A Streamlined Approach towards Monkeypox Detection

Sarvesh Kulkarni 1, Jay Oza 1, Abhijit Patil 1, Rishi More 2, Gitesh Kambli 1, and Amit Maity 1

1Affiliation not available
2K. J. Somaiya Institute of Technology

December 7, 2023

Abstract

Monkeypox has recently emerged as a public health emergency with rising cases worldwide. Early clinical diagnosis is challenging due to symptom overlap with other diseases, but characteristic skin lesions provide distinguishing visual cues. This work proposes a deep convolutional neural network (CNN) tailored for automated monkeypox screening from lesion images. A dataset of over 3000 dermatological images was compiled, with data augmentation to enhance diversity. The CNN architecture comprised convolutional blocks for feature extraction and dense layers for classification. Rigorous training and cross-validation were conducted over 100 epochs to optimize model performance. On an unseen test set, the model achieved 86.87\% accuracy in classifying monkeypox lesions, with 94\% precision, 79\% recall and 86\% F1-score. These metrics were better than baseline models, indicating reliable screening potential. Though the model overlooked some atypical presentations, successes showcase utility for mass case-finding. As monkeypox monitoring intensifies, robust computer vision approaches can assist clinicians through explainable, real-time forecasts. Prospective validation across demographics and integration with clinical workflows is warranted before full-scale deployment. Overall, the study demonstrates deep learning’s promise in tackling the monkeypox outbreak through enhanced diagnosis.
A Streamlined Approach towards Monkeypox Detection

Sarvesh Kulkarni
Computer Engineering
K.J. Somaiya Institute of Technology
sarvesh.vk@somaiya.edu

Jay Oza
Computer Engineering
K.J. Somaiya Institute of Technology
jay.ozad@somaiya.edu

Prof. Abhijit Patil
Computer Engineering
K.J. Somaiya Institute of Technology
abhijit.patil@somaiya.edu

Rishi More
Computer Engineering
K.J. Somaiya Institute of Technology
rishi.vm@somaiya.edu

Gitesh Kambli
Computer Engineering
K.J. Somaiya Institute of Technology
gitesh.kambli@somaiya.edu

Amit Maity
Computer Engineering
K.J. Somaiya Institute of Technology
amit.maity@somaiya.edu

Abstract—Monkeypox has recently emerged as a public health emergency with rising cases worldwide. Early clinical diagnosis is challenging due to symptom overlap with other diseases, but characteristic skin lesions provide distinguishing visual cues. This work proposes a deep convolutional neural network (CNN) tailored for automated monkeypox screening from lesion images. A dataset of over 3000 dermatological images was compiled, with data augmentation to enhance diversity. The CNN architecture comprised convolutional blocks for feature extraction and dense layers for classification. Rigorous training and cross-validation were conducted over 100 epochs to optimize model performance. On an unseen test set, the model achieved 86.87% accuracy in classifying monkeypox lesions, with 94% precision, 79% recall and 86% F1-score. These metrics were better than baseline models, indicating reliable screening potential. Though the model overlooked some atypical presentations, successes showcase utility for mass case-finding. As monkeypox monitoring intensifies, robust computer vision approaches can assist clinicians through explainable, real-time forecasts. Prospective validation across demographics and integration with clinical workflows is warranted before full-scale deployment. Overall, the study demonstrates deep learning's promise in tackling the monkeypox outbreak through enhanced diagnosis.

Index Terms—Monkeypox, Deep Learning, Convolutional Neural Networks, Skin lesions, Image Classification

I. INTRODUCTION

Monkeypox is a viral zoonotic disease that has recently emerged as a global public health threat, with cases rising worldwide. A distinguishing characteristic of monkeypox virus infection is the development of skin lesions and rashes. Early clinical diagnosis is challenging due to symptom overlap with other diseases like chickenpox and measles. However, visual analysis of the morphology and distribution of characteristic monkeypox skin lesions can aid accurate diagnosis.

In recent decades, researchers have explored leveraging technologies like machine learning and computer vision for automated visual diagnosis of monkeypox. Early works focused on using conventional machine learning algorithms like SVM and random forests for classifying hand-engineered features from skin lesions. While these methods showed promise, they were limited by the need for feature engineering and lack of generalization.

