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Corn Leaf Diseases Classification Using CNN with GLCM, HSV, and L*a*b* Features

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Abstract

Corn leaf diseases can damage plants and reduce crop yields, thus affecting the quality and quantity of corn production. This study aims to classify corn leaf diseases using the Convolutional Neural Network (CNN) method with different color features, namely Gray Level Co-Occurrence Matrix (GLCM), HSV, and L*a*b*. The dataset consists of 1,739 corn leaf images, which are divided into four disease classes: Blight, Common Rust, Gray Spot, and Healthy. The data is split into training and testing sets using an 80:20 ratio. Two testing scenarios were conducted: individual feature evaluation and feature combination. The results show that in the first scenario, the L*a*b* feature provides the best accuracy at 91.75%, followed by the HSV feature with an accuracy of 90.29%, and GLCM with an accuracy of 78.40%. In the second scenario, the combination of HSV and L*a*b* features results in the highest accuracy of 92.48%, indicating that combining color and brightness information can improve the model's performance. The combination of GLCM and L*a*b* features results in an accuracy of 91.75%, while the combination of GLCM and HSV results in an accuracy of 90.29%. These findings demonstrate that integrating HSV and L*a*b features enhances CNN performance in corn leaf disease classification, outperforming individual feature-based approaches, thus contributing to more effective AI-based agricultural disease diagnosis.

Keywords : *Convolutional Neural Network , Corn Leaf Diseases, GLCM, HSV, L*a*b*.*

1. INTRODUCTION

Corn is a key staple crop in Indonesia, essential for both food and industrial needs. It serves as a major carbohydrate source and raw material for industries like animal feed, bioethanol, and processed foods. With demand rising by 10 to 15 percent annually, ensuring high productivity and quality in corn cultivation is crucial[1]. Corn thrives in areas with low to moderate rainfall, though it remains susceptible to diseases that can impact growth[2]. However, diseases such as Blight, Common Rust, and Gray Spot significantly impact production[3]. Blight, caused by the *Helminthosporium turcicum* fungus, affects corn leaves, stems, and roots, causing yellowing, drying, and leaf death, with severe infections leading to plant wilting. It spreads through fungal spores carried by wind or rain. Common Rust, caused by *Puccinia sorghi* and *Puccinia polypore Underw*, creates orange or reddish spots on leaves, reducing photosynthesis and crop yields. Though it rarely kills the plant, it impacts both quality and quantity. Gray Spot, caused by *Cercospora zeae-maydis*, creates gray or brown spots, eventually killing leaves[4] and reducing photosynthesis, potentially cutting yields by up to 30%. If not managed, these diseases can cause significant crop and quality losses, making early detection and management essential for sustaining optimal production. Farmers traditionally rely on manual observation to detect diseases, but this method is limited by the farmer's experience and delays in detection, resulting in crop yield losses[2]. Advances in machine learning and technologies like image processing, deep learning, and computer vision offer more efficient, automated disease detection and faster diagnoses.

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Many previous studies have conducted disease detection on corn using different algorithms with good accuracy results [5]-[9]. The research conducted by Khaled Adil Dawood Idress and colleagues focuses on detecting diseases in maize plants using machine learning techniques and image processing. The study utilized the Plant Village image dataset to identify maize leaves infected with common rust and gray leaf spot. Based on the research findings, machine learning algorithms have been shown to be effective in detecting diseases, with accuracy ranging from 90% to 92.7%. The highest accuracy was achieved by the support vector machine (SVM) and artificial neural networks (ANN) algorithms.. This research demonstrates that these methods can accelerate disease detection, improve accuracy, and reduce the risk of crop failure[10]. Chaudhary and Kumar (2024) conducting disease detection in rice plants by utilizing Gray-Level Co-occurrence Matrix (GLCM) and Neuro-GA classifier. The study revealed that the Neuro-GA method successfully achieved a very high level of accuracy, which is above 90%. The method has proven effective in automatically integrating various aspects of crop production, reducing losses due to crop damage, and increasing the efficiency of agricultural production as a whole. [11]. The same study was conducted by Patel et al., who used GLCM features in maize leaf disease classification, but applied the algorithms Decision Trees, Gradient Boosting, Support Vector Machines (SVM), and K-Nearest Neighbors (KNN). The results showed that the Decision Trees and Gradient Boosting algorithms achieved an accuracy of 95.05% using GLCM features at a 135° angle[12]. Reno et al. developed a deep CNN model for classifying vegetable leaf diseases. The proposed model, utilizing transfer learning with VGG-16 and ResNet-50, achieved a Mean Average Precision (mAP) accuracy of 99.80%[13]. A similar study was also conducted by Trivedi, dkk using the Convolutional Neural Network algorithm for disease attacks on vegetable plants. The results of the study show that the system performance is predicted to reach a very significant level[14]. The development of an effective classification model for detecting diseases in corn leaves using HSV color space and Support Vector Machine (SVM) algorithm successfully achieved the highest accuracy of 98.53% with an error rate of 0.10%, surpassing other algorithms such as Logistic Regression, LDA, and Naïve Bayes[15]. The research conducted by S. Pancono et al. utilized transfer learning and fine-tuning on Convolutional Neural Network (CNN) with DenseNet169 architecture integrated with Internet of Things (IoT) technology. Based on the test results, this model obtained an accuracy of 94%, while the application to detect tomato leaf disease achieved an accuracy of 92.80%, with a response time of around 1077.56 ms. This application is also able to monitor plant conditions in real-time with a delay of around 1998 ms. [16].

