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MPCNN: a novel approach for detecting human Monkeypox from skin lesion images leveraging deep neural network

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ABSTRACT

The global healthcare scenario encounters a substantial challenge caused by the widespread outbreak of Monkeypox affecting over 65 countries. Limited availability of polymerase chain reaction (PCR) tests and biochemical assays necessitates alternative strategies. This study explores the viability of computer-aided identification of Monkeypox through the analysis of skin lesion images, offering a potential solution, particularly in resource-constrained settings. Employing data augmentation techniques, we augment the dataset to enhance its robustness. Subsequently, we utilize various pre-trained deep learning models, including EfficientNetB3, VGG16, ResNet50, AlexNet, and EfficientNet for classification tasks related to Monkeypox and other diseases. The achieved accuracies for these models are 98.48%, 69.19%, 91.41%, 78.38%, and 94.44%, respectively. We introduce a novel modified convolutional neural network (CNN) architecture named MPCNN to further improve performance. Our proposed MPCNN model demonstrates exceptional accuracy, precisely identifying Monkeypox patients with a remarkable precision of 99.49%. This technological advancement in disease identification holds significant promise for enhancing healthcare strategies and response mechanisms in the context of global health concerns.

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1. INTRODUCTION

The emergence of COVID-19 has drawn global attention to pressing health challenges, among them the resurgence of Monkeypox, a viral disease affecting numerous countries. Caused by a Zoonotic Orthopoxvirus with links to smallpox and cowpox, Monkeypox poses a significant threat to human health [1]-[3]. Its transmission occurs through direct contact with infected animals or humans, prompting concerns due to its potential for rapid spread and impact on human populations [4]-[7]. Compounding the issue is the limited availability of diagnostic tools like polymerase chain reaction (PCR) tests and biochemical assays, hindering early detection and containment efforts [8].

In response to the escalating cases of Monkeypox, the World Health Organization (WHO) convened an emergency meeting to assess the situation's severity [9]. The possibility of designating Monkeypox as a Public Health Emergency of International Concern underscores the urgency of the situation, reminiscent of responses to previous global health crises such as COVID-19 and Ebola [10]. Despite efforts by organizations like the United States Center for disease control (CDC) to elevate awareness and provide treatment options, including repurposed drugs, Monkeypox remains a pressing concern with no specific treatment available [11].

Recognizing the urgent need for improved diagnostic methods, this research endeavors to propose an automatic detection system, namely the Monkeypox convolutional neural networks (MPCNN). Unlike conventional diagnostic approaches, MPCNN leverages deep learning techniques to efficiently discern and differentiate Monkeypox lesions from similar dermatological conditions. By capitalizing on CNN models, MPCNN aims to achieve elevated prediction accuracy while reducing validation loss within the Monkeypox skin lesion dataset (MSLD). This novel approach transcends the limitations of traditional diagnostic methods, offering a promising avenue for accurate and accessible disease identification, particularly in resource-limited areas.

The core objective of this research extends beyond technological innovation; it seeks to provide a life-saving solution capable of revolutionizing disease identification and healthcare delivery. By amalgamating cutting-edge technology with purpose-built datasets, MPCNN offers hope for enhancing disease surveillance and response mechanisms, ultimately contributing to improved healthcare outcomes worldwide.

This work is structured as follows: section 2 presents a concise overview of related work, discussing existing research contributions. In section 3 outlines the methodology for developing and evaluating the MPCNN for automatic detection. In section 4, we conduct a comparative analysis of results, comparing MPCNN's performance with other methods and models. Finally, section 5 concludes the paper, summarizing key findings, contributions, and suggesting potential future work.

2. RELATED WORKS

The related works in the field of automatic detection of infectious diseases, particularly Monkeypox, encompass a variety of approaches and methodologies focused on enhancing diagnostic accuracy and efficiency. Numerous studies have utilized machine learning, including deep learning techniques, for the analysis of medical images to identify specific diseases and conditions.

