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Classification of Skin Diseases using Digital Image Processing with MobileNetV2 Architecture

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INFORMATION

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ABSTRACT

Skin diseases are prevalent in tropical countries like Indonesia, where geographical and climatic conditions facilitate their spread. This research aims to classify skin diseases using digital image processing with the MobileNetV2 architecture. The DermNet dataset is used to develop and test the model. Various image preprocessing techniques, including resizing, augmentation, and normalization, were applied to the dataset, which consists of 300 images categorized into dermatitis, psoriasis, and scabies. The model achieved a training accuracy of 90% and a validation accuracy of 70%, with notable success in classifying psoriasis. The findings suggest that MobileNetV2, when combined with CNN, is a promising tool for diagnosing skin diseases early and efficiently.

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1. INTRODUCTION

The skin is the first organ to be exposed to external stimuli such as temperature, touch, and extreme climate change. Therefore, skin diseases are the most common and most easily transmitted diseases in humans, especially in Indonesia. Head of the Meteorology, Climatology and Geophysics Agency (BMKG) Dwikorita Karnawati revealed that 2024 is officially the hottest year in instrumental recording history, with global average temperatures reaching 1.55°C above pre-industrial levels. This figure exceeds the Paris Agreement threshold that has been agreed globally to prevent a climate crisis.

Skin disease is a skin disorder that occurs in humans. The lack of awareness to maintain hygiene is one of the main reasons why fungi, bacteria and viruses can develop rapidly [1]. According to the Indonesian Ministry of Health in 2011, the national prevalence of the largest case of skin disease in Indonesia is dermatitis with a percentage of around 6.8% based on respondents' complaints. This is in line with the importance of maintaining cleanliness in the environment. Although skin diseases are not deadly, they can affect a person's quality of life [2].

The medical field is currently growing rapidly due to technological advancements, especially in the utilization of medical images such as x-rays, MRIs, CT scans, and skin photos to help diagnose and monitor

diseases[3]. This medical image processing used to rely on conventional image processing, which is an approach based on basic algorithms such as filtering, thresholding, edge detection, and morphological operations, which work directly on image pixels to improve quality, extract features, or separate certain areas. However, conventional methods have limitations in capturing complex patterns that often appear in medical images. To overcome this challenge, deep learning emerged as a solution capable of automatically learning important patterns from image data using architectures such as Convolutional Neural Network (CNN).

The potential of deep learning in the medical field is enormous, ranging from disease classification, lesion or tumor detection, to severity prediction. CNN was able to classify skin cancer with the accuracy of a dermatologist [4]. In addition, deep learning has played an important role in medical image analysis, particularly for detecting and analyzing lung cancer in CT scan data, with very promising results in improving diagnosis accuracy. With this potential, deep learning continues to drive innovation in the medical world, opening up new opportunities for faster, more accurate and efficient diagnosis [5][6].

This research aims to develop a skin disease classification model using CNN with the MobileNetV2 architecture. The model is trained using medical image datasets obtained from DermNet, tested to recognize common skin disease patterns, and evaluated to assess its accuracy, precision, recall, and F1-Score.

2. METHODOLOGY

This research follows a structured methodology to ensure the reliability and accuracy of the developed skin disease classification model an experimental approach using a Convolutional Neural Network (CNN) with the MobileNetV2 architecture for skin disease classification[7][8]. The workflow includes dataset, preprocessing, pre-trained, classification, and evaluation.

2.1 Dataset

The image data used is obtained from the DermNet dataset on the Kaggle website. There are 3 disease classes with a total of 300 image data, namely, 100 Atopic Dermatitis, Psoriasis, and Lyme Scabies. For each class of data has 2 classes each, namely train data of 80 images and test of 20 images.

Each class was divided into 80 image per class for training data dan 20 images per class for test data. With sample images of disease types: [A] Atopic Dermatitis, [B] Psoriasis, [C] Lyme Scabies, and [D] Example of augmentation results.