However, although various studies have explored different classification algorithms and feature extraction techniques, there has been no research comparing the CNN classification method results with the GLCM, HSV, and L*a*b* features individually, or the combination of two features such as HSV and L*a*b*, GLCM and HSV, and GLCM and L*a*b* for disease detection in corn. Most studies focus on a single feature, so there is no comprehensive study that compares and combines multiple features, particularly in the context of disease detection in corn. Additionally, while deep learning models such as CNN have been used in several studies, the use of transfer learning and the combination of GLCM, HSV, and L*a*b* feature extraction for corn disease detection remains limited. Therefore, this research focuses on a comparative exploration of GLCM, HSV, and L*a*b* feature extraction, and how these three features can improve the accuracy of disease detection in corn, particularly for Blight, Common Rust, and Gray Spot diseases.

2. METHOD

Diseases in corn leaves are detected and classified by utilizing Convolutional Neural Network (CNN) by comparing three primary features: Gray Level Co-Occurrence Matrix (GLCM), HSV, and L*a*b*. CNN was chosen for its exceptional ability in image classification, supported by its deep and

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complex neural network structure[17]. As one of the top algorithms in deep learning, CNN has demonstrated its superiority in various studies, particularly in image recognition and classification. In the context of identifying plant species and their diseases, CNN has proven to outperform feature extraction methods such as Support Vector Machine (SVM) and K-Nearest Neighbors (KNN), which rely more on predefined features and are less flexible in handling complex and diverse data. Compared to other algorithms like Decision Trees or Logistic Regression, CNN is able to handle large datasets more effectively and provides more accurate results due to its ability to learn automatically from data without requiring explicit programming. Therefore, the application of CNN in this research is expected to achieve high accuracy in detecting and classifying diseases on corn leaves, particularly in handling more complex and dynamic image variations. This study uses the 8BJU06B7 laptop model with an AMD Athlon Gold 3150U processor, AMD Radeon R3 graphics, 4 GB RAM, and 128 GB SSD, running Windows 11 Home Single Language 64-bit. The software used includes Visual Studio 2022 and Python 3.10. The methodological procedures applied can be seen in the following Figure 1:

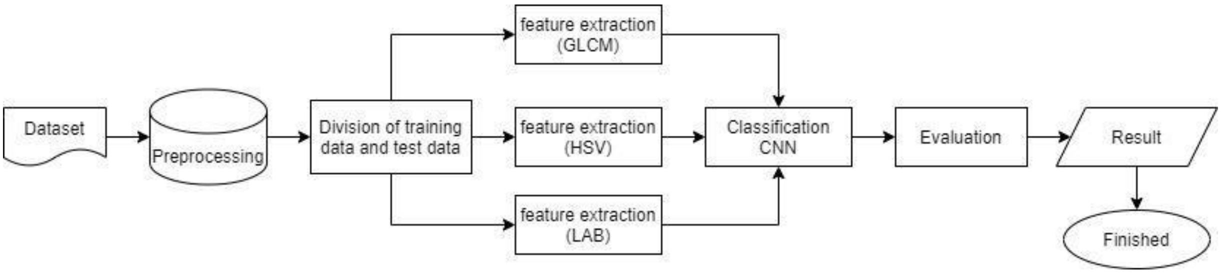

Figure 1. Methodological Steps Implemented in This Study.

A detailed explanation of the methodological steps applied is as follows:

2.1. Data Collection

The data used in this study were obtained from Kaggle, consisting of 1,739 corn leaf images divided into four categories: 512 images for Blight, 512 images for Common Rust, 512 images for Gray Spot, and 512 images for Healthy. The data was then separated into 409 images for training and 103 images for testing in each category. To ensure objective evaluation, training data is used to train the model, while testing data is used to measure the accuracy level of the model. This structured data division allows the model to be better at generalizing across different types of diseases and health conditions. Example data for each category is shown in Figure 2 below.

Blight *Common Rust* *Gray Spot* *Health*

Figure 2. Example Data for Each Class Category

2.2 Preprocessing

At the pre-processing stage, the original images are resized to 256x256 pixels. This is done to standardize the image size, making it easier for the model to process the data, speeding up the computation time during training, and improving consistency in the prediction results[18].

