

Original Research

CLASSIFICATION OF DISEASES ON MANGGO LEAVES USING ARCHITECTURE VGG16 AND SUPPORT VECTOR MACHINE (SVM)

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Abstract

Indonesia is one of the countries that has a diversity of mango plants. Mango fruit is in great demand throughout the world, but pest control of mango diseases is still not too optimal, one of which is on the leaves. So the automatic recognition of diseases on mango leaves will have a very important role in achieving satisfactory yields. With these problems, this study evaluates models using Convolutional Neural Network (CNN) architecture VGG16 + SVM and VGG alone. The dataset consists of 4000 digital images with seven (7) disease classes and one (1) healthy class. This study shows that the VGG16 + SVM model has a fairly good performance in disease detection on mango leaves with accuracy, precision, recall, and F1-Score values of 99.50%, 99.50%, 99.50%, and 99.50%, respectively

Keywords

Mango, Leaves diseases, CNN, VGG16, SVM

1. Introduction

Mango is an annual fruit plant in the form of a tree that originated in India. Now, this plant is spread in various parts of the world including Indonesia. Mango plants can grow well in lowlands and hot weather. Many observations state that there are various types of mangoes spread across Indonesia that have their own characteristics and economic prices [1]. Mango fruit is in high demand. So, timely control of mango plant diseases is necessary to get high returns [2].

According to data from the Central Statistics Agency (BPS) in 2021, it is known that the amount of mangoes obtained from production is 2.8 million tons. And in 2022 there was an increase in the amount of production

to 3.3 million tons. In order for the amount of mango production to increase every year, it is necessary to deal with various diseases that may occur. With technological advances in image processing and artificial intelligence, automated solutions for disease detection can be implemented. Automatic recognition of foliar diseases of mango plants is still a challenge and manual disease detection is not a viable option in this computerized era due to its high cost and unavailability of mango experts and the variety of symptoms [2].

In the era of evolving technology, many studies have been conducted to develop digital image processing in agriculture. Research conducted by (O'Shea & Nash,

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2015) entitled “An Introduction to Convolutional Neural Network” to identify diseases and agricultural production using digital image technology. One of the main benefits of this research is its use in identifying diseases on mango leaves using Convolutional Neural Network (CNN). CNNs are primarily used to solve difficult image-based pattern recognition tasks and with their precise yet simple architecture, offer a simplified method to get started with CNN.

One of the widely used CNN architectures is VGG-16 which was developed in 2014. The architecture includes 13 convolutional layers, three (3) fully connected layers, and a total of about 138 million parameters [3]. In another study, the model was used as a disease classification model in eggplant plants. The Transfer Learning approach used in this study, and obtained satisfactory results [4]

The transfer learning approach has proven effective in various classification studies in plants. The advantage of this architecture lies in its ability to extract features from an image. Based on previous research, similar approaches can be applied to other plants, including leaf diseases in mangoes, which also have the potential to be infected with various diseases. With this method, it is expected to contribute to the development of a plant disease detection system that can be a reference for further research.

2. Research Method

The research used is applied which aims to develop a model and test the effectiveness of the model. This research analyzes the comparison of CNN VGG16 and CNN VGG16 + SVM on disease classification on mango leaves using digital images with a total of 7 disease classes and 1 class of healthy leaves.

2.1. Manggo Leaves Disease

2.1.1. Anthracnose

This disease is caused by *Colletotrichum species complex* which can spread widely before it is detected because this disease cannot be eradicated easily until it passes the latency period. The disease can be characterized by the appearance of black spots on mango plant parts including leaves, fruits, flowers, petioles, twigs, and stems [5].



Figure 1 Anthracnose

2.1.2. Bacterial Canker

This disease is caused by *Xanthomonas citri pv* which causes leaf growth on mango plants to experience disease with the characteristics of leaves having black spots, jagged and sometimes changes the color of the leaves to yellow (*chlorosis*) [6].



