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Deep Learning for Viral Detection: Affordable Camera Technology in Public Health

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Viral infections like chickenpox, measles, and monkeypox pose significant global health challenges, affecting millions with varying severity. This study presents a novel deep-learning approach using widely available low-cost RGB camera technology to accurately identify these infections based on skin manifestations. We aim to enhance diagnostic capabilities and enable timely interventions, thus improving public health outcomes and individual well-being. Using MobileNetV3 for data classification, our model achieved a precision of 95% for positive cases, an overall accuracy of 95.73%, a recall of 88.37%, and an F1-score of 91.56%, indicating balanced performance between precision and recall. Notably, the model demonstrated exceptionally high specificity at 98.34%, effectively identifying negative cases. This deep learning approach holds promise for improving diagnostic accuracy and efficiency, especially in resource-limited settings with limited access to specialized medical expertise. By leveraging low-cost RGB camera technology, our method enables broad deployment, facilitating early detection and treatment of viral infections. We focus on the potential of deep learning in public health by emphasizing the critical role of early detection and intervention in mitigating the impact of viral infections. Our findings contribute to advancing healthcare technology and lay the groundwork for future innovations in disease detection and management.

Keywords: Deep Learning; Contagious Infections; Mobile Net Architecture; Infection Diagnosis; Image Classification.

Introduction:

Viral infections are a significant global health issue, affecting millions of people with a wide range of severity, from mild conditions to severe, life-threatening diseases. These infections, caused by pathogenic viruses, can target various systems and organs within the human body. Prominent examples include chickenpox, measles, and monkeypox, each characterized by distinct symptoms and transmission methods. These viral illnesses have a considerable impact worldwide, particularly affecting children due to their developing immune systems, which are less capable of effectively combating these infections at an early age [1].

Chickenpox, measles, and monkeypox are notable viral infections, each with distinct characteristics. Chickenpox, induced by the Varicella-Zoster Virus, is highly contagious and predominantly affects children. It is marked by an itchy rash featuring red spots and blisters, usually starting on the face and spreading to other body parts. Measles, triggered by the rubeola virus, is another highly contagious respiratory illness. Its symptoms include fever, cough, runny nose, and red, watery eyes that are followed by a distinct rash that covers the body. Monkeypox, caused by the monkeypox virus, resembles smallpox but tends to be milder. Initial symptoms include fever, headache, and muscle aches, followed by a rash that often starts on the face before spreading elsewhere.

The landscape of infectious diseases is constantly changing, with recent outbreaks such as Monkeypox underscoring the persistent challenges faced by public health systems worldwide. Since its resurgence in May 2022 [2], Monkeypox has re-emerged as a notable viral threat, with over 200 cases reported globally in the past month alone. This virus, originating from wild animals like rodents and primates, spreads primarily through animal-to-human transmission but can also be transmitted between humans. As a zoonotic disease, Monkeypox presents significant public health risks due to its potential for rapid spread and diverse clinical symptoms.

Alongside Monkeypox, chickenpox and measles persist as significant health challenges worldwide. Chickenpox remains widespread, especially in countries like Pakistan where it impacts a large segment of the population. Measles, a highly contagious viral infection, is notorious for causing severe complications, particularly in young children [3]. These illnesses highlight the critical need for strong surveillance systems, early detection, and effective public health measures to reduce their impact and prevent future outbreaks.

Identification of these viral infections is crucial due to their frequent manifestation of skin symptoms. Studying these diseases encompasses their epidemiology, transmission patterns, clinical presentations, and potential complications. This introduction aims to delve into these areas, emphasizing the impact of these viral illnesses on public health and individual well-being. Utilizing deep learning technology for disease identification, we can leverage low-cost RGB cameras to detect these infections efficiently. This approach facilitates timely interventions, including appropriate medication and preventive measures, to effectively manage and curb these diseases' spread.

The structure of this paper is organized as follows: First, a literature review is provided followed by the methodology, highlighting the use of MobileNetV3 for deep learning. Next, an overview of the datasets, experimental setups, configurations, evaluation criteria, and results is provided. The final section concludes the paper and suggests future research directions.

Objectives of Research:

The following are the research objectives for this study.

Research Scope:

The study aims to explore the application of deep learning technologies in combination with low-cost RGB cameras for the identification of viral infections such as chickenpox, measles, and monkeypox, focusing on skin symptoms. This specific scope ensures the research remains targeted and manageable.

Development of an Innovative Diagnostic Tool: By concentrating on the integration of deep learning and affordable imaging technology, the study seeks to create an innovative diagnostic tool. This direction guides the research toward developing a practical solution that addresses current diagnostic challenges in detecting viral infections based on visible symptoms.

Focused Research on Viral Infection Identification:

The objective delineates the study's focus on viral infection identification using specific technologies, thus helping to maintain a concentrated effort on relevant experiments, data collection, and analysis. This focus helps in avoiding deviations into unrelated areas or broader, less manageable topics.

Efficient and Economical Research Approach:

By establishing a clear and concise objective, the research ensures efficient use of time, money, and energy. Targeting the use of low-cost RGB cameras combined with deep learning not only makes the research economically viable but also ensures that efforts are streamlined toward achieving specific, impactful outcomes.