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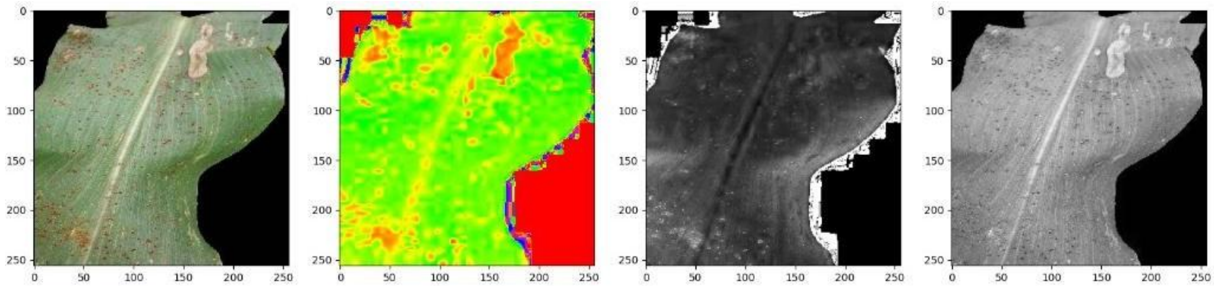
2.2. Feature Extraction

In the feature extraction stage, three different methods are used to analyze the texture and color of leaf images, namely HSV (Hue, Saturation, Value), GLCM (Gray Level Co-Occurrence Matrix), and L*a*b*. Each of these methods provides a unique approach in describing the characteristics of the leaf images. The results from these three methods will be compared using the Convolutional Neural Network (CNN) algorithm to evaluate their impact on the accuracy of disease classification in corn leaves.

2.2.1. HSV (Hue, Saturation, Value)

At this stage, the RGB image will be converted to an HSV image. HSV is a color model that describes how colors are formed, with the main components including hue, saturation, and value. The HSV color model was designed to improve the quality of computer graphics. The HSV color wheel is constructed using circles and triangles, where the circle represents hue and the triangle depicts the relationship between hue and saturation on the horizontal axis, while value is located on the vertical axis. This allows for more specific color selection for a particular image. Value or brightness levels can be selected via the horizontal triangle axis. The HSV model is translated into a cone shape, with saturation curving along the radius of the cone and value following the height of the cone[19]. Hue describes the type of color, such as red, green, or yellow, which serves as a color distinguisher and determines how far the color tends to red or green. Saturation describes the clarity or strength of the color, while Value indicates the level of brightness or darkness of the color[20]. In detecting diseased leaves, the HSV model can be used to differentiate healthy leaf colors from areas showing signs of infection by utilizing differences in Hue, Saturation, and Value within the affected regions. The example of the RGB image of corn leaves converted to an HSV image is shown in Figure 3.



RGB Image *Hue* *Saturation* *Value*

Figure 3. Feature Extraction from The RGB Image to The HSV Image

2.2.2. GLCM (Gray Level Co-Occurrence Matrix)

The Gray Level Co-Occurrence Matrix (GLCM) method is an effective technique in analyzing texture features in images, namely by describing texture through computing the frequency of pixel pairs with certain values that appear in certain spatial relationships in the image [21]. When applied to plant disease image datasets, this method helps capture various texture aspects that are crucial for identifying disease patterns. In this study, the main focus is on several GLCM metrics used to explore the textural characteristics of maize leaf images affected by diseases as follows [22]:

a. Energy: Describes the number of square elements in GLCM, which describes the level of texture complexity. Higher energy values indicate more complex textures with a greater variety of pixel pairs. The calculation is done using the following equation:

$$\sum_{i,j}^{K-1} P(i,\, j)^2 \qquad (1)$$

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b. Contrast: Assesses local variations in the image, with higher values indicating greater differences in pixel intensity and clearer surface texture. Contrast is calculated using the following formula:

$$\sum_{i,j}^{K-1} |i-j|^2 \, p(i,j) \qquad (2)$$

c. Correlation: Describes the linear relationship between gray levels in an image. A larger value indicates a stronger linear association between pairs of pixels, which is calculated using the Equation:

$$\sum_{(i,j)}^{K-1} \frac{(i,j)P(i,j)-\mu_x\,\mu_y}{\sigma_x\,\sigma_y}) \qquad (3)$$

d. Homogeneity: Describes the distance at which GLCM elements are close to the diagonal, indicating consistency in image texture. It is calculated using the following equation:

$$\sum_{(i,j=0)}^{K-1} \frac{P(i,j)}{1+|i-j|^2}) \qquad (4)$$

e. Variance: Reflects the variance in GLCM, which provides a more complete understanding of texture complexity. Higher values indicate more complex textures. The calculation is done using the following equation:

