 92.41% and 85.17% accuracy, respectively [27].

2. Materials and Methods

In this study, feature selection based on the Minimum Redundancy Maximum Relevance (mRMR) algorithm was hybridly combined with transfer learning architectures. This approach enables faster and more accurate results in the medical diagnosis process of monkeypox. The goal was to facilitate the detection of the disease by doctors using this method. Figure 2 presents the experimental stages of the study. The experimental stages of the study and the methodology followed are detailed below:

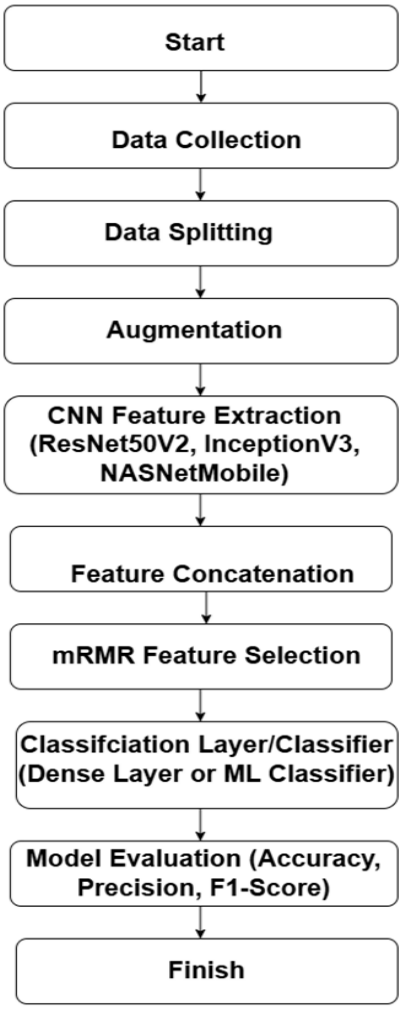


Fig. 2. Research methodology

2.1. Dataset and Preprocessing

In this study, three different datasets—MSID, MSCI, and MSLD—are used, as shown in Table 1. The performance of the developed model was evaluated using these datasets. The data was split into training, validation, and testing sets in an 80-10-10 ratio. To match the input dimensions of the model, the image data was rescaled to 224×224 pixels. The data augmentation techniques listed in Table 2 were applied only to the training data. Data augmentation helps prevent overfitting by ensuring the model does not memorize the training data excessively, thereby improving the general performance of the model. The hyperparameter values used in the study are presented in Table 3. The ReduceLROnPlateau callback reduces the learning rate by half when the performance plateaus. The categorical_crossentropy loss function used in this study is commonly preferred for multi-class classification problems. This function calculates the difference between the predicted probability for each class and the actual class label. To achieve high classification accuracy, the value of this loss function should be as low as possible.

Table 1. Distribution of datasets used in the study

Data Set	Class	Count
MSLD	Monkeypox	102
	Others	126
MSID	Monkeypox	279
	Normal	293
	Chickenpox	107
	Measles	91
MSCI	Monkeypox	100
	Normal	100
	Acne	100
	Chickenpox	100

Table 2. Summary of preprocessing and data augmentation methods

Augmentation Type	Configuration	Description
Rotation Range	40° (Clockwise & Counterclockwise)	Random image rotation up to ±40 degrees
Width Shift	0.2 (20%)	Horizontal shift up to 20% of image width
Height Shift	0.2 (20%)	Vertical shift up to 20% of image height
Zoom Range	0.2 (20%)	Random zoom in or out by up to 20%
Shear Range	0.2 (20%)	Shear transformation applied within 20% range
Horizontal Flip	Enabled (True)	Random horizontal flipping
Vertical Flip	Not Applied	No vertical flipping performed
Brightness Range	[0.8, 1.2]	Adjust brightness between 80% and 120%
Channel Shift	Not Applied	No shift in color channels
Fill Mode	Nearest	Fill empty pixels using nearest neighbor method

Table 3. Model training parameters

Parameter	Value
Input Size	(224, 224, 3)
Batch Size	8
Epochs	32
Learning Rate	1e-4
Optimizer	Adam
Learning Rate Scheduler	ReduceLROnPlateau
Loss Function	categorical_crossentropy