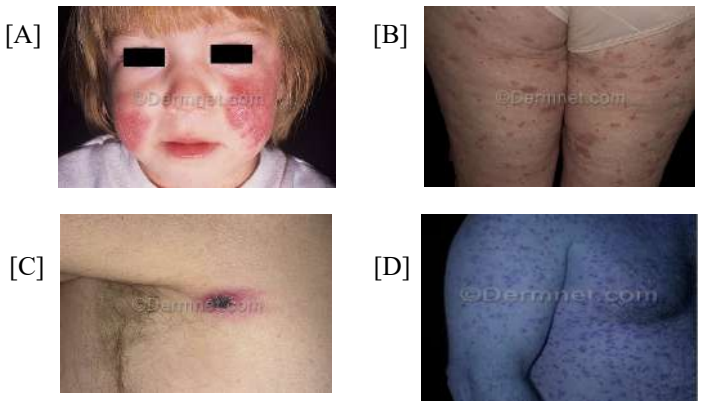

Figure 1. Dataset sample

2.2 Preprocessing

Preprocessing is the preparation stage before starting the process which consists of various stages such as mounting Google Drive which is used to connect Google Colab (execution platform) and Google Drive (dataset storage), calculating image data, resizing image data from the initial 720 x 480 pixels to 224 x 224 pixels, and augmentation. Data augmentation is a technique to increase the number of training data variations by applying transformations such as rotation, flipping, zooming, and shearing[9][10]. This technique helps in expanding the dataset by creating new variations of existing image data which is useful for improving the generalization ability of the ImageDataGenerator or Albumentations library models. Data preprocessing was performed to optimize image quality and enhance model performance[11][12]. The following steps were applied:

Table 2. Augmentation

Variable	Value
Rescale	1./255
Rotation Range	40
Width Shift	0.2
High Shift	0.2
Shear Range	0.2
Zoom Range	0.2
Validation Split	0.4
Horizontal Flip	TRUE

Validation data was split from training data using validation split = 0.4, resulting in 48 training images and 32 validation images per class.

2.3 Pre-trained

After preprocessing, the data was fed into a pre-trained model for feature extraction[13]. MobileNetV2 from TensorFlow, trained on a large dataset, was used as a feature extractor to recognize patterns and features in images [14]. These extracted features were then processed by additional layers for classification tasks, reducing the need to train the model from scratch.

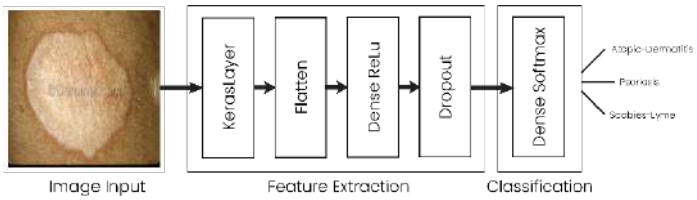

Figure 2. The proposed MobileNetV2 architecture

The pre-trained model first defined parameters such as the models name (mobilenet_v2), input image size (224 × 224 pixels), and feature vector size (1280). It was loaded using hub.KerasLayer from TensorFlow Hub, taking RGB images (224 × 224 pixels, 3 channels) as input and outputting feature vectors. Fine-tuning was then applied by setting do_fine_tuning = TRUE, allowing the last 30 layers of the base model to be trained. If set to FALSE, the model used only pre-learned features without updating weights[13]. The model was built as follows:

1. Feature Extractor: Pre-trained MobileNetV2 layers (excluding the top layer).
2. Flatten Layer: Converts extracted features into a 1D array.
3. Dense Layer: 1024 neurons with ReLU activation for feature learning.
4. Dropout Layer: 0.5 dropout rate to prevent overfitting.
5. Output Layer: Softmax activation to classify the images into three categories.

Fine-tuning was applied to adjust the pre-trained model to the specific skin disease dataset.

2.4 Classification

The classification process involves several pre-trained processes including adding the MobileNetV2 module and fine-tuning. Fine-tuning is the process of retraining an existing model, usually a pre-trained model, to suit a more specific task or dataset[15][16]. This classification process uses training data and validation data to measure how well the model learns. After the pre-trained process, it will produce several main components such as training accuracy, training loss, validation accuracy, validation loss, and graph results [17]. These metrics were visualized using graphical plots to track improvements over time and identify potential overfitting or underfitting issues.