$$\sum_{(i,j)}^{K-1} |i-\mu|^2 \, p(i,j) \qquad (5)$$

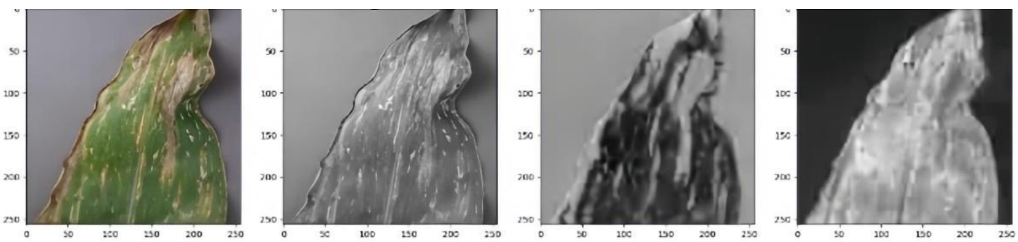
f. Dissimilarity: This metric measures the average difference between gray levels in an image. Dissimilarity calculates the intensity difference between adjacent pixel pairs.
Examples of values for each feature are presented in Table 1.

Table 1. Sample Results of GLCM Feature Extraction

Class	Contrast	Dissimilarity	Homogeneity	Energy	Correlation
Blight	291,887	11,0251	0,2136	0,0003	11872,156
Common Rust	398,166	9,15085	0,5593	0,2272	10291,151
Gray Spot	416,571	13,5730	0,2145	0,0003	13875,618
Health	75,535	6,33821	0,25532	0,0003	22378,931

2.2.3. L*a*b*

The Lab color space (Lightness, a*, b*) is a three-dimensional model that represents color based on lightness (L*), green/red spectrum (a*), and blue/yellow spectrum (b*). The L* component indicates the level of brightness, a* represents the dominance of green or red, and b* shows the dominance of blue or yellow. This model better reflects human color perception by separating luminance and chrominance information, making it highly useful in image processing for color analysis and object classification based on color[23]. The example of the RGB image of corn leaves converted to an L*a*b* image is shown in Figure 4.



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RGB Image L* *a** *b**

Figure 4. Feature Extraction from The RGB Image to The L*A*B* Image

2.3. Classification using Convolutional Neural Network

The design of this model uses a Convolutional Neural Network (CNN), which is a type of supervised learning model that processes input in the form of images or photos[24]. CNN is particularly effective in handling data with a grid-like structure, such as two-dimensional images, and can also process high-dimensional data, such as videos[25]. Multilayer CNNs are highly capable of extracting various features from images. Initially, an image is converted into a digital representation, forming a two-dimensional matrix, which is then subjected to sampling. To analyze input features, CNNs use a series of filters to examine local components in the image. Different kernel sizes are used to capture different image attributes, both kernel size and stride can affect information preservation. Each neuron in a convolutional layer processes only a small portion of the output of the previous layer that has been processed by the kernel. The "receptive field" of the neuron determines the area of output that can be processed. Next comes the "pooling layer," which combines the outputs of the previous layers into a single neuron. Common combination techniques, such as maximum and average combination, serve to reduce the dimensionality of the feature map and are often used for downsampling in CNNs. Additional layers are added to improve the model's ability to distinguish features, while improving overall performance and functionality. These layers also play a role in preventing overfitting and reducing spatial parameter complexity. In this configuration, the CNN consists of eight convolutional layers and eight pooling layers, with a normalization layer in between to optimize the training process and reduce the model's dependence on initialization. Normalization is applied to the gradient values throughout the network to improve stability and efficiency[26].

2.4. Model Evaluation

The evaluation metrics used to assess the performance of the model in this study include accuracy, precision, recall, and F1-Score. These metrics provide an overview of the extent to which the model is able to classify diseases in corn leaves effectively. The formula for calculating accuracy can be found in equation 6, while precision is calculated using equation 7. The calculation of recall is explained in equation 8, and the formula for F1-Score is available in equation 9[27].

$$accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (6)$$

$$precision = \frac{TP}{TP+FP} f_{baud} = \frac{2^{SMOD}}{64} x f_{osc} \quad (7)$$

$$recall = \frac{TP}{TP+FN} \quad (8)$$

$$F1 - Score = 2x\frac{Precision \ x \ Recall}{Precision + Recall} \quad (9)$$

TP (True Positives) Refers to correct predictions that are considered positive. TN (True Negatives) refers to correct predictions that are categorized as negative. Meanwhile, FP (False Positives) are incorrect predictions but are classified as positive, and FN (False Negatives) are incorrect predictions but are classified as negative.

3. RESULT

At this stage, disease classification testing was carried out on corn leaves using the Convolutional Neural Network method with several scenarios. The first scenario compares the results of three color features: Gray Level Co-Occurrence Matrix (GLCM), HSV, and L*a*b*. The second scenario compares the results of combining features: GLCM and HSV, GLCM and L*a*b*, and HSV and L*a*b*. The dataset used consists of 1,739 corn leaf images, with 512 images for each class category. This dataset is

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divided into two sets: training data and test data with a ratio of 80:20, consisting of 409 training data and 103 test data. The parameters of the CNN algorithm are shown in Table 2.