2.2. Transfer Learning Architectures

In the developed model, the feature extraction capabilities of three different convolutional neural network (CNN) architectures—ResNet50V2, InceptionV3, and NASNetMobile—were combined to enhance overall performance. These pre-trained models, initialized with ImageNet weights, were used exclusively for feature extraction by freezing all their layers during training to prevent weight updates. This approach allows the model to leverage learned representations while reducing the risk of overfitting given the dataset size. Compared to other deep CNN architectures, ResNet50V2 is more advantageous due to its easier training and higher accuracy performance. It includes various layers such as Dense, Flatten, and Dropout [9]. Through the use of residual blocks, the model enables information to pass through a "residual block" to another layer instead of directly

forwarding it to the next, allowing for the construction of more complex structures, increasing network depth, and supporting a healthier learning process [10]. The output feature map from ResNet50V2 is pooled using a Global Average Pooling layer, producing a 2048-dimensional feature vector. InceptionV3 is a deep neural architecture consisting of 42 layers. This architecture includes convolutional layers, batch normalization, and max pooling layers [11]. Unlike InceptionV2, InceptionV3 introduces convolutional factorization, which improves computational efficiency by decomposing 3×3 convolutions into 1×3 and 3×1 convolutions, thereby reducing the number of parameters [12]. The output of InceptionV3 is similarly passed through a Global Average Pooling layer, resulting in a 2048-dimensional vector. NASNetMobile is a neural network model designed through a Deep Learning-based Neural Architecture Search (NAS) approach. Due to the significant difference in the number of parameters, NASNetMobile is considered much more reliable compared to NASNetLarge. It consists of cells that can be developed using reinforcement learning. These cells repeat convolution and pooling operations multiple times based on the network's capacity [13]. The architecture of NASNet is formed by combining these cells. In addition, this approach includes a Recurrent Neural Network (RNN) component called the "Controller," which acts as the parent AI, and evaluates the performance of a model called the "Child Network" within the CNN to optimize its architecture for better efficiency [14]. The Controller RNN optimizes the cells in blocks, making the structures adaptive rather than fixed, based on the dataset. Each block is treated as a functional module and can perform the following operations [15]:

- Convolutions,
- Max Pooling,
- Average Pooling,
- Separable Convolutions,
- Identity Mapping and others.

2.3. Minimum Redundancy Maximum Relevance (mRMR) Algorithm

It is a feature selection method that filters the existing features to ensure maximum relevance to the target classes, rather than using all the features. Feature selection reduces computational costs, enabling the model to run faster, minimizes noise, increases the accuracy of class predictions in the dataset, and provides more useful features, thus allowing function types to be defined and traceable [16]. Using the combined feature vector obtained from the final dense layer (with 1024 features), the 10 most significant features were selected using the mRMR algorithm. For this purpose, a subset of 100 samples from the training data was extracted to compute feature relevance and redundancy efficiently. Figure 3 illustrates that the input images are processed through the three different CNN models (NASNetMobile, ResNet50V2, InceptionV3), and their extracted features are concatenated. The combined features are then subjected to the mRMR algorithm to select the most informative subset, which is subsequently passed to the classification layer for improved performance and reduced computational complexity.

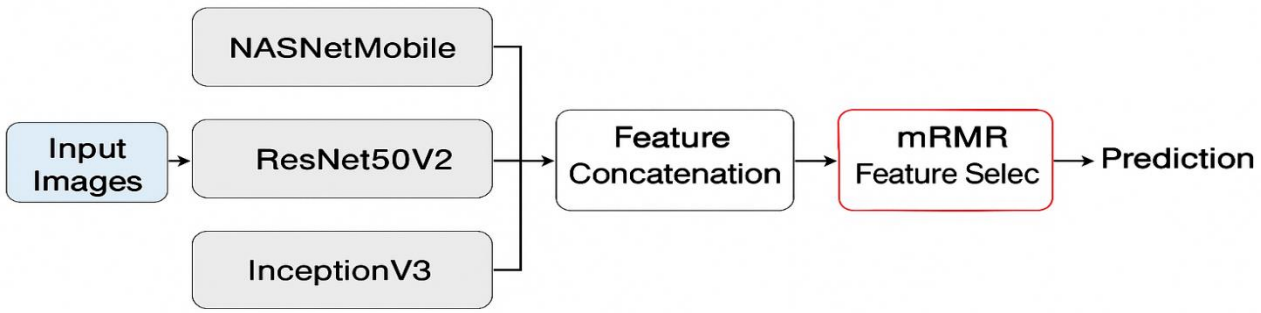


Fig. 3. The integration process of the mRMR algorithm in the proposed hybrid model