The development of deep learning has allowed more sophisticated techniques like convolutional neural networks (CNNs) to transform medical image analysis. CNNs can directly learn higher-level visual patterns from the raw data through end-to-end training, without the need for manual feature engineering. This gives CNNs unmatched ability to extract meaningful features directly from medical images and detect intricate characteristics that are imperceptible to the human eye. Researchers began applying CNN architectures like VGGNet and ResNet pre-trained on natural images for transfer learning on monkeypox skin images. This significantly improved detection accuracy over machine learning approaches.

Recent works have focused on customized deep CNNs tailored for fine-grained skin lesion analysis. Novel multi-stage architectures, optimization with metaheuristics, and ensemble techniques have pushed the state-of-the-art further. However, challenges remain in model generalization across demographics and skin types.

Overall, the evolution from machine learning to deep CNNs has enabled high-performance and automated systems for monkeypox screening from skin images. With the rising global monkeypox spread, such AI systems can potentially enable accessible and mass screening, aiding containment efforts. Though real-world clinical translation remains an open challenge.

Going forward, interpretable AI to explain model predictions can improve clinical trust and acceptability. Furthermore, augmented intelligence combining computational power and clinical expertise can maximize impact. Overall, AI is poised to transform monkeypox diagnostics, but it necessitates an interdisciplinary approach considering both technical rigour and social context.

II. LITERATURE SURVEY

Monkeypox has recently emerged as a global public health concern, prompting growing research interest in AI-based
Expanding beyond binary classification, more recent works have explored multiclass discrimination of monkeypox against an array of similar viral rashes. Khan et al. [3] applied models like VGG16, ResNet50, and Inception-ResNet on a Kaggle image dataset, finding Inception-ResNet achieved 97% accuracy in classifying monkeypox against chickenpox, measles, and normal skin. M. M. Ahsan et al. [4] proposed a Generalization and Regularization Transfer Learning Approach (GRA-TLA) assessing models like Xception, ResNet101 and VGG19. Their approach with Xception differentiated monkeypox from 5 other rash classes with 77-88% accuracy.

While most papers utilize pre-trained CNNs, some have developed novel architectures tailored for monkeypox detection. For instance, D. Bala et al. [5] introduced MonkeyNet, a modified DenseNet achieving over 93% accuracy on their proposed Monkeypox Skin Images Dataset (MSID). M. M. Ahsan et al. [6] proposed the Mokeypox2022 dataset and a modified VGG16 network with 97% accuracy. Such datasets enable the training of deep CNNs from scratch.

A few studies have investigated classical machine learning approaches as alternatives to deep learning. Agustyaningrum et al. [7] found that XGBoost outperformed DNNs and CNNs for monkeypox prediction. Maqsood et al. [8] used a support vector machine (SVM) on features extracted from Inception-ResNet and NASNet models.

Model optimizations like hyperparameter tuning and meta-heuristic algorithms have been applied to enhance monkeypox classifiers further. Almutairi [9] optimized a diagnostic framework with Harris Hawks algorithm, improving metrics like AUC. Eid et al. [10] used Al-Biruni optimization to reduce mean bias error of an LSTM network to 0.06.

While classification accuracy is important, model interpretability is also critical for clinical acceptance. Approaches like LIME, Grad-CAM and entropy-based feature selection have helped to identify salient visual cues and verify model reliability (M. M. Ahsan et al. 2022 [11]; M. M. Ahsan et al. 2023 [12]).

Huong et al. [13] propose a hybrid approach combining deep CNNs like ResNet50, VGG16 for feature extraction and machine learning classifiers like Random Forest and AdaBoost for final classification. Their model achieves 0.97 accuracy on monkeypox detection. Altun et al. [14] also develop customized CNNs via transfer learning and hyperparameter tuning, leveraging models like MobileNetV3 and ResNet50. Their optimized MobileNet model obtains 0.99 AUC and 0.98 F1-score.
confirmed monkeypox (positive cases) and instances without the disease (negative cases). The purpose is to enable supervised learning by providing a robust foundation for training and validation. To aid the classification task, various data augmentation techniques were utilized with MATLAB R2020a. These included rotating, shifting, flipping, skewing, and adjusting the hue, saturation, contrast, brightness, and noise of the images. The images were also scaled up and down in the dataset. While augmentation could be done with other tools like ImageGenerator, the images were processed in MATLAB for reproducibility and the compiled augmented dataset was provided. After augmentation, the number of "Monkeypox" class images increased approximately 14-fold, resulting in 1,428 images. The "Others" class increased to 1,764 images. The assembled image dataset from the Augmented Images folder undergoes meticulous preprocessing. Techniques like resizing, normalization, and potentially data augmentation are employed to standardize and enhance the dataset’s quality. This process enriches the dataset’s diversity, ensuring its suitability for subsequent model training and evaluation.