Table 2. Sample Results of GLCM Feature Extraction

Layer	Type	Output Shape	Parameter
Conv1D (Layer 1)	Convolution	(5,32)	64
MaxPooling1D (Layer 1)	Pooling	(2,32)	0
Conv1D (Layer 2)	Convolution	(2,64)	416
MaxPooling1D (Layer 2)	Pooling	(2,64)	0
Conv1D (Layer 3)	Convolution	(2,128)	832
MaxPooling1D (Layer 3)	Pooling	(2,128)	0
Flatten	Flatten	(256,)	0
Dense (Layer 1)	Fully Connected	(64,)	16,448
Dropout	Dropout	(64,)	0
Dense (Output)	Fully Connected	(4,)	260

In Table 2, The CNN architecture used consists of several layers designed to extract and classify features from input data. The first layer is a 1D convolutional layer (Conv1D) with a kernel size of 5 and 32 filters, which serves to extract basic features from input data. Then, a max-pooling layer (MaxPooling1D) with a pool size of 2 is used to reduce the spatial data dimension while retaining the most important features. The second convolutional layer (Conv1D) uses a kernel size of 2 and 64 filters, which improves feature extraction, followed by a max-pooling layer to reduce the output size. The third convolutional layer (Conv1D) has a kernel size of 2 and 128 filters, which allows the model to extract more complex features, followed by another max pooling layer. After the convolutional and pooling layers, a Flatten layer transforms the 2D output from the previous layer into a 1D vector. Next, a dense layer with 64 neurons combines the extracted features. Dropout layers are applied to prevent overfitting by randomly deactivating some neurons during the training process. Finally, the output layer is a Dense layer with 4 neurons that classifies the input into one of four classes. This architecture includes a total of 16,448 parameters in the first dense layer and 260 parameters in the output layer, with the use of dropout to improve generalization. This structure allows CNN to extract and classify features from input data effectively.

Comparison of individual and combined features can be seen in Tables 5, 6, 7, 8, 9, and 10, which present the results of model performance evaluation based on accuracy, precision, recall, and F1-score for each test scenario. Tables 5 to 7 show the evaluation results when GLCM, HSV, and L*a*b* features are used individually in the classification of corn leaf diseases, with parameters reflecting the effectiveness of each feature in distinguishing disease categories. Meanwhile, Tables 8, 9, and 10 present the evaluation results of the model using feature combinations: GLCM and HSV, GLCM and L*a*b*, and HSV and L*a*b*. These combinations aim to analyze classification performance improvements by integrating texture and color information. This comparison provides insights into which features are the most optimal in enhancing classification accuracy and effectiveness. The results of the GLCM, HSV, and L*a*b* features are shown in Figures 5 to 10.

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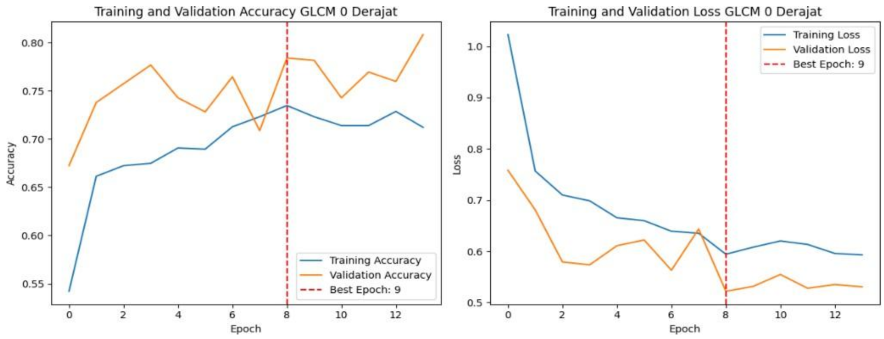

Figure 5. Accuracy and Loss Results in The Training and Validation Process of Use GLCM Features

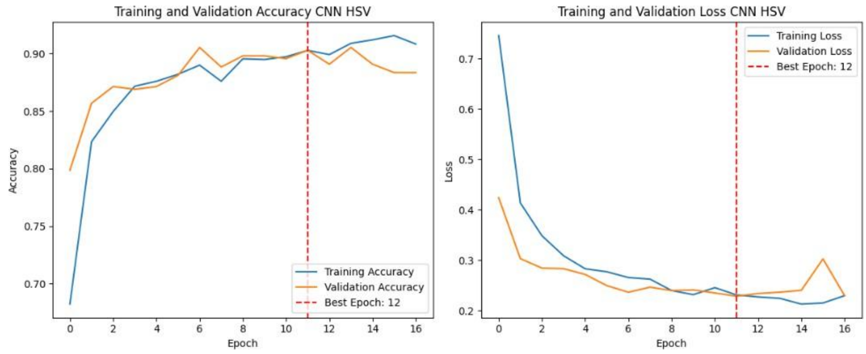

Figure 6. Accuracy and Loss Results in The Training and Validation Process of Use HSV Features