3. Results and Discussion

In this study, the PyCharm IDE was utilized. Python was chosen as the programming language, and the Keras and TensorFlow libraries were employed. The input dimensions of the model were set to 224×224, and the batch size and number of epochs were set to 8 and 32, respectively. The learning rate was defined as 1×10^{-4}. To prevent overfitting and improve generalization performance, the ReduceLROnPlateau callback function was applied: if no improvement in validation accuracy was observed for three consecutive epochs, the learning rate was reduced by half. The fully connected (dense) layer before the output consisted of 1024 neurons, and a 50% dropout rate was applied. In this study, transfer learning architectures ResNet50V2, InceptionV3, and NASNetMobile were selected and integrated. The final layers of these architectures were used as feature extractors. The feature vectors obtained from the three models were concatenated to form a single unified feature vector. The Minimum Redundancy Maximum Relevance (mRMR) algorithm was applied to the combined feature vector extracted from the dense layer of the model to select the 10 most informative features, aiming to enhance classification performance. Additionally, data augmentation techniques, as presented in Table 3, were applied to the training data to improve the model's robustness. The

classification results and related performance metrics obtained from the study are detailed in Table 4. Table 4 shows the classification performance of the proposed hybrid model applied to three different datasets (MSCI, MSLD, MSID), including accuracy, F1-score, precision, and sensitivity values. From the table, it can be observed that the accuracy percentages vary depending on the diversity of the datasets used.

Table 4. Testing results

Model	Dataset	Optimizer	Accuracy (%)	F1-Score (%)	Precision	Sensitivity	Total Training Time (min)	FLOPs (Billions)
Proposed Hybrid Model	MSCI	Adam	%92,50	%90,05	%94,25	%92,50	10 min 43 s	13.84
	MSLD	Adam	%92,00	%92,00	%92,50	%93,00	21 min 53 s	13.84
	MSID	Adam	%87,65	%85,26	%87,76	%85,00	6 min 0 s	13.84

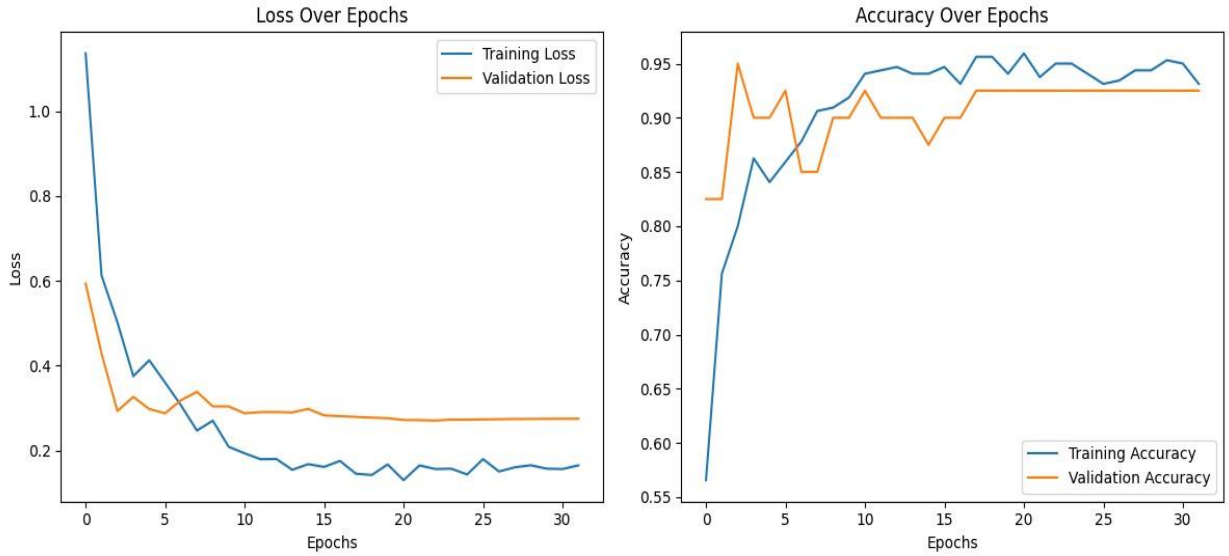


Fig. 4. Hybrid model performance success status and loss status for the MSCI dataset

