

Performance of majority voting transfer learning deep learning monkeypox disease detection

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ABSTRACT

Global health concerns have been raised by the advent of monkeypox following the COVID-19 epidemic, highlighting the need for reliable automated systems to support early skin disease screening. This study proposes a monkeypox skin disease classification framework using a majority voting ensemble based on transfer learning. The ensemble combines predictions from multiple pretrained convolutional neural networks (CNNs) to improve classification robustness. A publicly accessible dataset comprising four classes: monkeypox, chickenpox, measles, and normal skin was used for the experiments. The results indicate that while a single ResNet50 model achieved the highest overall accuracy (99.15%), the majority voting approach yielded higher precision than several individual models, demonstrating improved reliability in distinguishing monkeypox cases. These findings suggest that ensemble-based majority voting can enhance the robustness of monkeypox skin disease classification and may support computer-aided screening systems.

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1. INTRODUCTION

The apparent similarity and variety in lesion appearance of skin cancer and other dermatological illnesses make diagnosis extremely difficult. The application of deep learning and convolutional neural networks (CNN) for skin lesion categorization has been thoroughly studied in the past to help dermatologists increase the accuracy of their diagnoses. For instance, studies using densely connected convolutional network (DenseNet)-201 and skin lesion augmentation style-based generative adversarial network (SLA-StyleGAN) obtained a balanced multiclass accuracy (BMA) of 93.64%, showing that generative models can improve dataset diversity and model robustness [1]. Other research has developed automated image-based systems using CNNs and softmax classifiers to produce faster and more reliable diagnostic results, which can also serve as real-time educational tools for medical students [2]. Similarly, deep neural network (DNN)-based research combining image preprocessing, segmentation, feature extraction, and classification has achieved accuracy up to 84.45% on ISIC 2017 dataset [3]. Additionally, on the HAM10000 dataset, deep CNN trained using preprocessing, normalization, and augmentation strategies achieved 91.93% testing accuracy [4]. Using EfficientNet with transfer learning and the ranger optimizer, more recent study achieved a high area under the curve (AUC)-receiver operating characteristic (ROC) score of 0.9681 on ISIC-2019 and ISIC-2020 datasets [5]. These research findings demonstrate that deep learning based image analysis provides reliable performance in skin lesion classification tasks.

Classifying melanoma and other skin malignancies has advanced significantly, but little study has been done on infectious skin conditions like monkeypox, which has resurfaced as a worldwide health concern since the COVID-19 pandemic. Most common in Central and West Africa, monkeypox is a zoonotic viral illness that can transfer from wild animals to humans. However, it can also travel to tropical areas like Indonesia. Delayed identification of monkeypox can accelerate transmission and increase mortality. Therefore, early and accurate detection using artificial intelligence (AI) and computer vision is crucial for preventing further spread [6]. Monkeypox may be successfully distinguished from superficially similar illnesses like chickenpox and measles with the use of AI-based medical image analysis [7].

High accuracy rates have been attained in earlier studies on deep learning-based monkeypox categorization. For example, MobileNetV2 attained 98.16% accuracy and modified DenseNet-201 98.91% [7]–[9]. However, these approaches rely heavily on large and balanced datasets to avoid overfitting, which remains a significant limitation. Researchers have used picture augmentation approaches involving several skin disease classes (chickenpox, measles, monkeypox, and normal) to resolve data imbalance [7]. In order to get 93.39% accuracy, some research has also looked into ensemble approaches that include many deep learning models, including extreme inception (Xception), InceptionV3, and DenseNet169 [10]. Although ensemble learning improves classification reliability, there is still room to enhance precision and stability, particularly when dealing with complex skin lesion variations.

In light of these constraints, this study suggests a majority voting-based classification framework that incorporates several transfer learning models, including ResNet50, VGG16, MobileNet, InceptionV3, and Xception, to increase the precision and consistency of the categorization of monkeypox skin diseases. Additionally, an image preparation step called contrast limited adaptive histogram equalization (CLAHE) is included to improve image quality by balancing contrast and brightness before to classification. This study attempts to address the shortcomings of earlier approaches and achieve more precision and resilience in the detection of monkeypox skin illness by combining CLAHE preprocessing with majority voting.