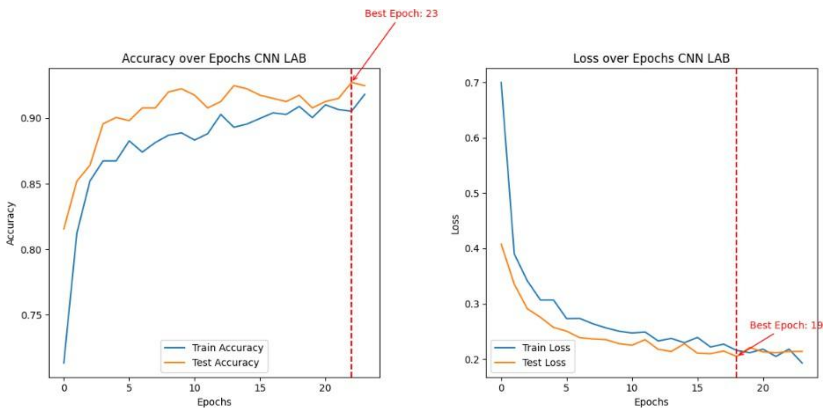

Figure 7. Accuracy and Loss Results in The Training and Validation Process of Use L*a*b* Features

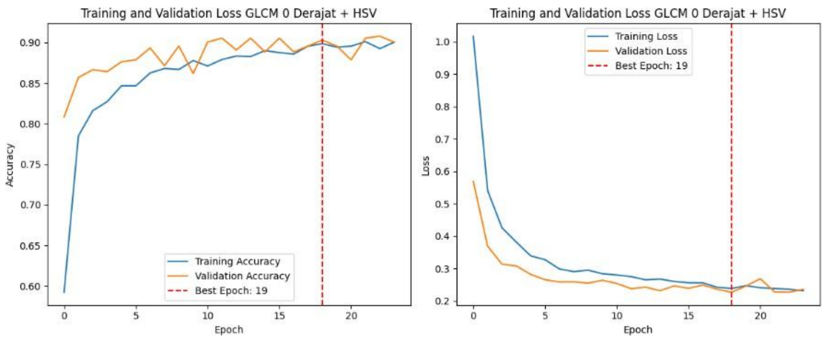

Figure 8. Accuracy and Loss Results in The Training and Validation Process of Use GLCM and HSV Features

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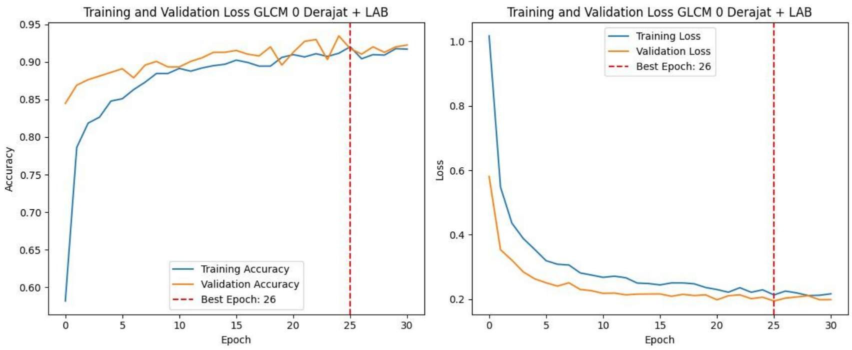

Figure 9. Accuracy and Loss Results in The Training and Validation Process of Use GLCM and L*a*b* Features

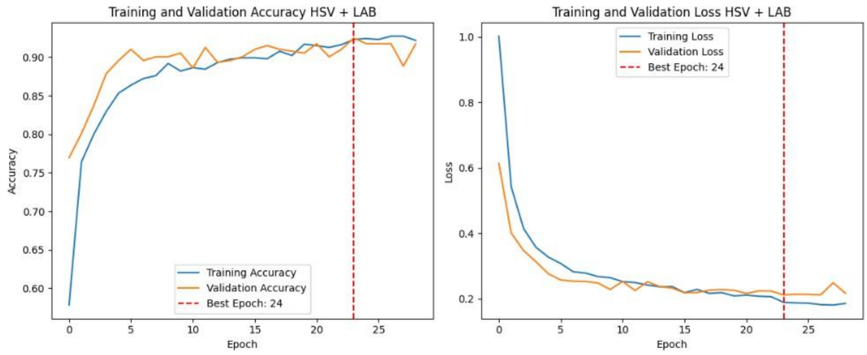

Figure 10. Accuracy and Loss Results in The Training and Validation Process of Use HSV and L*a*b* Features

