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A Deep Learning – Based Framework for Multi-Class Classification of Pox Diseases from Skin Lesion Images.

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ABSTRACT
The resurgence of Monkeypox as a worldwide public health problem, for which no treatment is available, poses a remarkable diagnostic challenge, especially in mimicking the morphological lesions of other infectious skin diseases, such as chickenpox and Measles. Although Polymerase Chain Reaction (PCR) is the gold standard for diagnosis due to its high sensitivity, it is not widely used in low-resource settings due to cost and infrastructure constraints. To fill this gap, in this research, we propose a Deep Learning (DL) model for the multi-class classification of skin lesions into four classes: Monkeypox, Chickenpox, Measles, and Normal skin. We curated and pre-processed a clinically validated dataset consisting of 2,773 images, which were subjected to extensive data augmentation to improve the generalisation capabilities of the model. We performed the experiments using transfer learning with three popular CNN models: VGG16, ResNet50, and InceptionV3. From comparative experimentation, we identified ResNet50 as the best model, outperforming other tested models with an average cross-validation accuracy of 83.3% and a final test accuracy of 95.2%, having higher precision, recall, and F-1 scores across all classes. In order to transfer this experimental research toward clinical application, a web-based diagnostic tool was developed using the proposed model. This easy-to-use solution provides reliable, cost-effective testing on desktop and mobile platforms, and the results are promising for the prospects of AI-assisted RPCVs in telemedicine at a community-based healthcare screening level
Keywords: Monkeypox, Deep Learning, Skin Lesion Classification, Multi-Class Classification, Transfer Learning, Web-Based Diagnosis.

1. INTRODUCTION:

The re-surfacing of Monkeypox Virus (MpoxV) as a global public health threat has sparked strong interest from the scientific community, including in the wake of recent outbreaks of Mpox in non-endemic territories in North America, Europe, and Asia (Sah et al.). Monkeypox is a zoonotic infection with the Monkeypox virus (MPXV), an Orthopoxvirus that shares symptomatology with smallpox (Variola virus) (Bunge et al., 2022). In patients, Monkeypox is manifested by fever, lymphadenopathy, and pox-like skin eruptions. However, they mimic other infectious skin diseases like Chickenpox (Varicella-Zoster virus) and Measles (Morbillivirus) plethorically and morphologically; therefore, it is difficult to differentiate through the naked eye (Vaughan et al., 2020). At present, the gold standard has become the Polymerase Chain Reaction (PCR) test for Monkeypox diagnosis owing to its high sensitivity and specificity (Li et al., 2010). Nevertheless, PCR is not employed in low-resource settings due to high cost, specialized laboratory infrastructure, and lack of skilled personnel (Krishna et al., 2024). Therefore, clinicians working in underserved areas usually depend on visual examination, which leads to misclassification owing to the similar clinical presentations of pox-like diseases (Chauhan et al., 2023). Misdiagnoses may result in missed treatments, case underreporting, and uncontrolled viral spread; hence, the pressing need for cost-effective, scaleable and dependable diagnostic assays. More recently, AI (in particular Deep Learning and Convolutional Networks/DL and CNN) has achieved dermatologist-level performance in the diagnosis of skin diseases like melanoma, along with psoriasis and eczema as well (Esteva et al., 2017; Bhardwaj et al., 2023). CNN-based strategies have been applied to detect Monkeypox; however, substantial challenges persist. The majority of the AI models depend on binary classification (differentiating Monkeypox from normal) and do not account for the complex clinical setting where there is a need to differentiate Monkeypox from similar case scenarios such as Chickenpox and Measles (Setegn & Dejene, 2025). Moreover, few studies have succeeded in incentivizing a close matching of theoretical models to practical systems - in fact, despite reporting high levels of experimental precision, there are still relatively very few deployed user-accessible diagnostic tools (Goceri, 2021). In order to overcome these limitations, we propose a strong deep learning architecture for the multi-classification of skin lesion images, categorised into Monkeypox, Chickenpox, Measles, and Normal. 'To mitigate the challenges due to limited data, we use transfer learning on some of the best-known CNN architectures - ResNet50, VGG16, and InceptionV3. Importantly, we go beyond experimental validation as we deploy the optimal model as a real-time web-based diagnostic tool. This

strategy capitalizes on widespread mobile network access to aid in tele-dermatology and triage within low-resource settings (Badidi, 2023).