Ali *et al.* [12] developed the 'MSLD,' containing images of lesions from Monkeypox, chickenpox, and measles. The research employs a 3-fold cross-validation approach and leverages pre-trained deep learning models specifically VGG-16, ResNet50, and InceptionV3 for the categorization of Monkeypox and other ailments. ResNet50 demonstrates the highest overall accuracy at 82.96 (±4.57%), followed by VGG-16 at 81.48 (±6.87%), with the ensemble system achieving 79.26 (±1.05%).

Haque *et al.* [13], address the challenges of early detection in Monkeypox, a rare viral disease sharing symptoms with measles and chickenpox. Training and evaluation involve two datasets, "Monkeypox Skin Images Dataset (MSID)" and "Monkeypox-dataset-2022(MD-2022)," with stratified cross-validation ensuring representative samples. Five pre-trained models are individually trained on each dataset, including DenseNet121, ResNet152V2, ResNet50, InceptionV3, and EfficientNetV2B3. Their ensemble model, using majority voting, outperformed individual models, achieving high accuracy scores of 89.4% and 98.7% for the respective datasets.

Ahsan *et al.* [14] explore the application of machine learning for diagnosing Monkeypox-related diseases through image-based diagnoses. Utilizing the publicly available "Monkeypox2022" dataset, sourced from various open-access portals without usage restrictions, the authors propose and assess a modified VGG16 model for identifying Monkeypox patients. Computational results demonstrate the model's effectiveness, achieving an accuracy of 97% (AUC=97.2) and 88% (AUC=0.867) across two distinct studies. To enhance interpretability, the authors employ Local Interpretable model-agnostic explanations (LIME), shedding light on the specific features indicative of Monkeypox virus onset.

Mohbey *et al.* [15] investigate public reactions to Monkeypox illnesses and utilizing a dataset of Monkeypox-related tweets, the researchers developed an architecture based on CNN and LSTM to predict sentiment polarities (positive, negative, and neutral) in tweets, achieving an impressive accuracy of 94%. The study contributes valuable insights into public awareness of Monkeypox infection, shedding light on sentiment patterns through social media analysis.

Örenç *et al.* [16] escalating global prevalence of Monkeypox has necessitated swift disease identification to curb its rapid transmission. This study employs deep learning models, specifically EfficientNetB3, ResNet50, and InceptionV3, for the accurate detection of Monkeypox. Notably, ResNet50 outperforms its counterparts, exhibiting an impressive accuracy of 94%. The evaluation criteria encompass precision, recall, F1-score, and support, revealing the models' robust performance in classifying Monkeypox with high precision. These findings underscore the suitability of the employed models for prospective research and applications in combatting the spread of Monkeypox.

Sahin *et al.* [17] Introduced a system utilizing body lesions to enable swift preliminary diagnoses, facilitating prompt actions for Monkeypox-infected individuals to seek a diagnosis. Based on the test outcomes, their proposed system demonstrates an image classification accuracy of 91.11%. They also

proposed a mobile application to train preliminary diagnosis of different skin type diseases. Table 1 presents a comprehensive overview of studies focused on the identification of Monkeypox, offering a summary of key findings and methodologies utilized in previous research endeavors.

Table 1. Overview of studies pertaining to the identification of Monkeypox

References	Algorithm	Result
Ali *et al.* [12]	VGG-16, ResNet50, InceptionV3, ensemble	Highest accuracy: 82.96%, early detectionfeasibility using transfer learning
Haque *et al.* [13]	Modified transfer learning, ensemble of pre-trained models	Impressive accuracy (89.4% and 98.7%) for two datasets
Ahsan *et al.* [14]	Modified VGG16, local interpretable model-agnostic explanations	High accuracy (97%) and AUC (97.2%), insights through LIME
Mohbey *et al.* [15]	CNN and LSTM architecture, sentiment analysis	High accuracy (94%), contribution to public awareness analysis
Örenç *et al.* [16]	EfficientNetB3, ResNet50, InceptionV3	High accuracy (94%), robust performance in classifying Monkeypox
Sahin *et al.* [17]	DCNN	91.11% classification accuracy

In conclusion, while the reviewed studies present significant progress in Monkeypox detection, further research should focus on integrating multi-modal data, assessing scalability in real-world settings, ensuring model robustness across diverse populations, and exploring collaborative training approaches like federated learning for improved healthcare outcomes.