2. METHOD

This section outlines the study's general methodology, which includes the collection of datasets, preprocessing techniques, transfer learning-based model training, and majority voting-based ensemble classification. By merging predictions from several CNN models, the suggested approach seeks to increase the robustness of monkeypox skin disease classification. An overview of the methodological pipeline is presented before detailing each component.

2.1. Datasets

This study's skin picture collection came from a publicly accessible dataset that had been used in earlier studies [7]. Table 1 summarizes the 770 original photos, which are divided into four classes: chickenpox (107 images), measles (91 images), monkeypox (279 images), and normal skin (293 images). Sample photographs from each class are shown in Figure 1.

Table 1. Original dataset distribution

No	Type	Total
1	Chickenpox	107
2	Measles	91
3	Monkeypox	279
4	Normal	293
	Total	770

The training data was subjected to data augmentation-based oversampling in order to correct the class imbalance. Horizontal and vertical flipping, rotation, center cropping, brightness and contrast alteration, saturation and hue jittering, width and height shifting, and noise addition were among the augmentation techniques used. The dataset was expanded to approximately 1,200 images per class to ensure sufficient representation while maintaining class balance. As a result, the final augmented dataset consisted of 4,692 images, as shown in Table 2. After that, the dataset was split 80:20 into training and testing sets, yielding 4,222 training images and 470 testing images. To avoid data leaking, data augmentation was only used on the training set. Examples of augmented photos are shown in Figure 2.



Figure 1. Dataset research

Table 2. Augmented dataset distribution

No	Type	Train	Test	Total
1	Chickenpox	1,080	120	1,200
2	Measles	982	110	1,092
3	Monkeypox	1,080	120	1,200
4	Normal	1,080	120	1,200
Total		4,222	470	4,692

2.2. Proposed model

This study uses an ensemble architecture based on majority voting from several transfer learning models, including ResNet50, VGG16, MobileNet, InceptionV3, and Xception, to classify four skin conditions: chickenpox, measles, monkeypox, and normal skin. The overall research framework is illustrated in Figure 3. According to earlier research, the majority voting method uses a hard voting scheme in which the final class label is decided by the class that each model predicts the most frequently [11]. Without weighting, each model makes an equal contribution to the ultimate choice. The chosen transfer learning architectures have proven to perform well in previous medical picture categorization studies [7]. ImageNet pre-trained weights were used to initialize each model, and it was set up to take input photos with 224×224 pixels. A GlobalAveragePooling2D layer, a fully connected Dense layer with 256 neurons and rectified linear unit (ReLU) activation, batch normalization, dropout with a rate of 0.5, and a final Dense layer with softmax activation for four-class prediction were added to the basic networks.

As illustrated in Figure 4, image preprocessing was carried out using CLAHE to improve contrast and lessen light variability before training. The Adam optimizer was used to train the model at a learning rate of 0.0001. Accuracy, which was computed using (1), was the main metric used to assess model performance [9]. This study contributes by investigating the effectiveness of individual transfer learning models and assessing the resilience of a majority voting ensemble in conjunction with contrast enhancement preprocessing for the categorization of monkeypox skin diseases.

2.3. Model evaluation

Accuracy (1) was used to assess the performance of the ResNet50, VGG16, MobileNet, InceptionV3, and Xception models. This metric offers a thorough evaluation of the model's efficacy in picture detection and classification. True positives (TP), true negatives (TN), false positives (FP), and false negatives (FN) are all included in this equation. Whereas FP and FN represent inaccurate forecasts, TP and TN represent accurate predictions.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (1)$$