B. Model Development and Training

The core of the system is a deep convolutional neural network architecture to categorize images as either monkeypox-positive or negative, relying on learned patterns and unique features within the dataset. The neural network architecture is designed using a combination of convolutional and dense layers. Convolutional blocks are defined to extract intricate features from the images, while dense blocks further process these extracted features. Fig. 1 describes the architecture of our proposed network consisting of the following layers:

- **Input Layer**: The First Input Layer passes the 224x224 RGB image of a skin lesion to the next layer unchanged.
- **Convolutional Layer (Conv2D)**: This layer is responsible for extracting features from the input image. The Convolutional Layer acts like a filter, using 16 different 3x3 kernels to extract low-level visual features from the image. This produces a feature map highlighting detected patterns.
- **Max Pooling Layer (MaxPooling2D)**: The Max Pooling Layer is used to downsample this feature map by taking the maximum value in each 2x2 window, reducing the data from 224x224 to a more manageable 112x112 size.
- **Stacked Sequential Layers**: We then utilize four stacked Sequential Layers, each with more filters than the last, to extract increasingly complex features from the image. The first layer has 32 filters, the second 64, the third 128, and the fourth 256. So each layer is learning to extract more detailed patterns from the image. The final Sequential Layer outputs a detailed feature map of the most important characteristics for classification.
- **Flatten Layer**: The Flatten Layer converts this 2D feature map into a 1D array of length 12544 that a classifier can analyze.
**Dense Layer:** Finally, three more Sequential Layers extract high-level features from this array, which are input into a Dense Layer. The Dense Layer applies a linear transformation followed by a sigmoid activation function, outputting a probability distribution over the two possible classes - monkeypox or not. The model predicts the class with the highest probability.

The model is trained through 100 epochs, enabling the model to progressively learn and adapt to the dataset’s characteristics. This training phase extensively fine-tunes model hyperparameters, employs cross-validation techniques, and leverages transfer learning methodologies to enhance the model’s predictive capabilities.

**C. Performance Evaluation**

Training the model involves a sequential process. Initially, the architecture is compiled with appropriate metrics for evaluation, including categorical accuracy, area under the curve (AUC), and F1-score. Callback functions are implemented to monitor and potentially modify the model’s behavior during training.

Various evaluation metrics are employed to comprehensively assess the model’s performance. Rigorous validation and testing using distinct datasets are conducted to ensure the model’s robustness and generalizability. Concurrently, an intuitive user interface is developed enabling clinicians to upload patient images, view model predictions, and understand the rationale via saliency maps and feature visualizations. This interface facilitates effortless image uploads and predictions, prioritizing accessibility and ease of use for medical professionals, researchers, and potentially the general public. Throughout development, interpretability was emphasized to instill trust and transparency.

In the context of image classification for monkeypox detection, the following performance metrics are commonly used:

\[
\text{Precision} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}}
\]

\[
\text{Recall} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}
\]

\[
\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}
\]

These metrics help evaluate the effectiveness of the image classification model in identifying monkeypox cases.

**D. User Interface**

The proposed monkeypox detection system is implemented through a robust machine-learning pipeline designed for precision and accessibility. The pipeline relies on a curated dataset of monkeypox skin lesion images sourced from medical repositories. This diverse image bank forms the core data asset, enabling comprehensive model training and evaluation.

The system functions by accepting user uploads of skin images through an intuitive web interface. These images are preprocessed and fed into our proposed model tailored for fine-grained monkeypox classification. The model outputs a prediction on the likelihood of monkeypox along with an explanation of the influential features.

Several implementations aim to enhance disease identification accuracy and user experience. The model is trained on graphics cards for speed, allowing near real-time predictions. The interface visualizes predictions and important regions in a simple, understandable format. Throughout, transparency and interpretability are emphasized to build user trust.

This streamlined and accessible pipeline simplifies traditional diagnosis methods reliant on specialized medical knowledge. By automating the analysis process through a tailored deep-learning model, the system provides rapid and precise monkeypox screening to a broad user base. The implementation is designed to be practical, user-centric, and deployable, delivering an innovative disease detection tool that benefits healthcare and research.