2.5 Evaluation

As part of the evaluation process, the classification report provided an overview of precision, recall, and F1-score for each skin disease category. Here is the formula for the confusion matrix:

$$\text{Accuracy} = \frac{\text{Total True Positives}}{\text{Total Data}} \qquad Precision_i = \frac{\text{TP}_i}{\text{TP}_i + \text{FP}_i}$$

$$Recall_i = \frac{\text{TP}_i}{\text{TP}_i + \text{FN}_i} \qquad F1 - Score_i = 2\,x\,\frac{(Precision_i \text{ x } Recall_i)}{Precision_i + Recall_i}$$

Accuracy indicated the proportion of total predictions (both positive and negative) that the model correctly identified, precision indicated how many of the model's positive predictions were correct, recall measured the proportion of actual cases that were correctly identified, and F1-score represented a balance between precision and recall [17]. These metrics helped determine how well the model distinguished between the different skin diseases. In addition, a confusion matrix was generated to analyze the model's misclassifications, displaying the number of correctly and incorrectly predicted cases for each category[18][19]. By examining the confusion matrix, it was possible to identify which diseases were most frequently misclassified and assess the overall reliability of the model.

3. RESULTS AND DISCUSSION

This section presents the research findings along with a comprehensive discussion. The results are displayed using tables, figures, and graphs to enhance readability and clarity for the reader.

3.1. Classification Analysis

This research uses MobileNetV2 architecture as a skin disease classification. The data division used is 100 image data (except for analysis 1) as train, val, and test data using Adam optimizers. To produce optimal accuracy in this study, several experiments were carried out on the implementation and parameters used.

Analysis 1

Batch Size : 16
Epochs : 15
Dropout : 0.5
Learning Rate : 0.001
Early Stopping : *TRUE*

Table 3.1. Analysis 1

Model	Split Data			Train Acc	Train Loss	Val Acc	Val Loss
	Train	Val	Test				
A1	30	30	30	0.94	0.19	0.50	1.88
A2	50	30	20	0.93	0.23	0.53	0.86
A3	175	37	38	0.75	1.23	0.57	1.73

Analysis 1 results suggest that the A2 model performs best in terms of accuracy although there are signs of overfitting that need to be addressed, perhaps using additional regulation techniques and better validation.

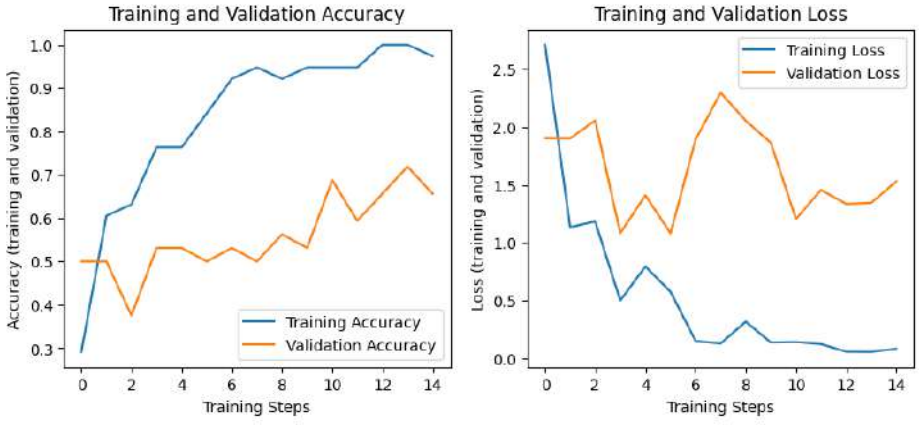

Figure 3.1. Analysis 1 Accuracy and Loss Graph

Analysis 2

Epochs : 15
Dropout : 0.2
Learning Rate : 0.001
Total *Dataset* : 300

Table 3.2. Analysis 2

Model	*Batch Size*	*Learning Rate*	*Train Acc*	*Train Loss*	*Val Acc*	*Val Loss*
B1	16	0.001	0.97	0.08	0.71	1.89
B2	16	0.0001	1.00	0.00	0.65	2.10
B3	32	0.001	1.00	0.04	0.65	1.49
B4	32	0.0001	0.93	0.20	0.53	1.17