Enhancing Diagnostic Precision for Public Health:

The primary goal emphasizes enhancing diagnostic precision and facilitating prompt medical responses. This objective aligns the research with broader public health goals, aiming to contribute significantly to individual and community health by reducing the burden of viral infections through early and accurate diagnosis.

Novelty of Work:

The novelty of this research lies in the application of deep learning with low-cost RGB camera technology to accurately identify viral infections based on skin manifestations. This method presents a promising solution to enhance diagnostic accuracy and efficiency, particularly in resource-limited settings with restricted access to specialized medical expertise.

Literature Review:

Classical Machine Learning Approaches:

V. Vasudha Rani et al. [4] explain that skin, a remarkable human structure, often suffers from neglected conditions due to inherited traits and environmental factors. Identifying skin diseases is challenging due to the complexity of human skin and the similarity of conditions. Early detection is crucial, yet it remains a difficult scientific field. Machine learning (ML) techniques are used for segmentation and diagnosis, relying on image features. This analysis discusses using ensemble data mining and ML algorithms to classify skin diseases, employing multiple ML techniques to enhance reliability.

Pakkapat Banditsingha et al. [5] explain that in recent decades, skin disorders have been on the rise. Most are infectious and rely on visual perception. They proposed a Decision Machine Learning Support System to classify five types of skin diseases using 750 images from the dataset. They preprocess, resize, interpolate, and augment images for all models. Extensive experiments show that ResNet50 significantly outperforms other methods in accuracy, precision, recall, and F-measure. Bisahu Ram Sahu et al. [4] said that skin disease is a significant global health issue. Advances in technology and machine learning have improved the accuracy of dermatological disease categorization. Developing machine learning methods to accurately classify skin diseases is crucial. This research introduces a novel approach using four data mining techniques: support vector machine, k-nearest neighbor, random forest, and naive Bayes. An ensemble model combining these techniques via a voting scheme classifies skin diseases into five categories: acne, skin allergies, nail fungus, hair loss, and healthy skin. The proposed model achieved 97.33% accuracy, outperforming other classifiers.

In [6], Rinci Kembang Hapsari explains that Monkeypox, caused by the orthopoxvirus, presents symptoms like fever, headache, muscle aches, back pain, fatigue, and swollen lymph nodes. This research uses a Particle Swarm Optimization-enhanced Random Forest algorithm (PRFO) to predict Monkeypox. PRFO improves accuracy and reduces runtime. Testing on three

datasets showed accuracy increases: the Monkey Pox dataset (25,000 data points) improved by 2.08% to 69.88%, the Health dataset (20,000 data points) by 0.89% to 93.67%, and the PulsarStar dataset (12,000 data points) by 0.27% to 98.16%. PRFO's efficiency was achieved using 30 particles and 50 iterations, making it effective for large datasets.

Azka Mir in [7] predicts monkeypox outbreaks to manage them before they become a health hazard. Monkeypox cases are classified as confirmed, discarded, or suspected. Using a supervised machine learning model, this study predicts the status of monkeypox cases based on clinical parameters. The dataset used includes parameters from April 2022 onwards. Supervised machine learning techniques, including Decision Tree and Naïve Bayes classifiers, were used to analyze the dataset's performance. The proposed K-NN classifier model achieved the highest accuracy rate of 93.51% with k=5 neighbors. The RapidMiner platform was used for applying machine learning tools and techniques. This research emphasizes effective steps in machine learning to develop highly accurate models for predicting monkeypox outbreaks.

Deep Learning Approaches for Skin Disease & Viral Infection Classification:

Someswar Pal and Amit Kumar Mishra [8] explain that Monkeypox is a zoonotic disease, less severe than smallpox, primarily found in tropical African jungles but increasingly common in cities. Its primary hosts are animals, such as rats and other primates. Due to its spread, there is concern it might circulate like COVID-19, making early detection crucial. This paper explores a monkeypox image classification task using various CNN models, achieving 94.99% accuracy with Inception V3.

According to Md. Enamul Haque et al. [9] highlighted that amidst the global recovery from COVID-19, there is a concerning rise in monkeypox outbreaks, presenting a potential new pandemic threat. Monkeypox shares symptoms with chickenpox and measles but is distinguished by its characteristic skin blisters. Deep learning algorithms have shown promise in diagnosing COVID-19, tumors, and skin diseases. The paper integrates deep transfer learning and a convolutional block attention module to enhance image-based monkeypox classification, including five deep learning models i.e, VGG19, Xception, DenseNet121, EfficientNetB3, and MobileNetV2 that were tested with channel and spatial attention processes. The Xception-CBAM-Dense architecture achieved the highest accuracy at 83.89%.

Ashish Kumar Nayak in [10], warns that with humanity recovering from COVID-19, monkeypox emerges as a potential new pandemic threat. While not as lethal or contagious as COVID-19, unchecked spread could lead to a global epidemic. Deep learning (DL) techniques in medical imaging show promise for early disease identification, using images of monkeypox-infected skin. However, the lack of a reliable public database for training DL models remains a challenge. This research proposes the Mpox Classifier, an improved DenseNet-201 deep transfer learning model. It achieves accuracy rates of 94% and 99.1% on initial and enhanced datasets, respectively, for identifying monkeypox.