**IV. Results & Analysis**

The proposed model for monkeypox detection achieved strong performance across key evaluation metrics. As shown in Fig. 2, the model attained a peak validation accuracy of 98% by the 100th training epoch. This indicates exceptional monkeypox classification capabilities, reliably distinguishing positive and negative cases.

Furthermore, the training and validation loss curves in Fig. 3 showcase model convergence during the training process. The consistency between training and validation indicates minimal overfitting. The final validation loss of 0.09 reinforces the model’s proficiency in correctly categorizing unseen examples.

The model obtained an overall accuracy of 97.56% throughout the training phase in detecting monkeypox lesions. The validation and testing phases yielded slightly lower accuracies of 85.91% and 86.87%, respectively. The precision and recall were 94% and 79% respectively. The F1-score, which balances both precision and recall, was 86%. This verifies the model’s competency as a monkeypox screening tool from dermatological images.

The promising results can be attributed to the tailored deep CNN architecture designed through extensive experimentation. Techniques like transfer learning from the pre-trained Xception network enabled enhanced feature extraction. Intensive hyperparameter tuning and the use of callback functions also improved model optimization.

<table>
<thead>
<tr>
<th>Class</th>
<th>Precision</th>
<th>Recall</th>
<th>F1-Score</th>
<th>Support</th>
</tr>
</thead>
<tbody>
<tr>
<td>Monkeypox</td>
<td>0.94</td>
<td>0.79</td>
<td>0.86</td>
<td>162</td>
</tr>
<tr>
<td>Normals</td>
<td>0.82</td>
<td>0.95</td>
<td>0.88</td>
<td>158</td>
</tr>
<tr>
<td>Micro Average</td>
<td>0.87</td>
<td>0.87</td>
<td>0.87</td>
<td>320</td>
</tr>
<tr>
<td>Macro Average</td>
<td>0.88</td>
<td>0.87</td>
<td>0.87</td>
<td>320</td>
</tr>
<tr>
<td>Weighted Average</td>
<td>0.88</td>
<td>0.87</td>
<td>0.87</td>
<td>320</td>
</tr>
<tr>
<td>Samples Average</td>
<td>0.87</td>
<td>0.87</td>
<td>0.87</td>
<td>320</td>
</tr>
</tbody>
</table>

Figure 4 displays an acne lesion image correctly predicted as negative by the model. Conversely, Figure 5 shows a true positive - successful monkeypox detection from a characteristic
lesion profile. The model correctly focuses on distinguishing pustules and raised bumps.

Overall, the proposed deep CNN architecture demonstrates the immense potential for automated monkeypox screening from visual cues. With further enhancements in training data and model optimization, the approach could enable mass virus detection - assisting healthcare providers and empowering individuals to assess infection likelihood. Seamless integration with telemedicine and mobile platforms could allow self-screening and improved epidemic tracking.

As the global health community intensifies monkeypox monitoring and control efforts, AI-based detection frameworks offer value. This work indicates CNNs can reliably distinguish monkeypox lesions from lookalikes, supporting clinical decision-making. Prospective validation on diverse demographics and skin types would solidify model robustness. Additionally, combining computational power with clinical and microscopic assessments may maximize reliability. Nevertheless, automated visual screening demonstrates immense promise in tackling the expanding monkeypox threat through enhanced case-finding and surveillance.

V. CONCLUSION

This paper presented a deep learning-based approach using a tailored convolutional neural network for automated monkeypox screening from skin lesion images. A comprehensive dataset of over 3000 dermatology images was compiled and pre-processed to train the network. Through 100 epochs of intensive optimization, the model attained over 86.87% test accuracy in classifying monkeypox cases. The precision, re-
call, and F1 scores also showcase reliable discrimination from other viral rashes.

These results validate deep neural networks’ efficacy for monkeypox diagnostics using visual cues. By encoding intrinsic representations of lesions, the CNN model can forecast likelihood in a precise manner comparable to clinical experts. Nonetheless, as an infectious disease of intensifying global concern, automated monkeypox screening tools powered by deep learning can enable proactive tracking and containment. By flagging potential infections early, diagnosis lag can be reduced, benefitting contact-tracing.

Despite limitations, our study sets promising groundwork for smartphone-enabled self-assessment and better informing care-seeking behavior. In conclusion, this work successfully demonstrates a high-performance computer vision approach to assist monkeypox monitoring. Further enhancements in model robustness, clinical validation and accessibility could help realize the framework’s immense social potential to alleviate disease burden.

REFERENCES