Based on this analysis, B3 seems to be the better choice as it has a better balance between validation accuracy and validation loss. Although the validation accuracy is not as high as B1, the validation loss is lower, suggesting this model can generalize better.

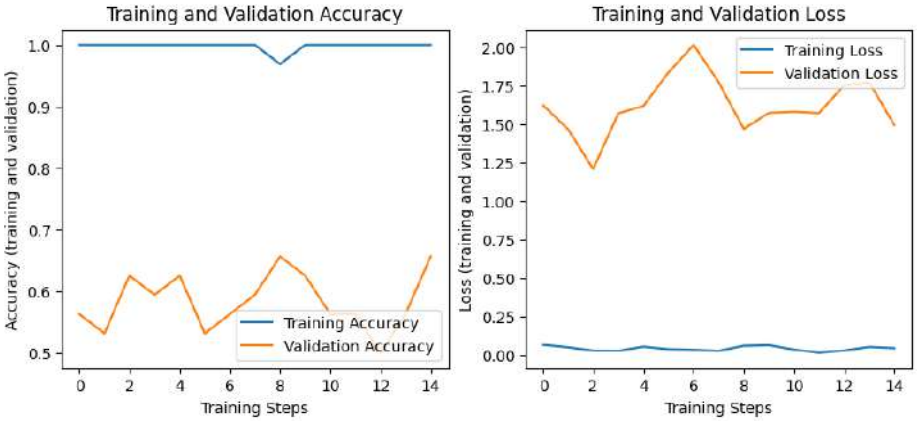

Figure 3.2. Analysis 2 accuracy and loss graph

Analysis 3

Epochs : 50
Dropout : 0.5
Learning Rate : 0.001
Total *Dataset* : 300

Table 3. 3 Analysis 3

Model	*Batch Size*	*Learning Rate*	*Train Acc*	*Train Loss*	*Val Acc*	*Val Loss*
B5	16	0.001	0.97	0.04	0.68	2.18
B6	16	0.0001	0.89	0.21	0.65	1.16
B7	32	0.001	1.00	0.23	0.59	2.41
B8	32	0.0001	0.86	0.41	0.59	1.05

For this analysis, B6 seems to be the best choice as it provides a balance between good validation accuracy and low validation loss. This illustrates that the data generalization ability of B6 is better than other models.

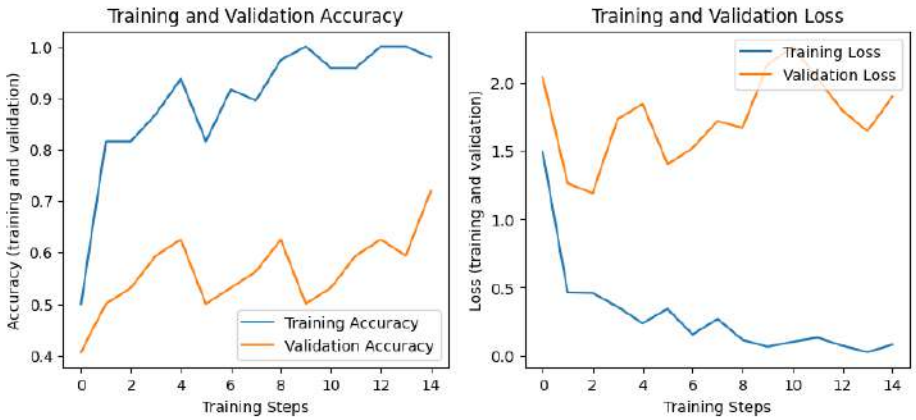

Figure 3.3. Analysis 3 accuracy and loss graph

Analysis 4

Batch Size : 16
Epochs : 15
Dropout : 0.5
Total *Dataset* : 300
Early Stopping : *TRUE*