Namirah Nazmee [11] focuses on using Machine Learning (ML) to classify and detect monkeypox, a skin illness caused by the varicella-zoster virus. Using a Kaggle dataset of monkeypox lesion images, the images were augmented to develop and test custom models. A web app was created for users to submit images for analysis and classification. The study evaluates the effectiveness of ML models, comparing ResNet50, InceptionV3, Xception, DenseNet121, and MobileNet. MobileNet and Xception showed the best performance, with MobileNet achieving a mean accuracy of 0.97, precision of 0.96, F-1 score of 0.968, and recall of 0.968. The aim is to assess the efficacy of ML models for monkeypox categorization and evaluation.

Z. Wu et al. in [12] investigate various CNN algorithms for classifying facial skin diseases from Xiangya—Derm, China's largest clinical imaging dataset for skin diseases, comprising 2,656 face images from six common skin diseases. They evaluated five mainstream CNN algorithms and observed that models achieved higher average precision and recall. In a test dataset of 388

facial images, the best model achieved recalls of 92.9%, 89.2%, and 84.3% for lupus erythematosus, basal cell carcinoma, and seborrheic keratosis, respectively, with mean recall and precision reaching 77.0% and 70.8%.

Evgin Goceri [13] investigates the impact of residual connections and activation functions (ReLU and SELU) on image classification. Four network models were implemented and evaluated for automated skin disease classification from colored digital images. Experimental results indicate that ResNET with SELU and without residual blocks achieved the highest validation accuracy of 97.01%. The models using the SELU activation function exhibited stable performance, while those with residual blocks minimized validation loss. These findings demonstrate that deep networks can effectively classify five skin diseases with high accuracy, paving the way for further testing with larger and more diverse datasets.

Adnan Afroz et al. [14], utilized a deep learning approach employing Convolutional Neural Networks and the LeNet-5 architecture to enhance the accuracy and speed of classifying dermoscopy test results. The application was developed using Python and the Keras library, with TensorFlow as the backend. By experimenting with different training epochs and a dataset comprising 176 images, the model achieved a training success rate of 93% and a perfect testing accuracy of 100%.

Other Approaches for Skin Disease & Viral Infection Classification:

Electrical impedance has been explored by P. B. Manoorkar et al. [15] as a method to distinguish between skin cancer and normal tissue based on structural and chemical differences. Studies show that bio-electric properties vary significantly due to factors such as irritation, allergic reaction, location, sex, age, and hydration. Clinical studies using impedance measurements have successfully differentiated affected and normal skin, employing magnitude, phase, real part, and imaginary part indexes. The bio-impedance method proves effective for diagnosing early-stage skin diseases, including melanoma, basal cell carcinoma, squamous cell carcinoma, scabies, and acne. It offers the ability to compare affected and normal skin, helping to control body parameters and prevent various diseases, including early-stage skin cancer. This low-power, cost-effective, and portable method operates well across different skin diseases, achieving an approximately 75% accuracy rate in experimental settings.

Anik Pramanik in [16], predicts infectious disease outbreaks, including monkeypox using explain time series forecasting. Despite its analytical limitations, it supports both single-step and multi-step forecasting. This study uses ARIMA and SARIMA models to forecast the spread of monkeypox. Various analytical methods validated the models, yielding RMSE values of 3.6818 for ARIMA and 3.1180 for SARIMA. The results indicate an increase in active cases. These models can predict future daily and cumulative cases, aiding in the development of effective public health strategies for the monkeypox outbreak.

Methodology:

The dataset for this study comprised input images containing various diseases (chickenpox, measles, monkeypox) and normal cases. Data preprocessing is then applied for data cleaning and feature selection. Once the data is preprocessed, it is ready to train the model, which in this case is MobileNetV3. Testing is performed on new, unseen images, and classification is conducted for each class. Finally, assessment criteria were established, and various measures were calculated to evaluate the model's performance. Figure 1 shows the workflow of our study.

MobileNetv3:

In this section, we elaborated on MobileNetV3. MobileNetV3 builds upon the MobileNet series, incorporating enhancements from MobileNetV1 and MobileNetV2, as well as innovative architecture search techniques and optimizations such as squeeze-and-excitation modules. This version is specifically designed to be highly efficient and powerful for applications in mobile and embedded vision.