Figure 4 presents the accuracy and loss graph of the MSCI dataset, which achieved the highest performance among the datasets with an accuracy rate of 92.50%. Examining the graphical trend of the loss values, the training loss shows some fluctuating increases at certain points but eventually decreases to around 0.15. Although the validation loss initially exhibits fluctuations, it gradually stabilizes and levels off around 0.25 after the 15th epoch. These results indicate that the model has a strong generalization capability, as reflected by the achieved accuracy and loss values. The training accuracy initially starts at approximately 57–58% and increases rapidly, surpassing 90% after 10 epochs. Following the 10th epoch, it remains between 90–95%, indicating high performance. The validation accuracy reaches around 95% in the early epochs and then stabilizes at approximately 92%, demonstrating the overall strong performance of the model and suggesting that overfitting is not evident.

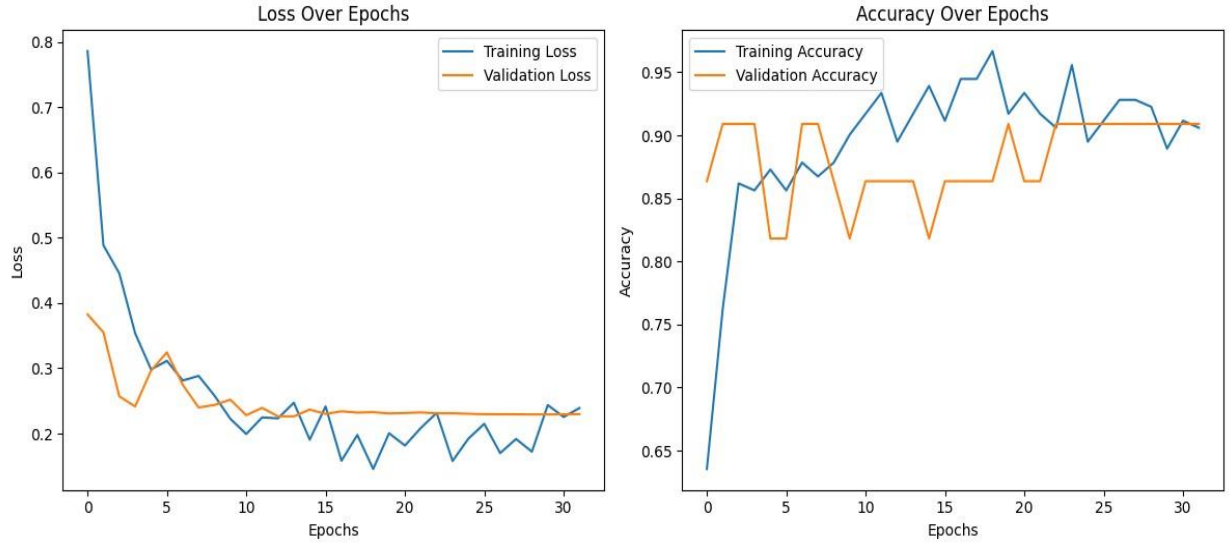


Fig. 5. Hybrid model performance success status and loss status for the MSLD dataset

Figure 5 shows the accuracy and loss graph of the MSLD dataset, which achieved the second-best performance among the datasets with an accuracy rate of 92.00%. The training loss starts at around 0.80 and decreases rapidly, reaching approximately 0.20. Similar to the MSCI dataset, the validation loss gradually decreases and stabilizes around 0.25 after the 15th epoch. These results indicate that the model also performs well on this dataset, demonstrating strong generalization capability. The training accuracy initially ranges between approximately 60–65% and rapidly increases, surpassing 85% after the 5th epoch. After this point, the accuracy begins to fluctuate, continuing this pattern until the final epoch while maintaining a high-performance level between 90–95%. Validation accuracy initially reaches around 87% but then fluctuates, dropping to around 82%. After the 22nd or 23rd epoch, it stabilizes at 92%, indicating strong overall model performance and suggesting that overfitting is not present.

Figure 6 presents the accuracy and loss graph for the MSID dataset, which achieved the lowest performance among the datasets with an accuracy rate of 87.65%. Observing the graphical trend of the loss values, the training loss, despite showing some fluctuations at certain points, decreased to approximately 0.10–0.15. Although the validation loss initially exhibited a fluctuating pattern, it stabilized around 0.26 after the 5th epoch. These results suggest that, despite a slightly lower accuracy, the model still demonstrates a strong generalization capability. The training accuracy initially starts below 70% and increases rapidly, reaching around 87% by the 5th epoch. It then continues to rise with fluctuations until the final epoch, maintaining a high-performance level between 90–95%. The validation accuracy reaches approximately 92% in the early stages but slightly drops to around 90%, continuing with minor fluctuations. After the 20th epoch, it stabilizes at around 90%, indicating strong overall model performance and providing evidence that overfitting is not observed.