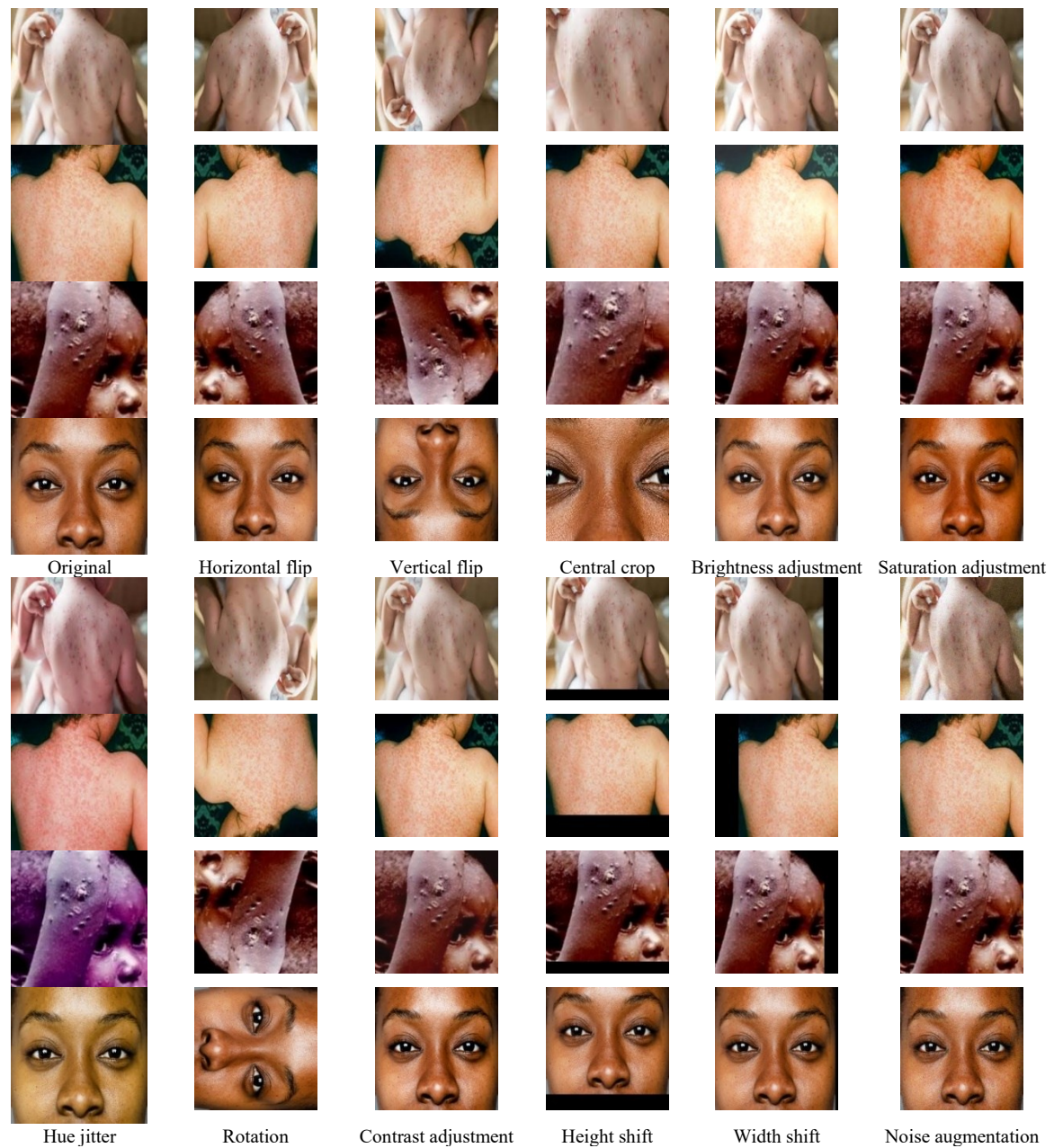


Figure 2. Dataset augmentation

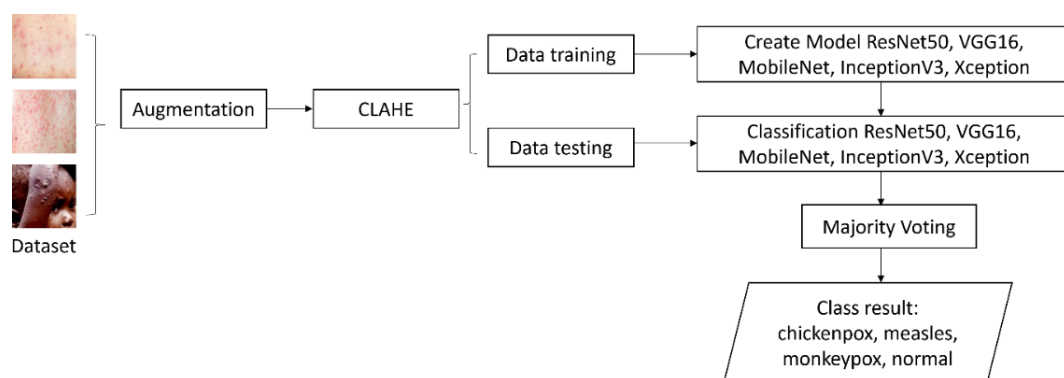


Figure 3. Research proposed



Figure 4. Results CLAHE

3. RESULTS AND DISCUSSION

3.1. Training methodology

In order to categorize four kinds of skin diseases: chickenpox, measles, monkeypox, and normal skin, this study assesses the effectiveness of transfer learning models: ResNet50, VGG16, MobileNet, InceptionV3, and Xception in addition to an ensemble method based on majority voting. The majority voting strategy combines the predicted class labels from all individual models, following a hard voting scheme as described in previous studies [11]. Each model's classification accuracy is shown in Table 3. ResNet50 had significant discriminative capacity, achieving the best accuracy of 99.15% among the individual architectures. With an accuracy of 98.94%, the suggested majority voting ensemble outperformed VGG16, MobileNet, and InceptionV3 and was on par with the top-performing single model.

Table 3. Evaluation results

No	Model	Accuracy (%)
1	ResNet50	99.15
2	VGG16	96.59
3	MobileNet	97.87
4	InceptionV3	98.29
5	Xception	98.93
6	Majority voting	98.94

Although the ensemble did not surpass ResNet50 in terms of overall accuracy, majority voting provides improved robustness by aggregating predictions from multiple models, thereby reducing the influence of individual model errors. This characteristic is particularly important in medical image classification, where prediction reliability is critical. The accuracy and loss curves for each transfer learning model during training and validation are shown in Figure 5. ResNet50 demonstrates fast convergence and stable loss reduction, while InceptionV3 and Xception exhibit smoother convergence behavior with relatively low validation loss. These results indicate that the selected architectures are well-suited for the skin disease classification task.