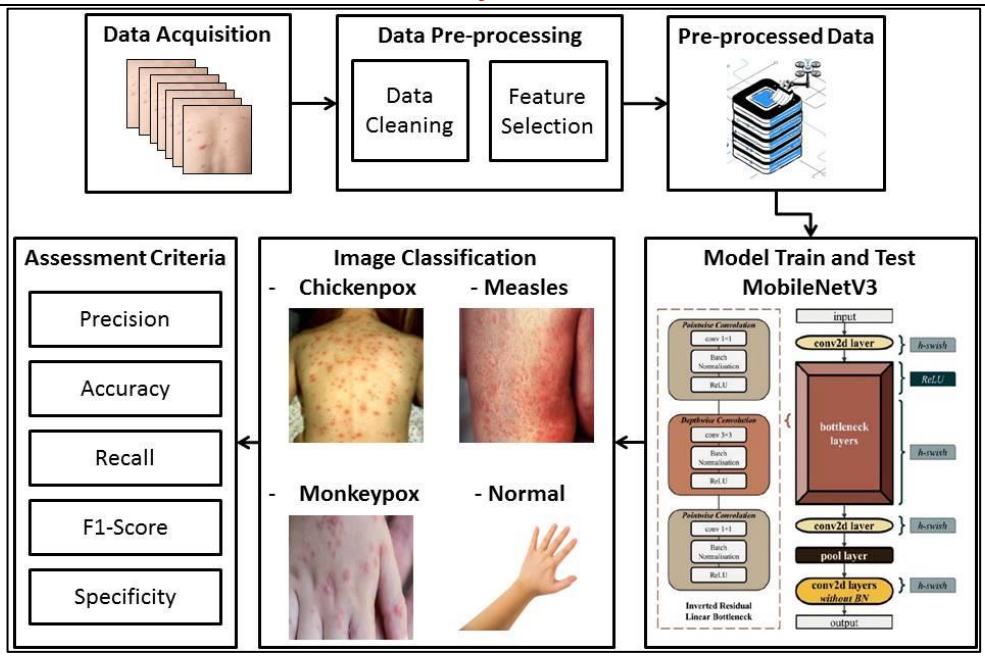

Figure 1: Workflow of Disease Classification Using MobileNetV3

Core Attributes of MobileNetV3:

Table 1 shows the core attributes of MobileNetv3 architecture. The table provides essential details about the structure and design principles of MobileNetV3, highlighting its key features and specifications.

Table 1: Core Attributes of MobileNetv3 Architecture

S.No.	Attributes	MobileNetV3
1	Inverted Residuals and Linear Bottlenecks:	Like MobileNetV2, MobileNetV3 employs inverted residual blocks with linear bottlenecks. This design maintains high efficiency and minimizes the number of operations required.
2	Squeeze-and-Excitation (SE) Modules:	MobileNetV3 integrates SE modules to enhance representational power through adaptive recalibration of channel-wise feature responses.
3	Architecture Search	The architecture of MobileNetV3 incorporates Neural Architecture Search (NAS) techniques to automatically optimize for both performance and efficiency. This approach helps achieve a balance between accuracy and computational resources.
4	Non-Linearities	MobileNetV3 utilizes a mix of ReLU and hard-swish activation functions, where hard-swish strikes a good balance between performance and efficiency.
5	Network Variants	MobileNetV3 is available in two primary versions: MobileNetV3-Large and MobileNetV3-Small, designed to meet varying requirements for accuracy and efficiency.

Detailed Architecture:

The MobileNetV3-Large model is optimized for higher accuracy while maintaining efficiency in computational resources. Table 2 provides a summary of its architecture, detailing the key components and design principles that contribute to its enhanced performance. Figure 2 provides the visual overview of the MobileNetV3 Architecture. The diagram illustrates the structural components and flow of information within the MobileNetV3 model, offering a clear depiction of its design and operational characteristics.

Table 2: Detailed Architecture of MobileNetv3

S.No.	Main Blocks	MobileNetv3
1	Stem	A 3x3 convolution with 16 filters, applied with a stride of 2, followed by batch normalization and ReLU activation.
2	Inverted Residual Blocks	Comprises multiple stages with various configurations of kernel sizes, expansion factors, filter numbers, and strides. Certain blocks incorporate SE modules and hard-swish activations.
3	Stages	
	Stage 1	Convolution with a 3x3 kernel and 16 channels, using a stride of 1.
	Stage 2	Inverted residual block with 24 channels, utilizing a 3x3 convolution and a stride of 2. Followed by another inverted residual block with 24 channels, employing a 3x3 convolution and a stride
	Stage 3	Inverted residual block with 40 channels, featuring a 5x5 convolution and a stride of 2. Includes an SE module and hard-swish activation.
	Stage 4	Inverted residual block with 80 channels, applying a 3x3 convolution with a stride of 2. Followed by multiple repeated inverted residual blocks with 80 channels, utilizing a stride of 1.
	Stage 5	Inverted residual block with 112 channels, featuring a 3x3 convolution with a stride of 1. It includes an SE module and uses hard-swish activation.
	Stage 6	Inverted residual block with 160 channels, utilizing a 5x5 convolution with a stride of 2. Includes an SE module and employs hard-swish activation.
4	Head	1x1 convolution with 960 channels, incorporating an SE module and hard-swish activation. This is followed by global average pooling, then a fully connected layer with 1280 channels and hard-swish activation. Dropout is applied if necessary, followed by the final fully connected layer for classification.