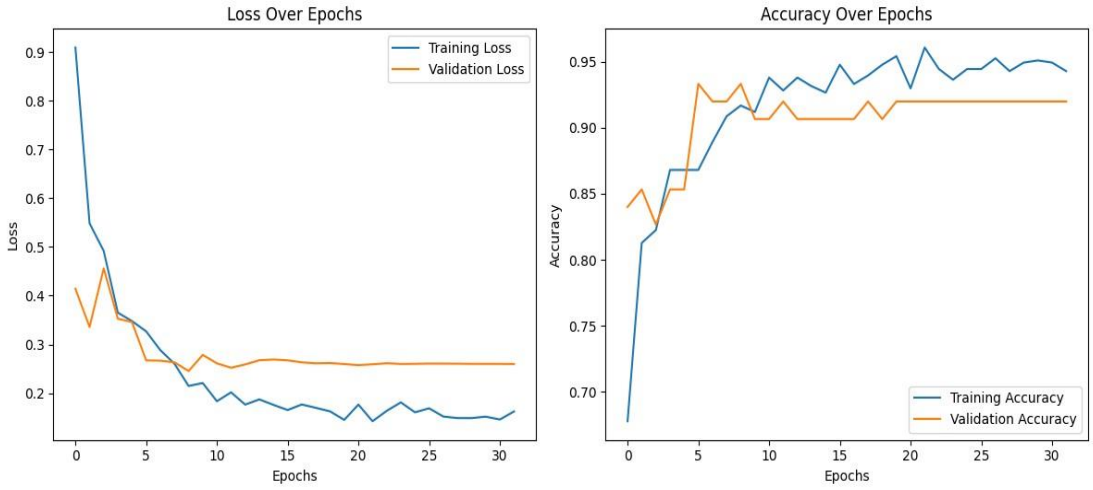


Fig. 6. Hybrid model performance success status and loss status for the MSID dataset

Table 5. Confusion matrix of the hybrid model for the overall performance on the MSLD dataset

		Predicted Class		
		Monkeypox	Others	Total
Actual Class	Monkeypox	11 (TP)	0 (FN)	11
	Others	2 (FP)	12 (TN)	14

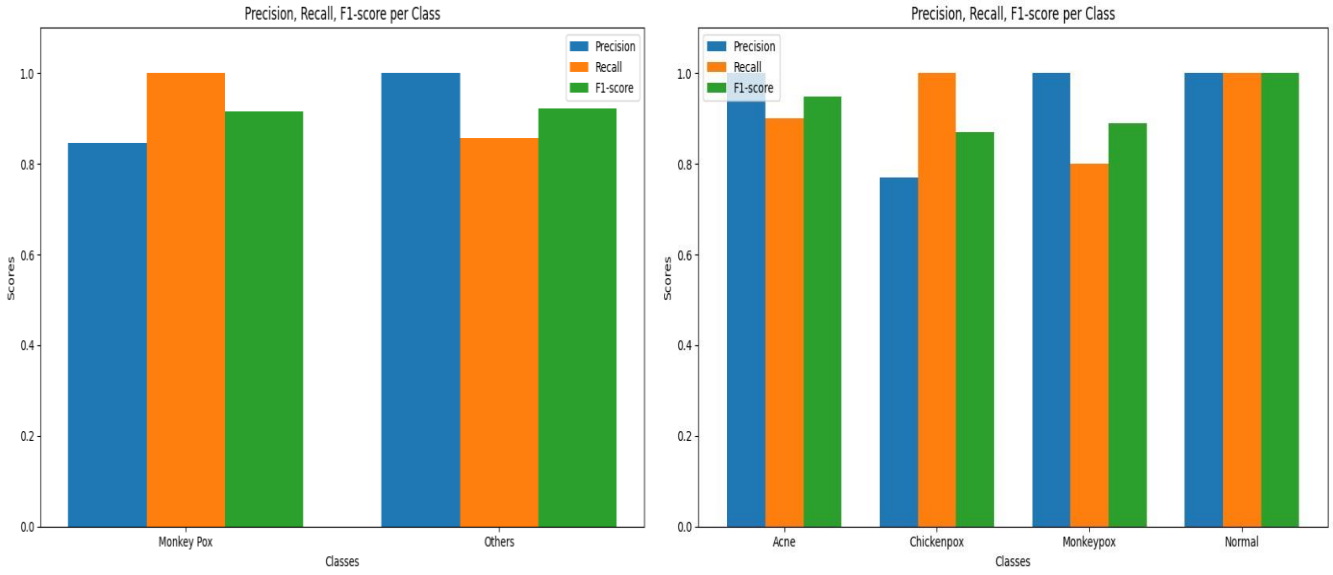
Table 6. Confusion matrix of the hybrid model for the overall performance on the MCSI dataset