3. METHOD

This research constructs an automated model for detecting Monkeypox utilizing a customized CNN architecture. The model is trained using the feature representation approach of transfer learning. The flow diagram of our suggested methodology for Monkeypox classification is depicted in Figure 1.

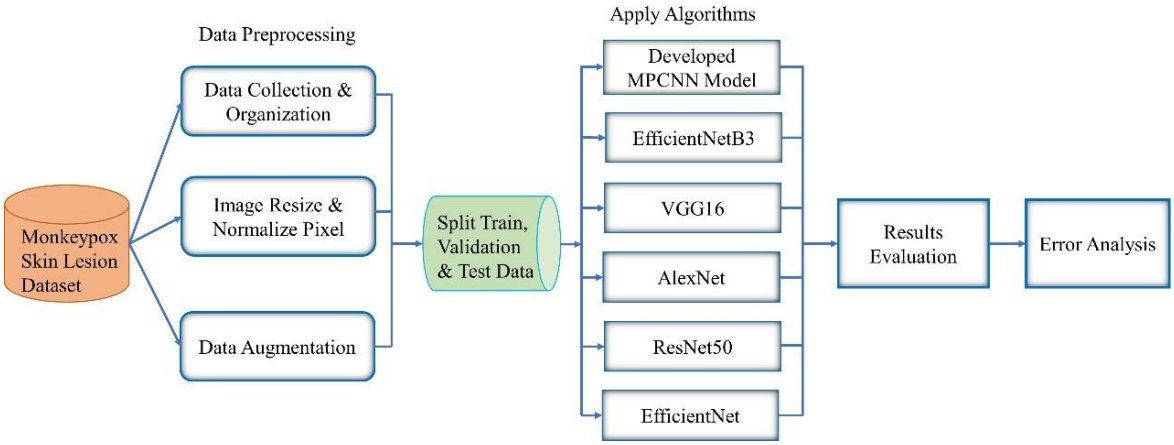

Figure 1. Flow diagram of the proposed system

3.1. Data set collection and organization

The dataset utilized in this study, sourced from Kaggle [18], has been meticulously curated for the computer-aided identification of human Monkeypox through the analysis of skin lesions. It consists of a total of 228 images, categorized into two primary classes: images depicting Monkeypox skin lesions and comparator images representing diseases such as Chickenpox and Measles. Each image in the dataset has been standardized to a resolution of 256×256 pixels with RGB color channels. Figure 2 provides a visual representation of a sample from the dataset used in this research. This figure showcases various images that are part of the dataset, highlighting the diversity and complexity of the data.

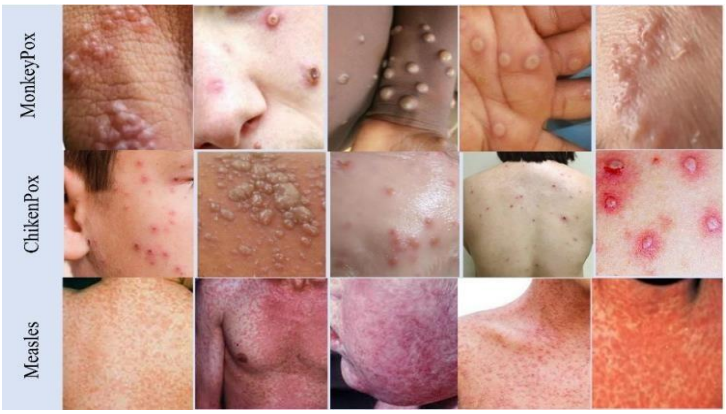

Figure 2. Sample of images within the dataset: Monkeypox, Chickenpox, and Measles

3.2. Pre-processing

Preprocessing is essential to standardize and enhance the quality of images before training the model [19]. This involves image resizing and normalization techniques to mitigate variability in original images. In this study, images are resized to 224×224 pixels while preserving the aspect ratio. The normalization process addresses significant fluctuations in image appearance, including contrast and brightness.