Table 3.4. Analysis 4

Model	*Learning Rate*	*Acc Train*	*Loss Train*	*Acc Val*	*Loss Val*
C1	0.001	0.89	0.17	0.62	1.19
C2	0.0001	0.84	0.43	0.56	1.00

As for Analysis, it is a combination of models B1-B8 by taking one of the samples and trying it by calling Early Stopping. It can be concluded that model C1 is a better choice than model C2 because the performance on validation data is better despite the trade-off with higher validation losses.

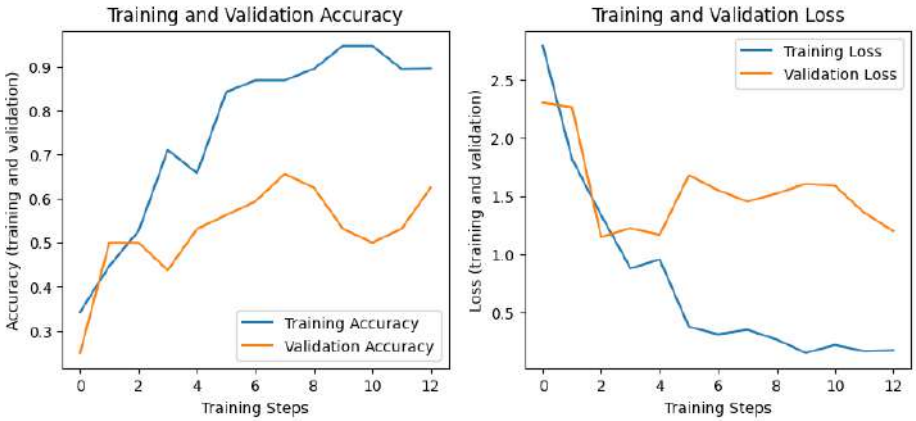

Figure 3.4. Analysis 4 accuracy and loss graph

Analysis 5

Epochs : 15
Dropout : 0.5
Total *Dataset* : 300
Early Stopping : *TRUE*
Conv2D : *TRUE*
Maxpooling2D : *TRUE*

Table 3.5. Analysis 5

Model	*Batch Size*	*Learning Rate*	*Train Acc*	*Train Loss*	*Val Acc*	*Val Loss*
D1	16	0.001	0.37	3.36	0.43	3.36
D2	16	0.0001	0.31	1.81	0.37	1.61
D3	32	0.001	0.45	3.58	0.37	3.23
D4	32	0.0001	0.31	2.69	0.28	2.17

The D2 model is the best choice because it has the lowest validation loss and good accuracy, indicating that it learns better and generalizes better than other models.

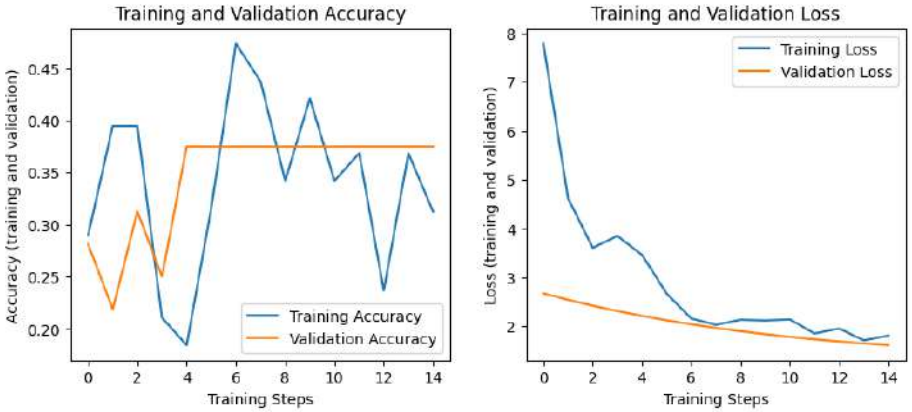

Figure 3.5. Analysis 5 accuracy and loss graph

Analysis 6

Batch Size : 16
Learning Rate : 0.0001
Total *Dataset* : 300
Early Stopping : *TRUE*
Conv2D : *TRUE*
Maxpooling2D : *TRUE*