Figure 2 Bacterial Canker

2.1.3. Cutting Weevil

This disease is characterized by cutting off most of the leaves and leaving only the base of the leaves caused by *Deporaus marginatus* Pascoe (*Coleoptera: Curculionidae*) or leaf beetles [7].



Figure 3 Cutting Weevil

2.1.4. Die Back

The disease is difficult to eradicate when it appears, and will be worse in the event of drought, heat, sunburn, lack of water, lack of nutrients. caused by the *fungus Lasiodiplodia theobromae* which causes leaves to turn brown or black, angular leaves, chlorosis

(yellowing), or defoliation (drying and wilting) [8].



Figure 4 Die Back



Figure 7 Sooty Mould

2.1.5. Gall Midge

This disease is characterized by the appearance of quite a lot and quite large black spots on mango leaves which cause damage to mango leaves and interfere with growth. this disease is caused by *Procontarinia mangicola* (Shi) which is a type of mango mite, a small insect species [9].



Figure 5 Gall Midge

2.1.6. Powdery Mildew

This disease is caused by *Pseudoidium anacardii* (formerly *Oidium mangiferae* Berthet) which is a type of fungus known as “iodine” in mango plants characterized by the appearance of white spots on the leaves [10].



Figure 6 Powdery Mildew

2.1.7. Sooty Mould

This disease is characterized by the appearance of black and white spots on the leaves and a thin layer on the outside of the leaves. The disease is caused by *Meliola mangiferae* [11].

2.1.8. Healty



Figure 8 Healthy

2.2. Architecture

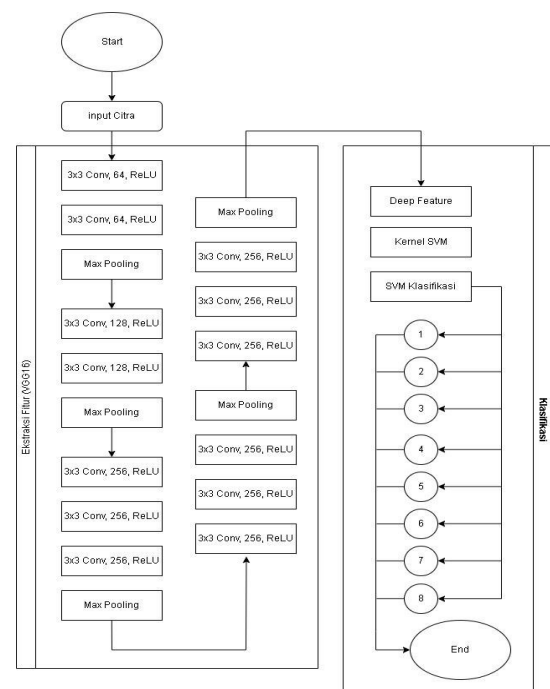


Figure 9 Architecture VGG16 + SVM

Model design is done by replacing the default fully connected layer structure of VGG16 by using SVM which is used as a classifier with some adjustments for its use.

3. Results and Analysis

Table 1 Configuration

Parameter	Configuration
Rescale	1./255
Rotation_range	30
Width_shift_range	0.2
Height_shift_range	0.2
Shear_range	0.2
Zoom_range	0.2
Horizontal_flip	True
Batch_size	32
Picture ratio	224x224
Patience	3
Epoch	10
Learning_rate	0.0001

Table 2 VGG16 Data Validation

MODEL	CLASS	EVALUATION METRIX (%)			
		ACCURACY	PRECISION	RECALL	F1-SCORE
VGG16	Anthracnose	100	100	100	100
	Bacterial Canker	100	89	100	94
	Cutting Weevil	100	100	100	100
	Die Back	100	98	100	99
	Gall Midge	86	100	86	92
	Healthy	98	89	98	93
	Powdery Mildew	94	100	94	97
	Sooty Mould	92	96	92	94
	Average	96.25	96.5	96.25	96.125

CNN models will be trained using VGG16 for extraction and classification. Datasets that have been divided into 80:10:10 will be trained on VGG16 using python programming language on google colab GPU T4 with libraries that facilitate the model training process. Before entering into training both models are adjusted by several parameters, see on table 1. The configuration can be changed according to the capabilities and complexity of each model to be used.