The development of a generalized CNN-based model requires a substantial volume of data, which is challenging due to the scarcity of clinical imaging information. To address this, image augmentation techniques are employed to increase the diversity of the dataset and enhance model robustness. These techniques encompass a variety of transformations, including rotation range, height shift, zoom range, width shift, fill mode, horizontal flip, shear range, and brightness jitter. By applying these augmentation strategies, the dataset is enlarged, improving the model's ability to generalize and reducing the risk of overfitting. Table 2 presents the methods for augmenting data employed in this investigation.

Table 2. Methods for augmenting data employed in this investigation

Generator type	Facility
Rotation range	Randomly
Height shift	Up to 2%
Zoom range	2%
Width shift	Up to 2%
Fill mode	Reflective
Horizontal flip	True
Shear range	2%
Brightness jitter	Up to 2%

An insightful breakdown of the MSLD is provided in Table 3, offering a comprehensive overview of the distribution of key parameters within the dataset. This includes information on lesion types, anatomical locations, age groups, and gender representation. The dataset is systematically organized into training, validation, and test sets to ensure a well-balanced and representative distribution, contributing to the robustness and reliability of the model evaluation process.

Table 3. Arrangement of the MSLD

Class label	Original images no.	Augmented images no.
Monkeypox	102	1428
Others (Chickenpox and Measles)	126	1764
Total	228	3182

3.3. Proposed model

The proposed MPCNN adopts a sequential architecture, beginning with an input layer configured with a 32-batch size and 256×256 RGB image dimensions. The model comprises six convolutional blocks, each contributing to the extraction of intricate features from the input data. Subsequently, a flattening layer

prepares the data for two dense layers: Dense_2 and Dense_3. Dense_2, housing 64 neurons, introduces non-linearity to the model, while Dense_3, the output layer, contains two neurons representing the binary classes-Monkeypox or not. With a total of 183,682 trainable parameters, the model demonstrates its adaptability and potential for accurate skin lesion classification. Figure 3 shows the architecture of the proposed MPCNN model.

Layer (type)	Output Shape	Param #
sequential_3 (Sequential)	(32, 256, 256, 3)	0
conv2d_6 (Conv2D)	(32, 254, 254, 32)	896
max_pooling2d_6 (MaxPooling2D)	(32, 127, 127, 32)	0
conv2d_7 (Conv2D)	(32, 125, 125, 64)	18496
max_pooling2d_7 (MaxPooling2D)	(32, 62, 62, 64)	0
conv2d_8 (Conv2D)	(32, 60, 60, 64)	36928
max_pooling2d_8 (MaxPooling2D)	(32, 30, 30, 64)	0
conv2d_9 (Conv2D)	(32, 28, 28, 64)	36928
max_pooling2d_9 (MaxPooling2D)	(32, 14, 14, 64)	0
conv2d_10 (Conv2D)	(32, 12, 12, 64)	36928
max_pooling2d_10 (MaxPooling2D)	(32, 6, 6, 64)	0
conv2d_11 (Conv2D)	(32, 4, 4, 64)	36928
max_pooling2d_11 (MaxPooling2D)	(32, 2, 2, 64)	0
flatten_1 (Flatten)	(32, 256)	0
dense_2 (Dense)	(32, 64)	16448
dense_3 (Dense)	(32, 2)	130

Total params: 183,682
Trainable params: 183,682
Non-trainable params: 0

Figure 3. Architecture of the proposed MPCNN model

The model's effectiveness is demonstrated by its accuracy in classifying skin lesions as either indicative of Monkeypox or not. By leveraging the learned features from the dataset and employing a sequential architecture with multiple convolutional blocks, the model can discern subtle patterns and characteristics associated with Monkeypox lesions. This allows for precise classification, contributing to the model's overall effectiveness in aiding the identification and diagnosis of Monkeypox cases.