In the first scenario depicted in Figure 5 using GLCM features, early stopping was applied at epoch 14 because there was no significant improvement in validation accuracy and validation loss after epoch 9. The model was reverted to epoch 9, which had the highest validation accuracy (0.7840) and the lowest validation loss. Although there was some improvement in validation accuracy at epoch 14 (0.8083), the model chose epoch 9 as the best epoch to avoid overfitting and maintain optimal performance. In Figure 6 using HSV features, early stopping was applied at epoch 17 because there was no significant improvement in validation accuracy and validation loss after epoch 12. The model was reverted to epoch 12, which had the highest validation accuracy (0.9092) and the lowest validation loss. The final result shows an accuracy of 90.29%, with precision of 90.5%, recall of 90.29%, and F1-score of 90%, indicating that the model performs very well in classifying data, minimizing classification errors, and capturing most of the relevant data. In Figure 7 using L*ab* features, early stopping was applied at epoch 24, and the model was reverted to epoch 19, which had the best validation accuracy (0.9175) and the lowest validation loss (0.2048). The final performance shows accuracy of 91.75%, precision of 91.74%, recall of 91.75%, and F1-score of 91.69%, indicating excellent classification performance with minimal errors. The confusion matrix confirms the model's effective classification with few misclassifications. Based on the testing results in Scenario 1, L*a*b* features are the most effective for this classification task, achieving the highest accuracy and demonstrating strong overall performance.

In the second scenario depicted in Figure 8 by combining GLCM and HSV features, early stopping was applied at epoch 24, and the model was reverted to epoch 19, which showed the best validation accuracy of 90.29%. The final performance metrics include 90.29% accuracy, 90.5% precision, 90.29% recall, and F1-score of 90%, indicating that the model performed well in classifying

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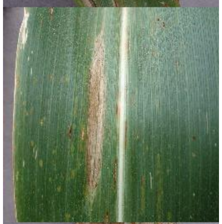
the data, minimizing errors, and capturing most of the relevant instances. In Figure 9 using the combination of GLCM and L*a*b* features, the model achieved its best performance at epoch 26, with a validation accuracy of 91.75% and a validation loss of 0.1940. The final metrics, including 91.75% accuracy, 91.85% precision, 91.75% recall, and F1-score of 92%, demonstrate the model's exceptional classification performance with minimal errors, highlighting the effectiveness of using combined features for this scenario. In Figure 10, using the combination of HSV and L*a*b* features, early stopping was applied at epoch 29, and the model was reverted to epoch 24, which achieved the best validation accuracy of 92.48%. The final performance metrics include 92.48% accuracy, 92.45% precision, 92.48% recall, and F1-score of 92%, demonstrating the model's excellent classification performance. Thus, the combination of HSV and L*a*b* features resulted in the best performance, with the highest accuracy of 92.48%, demonstrating superior classification ability compared to the other feature combinations.

Table 3. Results of Prediction Error Classification

Data	Feature Extraction	Actual Data	Prediction	Description
	GLCM	Corn Blight	Corn Gray Spot	False
	GLCM	Corn Blight	Corn Health	False
	HSV	Corn Gray Spot	Corn Blight	False
	HSV	Corn Blight	Corn Gray Spot	False
	L*a*b	Corn Blight	Corn Gray Spot	False

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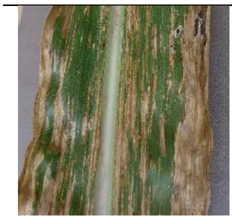
Data	Feature Extraction	Actual Data	Prediction	Description
	L*a*b	Corn Gray Spot	Corn Blight	False

4. DISCUSSIONS

The results of this study indicate that the application of various features in the classification of diseases in corn leaves using the Convolutional Neural Network (CNN) method produces a variety of results, both when using single features and combinations of features. In general, the CNN model performed well in classifying corn leaf images based on the three color features used: Gray Level Co-Occurrence Matrix (GLCM), HSV, and L*a*b*, both individually and in combination. In Scenario 1, where each feature was tested separately, the results show that *L*a*b** feature delivered the best performance with an accuracy of 91.75%. This suggests that the L*a*b* feature is better at capturing important information related to corn leaf disease classification compared to GLCM and HSV features. In this case, L*a*b*, as a color model that separates the color components into L (lightness), a (red-green component), and b (yellow-blue component), provides a better representation of images of corn leaves affected by disease. Meanwhile, GLCM feature showed a lower accuracy at epoch 9 with an accuracy of 78.40%. This could be due to the inability of GLCM to capture finer spectral color information, which is better addressed by HSV and L*a*b* features. However, despite GLCM not achieving as high an accuracy as L*a*b*, GLCM still provides significant contributions in classifying surface textures of leaves, which could be distinctive for certain diseases. HSV feature also showed a fairly good result with 90.29% accuracy, indicating that color information (Hue), saturation (Saturation), and brightness value (Value) can aid in detecting corn leaf diseases. In some cases, color changes caused by diseases on corn leaves can be more clearly detected using the HSV representation.