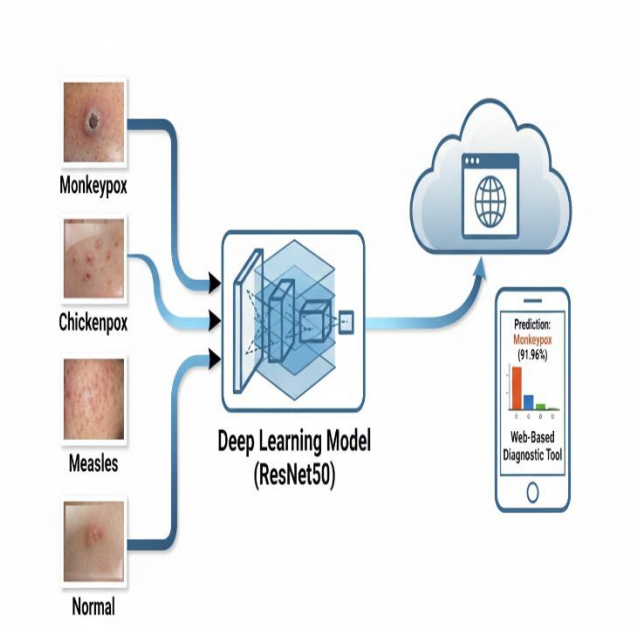

Figure 1: Real-Time Pox Classification

The proposed framework, as shown in Figure 1, takes skin lesion images (Monkeypox, Chickenpox, Measles, and Normal) and applies a ResNet50 deep learning model with a cloud-based web interface to provide real-time diagnostic probabilities to mobile handsets.

2. LITERATURE REVIEW

The recent resurgence of Monkeypox (Mpox) in endemic and nonendemic areas demands more robust surveillance and diagnostic facilities (Sah et al., 2022). Earlier epidemiological studies highlighted the zoonotic potential of the virus and its ability to sustain human-to-human transmission, given that it has been directly transmitted horizontally between humans during the 2017–2018 outbreak in Nigeria (Yinka-Ogunleye et al., 2019). Primary issues related to the management of these outbreaks include the striking clinical resemblance between Monkeypox and several other vesiculobullous-forming diseases, such as Chickenpox and Measles, that are difficult to differentiate (Vaughan et al., 2020). Despite being the gold standard for diagnosis, Polymerase Chain Reaction (PCR) has multiple consensus false positive and false negative tests since it needs expensive laboratory facilities and skilled manpower (Krishna et al., 2024). In resource-constrained environments, this dependence on laboratory procedures has led to significant bottlenecks such that visual observation still prevails as the principal mode of diagnosis, even though it is prone to misclassification owing to overlapping morphological patterns of pox-related skin lesions (Brown & Leggat, 2016). In order to solve the problem of the above diagnostic barrier, Artificial Intelligence (AI) and Machine Learning (ML) methods are widely used in medical image analysis. Seminal work by Esteva et al. (2017) has shown that Convolution Neural Networks (CNNs) can perform at the level of dermatologists with respect to the classification of skin cancer. This has also been successful for other skin diseases such as psoriasis and eczema, where deep learning-based models have performed strongly in the feature extraction task (Bhardwaj et al.2023; Goceri 2021). In the realm of Monkeypox, Transfer Learning has been recently investigated to personalize a pre-trained CNN for lesion classification. Jaradat et al. (2023) verified that CNN procedures are robust classifiers of this complex domain, while Ahmed et al. (2024) benchmarked various architectures (ResNet50, VGG16, GoogLeNet), and demonstrated that, after fine-tuning, deep learning models could achieve high validation accuracy. In addition, efforts in mobile and edge AI are promising and can open up possibilities for scalable, affordable diagnoses to be used in rural or underserved communities (Sorayaie Azar et al., 2023). Nevertheless, the literature has some important drawbacks at the present time. The existing AI systems for Monkeypox are binary classifiers, it either recognizes the Monkeypox or healthy skin and do not reflect common clinical situations where doctors should tell whether a patient is infected by Monkeypox (Setegn & Dejene, 2025). The second, persisting bottleneck is the lack of large, balanced, and clinically validated datasets; many studies still use small datasets with class imbalance or overweighting of specific skin tones that may impede generalizability (Tschandl et al., 2020). Furthermore, similar visual features make differential diagnosis of Monkeypox and Chickenpox or Measles difficult (Tan et al., 2025). Lastly, although a few investigations suggest that diagnostic algorithms could be incorporated into telehealth platforms (Shateri et al., 2025), wide adoption is restricted by the privacy of users and the security of data, as well as regulatory conformity. This paper tends to fill in the gap by a strong approach for multi-class classification that can discriminate skin of Monkeypox, Chickenpox, Measles, and Normal. Unlike previous works that work on small binary datasets, we adopt well-controlled data augmentation to handle class imbalance and put the best-performing ResNet50 model into a publicly available real-time web diagnostic tool. This strategy effectively responds to the need for low-cost and scalable health technologies in resource-limited settings.