4. RESULT AND DISCUSSION

This study investigated the efficacy of deep neural networks in detecting human Monkeypox from skin lesion images. Previous research has explored various diagnostic methods for Monkeypox, such as PCR tests and biochemical assays, but these methods are often resource-intensive and not readily available in all settings. Limited studies have investigated the potential of automated, image-based detection systems leveraging deep learning, particularly focusing on the comparative performance of different neural network architectures in identifying Monkeypox lesions. The proposed MPCNN model significantly outperformed existing deep learning architectures in accurately identifying Monkeypox from skin lesion images. Specifically, the MPCNN achieved an impressive accuracy of 99.49%, compared to 98.48% for EfficientNetB3, 69.19% for VGG16, 91.41% for ResNet50, 78.38% for AlexNet, and 94.44% for EfficientNet. The results, as depicted in Table 4, provided a detailed insight.

Table 4. Comparison of the proposed model with the pre-trained model

Model	Accuracy	Precision	Recall	F1-score
EfficientNetB3	0.9848	0.9800	0.9899	0.9849
VGG16	0.6919	0.6900	0.6969	0.6934
ResNet50	0.9141	0.9100	0.9192	0.9146
AlexNet	0.7838	0.7800	0.7879	0.7838
EfficientNet	0.9444	0.9400	0.9495	0.9447
Proposed CNN (MPCNN)	0.9949	0.9900	1.0000	0.9950

4.1. Analysis of training and validation accuracy

To further explore the learning dynamics of the models, we present the training and validation accuracy curves along with the training and validation loss curves for each model. Figure 4 displays these accuracy curves, offering important insights into each model's performance. EfficientNetB3 (Figure 4(a)) demonstrates high training accuracy, yet the validation loss suggests potential overfitting. VGG16 (Figure 4(b)) shows a performance gap between training and validation accuracy, suggesting susceptibility to overfitting. ResNet50 (Figure 4(c)) maintains a balanced profile, indicating robust learning without severe overfitting. While AlexNet (Figure 4(d)) exhibits reasonable training accuracy, a significant gap in validation accuracy raises concerns about overfitting. The generic EfficientNet (Figure 4(e)) performs strongly overall, yet the validation loss curve suggests a need for regularization. In contrast, MPCNN (Figure 4(f)) shines with the highest training accuracy, and both training and validation curves indicate a well-generalized model, minimizing the risk of overfitting.