In Scenario 2, which combines the features, the results show that the combination of HSV and L*a*b* features yielded the highest accuracy of 92.48%. This indicates that combining various types of information from the HSV and L*a*b* features provides a more complete and accurate representation for disease classification. The combination of these two features enriches the information that can be processed by the CNN model, enabling it to produce better predictions than when using a single feature. The combination of GLCM and L*a*b* also yielded 91.75% accuracy, which is nearly equivalent to the performance of L*a*b* alone. This indicates that while GLCM can provide important information about leaf texture, in this scenario, L*a*b* dominates in contributing more significantly to the model's performance. Overall, the results from both scenarios show that feature combinations provide significant advantages in improving model accuracy. Specifically, the combination of HSV and L*a*b* delivered the best results, suggesting that color, brightness, and contrast information in corn leaf images are extremely helpful in differentiating between various diseases more precisely. Thus, it can be concluded that using a combination of features yields better performance than using a single feature. This emphasizes the importance of selecting the right features to strengthen the ability of the CNN model to classify diseases in corn leaves.

Although many previous studies have been conducted on disease detection in plants using machine learning and deep learning methods, there are still several shortcomings in these studies. Research conducted by Khaled Adil Dawood Idress and colleagues using the Support Vector Machine (SVM) and Artificial Neural Networks (ANN) algorithms with the Plant Village dataset, produced an accuracy of between 90% and 92.7%. However, this study did not examine the effect of color features in improving the accuracy of disease classification in corn leaves. Likewise, research conducted by Patel

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and team used the Gray-Level Co-occurrence Matrix (GLCM) feature with classical classification algorithms such as Decision Trees and Gradient Boosting, which achieved a maximum accuracy of 95.05% at an angle of 135°. However, this study has not applied a more sophisticated deep learning approach in more complex feature extraction and classification.

Additionally, the study by Chaudhary and Kumar (2024) employed a combination of GLCM and the Neuro-GA method for disease detection in rice plants, achieving an accuracy above 90%. While effective in automatic agricultural production monitoring, this study did not specifically investigate corn diseases or explore the combination of color features to enhance classification model accuracy. The studies by Reno et al. and Trivedi et al. applied Convolutional Neural Network (CNN) models for vegetable disease classification using transfer learning, reaching up to 99.80% accuracy in some cases. However, these studies did not specifically evaluate the impact of color features on the classification accuracy of corn diseases.

Furthermore, some studies have used the SVM algorithm for corn leaf disease classification using the HSV color space, with the highest accuracy reaching 98.53%. However, these studies did not compare the effectiveness of other color features, such as L*a*b*, or explore feature combinations to improve classification performance. The study by S. Pancono et al. employed transfer learning with the DenseNet169 architecture integrated with Internet of Things (IoT) technology for tomato disease detection, achieving 94% accuracy for the CNN model and 92.80% for the IoT-based application. However, this study did not examine corn disease classification or conduct an in-depth evaluation of color features.

Therefore, this study contributes to addressing the existing gaps by evaluating and comparing the impact of various color features GLCM, HSV, and L*a*b* in classifying corn leaf diseases using the CNN method. Experimental results show that the L*a*b* feature individually provides the highest accuracy of 91.75%, followed by HSV at 90.29% and GLCM at 78.40%. Furthermore, the combination of HSV and L*a*b* features yields the highest accuracy of 92.48%, outperforming individual feature-based approaches. The combination of GLCM and L*a*b* achieves 91.75% accuracy, while GLCM and HSV achieve 90.29%. Thus, this study demonstrates that integrating color features can improve the accuracy of corn leaf disease classification, making a significant contribution to the development of a more accurate and efficient AI-based disease detection model in the agricultural sector.

This study has several limitations, including the use of a limited dataset that does not fully represent real-world environmental variations, such as lighting conditions and disease severity levels. Additionally, the model only utilizes color features (HSV, L*a*b*) and texture features (GLCM) without considering leaf morphological characteristics, which could enhance classification accuracy. The CNN model used has not been compared with more complex deep learning architectures and has not been tested on real-world data to evaluate its performance under field conditions. Moreover, broader data augmentation techniques have not been fully implemented to improve the model's generalization. Furthermore, this study has not integrated an IoT-based approach for real-time disease monitoring, which could enhance detection efficiency. Future research can address these limitations by expanding the dataset, considering environmental factors, exploring more advanced models, and testing model implementation in real-world conditions.

5. CONCLUSION

This study evaluates the use of GLCM, HSV, and L*a*b features in corn leaf disease classification using CNN. The results show that the L*a*b* feature provides the highest accuracy of 91.75%, while the combination of HSV and L*a*b* features yields the highest accuracy of 92.48%. Thus, the combination of color and texture features can improve the accuracy of the CNN model in classifying

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corn leaf diseases. Future researchers should explore real-time implementation and expand the dataset for better generalization.

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