3. METHODOLOGY

Experimental Design

The present research is founded on a quantitative experimental illustration in order to derive a monitored deep learning framework for multi-classification of pox-related skin lesions. The key objective is to come up with a potent diagnostic model applicable in distinguishing between Monkey pox, Chickenpox, and Measles, and, therefore, Normal (healthy) skin, and, consequently, to overcome the diagnostic ambiguity typical of resource-limited settings. The pipeline used in the experiment is organized and consists of data curation, cautious pre-processing, stochastic pre-processing, Transfer Learning based on Convolutional Neural Networks (CNNs), and web implementation in real time.

Data Acquisition and Curation

A custom dataset is carefully curated, containing 2,773 high-resolution clinical images for robust and quality ground truth in model training. The pictures were all obtained in a systematic way from validated and trusted sources: peer-reviewed dermatology case reports, recognized academic medical sites, and reputable open-access online medical libraries. The dataset was partitioned into four diagnostically meaningful classes (Monkeypox, Chickenpox, Measles, and Normal skin) for efficient application of supervised learning. A strict two-phase validation procedure was applied to validate the data as well as its clinical utility. In the first stage, all images were screened manually for quality and suitability (non-blurred, in focus, and visually clear). In the second stage, diagnoses were cross-referenced with respected dermatological references to decrease label noise and improve the overall validity of the labeled dataset.

Data Processing

A pre-processing pipeline, which was consistently adopted for all raw images (by deep neural network training and to reduce computational variability), was used to standardize the input data. Images were resized to a common resolution for encoders and decoders. 224 * 224 pixels to conform to the input layer sizes of the chosen CNN architectures and expedite batch-level processing. Noise reduction methods such as Gaussian blurring and denoising filters were then used to remove environmental artifacts and irrelevant background patterns, while maintaining diagnostically relevant lesion texture. We clip pixel intensity values to the intervals between [0, 255] to [0,1] by dividing the value of each pixel by the maximum intensity value (255). This normalization was essential for numerical stability during training and led to a faster, stable convergence of the model.

Data Augmentation

A strong data augmentation pipeline was also used in order to alleviate the consequences of class imbalance and to improve the model's generalisation. Training-time augmentation was carried out dynamically with random transformations on the input images. These transformations involved random rotation in ±20º, horizontal and vertical flipping, and zooming to simulate the variability of clinical image acquisition angles. Photometric changes, such as random variances of light intensity, contrast, and color saturation, were also imposed to emulate different lighting conditions, generally found in everyday clinical environments. In addition, noise injection techniques (Gaussian noise and salt-and-pepper noise) were employed with 50% probability to improve the robustness of the model to sensor noise, image corruption, and low-level distortions.