Table 3.6. Analysis 6

Model	*Epochs*	*Dropout*	*Train Acc*	*Train Loss*	*Val Acc*	*Val Loss*
E1	50	0.5	0.91	0.29	0.70	0.63
E2	50	0.2	0.98	0.14	0.79	0.67
E3	100	0.5	0.98	0.18	0.69	0.77
E4	100	0.2	0.98	0.06	0.71	0.69

Based on the data above, E1 seems to be a better fit because although its validation accuracy is not the highest, it has a low validation loss. This suggests that model E1 has a good balance between accuracy and generalization.

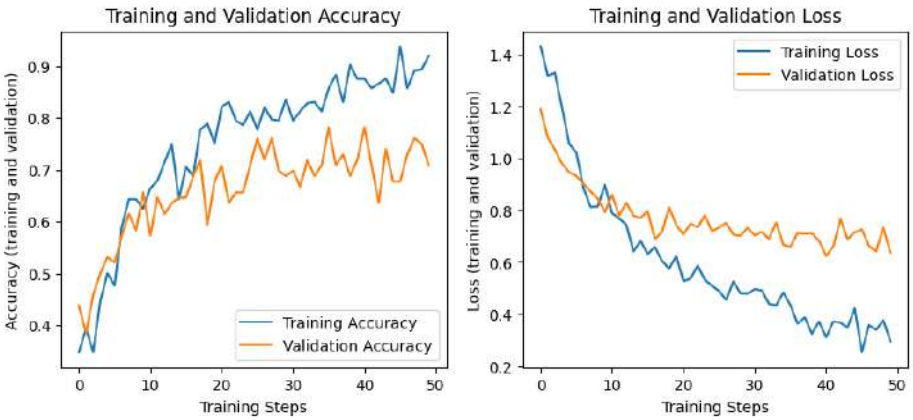

Figure 3.6. Analysis 6 accuracy and loss graph

After conducting various analyses with the specified epochs, batch size, learning rate, and other parameters, several of the best samples will be collected and reanalyzed to determine the final result and identify the best model.

Table 3.7. Final analysis result

Models	Train Accuracy	Train Loss	Validation Accuracy	Validation Loss
A2	0.93	0.23	0.53	0.86
B3	1.00	0.04	0.65	1.49
B6	0.89	0.21	0.65	1.16
C1	0.89	0.17	0.62	1.19
D2	0.31	1.81	0.37	1.61
E1	0.91	0.29	0.70	0.63

Overall, in the analysis of the best samples, model E1 was chosen as the best option due to its highest validation accuracy and lowest validation loss. However, model B6 can also be considered as an alternative if there is a preference for a specific batch size or learning rate used in that model.

3.2. Evaluation Result

After the model completes training, it will then be evaluated using test data, resulting in a classification report and a confusion matrix. In the previous stage, models E1 were identified as the best final results. However, upon reviewing the classification report, it was observed that model E1 performed better than model E4.

Table 4. Prediction result analysis E

Models	Predict Accuracy	Predict Loss
E1	0.73	0.67
E2	0.70	0.72
E3	0.71	0.72
E4	0.73	0.70

Models E1 and E4 exhibit balanced performance with a prediction accuracy of 0.73 and relatively low prediction losses (0.67 and 0.70). Models E2 and E3 have slightly lower prediction accuracy (0.70 and 0.71) and higher prediction loss (0.72). After considering all these factors—including accuracy and loss on training and evaluation data, as well as signs of overfitting—model E1 is selected as the final result. It provides the best balance between high accuracy and low loss while demonstrating good generalization ability with minimal signs of overfitting.

```
3/3 [==============================] - 7s 1s/step
Classification Report
                  precision    recall  f1-score   support

Atopic-Dermatitis       0.64      0.66      0.65        32
        Psoriasis       0.70      0.81      0.75        32
     Scabies-Lyme       0.69      0.56      0.62        32

         accuracy                           0.68        96
        macro avg       0.68      0.68      0.67        96
     weighted avg       0.68      0.68      0.67        96

3/3 [==============================] - 5s 1s/step - loss: 0.6786 - accuracy: 0.7396
[0.6786351799964905, 0.7395833134651184]
```