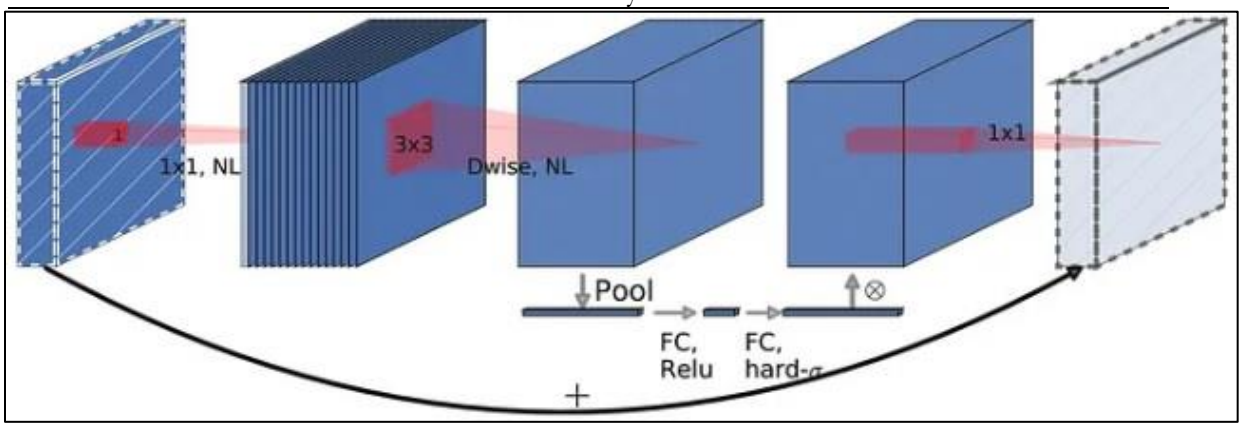

Figure 2: Visual Overview of MobileNetV3 Architecture [17].

Algorithm 2.1 presents the procedure for identifying chickenpox, measles, monkeypox, and normal cases from images using the MobileNetV3 model. This algorithm describes the step-

by-step process and criteria used by the model to classify and distinguish between different viral infections and normal skin conditions based on visual symptoms.

Algorithm 2.1. Image Classification using MobileNetV3

1 **Input:**
- Input images of various infections (chickenpox, measles, monkeypox) and normal cases.

2 **Preprocessing**:
- Resize the input images to the required input size for MobileNetV3.
- Normalize the pixel values of the images to the range [0, 1].

3 **Training & Fine-tuning**:
- Use transfer learning
- Load the pre-trained MobileNetV3 model.
- Fine-tune the model on a dataset containing images of chickenpox, measles, monkeypox, and normal cases to adapt it to this specific classification task.

4 **Model Evaluation**:
- Evaluate the trained model using a separate validation set or through cross-validation.
- Measure assessment criteria such as accuracy, precision, recall, etc.

5 **Testing**:
- Apply the trained MobileNetV3 model to new, unseen images.
- Obtain predictions for each image.
- Output the predicted class for each image (chickenpox, measles, monkeypox, normal).

Results & Discussion:

In this study, we introduced a cutting-edge, vision-based method for assessing skin disease using affordable RGB images. Our research aims to deliver valuable insights for developing practical solutions to manage contagious diseases. Utilizing advanced algorithms and image processing techniques, we aim to achieve high precision in distinguishing between healthy and diseased skin, providing a potential tool for improving public health safety.

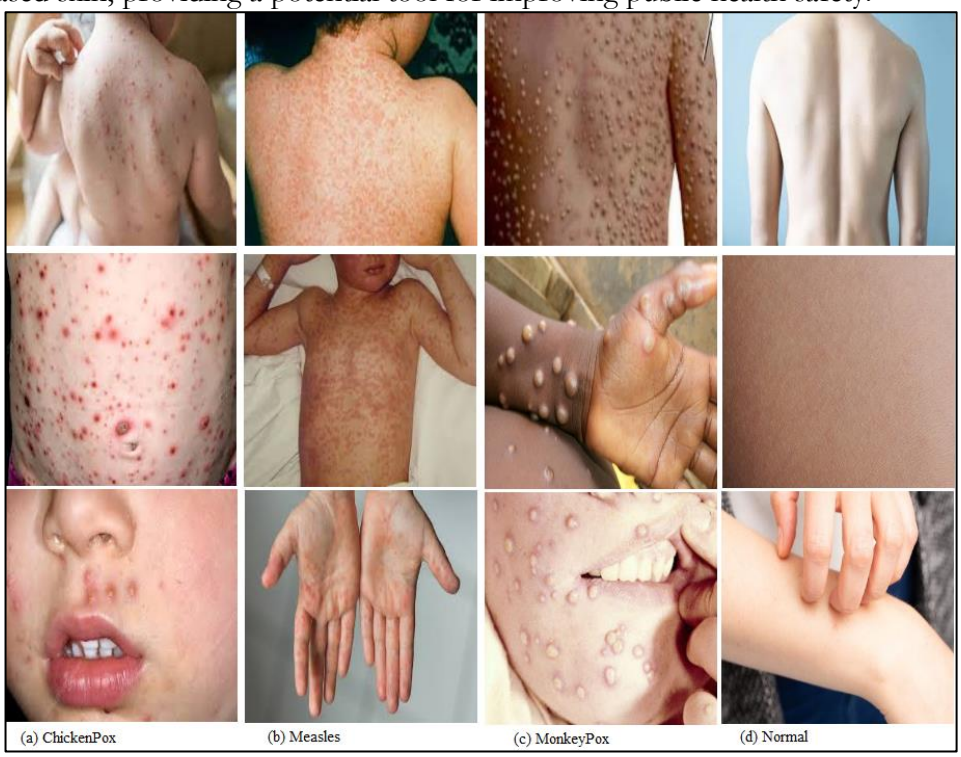

Figure 3: Dataset Sample

Dataset:

The dataset used in this study is sourced from Kaggle's Monkeypox Skin Image Dataset [18]. It is divided into four groups: Chickenpox, Measles, Monkeypox, and Normal. The Chickenpox category includes 107 images, the Measles category has 91 images, the Monkeypox category contains 279 images, and the Normal category comprises 293 images. Figure 3 illustrates a subset of the data, showcasing samples from each of the categories: Chickenpox, Measles, Monkeypox, and Normal. Figure 3 provides visual examples of the different skin symptoms associated with each condition, aiding in understanding the diversity of visual characteristics the model is trained to recognize.

Assessment Criteria:

The confusion matrix is an essential tool for evaluating the performance of classification models, providing a detailed analysis of correctly and incorrectly classified instances compared to the true outcomes within the test dataset. It includes four main components: True Occurrence (TO), where the model correctly predicts the occurrence of class when the condition is present; True Non-Occurrence (TNO), where the model accurately predicts the negative occurrence of class when the condition is absent; False Occurrence (FO), where the model incorrectly predicts the positive occurrence of class, falsely identifying the condition; and False Non-Occurrence (FNO), where the model incorrectly predicts the negative non-occurrence, failing to identify the condition.

This detailed breakdown helps in assessing the model's accuracy and its ability to distinguish between classes, highlighting its strengths and areas for improvement. It is a valuable tool in refining classification algorithms. Precision measures the proportion of correctly predicted positive instances among all instances predicted as positive and is calculated as:

$$\text{Precision} = TO / (TO + FO).$$

Accuracy represents the overall correctness of the model's predictions, defined as the ratio of correctly predicted instances to the total number of instances.

$$\textbf{Accuracy} = (TO + TNO) / (TO + TNO + FO + FNO).$$

Recall, or Sensitivity, measures the proportion of correctly predicted positive instances among all actual positive instances, calculated as:

$$\textbf{Recall} = TO / (TO + FNO).$$

Specificity, also known as the True Negative Rate (TNR), measures the proportion of correctly predicted negative instances among all actual negative instances and is calculated as:

$$\textbf{Specificity} = TNO / (TNO + FO).$$

The F1 Score, or F-score, is the harmonic mean of Precision and Recall, providing a balanced measure between the two metrics, calculated as:

$$\textbf{F1 Score} = 2 \times (\text{Precision} \times \text{Recall}) / (\text{Precision} + \text{Recall}).$$

Recent advancements in machine learning have improved these metrics' computation by integrating them into more sophisticated performance evaluation frameworks, enhancing the ability to fine-tune and optimize classification models.

Configuration:

Our deep learning model achieved remarkable results with a training time of just 35 seconds per epoch, trained over 50 epochs with a batch size of 16. Fine-tuned with a learning rate of 0.001, the model effectively learned intricate patterns in the data, showcasing its efficiency in both speed and accuracy. This configuration not only optimized our training process but also ensured that the model converged swiftly, providing robust predictions.

"Accuracy per epoch" and "loss per epoch" are metrics commonly utilized in the training of machine learning models, particularly neural networks. Accuracy per epoch refers to the model's accuracy on the training data at each epoch, with an epoch representing one complete pass through the entire training dataset. This metric is essential for monitoring the model's learning progress over time.

Loss per epoch quantifies the model's prediction error against the actual values for each training cycle. It represents the average loss (or error) on the training data at each epoch. A decreasing loss per epoch indicates that the model is improving in its predictions. These metrics play a critical role in evaluating and optimizing the performance of machine learning models during the training process. Figure 4 shows the accuracy and loss per epoch for our scenario. Figure 4 provides a visual representation of how the model's accuracy improves and loss decreases with each training epoch, demonstrating the effectiveness of the training process in optimizing the model's performance.

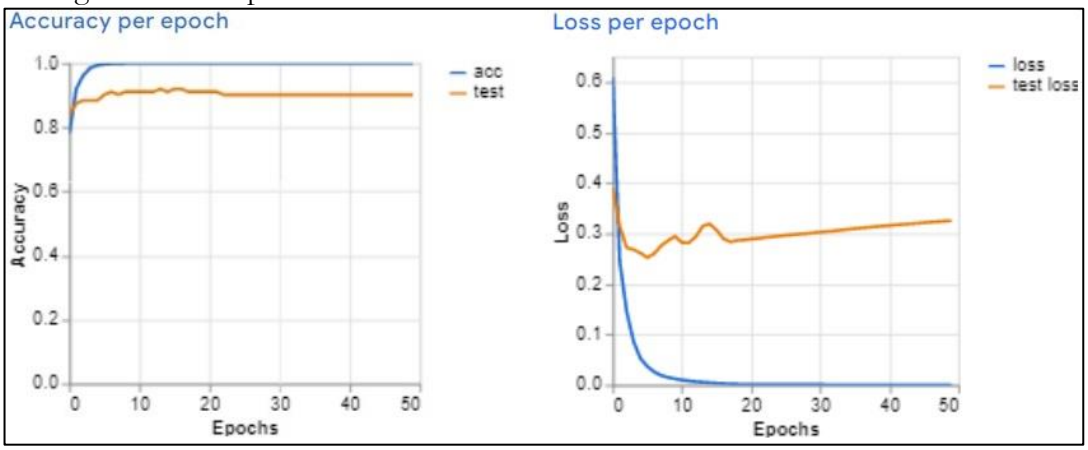

Figure 4: Training Progress Metrics: Accuracy and Loss per Epoch.