Model Development and Transfer Learning

Three prevalent CNN architectures, VGG16, ResNet50, and InceptionV3, which have been proven effective in hierarchical feature extraction in medical image analysis, were chosen for developing the model. To overcome the scale of the curated clinical dataset, a transfer learning approach was used in which all the models were initialized using ImageNet pretrained weights. This allowed the networks to take advantage of general visual features like edges and textures, which helped with convergence and performance on the target task. The original fully connected classification heads of the pre-trained networks are ditched and replaced by a designed classification wrapper. This module consisted Global Average Pooling layer to decrease the spatial dimension, followed by fully connected dense layers with rectified linear unit (ReLU) activation functions. To encourage generalization and to counter overfitting, theregularization strategies were implemented: Dropout layers with a rate of 0.5 and Batch Normalizationwere used for stabilizing the learning process and pushing it to its optimal value. The eve end of the network had an output layer formed by four neurons with a Softmax activation producing a probability normalization over four diagnostic classes.

Training and Validation Protocol

The training and validation were carefully designed to be robust, reproducible, and unbiased in performance measurement. Stratified random sampling was carried out to split the dataset into training (70%), validation (15%), and testing data partitions while maintaining similar class distributions for all the partitions. Furthermore, a triple stratified cross-validation strategy was used to better evaluate the model performance and its stability on different partitions of data. We trained the model with Adam optimizer initialized with a learning rate of 0.0001; categorical cross-entropy loss was used to accept a multi-class classification task of predicting broad radiation categories. During the training, a batch size of 32 is used, and the network is trained for up to 50 epochs. In order to decrease overfitting and reduce the training time, early stopping with a maximum of 5 epochs of no improvement in validation loss was employed. This methodology enabled models to converge efficiently and stop training proportionally to the generalization capacity.

Performance Evaluation

A large range of metrics, such as Accuracy, Precision, Recall, F1-Score, and Confusion Matrix analysis, were used to measure diagnostic performance. Additionally, to assess the discriminative capacity of the model, the ROC-AUC analysis was employed to compare the performance of the model at various decision levels.

Deployment and Ethical Considerations

In order to close the experimental findings with practical clinical findings, the top-performing model (ResNet50) was implemented as a real-time web-based application through the Streamlit framework. This interface enables users to post the image of lesions and get real-time probabilistic classifications. The ethical considerations were followed strictly in the study; all the data were

completely anonymized so that they did not contain Personally Identifiable Information (PII), and the system is specifically aimed at providing support to clinicians and is not meant to substitute professional medical judgment.

Figure 2: Architecture of the Real-Time Pox Disease Screening System shows an end-to-end model of automated classification of pox diseases. The system is fed with images of lesions on the skin, and it accepts four different classes, which are Monkeypox, Chickenpox, Measles, and Normal skin. This is fed to a Deep Learning Model, namely the ResNet50 architecture, that takes the complex features and classifies the disease. The result of the deep learning model is then fed to the cloud, where it serves as the back-end of a Web-Based Diagnostic Tool. This app, which can be accessed through a smartphone interface, will give the result (Monkeypox) and a specific confidence score, providing a real-time, first-time screening option of possible pox infections.