Figure 4.1. Classification report result

From the classification report results, model E1 shows good performance on the Psoriasis class with the highest F1-Score (0.75). However, it is less effective in the Scabies-Lyme class with the lowest F1-Score (0.62). In Overall, this model has fairly balanced accuracy and metrics, but can still be improved especially for the class with the lowest recall.

In the final step, the model will go through the confusion matrix process, where the classification model's performance is evaluated by comparing its predictions with the actual labels. This provides information on the number of correct and incorrect predictions for each class. The matrix is often used to calculate various performance metrics such as model accuracy, precision, recall, and F1-score.

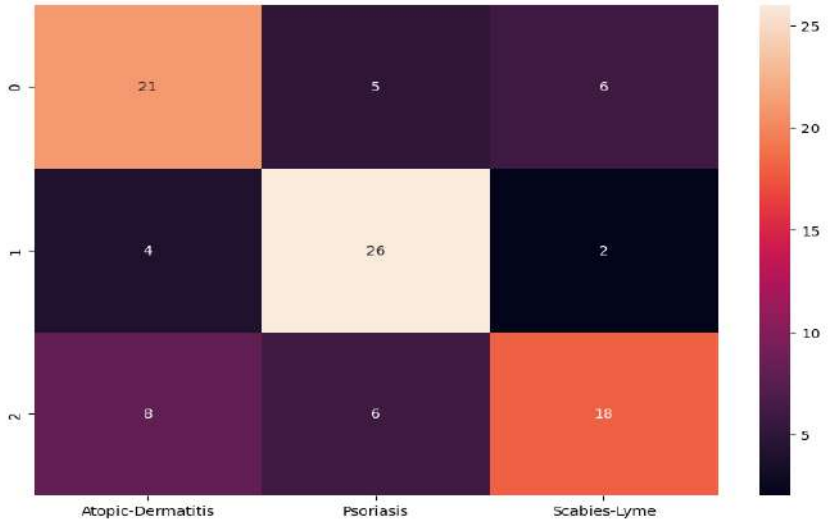

Figure 4.2. Confusion matrix result

Figure 4 above illustrates that the rows represent the true labels, while the columns indicate the predicted labels. The following section explains the elements of the matrix and the calculation of the model's performance. The confusion matrix consists of several elements, including True Positives (TP), False Positives (FP), False Negatives (FN), and True Negatives (TN) [20][21].

4. CONCLUSION

Based on the research conducted, starting from the introduction to the final results and analysis, several conclusions can be drawn. First, the use of the MobileNetV2 architecture in the Convolutional Neural Network (CNN) method for skin disease classification has shown fairly accurate results. Although there are some limitations in terms of accuracy, especially in certain classes, the model has proven capable of learning and recognizing patterns from the given images effectively. This capability is further enhanced by the application of data augmentation, which helps prevent overfitting. Second, during the training process, model E1 was identified as the best-performing model, as it demonstrated a well-fitted performance with a training accuracy of 0.90, training loss of 0.29, validation accuracy of 0.70, and validation loss of 0.63. The fact that the validation loss is higher than the training loss and the training accuracy is higher than the validation accuracy indicates that there are no signs of overfitting in the model. Third, in the first evaluation, the classification report showed that model E1 achieved a prediction accuracy of 0.73 with a prediction loss of 0.67, indicating that the model performs well in classifying skin diseases, particularly in the Psoriasis class. Lastly, in the second evaluation process, the confusion matrix revealed that the model successfully predicted 67 out of 96 correct data points, proving that it maintains balanced accuracy across various types of skin diseases.

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BIOGRAPHIES OF AUTHORS

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