3.2. Discussion

The experimental results are discussed in this section by contrasting the suggested approach with relevant research on the classification of skin diseases and monkeypox. As shown in Table 4, numerous studies have reported high classification accuracy using different deep learning architectures and problem formulations. Several studies have achieved very high accuracy, including PoxNet22 [12] with 100% accuracy and ResNet-based approaches [13]–[15]. It is crucial to remember that the majority of this research concentrate on binary classification tasks that separate instances of monkeypox from those that do not. Binary classification problems are generally less complex than multi-class scenarios. The suggested approach, on the other hand, tackles a more difficult four-class classification problem involving measles, chickenpox, monkeypox, and normal skin because of the visual similarities between skin disorders. The suggested majority voting ensemble achieves an accuracy of 98.94% despite this added complexity, which is on par with or better than a number of current four-class methods like MonkeyNet [7], MobileNetV2 [9], and other CNN-based models [16], [17].

Compared to previous ensemble-based studies, such as the work in [10], which combined multiple deep learning models for binary monkeypox classification and achieved an accuracy of 93.39%, the proposed method demonstrates superior performance while handling a more complex multi-class classification task. The majority vote ensemble provides better robustness by combining predictions from various architectures, even though a single ResNet50 model has the maximum accuracy. This ensemble approach improves

prediction stability and lessens the influence of individual model errors, which is crucial in medical image analysis where trustworthy decision assistance is needed.