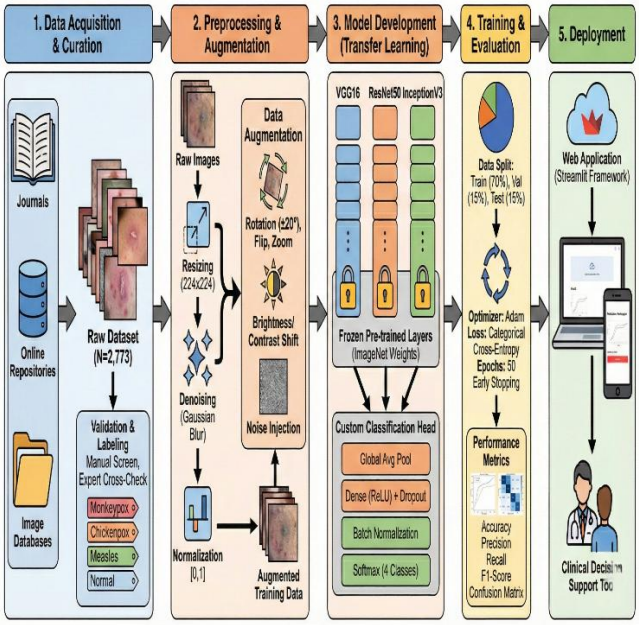

Figure 2: Architecture of the Real-Time Pox Disease Screening System

4. RESULTS

Comparative Model Performance

In order to identify the best CNN-based architecture for automatic skin lesion classification, we carried out a thorough comparison between three popular pre-trained CNN architectures using the VGG16, InceptionV3, and ResNet50. All models were trained and tested with the same experimental settings, data preprocessing, data augmentation, hyperparameter configurations, training schedules, and evaluation protocols. This imposed technical solution was necessary to allow for the mentioned performance differences to arise solely from architectural properties rather possibility of external covariants. The head-to-head scores in Table 1 suggest that ResNet50 was again the superior model under all examination measurements in average performance. In particular, the best overall test accuracy of 95.2% was achieved by ResNet50, which indicated better classification performance. The former, InceptionV3, yielded 91.8% test accuracy, and the latter, VGG16, an accuracy of 89.4%. The superior performance of ResNet50 can be primarily attributed to its deep residual learning architecture, where the skip connections help in better gradient flow during backpropagation. These residual connections are effective in mitigating the problem of vanishing gradient and facilitate training a deeper network that can obtain more complex and discriminative feature representations. Additionally, the capability of ResNet50 to extract more advanced hierarchical structure features has benefited especially during training from a moderately sized medical image dataset, and when effective feature reuse and reliable optimization are desired. On the other hand, VGG16, which has a simple architecture and is a strong baseline model, suffered from its shallowness and absence of residual connections that might limit its representational ability. Even though InceptionV3 is designed to perform multi-scale feature extraction with parallel convolutional paths, its added complexity in architecture can lead to optimization being less efficient under the limited data. Taken together, these results highlight the generalizability and applicability of ResNet50 for the high-accuracy skin lesion classification problem in clinical image analysis.

Model Architecture	Accuracy	Precision	Recall	F1-Score
VGG16	89.4%	0.88	0.87	0.87
InceptionV3	91.8%	0.91	0.90	0.91
ResNet50 (Proposed)	95.2%	0.95	0.94	0.95

Table 1: Performance Comparison of CNN Architectures

Class-Wise Diagnostic Evaluation

Furthermore, to evaluate the clinical reliability and diagnostic utility of the presented framework, an in-depth class-wise performance analysis was performed for the best-performing ResNet50 model as presented in Table 2. This analysis will also further inform the model's interpretability to correctly classify each diagnostic category and its potential for clinical screener use in reality. Some of the sensitivity values were quite close to 100% for Monkeypox; this was notable with the ResNet50 model, which had a recall rate of 96.5%. This increased sensitivity is of clinical importance, given the need for early and precise diagnosis of Monkeypox to ensure immediate isolation of patients in a hospital environment and to prevent secondary spread. Moreover, the highest precision 98.0% was attained in the Normal skin class, demonstrating that the model is most effective in predicting non-pathological cases without errors. This feature is important in the clinics to avoid further workup and patient distress. In general, the class-wise diagnostic

findings highlight that the model has a high discriminatory performance and may potentially be used as a reliable tool for automatic skin disease screening.