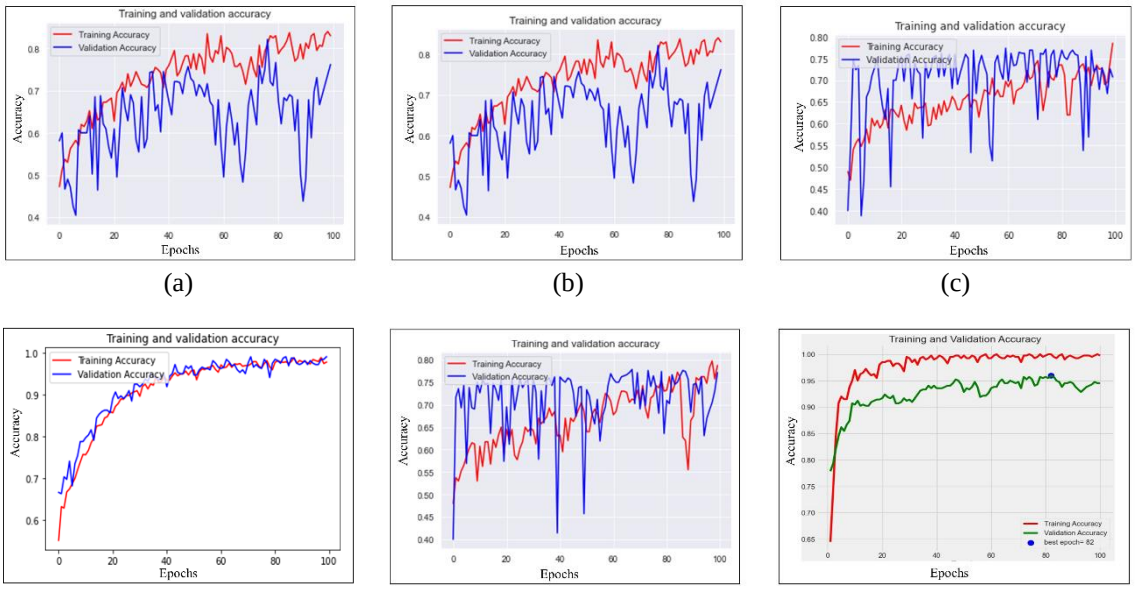

Figure 4. Training and validation accuracy curve of; (a) VGG16, (b) ResNet50, (c) Alexnet, (d) EfficientNetB3, (e) EfficientNet, and (f) MPCNN(proposed)

4.2. Analysis of training and validation loss

Training and validation loss are key metrics used to evaluate machine learning models. The training loss measures the error between the model's predictions and actual values during training, aiming to minimize this error [20]. Validation loss, computed on a separate dataset not seen during training, estimates how effectively the model generalizes to new data [21]. Figure 5 presents the training and validation loss curves, offering further insights into the model performance. VGG16 (Figure 5(a)) demonstrates a notable gap between training and validation loss, hinting at potential overfitting. In contrast, ResNet50 (Figure 5(b)) maintains a balanced loss profile, indicating robust learning. AlexNet (Figure 5(c)) shows reasonable training loss, but a considerable gap in validation loss raises concerns about overfitting. EfficientNetB3 (Figure 5(d)) exhibits high training loss, with the validation loss suggesting potential overfitting. While the generic EfficientNet (Figure 5(e)) performs strongly overall, the validation loss curve implies a need for

regularization. Lastly, MPCNN (Figure 5(f)) displays a minimal gap between training and validation loss, indicating a well-generalized model with a reduced risk of overfitting.