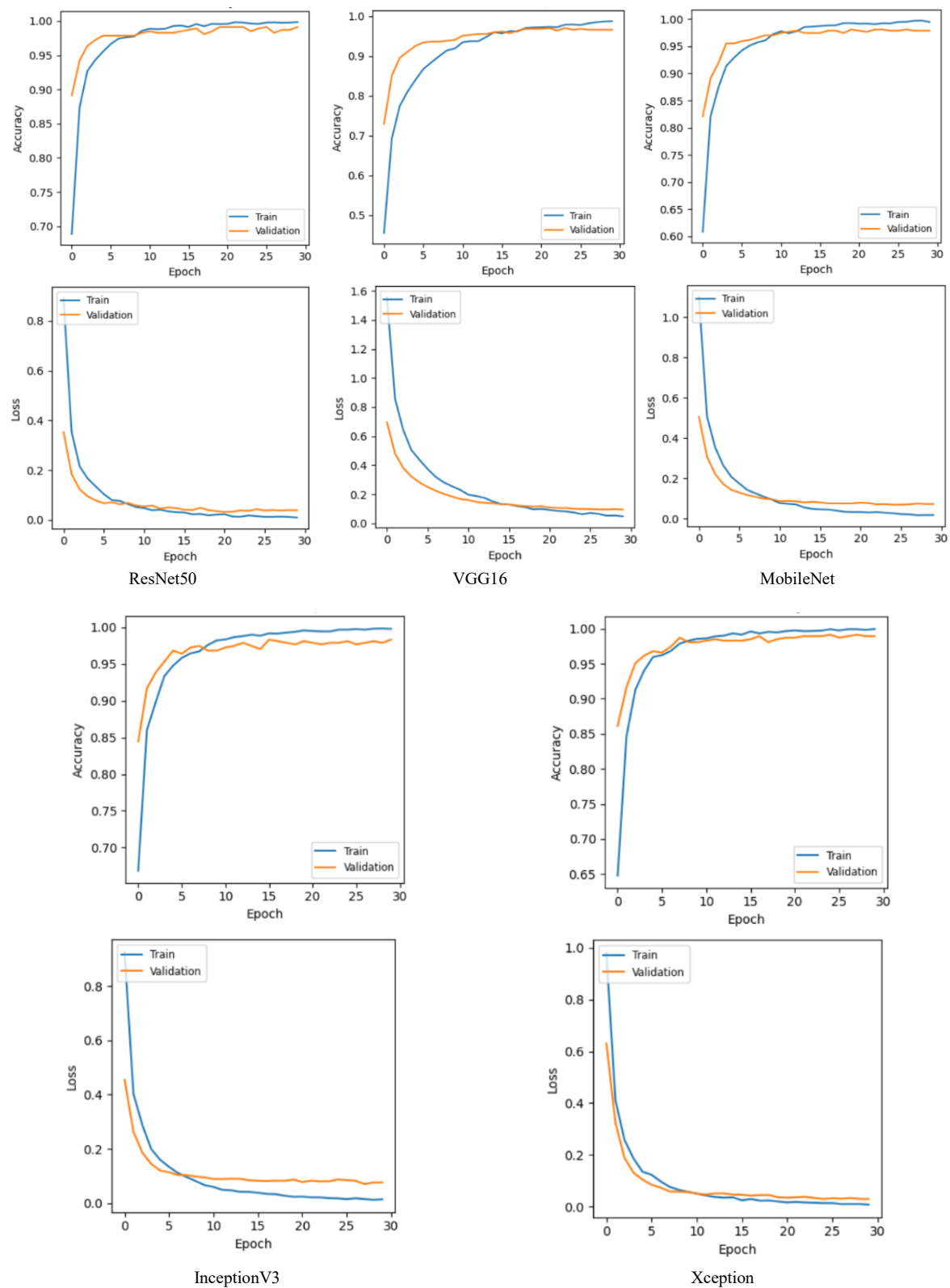


Figure 5. History training and validation transfer learning

Table 4. Evaluation comparison

No	Methods	Classification	Accuracy (%)
1	MonkeyNet is a deep learning-based CNN model that was modified from DenseNet-201 [7]	4 class (chickenpox, measles, monkeypox, normal)	98.91
2	Feature extraction with GoogleNet and Decision Tree classification [8]	4 class (chickenpox, measles, monkeypox, normal)	94.35
3	MobileNetV2 [9]	4 class (monkeypox, normal, scarlet fever, roseola)	98.16
4	Ensemble from Xception, InceptionV3, DenseNet169 [10]	2 class (monkeypox, non monkeypox)	93.39
5	ResNet101 [13]	4 class (chickenpox, measles, monkeypox, normal)	94.25
6	ResNet101 [14]	2 class (monkeypox, normal)	99.00
7	PoxNet22 [12]	2 class (monkeypox, non monkeypox)	100.00
8	ResNet18 [15]	2 class (monkeypox, non monkeypox)	99.49
9	CNN-LSTM hybrid model [18]	4 class (chickenpox, measles, monkeypox, normal)	87.00
10	Integrating deep neural networks with federated learning (FL) and CycleGAN [19]	4 class (chickenpox, measles, monkeypox, normal)	97.90
11	Feature extraction with deep learning and weighted naïve Bayes (WNB), weighted k-nearest neighbors (WKNN) classification [16]	4 class (chickenpox, measles, monkeypox, normal)	98.48
12	MobileNetV3-s [20]	2 class (positive, negative monkeypox)	99.00
13	DenseNet201 [17]	4 class (chickenpox, measles, monkeypox, normal)	95.18
14	MobileNetV2 [21]	2 class (monkeypox, normal)	99.00
15	DenseNet201 [22]	4 class (chickenpox, measles, monkeypox, normal)	99.94
16	AlexNet+VGG16 [23]	2 class (monkeypox, non monkeypox)	95.55
17	EfficientNet B3 [24]	6 class (chickenpox, cowpox, measles, monkeypox, healthy, smallpox)	87.00
18	MobileNetV2 [25]	4 class (chickenpox, measles, monkeypox, normal)	91.37
19	Proposed method	4 class (chickenpox, measles, monkeypox, normal)	98.94