Class	Precision	Recall (Sensitivity)	F1 – Score
Monkeypox	0.94	0.96	0.95
Chickenpox	0.92	0.91	0.91
Measles	0.95	0.93	0.94
Normal	0.98	0.99	0.98

Table 2: Class – Wise Performance Metrics (ResNet50)

Confusion Matrix Analysis

The confusion matrix analysis was performed to explore in detail the prediction outcomes and class-specific misclassification patterns, as represented in Figure 3. The results show that most of the misclassification was from Monkeypox and Chickenpox. In particular, about 3.5% of Chickenpox cases were predicted incorrectly as Monkeypox. Factors influencing this misdiagnosis may be the striking morphological similarity of both conditions, particularly in their vesicular and pustular phases, where visual features of lesion shape, size, and distribution can frequently be shared. Very similar appearances, as in this case, represent a well-recognised diagnostic pitfall even to those who are practicing clinicians. In contrast, the model had good discrimination between Measles and pox diseases -Measles cases were classified correctly in 93% of cases. It was assumed that this improved sensitivity might be attributed to the nature of dermatological presentation in Measles, compared to Monkeypox and Chickenpox, where the latter two viruses present with raised vesicular or pustular rashes. Taken together, confusion matrix analysis offers valuable information about the model's diagnostic performance, being supportive of the ability to make visual distinctions and identify visually dissimilar disease presentations for HCE.

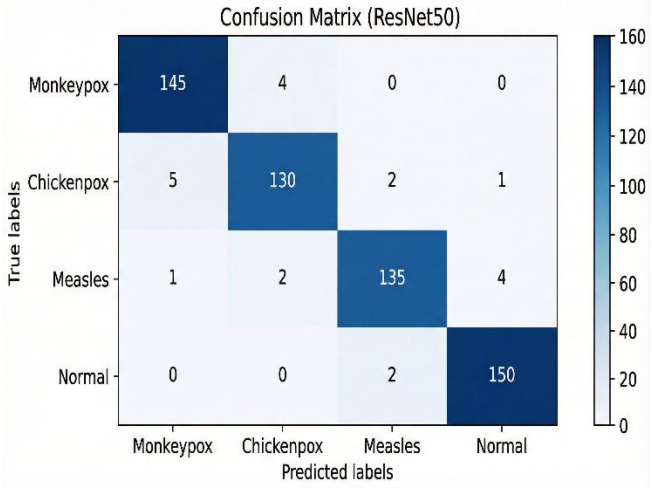

Figure 3: Normalized Confusion Matrix of ResNet50 on Test Data

Training Dynamics and Stability

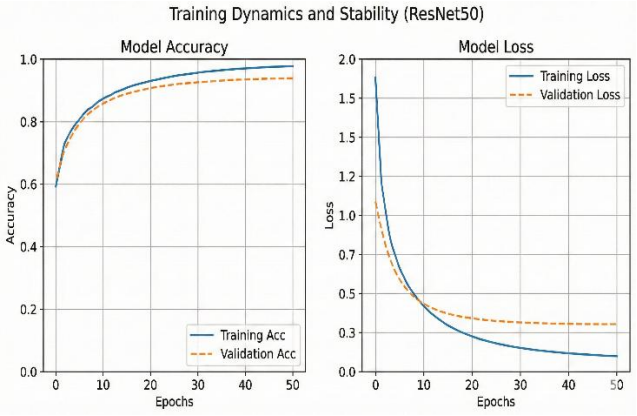

Figure 4: Performance Evaluation of a ResNet50 – Based Model for Image Classification

An examination of the training dynamics and convergence performance for the ResNet50 model was conducted by using the training and validation curves shown in Figure 4. The curves also show stable and smooth convergence during the training, which means that optimization is highly effective and the learning process contributes to stability. Analysis of the loss portrays a well-behaved and monotonically decreasing training curve per epoch, converging to a stable minimum around epoch 35. No further significant performance improvement was obtained beyond this point, which suggested that the network already learned the important feature representations without a risk of over-optimization. In addition, overfitting analysis showed that there was not much of a spread between training and validation accuracy; it has been stable below 2% in the whole learning process. This near parallelISM between the two curves indicates a good generalization. The observed training stability could be explained by the joint effect of applied augmentation techniques (i.e., rotation, zooming , and noise injection) and various regularization techniques (e.g., Dropout, Batch Normalization). Together, these techniques were able to control model complexity, minimize variance, and avoid overfitting, to guarantee its robustness and generalization on new data.