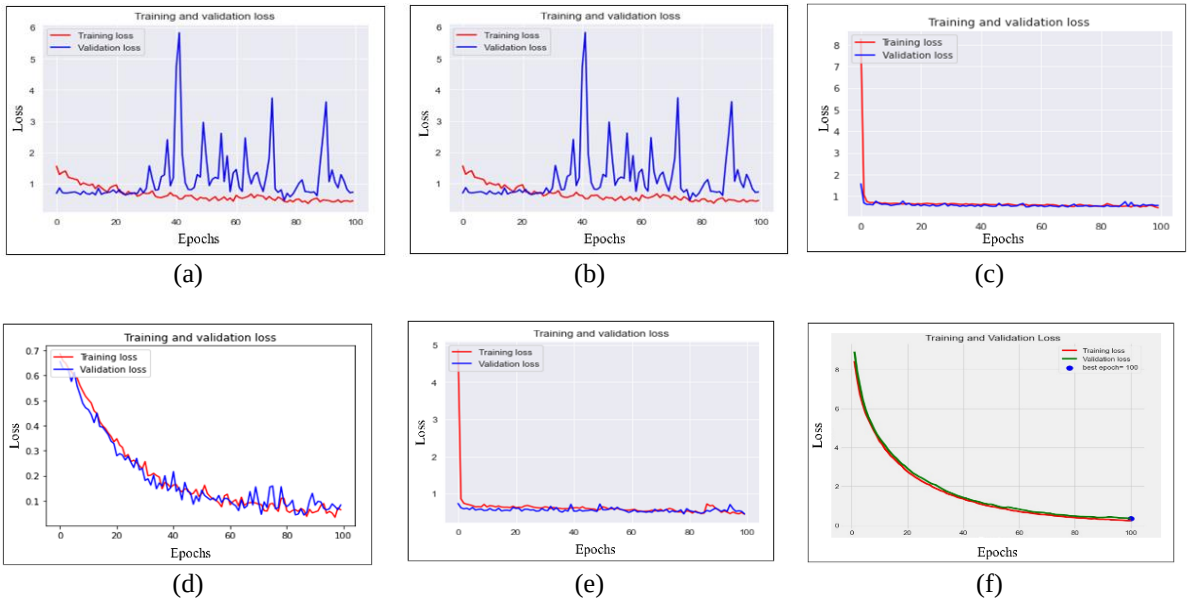

Figure 5. Training and validation loss curve of; (a) VGG16, (b) ResNet50, (c) Alexnet, (d) EfficientNetB3, (e) EfficientNet, and (f) MPCNN (proposed)

4.3. Analysis of confusion matrix

A confusion matrix, commonly used to assess the performance of a classification model, contrasts the actual dataset values with the predicted values produced by the model [22]. To better understand the performance of MPCNN, Figure 6 presents a confusion matrix that visually represents the model's classification results. This matrix provides insights into true positives, true negatives, false positives, and false negatives, allowing for a thorough evaluation of MPCNN's effectiveness in accurately classifying Monkeypox lesions.