The confusion matrices for the five transfer learning models: ResNet50, VGG16, MobileNet, InceptionV3, and Xception are shown in Figure 6. The high values along the major diagonal of each confusion matrix show that, overall, all models perform well in classification across the four skin disease classes (chickenpox, measles, monkeypox, and normal). With 118 images of chickenpox, 109 photographs of measles, 119 images of monkeypox, and 120 images of normal, the ResNet50 model has exceptional classification skill. Strong discriminative power and low misclassification rates across all classes are indicated by the large concentration of accurate predictions on the diagonal.

Similarly, VGG16 achieves robust performance, with 117 correctly classified chickenpox cases, 107 measles cases, 119 monkeypox cases, and 117 normal cases. Although a small number of misclassifications are observed, the overall pattern suggests consistent and reliable predictions. The MobileNet model also performs very well, correctly classifying 118 chickenpox, 108 measles, 119 monkeypox, and 120 normal images. This result highlights MobileNet's effectiveness despite its lightweight architecture, making it suitable for efficient classification tasks. For InceptionV3, the confusion matrix indicates strong performance, with 115 correct chickenpox predictions, 107 measles predictions, 119 monkeypox predictions, and 120 normal predictions. The relatively low number of misclassified samples suggests stable convergence and effective feature extraction. 113 photographs of chickenpox, 110 images of measles, 119 images of monkeypox, and 119 images of normal are correctly classified by the Xception model. Misclassification errors are minimal, with only a few chickenpox samples incorrectly predicted as measles, monkeypox, or normal. This further demonstrates the robustness of the model.

From a clinical perspective, the confusion matrices show that misclassification between monkeypox and other visually similar diseases is limited, which is particularly important for reducing false-positive and false-negative predictions. When these individual models are combined using the proposed majority voting ensemble, prediction reliability is enhanced by aggregating model decisions, thereby reducing the influence of isolated classification errors. Even when the ensemble accuracy is marginally less than that of the top-performing single model, this ensemble behavior explains the observed improvement in precision and overall robustness.