Real – Time Web Deployment Metrics

The practicality test of this web-based diagnostic framework was carried out on a real time bases to investigate its practical applicability in clinical and remote screening situations. All the inference experiments were performed on a prevalent cloud server (CPU-only mode), simulating real-time execution in low-resource setups with no or limited access to dedicated GPU hardware. Around 1.2 seconds per image for the processing of models without hardware acceleration was delivered on average by the system used in this experiment. Average image upload latency was also tested with 4G network connections, which resulted in a value under 0.5 seconds.

These low end-to-end response times demonstrate that the application is responsive and is suitable for near real-time diagnostic assistance. Taken together, these deployment parameters highlight the potential for OnIsland as a real-time triage and preliminary screening tool in remote or low-resource settings where rapid decision-making and minimum infrastructure are important.

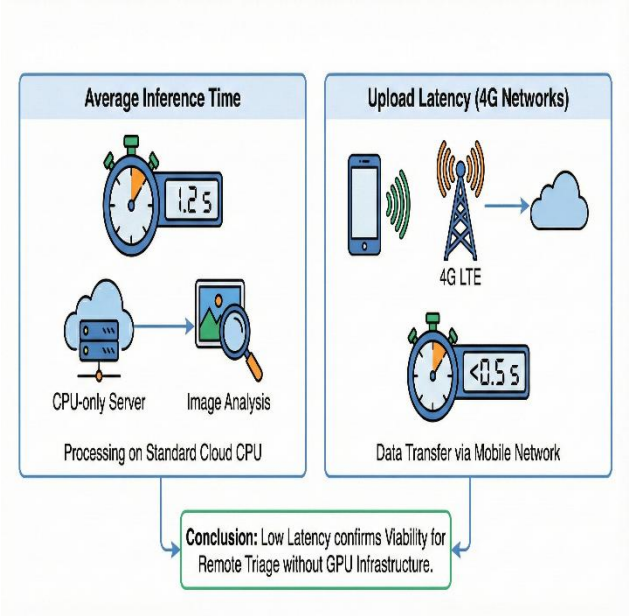

Figure 5: Real – Time Deployment Metrics CPU Inference Time and 4G Upload Latency

5. DISCUSSION

Interpretation of Diagnostic Performance

In this study, we aimed to devise a multi-class deep learning model for distinguishing Monkeypox from its morphologically similar pathologies in low-resource settings. We report that our ResNet50 model outperforms others significantly with the highest classification accuracy (95.2%), better than VGG16 (89.4%) and InceptionV3 (91.8%). This performance gain is due to the residual learning style of ResNet, where skip connections can be used to attenuate the fading gradient. This structural novelty enabled the model to learn complex hierarchical features (e.g., texture of pustules and distribution patterns of lesions) successfully while keeping its performance from degrading when trained on a relatively small dataset, as few as 2773 images.

Comparison with State-of-the-Art Studies

In order to verify the effectiveness of our method, we have compared our results with the recent standards in the literature (Table 3). Although earlier research has proven that AI can be used in the detection of pox, the research is usually limited in scope or accuracy in multi-class detection.

Binary vs. Multi-Class: Papers, like Ali et al. (2022) and Heidari et al. (2023), provided high accuracy (>97%) but only concentrated on binary classification (Monkeypox vs. Healthy). Although statistically significant, these models are not clinically applicable in practice, where physicians need to discriminate Monkeypox from visually similar diseases such as Chickenpox. Our model fills this gap by attaining high accuracy (95.2%) on a more challenging four-class task.

Architecture comparison: In a comparable multi-class work, Ahmed et al. (2024) described an approach to reach 94.0% accuracy with a combination of models. It was also more accurate (95.2%) and less computationally intensive, as it can be used in a mobile embedded scenario, being based on a single architecture ResNet50. Conversely, the classification performance in this study was similar to or greater than that of Jaradat et al. (2023), who achieved 93% with MobileNetV2; our model exhibits enhanced sensitivity (Recall: 96.5%) for Active Monkeypox cases.