Outcome Analysis:

Figure 5 displays the performance evaluation metric for four classes: Chicken Pox, Measles, Monkey Pox, and Normal. The figure indicates that Chicken Pox and measles were correctly identified 90% of the time, with 10% of instances misclassified as Monkey Pox while Monkey Pox and normal cases were correctly identified 100% of the time. These misclassifications are due to overlapping symptoms and visual similarities between the conditions, highlighting the challenges in distinguishing between these diseases based on their features.

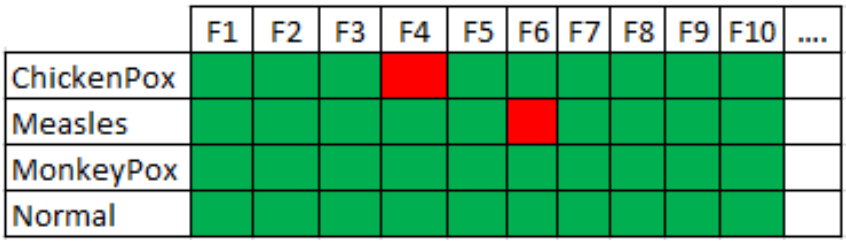

Figure 5: Performance Evaluation Metric.

The recognition results are detailed in Table 3 demonstrating strong performance across various measures. Precision is notably high at 95%, indicating that the model effectively identifies positive instances. Accuracy stands at 95.73%, reflecting the overall correctness of predictions. Recall, at 88.37%, alongside an F1-score of 91.56%, balances precision, and recall, providing a comprehensive measure of the model's performance. Specificity is exceptionally high at 98.34%, highlighting the model's proficiency in correctly identifying negative instances.

Table 3: Evaluation Metrics using MobileNetV3

Assessment Criteria	MobileNetV3 (%)
Precision	95
Accuracy	95.73
Recall	88.37
F1-score	91.56
Specificity	98.34

Figure 6 displays the performance metrics of our algorithm, Mobile Net, focusing on key indicators such as precision, accuracy, recall, F1-score, and specificity. The graphical representation of these metrics demonstrates the strong performance of our algorithm. These results suggest that our algorithm provides an effective and reliable solution for skin disease identification.

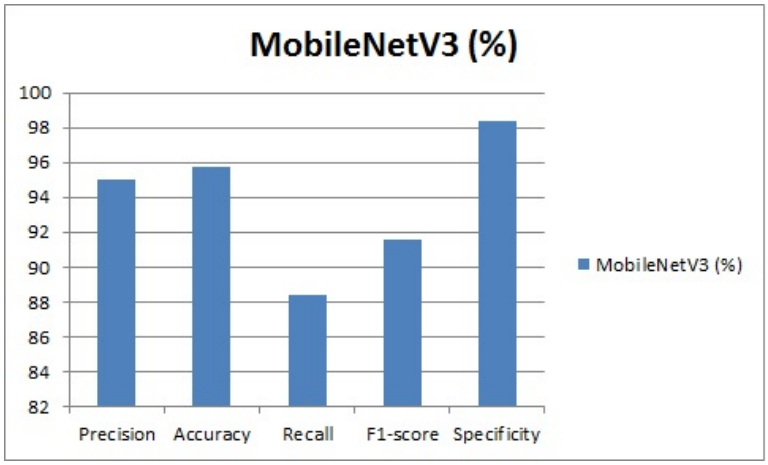

Figure 6: Mobile Net Performance Analysis: Key Metrics and Findings.

Comparison with Existing Methods:

The proposed approach using the MobileNetV3 model demonstrates significant advantages in the identification of Chicken Pox, Measles, Monkey Pox, and Normal cases. This section compares the effectiveness of the MobileNetV3 model with existing methods, particularly supervised machine learning techniques used exclusively for Monkey Pox detection.

Table 4: Comparison of Proposed Approach with Existing Methods

Parameters	**Proposed Approach**	**Classical Approach -Azka Mir et al.** [8] **Approach & Result**	**Deep Learning Approach - Md. Enamul Haque et al.** [10] **Approach & Result**
Model/ Classifier	MobileNetV3	Decision tree, Naïve Baye, K-NN (k=5 neighbors)	VGG19, Xception, DenseNet121, EfficientNetB3, MobileNetV2 with CBAM VGG19, Xception, DenseNet121, EfficientNetB3, MobileNetV2 with CBAM
Infection Coverage	Chickenpox, Measles, MonkeyPox, Normal	Monkeypox only	MonkeyPox and other diseases
Platform	Python – TensorFlow - Keras	RapidMiner	Not Specified
Precision	95%	Not Specified	Not Specified
Accuracy	95.73%	93.51%	83.89%
Key Findings	- Accurately identified ChickenPox and Measles 90% of the time, with a 10% misclassification rate as MonkeyPox	- Performed using various classifiers (Decision Tree, Naïve Bayes) - K-NN classifier achieved the highest accuracy rate among tested methods.	- An architecture consisting of Xception-CBAM-Dense layers performed better than the other models at classifying monkeypox and other diseases. Achieved a validation accuracy of 83.89%.