		Predicted Class				
		Acne	Chickenpox	Monkeypox	Normal	Total
	Acne	9 (TP)	1 (FN)	0	0	10
Actual Class	Chickenpox	0	10 (TP)	0	0	10
	Monkeypox	0	2 (FP)	8 (TP)	0 (FN)	10
	Normal	0	0	0	10 (TP)	10

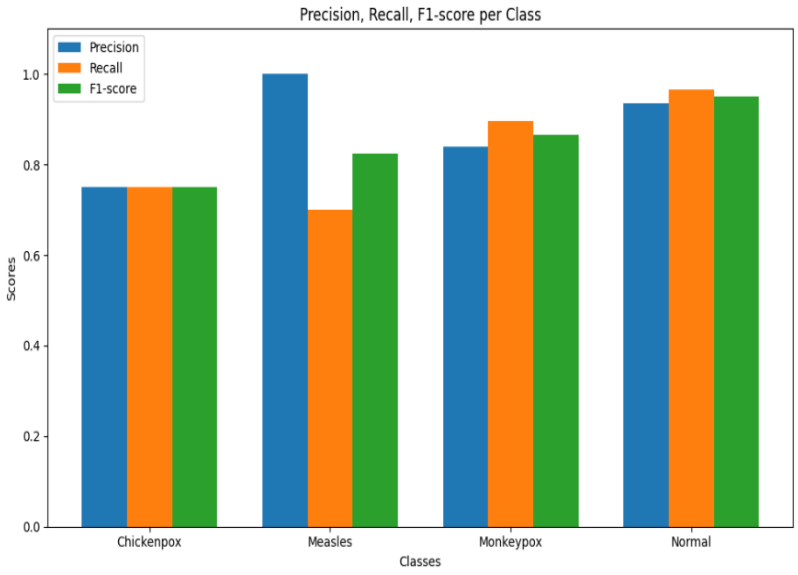
Table 7. Confusion matrix of the hybrid model for the overall performance on the MSID dataset

		Predicted Class				
		Chickenpox	Measles	Monkeypox	Normal	Total
	Chickenpox	9 (TP)	0	3 (FN)	0	12
Actual Class	Measles	1 (FN)	7 (TP)	1 (FN)	1 (FN)	10
	Monkeypox	2 (FN)	0	26 (TP)	1 (FN)	29
	Normal	0	0	1 (FN)	29 (TP)	30

The confusion matrices of the datasets used in the study are presented above. Table 5 shows the confusion matrix for the MSLD dataset, which includes two classes: Monkeypox and Others (comprising other skin diseases and healthy images). All samples in the Monkeypox class were correctly classified, indicating that the developed model performs exceptionally well in this category. In the Others class, 2 out of 12 samples were misclassified as Monkeypox. This misclassification may stem from visual similarities between certain skin conditions and Monkeypox. Overall, the model's ability to accurately detect Monkeypox confirms the effectiveness of the developed hybrid model. In Table 6, the confusion matrix for the MSCI dataset involves four classes: Acne, Chickenpox, Monkeypox, and Normal. The model accurately classified all samples in the Chickenpox and Normal classes, demonstrating strong performance in these categories. In the Acne class, one sample was misclassified, and in the Monkeypox class, two samples were confused with Chickenpox. This confusion may be attributed to visual similarities between different types of rashes. Overall, the model provides reliable predictions across all classes, particularly for Monkeypox detection. In Table 7, the confusion matrix for the MSID dataset includes four classes: Chickenpox, Measles, Monkeypox, and Normal (healthy). Within the Monkeypox class, 26 samples were correctly classified, and only 3 were misclassified into other classes, indicating robust model performance in this category. In the Normal class, only one sample was incorrectly labeled as Monkeypox. Some confusion was observed between the Chickenpox and Measles classes, likely due to visual resemblance. In general, the model achieves high accuracy across all classes and delivers dependable results, especially for identifying Monkeypox.About Title, Abstract, Author's Information



(a) **(b)**



(c)

Fig. 7. Class-wise precision, recall, and f1-score values: (a) MSLD, (b) MCSI, (c) MSID

Figure 7 presents a comparative analysis of the model's performance on the classes within the used datasets using Precision, Recall, and F1-score metrics.