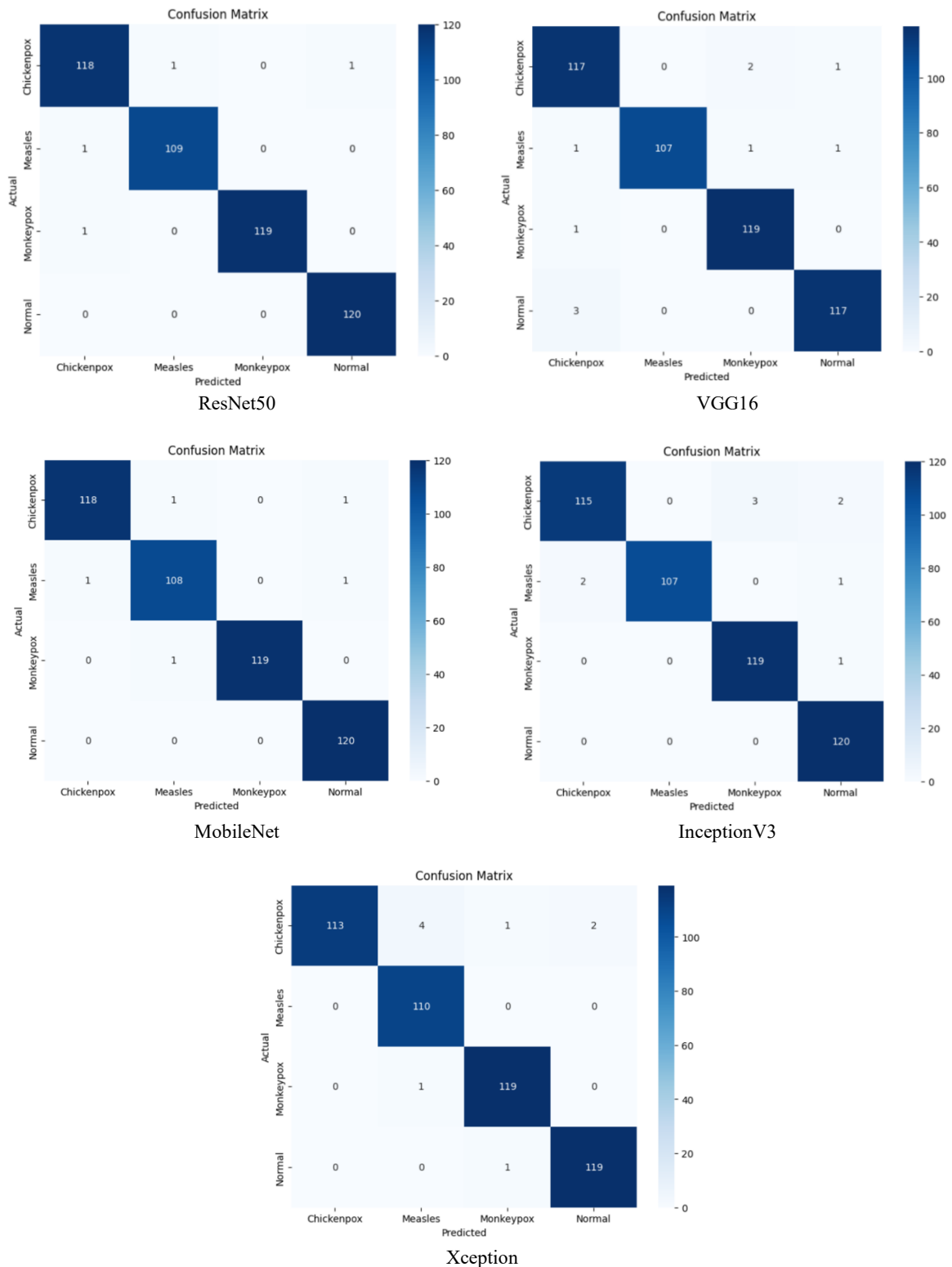


Figure 6. Confusion matrix of evaluation model

4. CONCLUSION

In order to classify monkeypox and other skin disorders, this work shows the efficacy of a majority voting ensemble that integrates five transfer learning models: ResNet50, VGG16, MobileNet, InceptionV3, and Xception. According to experimental data, the suggested majority voting strategy obtained a comparable accuracy of 98.94% and provided higher precision than various individual models, whereas ResNet50 earned

the best individual accuracy (99.15%). Majority voting improves prediction reliability by combining outputs from several architectures, so lessening the impact of individual model faults, even when the ensemble did not outperform the top-performing single model in terms of accuracy. When combined with CLAHE-based image preprocessing, this approach contributes to more robust classification performance, which is particularly relevant for medical image analysis tasks involving visually similar skin conditions. In order to increase generalizability, future work will concentrate on adding more varied real-world images to the dataset, investigating sophisticated ensemble techniques like weighted voting and stacking, and assessing extra performance metrics including recall, F1-score, and confusion matrices. Furthermore, integrating the proposed framework into web- or mobile-based computer-aided screening systems may support early and reliable monkeypox detection in practical healthcare settings.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

Name of Author	C	M	So	Va	Fo	I	R	D	O	E	Vi	Su	P	Fu
Nur Nafiiyah	✓	✓	✓	✓					✓	✓	✓	✓		✓
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C : Conceptualization

M : Methodology

So : Software

Va : Validation

Fo : Formal analysis

I : Investigation

R : Resources

D : Data Curation

O : Writing - Original Draft

E : Writing - Review & Editing

Vi : Visualization

Su : Supervision

P : Project administration

Fu : Funding acquisition

CONFLICT OF INTEREST STATEMENT

All researchers do not have a conflict.

DATA AVAILABILITY

The data availability from an open dataset that has been used previous research in Kaggle at <https://www.kaggle.com/datasets/dipuiucse/monkeypoxskinimagedataset>.

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