	- MonkeyPox and Normal cases correctly identified 100% of the time - Strong overall performance despite overlapping symptoms and visual similarities among diseases.

The proposed approach using the MobileNetV3 model demonstrates superior effectiveness in identifying multiple viral infections with higher precision and accuracy compared to existing methods focused solely on Monkey Pox detection. Moreover, some of the advantages of Deep Learning (MobileNetV3) Over Traditional Machine Learning Models (Decision Tree, Naïve Bayes, K-NN) are discussed below:

- MobilenetV3 is capable of handling high-dimensional data and complex patterns through its multiple layers, making it suitable for image recognition and other tasks requiring deep feature extraction. On the other hand Decision Trees, Naïve Bayes, and K-NN are generally less effective with complex, high-dimensional data, often requiring feature engineering to achieve good performance.
- MobilenetV3 automatically extracts and learns relevant features from raw data, eliminating the need for manual feature engineering while Decision Tree, Naïve Bayes, and K-NN rely on manually engineered features, which can be time-consuming and may not capture the underlying data patterns as effectively.
- MobilenetV3 scales well with large datasets, leveraging the increased data volume to improve model accuracy and robustness; while Decision Tree, Naïve Bayes, and K-NN may not scale as effectively with large datasets, and computational efficiency can become a concern, especially with K-NN which requires storing and comparing all training data.
- MobileNetV3 is more robust to noise and irrelevant features in the data due to its ability to learn discriminative features through multiple layers. On the other hand, Decision Trees, Naïve Bayes, and K-NN are sensitive to noise, with Decision Trees prone to overfitting and Naïve Bayes assuming feature independence, which may not hold in noisy data.
- MobileNetV3 tends to generalize better to new, unseen data due to its deep architecture and ability to learn hierarchical representations. Decision Tree, Naïve Bayes, K-NN: May overfit to training data and struggle with generalizing to new data, particularly when the dataset is complex or noisy.

These above-mentioned points highlight the superiority of MobilenetV3 models especially in tasks that involve complex data, such as image recognition, where deep learning can leverage its advanced architecture and learning capabilities. The comprehensive coverage of various diseases, coupled with the robust performance metrics, underscores the potential impact of this approach on public health diagnostics.

Discussion:

The MobileNetV3 model's performance evaluation, depicted in Figure 5 and detailed in Table 3, showcases its efficacy in identifying Chicken Pox, Measles, Monkey Pox, and Normal cases. It accurately identified Chicken Pox and measles 90% of the time, with a 10% misclassification rate as Monkey Pox. Conversely, Monkey Pox and normal cases were correctly identified 100% of the time, highlighting the model's strong overall performance despite challenges due to overlapping symptoms and visual similarities among these diseases. Table 3 underscores the model's robustness, achieving a precision of 95% for positive instances and an overall accuracy of 95.73%. Recent studies by Azka Mir in [8] report an accuracy rate exceeding

90% for similar diseases using machine learning models, aligning closely with our results. In contrast, Md. Enamul Haque et al. [10] achieved an 83% accuracy in identifying monkeypox and other diseases, which is consistent but lower than our findings. This suggests that MobileNetV3 competes favorably in disease identification tasks affirming its effectiveness and reliability in classifying viral infections based on skin manifestations.

Conclusion:

The evaluation metrics for MobileNetV3 indicate strong performance across multiple criteria. With a precision of 95%, accuracy of 95.73%, recall of 88.37%, an F1-score of 91.56%, and specificity of 98.34%, the model demonstrates its effectiveness and reliability in various aspects of classification. The use of MobileNetV3 in this methodology yields robust results. For future enhancements, exploring advanced techniques such as incorporating transfer learning, utilizing more diverse and representative training datasets, or integrating attention mechanisms could further boost the model's performance. Additionally, leveraging ensemble learning methods may enhance predictive accuracy and robustness. Employing real-time data augmentation and optimization techniques, such as hyperparameter tuning and model pruning, can also contribute to improved performance. These strategies can help refine the model and ensure its applicability across a broader range of scenarios, ultimately leading to more reliable and accurate outcomes in practical applications.

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Author's Contribution.

Shaheena Noor is responsible for the conception, design of the study, and analysis of the data. Muhammad Imran Saleem contributed to the development of the methodology, and execution of experiments, provided critical feedback on experimental design, and assisted with data analysis. Najma Ismat is responsible for data validation. Aneeta Siddiqui focused on data visualization and exploration. Humera Noor Minhas contributed to interpreting the results and drafting the manuscript.

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