4. Conclusions

In this study, Monkeypox disease was detected with accuracy rates of 92.50%, 92.00%, and 87.65% on three different datasets, namely MSCI, MSLD, and MSID, respectively. The datasets used in the study consist of images representing various skin lesions, including Monkeypox, Chickenpox, Measles, Acne, and healthy skin. Upon analyzing the results obtained from the developed hybrid model, it was observed that factors such as class imbalance, diversity of classes, and visual similarities between the skin diseases in the datasets significantly influenced the accuracy rates. This indicates that even with the application of image processing techniques, diseases with similar visual characteristics—particularly clinically important conditions like Monkeypox—can still be misclassified. Therefore, it is crucial to enrich the datasets as much as possible and to continuously improve image processing methods. In this study, a hybrid architecture was developed by combining three different transfer learning models (NASNetMobile, ResNet50V2 and InceptionV3), and feature selection was applied using the mRMR (Minimum Redundancy Maximum Relevance) algorithm. mRMR reduced the number of features derived from the combined transfer learning models, ensuring that only the most meaningful and relevant features were included in the final model. This led to a simplified learning process and improved model performance. The highest accuracy rate, 92.50%, was achieved on the MSCI dataset, which includes four balanced classes with 100 images each. The balanced distribution of classes provided an advantage in terms of class representation and contributed to the higher accuracy achieved. In contrast, the other datasets contained a varying number of classes and imbalanced distributions, which led to comparatively lower performance. An analysis of the confusion matrices and performance graphs for the three datasets demonstrated that the model exhibited strong discriminative performance, particularly in identifying Monkeypox cases. Furthermore, the correct and systematic application of data augmentation techniques had a positive impact on the overall performance of the model. In conclusion, the developed hybrid model achieved high accuracy across all three datasets and delivered reliable and effective results, especially in the identification of Monkeypox disease. In this study, successful results were achieved by combining the strengths of different transfer learning architectures and selecting the most relevant features using the mRMR algorithm. The use of multiple datasets revealed that higher performance was obtained particularly in those with balanced class distributions, emphasizing the influence of image quality and class representation on model performance. The developed model enables accurate and rapid diagnosis, reducing the reliance on costly and time-consuming laboratory tests such as PCR. This is especially important in low-resource settings—such as regions in Africa with limited healthcare infrastructure—where early detection and timely intervention are critical.

The observed performance differences across datasets are primarily attributed to variations in content diversity and data distribution. While the limitations of the datasets led to decreased model performance in some real-world scenarios, the use of multiple datasets allowed the model to generalize well, even in the presence of imbalanced classes and visually similar disease categories. These contributions support the development of more efficient and interpretable diagnostic systems. This study demonstrates practical usability, especially in real-world clinical settings with limited resources. These contributions distinguish our work from existing studies and highlight its value as a robust and innovative tool for diagnosing Monkeypox and other visually similar skin diseases.

5. Limitations and Future Work

Although the proposed hybrid model demonstrated high classification performance across three different datasets, there are several limitations that should be addressed in future studies. The most critical limitation is the issue of class imbalance observed in some datasets (MSID and MSLD). In particular, classes with a small number of samples or those that are visually very similar to other skin lesions—such as Chickenpox and Monkeypox—made accurate classification more challenging. To mitigate this issue, advanced data augmentation techniques such as Generative Adversarial Networks (GANs), Autoencoder-based approaches, and Neural Style Transfer (NST) can be utilized. Another limitation of the study is the high computational cost of the hybrid architecture. This may hinder its deployment in low-resource environments with limited hardware capabilities. In future work, efforts will focus on increasing the computational efficiency of the model by exploring more lightweight architectures and optimizing the implementation environment. Moreover, integrating the model into real-world applications, including mobile health platforms, is also planned to enhance its accessibility and usability.

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