3.1. VGG16 (Data Validation and Data Test)

table 2 shows the results for each evaluation. the average evaluation data on vgg16 shows results of 96.25% for accuracy, precision, recall, and for f1-score of 96.125%. for the accuracy results of each class can be seen in table 2.

VGG16 on test data can be seen in table 3. With an average result of 98%, these results are obtained for all evaluation results carried out, namely the accuracy, precision, recall and f1-score values.

Table 3 VGG16 (Data Test)

MODEL	CLASS	EVALUATION METRIX (%)			
		ACCURACY	PRECISION	RECALL	F1-SCORE
VGG16	Anthracnose	100	96	100	98
	Bacterial Canker	100	98	100	99
	Cutting Weevil	100	98	100	99
	Die Back	100	100	100	100
	Gall Midge	90	100	90	95
	Healthy	100	94	100	97
	Powdery Mildew	100	98	100	99
	Sooty Mould	94	100	94	97
	rata-rata	98	98	98	98

3.2. VGG16 + SVM (Data Validation and Data Test)

Table 4 VGG16 + SVM (Data Validation)

MODEL	CLASS	EVALUATION METRIX (%)			
		ACCURACY	PRECISION	RECALL	F1-SCORE
VGG16 + SVM	Anthracnose	100	100	100	100
	Bacterial Canker	100	98	100	99
	Cutting Weevil	100	100	100	100
	Die Back	100	100	100	100
	Gall Midge	96	100	96	98
	Healthy	100	100	100	100
	Powdery Mildew	100	100	100	100
	Sooty Mould	100	98	100	99
	Average	99.5	99.5	99.5	99.5

Table 5 VGG16 + SVM (Data Test)

MODEL	CLASS	EVALUATION METRIX (%)			
		ACCURACY	PRECISION	RECALL	F1-SCORE
VGG16 + SVM	Anthracnose	100	98	100	99
	Bacterial Canker	100	100	100	100
	Cutting Weevil	100	100	100	100
	Die Back	96	100	96	98
	Gall Midge	96	92	96	97
	Healthy	94	100	94	97
	Powdery Mildew	100	98	100	99
	Sooty Mould	98	96	98	99
	Average	98	98	98	98

table 4 shows the results for each evaluation. the average evaluation data on vgg16 shows results for accuracy, precision, recall, and for f1-score of 99.5%.

VGG16 on test data can be seen in table 5. With an average result of 98%, these results are obtained for all evaluation results carried out, namely the accuracy, precision, recall and f1-score values.

Table 6 Data Validation

MODEL	Accuracy	Precision	Recall	F1-Score
VGG16	96.25	96.5	96.25	96.125
VGG16 SVM	99.5	99.5	99.5	99.5

Table 7 Data Test

MODEL	Accuracy	Precision	Recall	F1-Score
VGG16	98	98	98	98
VGG16 SVM	98	98	98	98

The calculation used is macro average, with the following equation:

$$\text{Macro Average} = \frac{1}{n} + \sum_{i=1}^n M_i \quad (1)$$

with results shown in tables 7 and 8.

4. Conclusion

The VGG16 + SVM architecture CNN method can be applied by using VGG16 as feature extraction and replacing the fully connected layer with SVM used for classifier. The application of VGG16 + SVM to classify diseases on mango leaves gives the best results compared to VGG16 alone, with accuracy, precision, recall, and F1-Score values of 99.50%, 99.50%, 99.50%, and 99.50%, respectively.

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This journal only reports the results of the research conducted and hopefully can be used for further research and development.

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Biography



Achmad Muchdor Firdaus is a student from the University of Jember studying at the faculty of computer science, having attended SMA Negeri Balung

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