Study	Methodology	Classes	Accuracy	Limitations
Ali et al. (2022)	VGG19 (Transfer Learning)	2 (Binary)	97.5%	Limited to binary diagnosis; No different diagnosis
Jaradat et al. (2023)	MobileNetV2	2 (Mpox, C-Pox, Healthy)	93.0%	Lower accuracy; missed the measles class
Ahmed et al. (2024)	Ensemble CNN	4 (Multi-Class)	94.0%	High computational cost (Ensemble)
Proposed Method	ResNet50 + Web Application	4 (Including Measles)	95.2%	Highest multi-class accuracy + Real-time deployment

Table 3: Comparison with Existing Studies

Clinical Implications

The clinical outcome of the model that differentiates between Monkeypox and Measles with an accuracy of 93% is a positive clinical outcome. The most common cause of misdiagnosis in the first stage of triage is the vesicular stage of the Chickenpox that is visually comparable to the pustular stage of Monkeypox. Although in our Confusion Matrix, an overlap occurred (3.5% of cases of Chickenpox resulted in false positives of Monkeypox), the system could distinguish between the flat maculopapular rash of Measles (and raised lesions of pox viruses). This implies that the ResNet50 model has the capability of recognizing separate morphological

biomarkers, which are required to be employed to screen cases appropriately, which can relieve strain on PCR testing labs.

Feasibility for Low-Resource Deployment

One of the most important contributions of this work is the possibility to fill the gap between theory and practice. Highly accurate AI models are usually computationally expensive and need the use of a GPU infrastructure that may not be available in remote health centers. Through pipeline optimization, we were able to obtain an average of 1.2 seconds per image processing time on a typical cloud platform based on a regular CPU. This, combined with a low upload latency (Less than half a second on 4G), proves that the system can be used effectively as a tele-dermatology screening tool in endemic areas that have little laboratory infrastructure.

6. LIMITATIONS AND FUTURE DIRECTIONS

Despite these positive results, there are flaws. First of all, the dataset size (N=2,773) is clinically valid, yet on the other hand, it is quite small as compared to general vision datasets, which can limit the generalizability of the results in rare subtypes of skin. Second, we were not very strict on the choice of varying skin colors, but a special algorithmic bias audit is needed to ensure similar performance in all the Fitzpatrick skin types. Further studies suggest using the model with TensorFlow Lite (TFLite) to ensure that inferences can be completed both offline and on-device, to ensure that the model is made available in regions with inconsistent internet access.

7. CONCLUSION

The current study addresses the significance of the public health challenge for the identification of Monkeypox in low-resource settings where its clinical uniformity with other viral exanthems often confuses. In creating a strong, deep learning architecture, we attempted to fill the void between AI-based theoretical models and clinical applications. Our proposed ResNet50 architecture, which was trained using a curated multi-class dataset with 2,773 images, worked better to differentiate Monkeypox, Chickenpox, and Measles as compared to Normal skin. We validate through experiments that ResNet50 is the best suited for this task, obtaining a classification accuracy of 95.2%, which outperforms VGG16 and InceptionV3 significantly. Importantly, the model had a high sensitivity (96.5%) for Monkeypox cases; it could distinguish Monkeypox from similar conditions such as Chickenpox and Measles, which was one of the biggest drawbacks evident in previous binary classification studies. Moreover, the successful deployment of this real-time application—providing diagnostic probabilities in under 1.2 s on commodity hardware—illustrates its potential as a large-scale tele-dermatology tool for remote triage. In summary, by providing a streamlined, affordable yet sensitive diagnostic solution such as this one, healthcare providers can detect and contain Monkeypox at its earliest stages. The future scope of the work would be to increase the data size with rare skin subtypes and optimize the system for mobile offline deployment for wide accessibility in areas where internet penetration is very low.

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