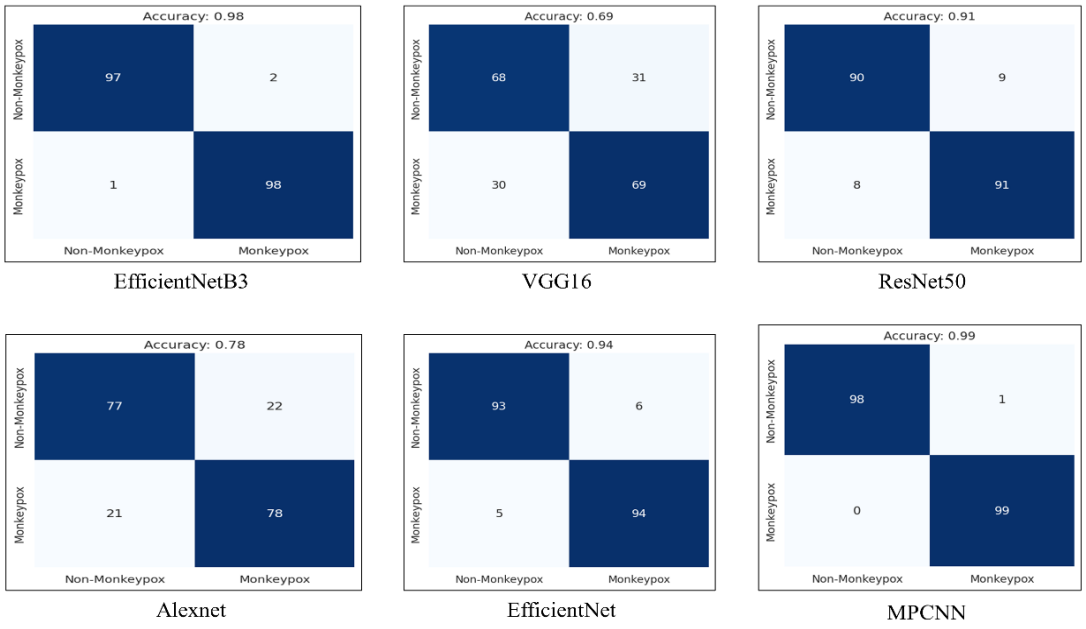

Figure 6. Confusion matrix of proposed and other model

4.4. Error analysis

In this section, this research performs an in-depth analysis of the performance of various machine learning models utilized for multiclass image classification tasks. Evaluation metrics such as hamming loss (HL), matthews correlation coefficient (MC), Jaccard Score (JS), and Cohen's Kappa (CK) are employed to assess the accuracy and effectiveness of the models in class prediction. Hamming Loss quantifies the average number of incorrect class predictions made by each classifier [23], while Matthews Correlation Coefficient considers the distribution of true positives (TP), false positives (FP), true negatives (TN), and false negatives (FN) predictions [24]. Additionally, the Jaccard score measures the similarity between predicted and actual class labels [25], and Cohen's Kappa evaluates the consistency between them, accounting for chance agreement [26]. By providing numerical representations of these evaluation metrics for each model, as depicted in Table 5, we gain valuable insights into their performance and ability to accurately classify images across multiple classes.

Table 5. Performance metrics comparison for a different model

Model	HL (%)	MC (%)	JS (%)	CK (%)
EfficientNetB3	0	97.94	97.03	95.97
VGG16	15.66	17.44	53.08	12.19
ResNet50	8.59	83.32	84.26	66.67
AlexNet	21.72	52.51	64.46	34.73
EfficientNet	5.56	85.43	89.52	70.46
Proposed CNN (MPCNN)	0	98.99	99	97.96

The proposed MPCNN model demonstrated a lower Hamming loss and higher Matthew's correlation coefficient, Jaccard score, and Cohen's kappa compared to other models. These results indicate that the MPCNN model excelled in predicting the presence of Monkeypox or other diseases within the same image and exhibited greater agreement with the ground truth labels. Overall, these outcomes underscore the potential efficacy of the proposed MPCNN model as a promising approach for accurate recognition of Monkeypox diseases and related conditions.

4.5. Comparison with other studies

To contextualize our findings, a comparison with other studies in the field was conducted. Our proposed MPCNN model demonstrates notable improvements in accuracy and precision compared to prior studies focusing on the automated detection of infectious diseases, particularly Monkeypox. While previous studies have reported accuracies ranging from 79.26% to 98.7%, our MPCNN model achieved a remarkable precision of 99.49%. These comparisons highlight the superior performance of our proposed MPCNN model in accurately identifying Monkeypox lesions, thus contributing significantly to the advancement of disease identification techniques in resource-constrained settings. The comparison of model performance across different studies is summarized in Table 6.

Table 6. Comparision with previous studies

Study	Name of sample	Technique	Accuracy
Ahsan *et al.* [14]	Monkeypox, Chickenpox,Measles, and Normal)	Modified VGG16	97±1.8%
Mohbey *et al.* [15]	61379 (tweets data)	CNN-LSTM	94%
Sahin *et al.* [17]	MSLD data	Mobile application	91.11%
Proposed CNN (MPCNN)	3192 (Monkeypox, Chickenpox and measles)	Modified CNN	99.49%

This table serves as a valuable tool for evaluating the effectiveness of different models across diverse studies, shedding light on their respective accuracies and precision. Specifically, it underscores the remarkable performance of the MPCNN model proposed in our research, showcasing its exceptional accuracy and precision in identifying Monkeypox lesions. This comparison not only highlights the efficacy of our model but also underscores its potential significance in advancing disease identification techniques, particularly in resource-constrained settings where accurate diagnosis is paramount.

5. CONCLUSION

In the context of Monkeypox detection, early prediction and detection play a crucial role in reducing financial burdens for patients and diagnostic time for medical professionals. The proposed modified CNN model exhibits promising outcomes with an exceptional accuracy, highlighting its potential in clinical

decision-making. Leveraging deep transfer learning methods holds promise for further enhancing Monkeypox detection. This research contributes significantly to advancing early disease detection and healthcare management, with implications for improved public health outcomes.

In future endeavors, emphasis could be placed on enhancing deep transfer learning methods for Monkeypox detection, expanding the dataset for more comprehensive training, integrating real-time data streams for dynamic interventions, and collaborating with healthcare institutions for real-world validation and deployment.

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