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Efficacy of chili plant diseases classification using deep learning: a preliminary study

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ABSTRACT

Plant disease classification using deep learning techniques is a popular research area due to the numerous opportunities for introducing advance and robust classifiers. Nevertheless, classifying chilli plant diseases accurately from images under uncontrolled environment and various imaging conditions remains unsolved due to the lack of chilli disease image datasets. In this study, the efficacy of three high-performance deep learning algorithms, namely VGG16, InceptionV3, and EfficientNetB0, in classifying three types of chilli leaves diseases, namely upward curling, mosaic/mottling, and the bacterial spot, is demonstrated. These methods are popularly used for other plant disease classifications due to their effectiveness. The experiments were performed on the 3,000 chilli plant disease images collected from three different field environments in Selangor, Malaysia. The images were captured with a complex background and various illuminations, angles, and distances to reflect the real-life scenarios. The complexity of the collected images was created based on the taxonomic information of chilli leaves diseases and the unavailability of chilli disease images under various imaging conditions in the publicly available plant disease databases. Experimented using appropriate specifications, the models demonstrated outstanding performance with more than 95% accuracy with the highest accuracy of 98.83% by InceptionV3.

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1. INTRODUCTION

Chilli or scientifically known as capsicum annuum L. is Malaysia's utmost cultivated crop [1] and has been recognized as among the top tenth of self-sufficiency ratio (SSR) in selected agricultural commodities with the highest import dependency ratio (IDR) of 73.6% [2]. The five widely domesticated species planted as annual crops are capsicum annuum, capsicum frutescense, capsicum chinense, capsicum baccatum, and capsicum pubescence [3], plagues and diseases easily infect these plants. The effects of the infection are a significant reduction in chilli production and deterioration of fruit quality, resulting in low returns for farmers [4]. According to [5], chilli plant diseases are mainly due to the infection caused by pathogenic microbes, namely fungus, bacteria, and viruses. The infection is visible but needs to be examined closely and adequately controlled to avoid the massive diseases spread on the farm. The conventional way of detecting and classifying plant diseases is time-consuming, and automatic detection and classification approaches have been introduced to tackle this problem. In the late 1990s, conventional computer vision techniques were used to resolve chilli plant diseases' automatic detection and identification [6]. The major weakness of the traditional computer vision technique was that it was only proven successful on simpler and controlled setups but struggled as the operational conditionschanged [7].

As the years passed, automatic detection and classification of plant diseases utilizing image processing and deep learning approaches have received significant consideration among the experts of the subject. Deep learning is a branch of artificial intelligence that allows machines to perform impressive recognition, prediction, and filtration [8]. Many practical and reliable deep learning algorithms for plant disease classification [9]–[13]. Typically, the classification is performed according to the infected leaf shape and a detectable change in the leaf colour caused by the fungus, bacteria, and virus infection. The application of the transfer learning approach for deep learning has received significant attention. Transfer learning has emerged as a powerful technique whereby the knowledge gained from the larger dataset is transferred to the new dataset [14], [15]. In scenarios within sufficient training data, this technique is beneficial, as presented in research by [16]. In transfer learning, pre-trained models are generally trained on a large scale, such as ImageNet that contains millions of actual images. The advantage is that the learned features are transferred by the weights and the architecture obtained from these models [17]. Inspired by these findings, the performance of the pre-trained model of VGG16, InceptionV3, and EfficientNetB0 in classifying chilli plant disease images captured under an uncontrolled environment with various imaging conditions and a small dataset is studied. This paper shows the performance of these models for classifying highly complex chilli plant diseases images. The findings in this paper will create more opportunities for developing more accurate classifiers in the future. This is because the existing studies have only shown less than 90% accuracy on a particular type of chilli disease [18], [19]. This paper is organized as follows. Section 2 describes chilli plant disease taxonomy, and section 3 provides the architectures of the used deep learning methods, materials, methods, and experimental setup, and section 4 discusses the results. Finally, the paper is concluded in section 5.

2. TAXONOMY OF CHILI DISEASES

Chilli is a type of plant that can be easily affected by fungi, bacteria, viruses, and pests. Besides, climate changes and the risk of a resistance breakdown can also affect the durability of disease resistance. The example of the fungi, bacteria, viruses, and pests commonly affected by chilli plants [5] are summarized in Figure 1.

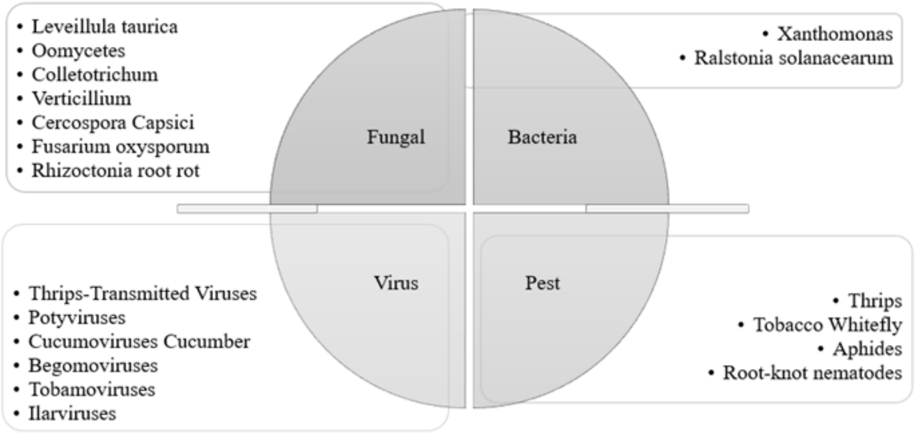


Figure 1. Taxonomy of chilli plant diseases according to [5]

In this study, three types of diseasewere considered: the bacterial spot, upward curling and mosaic/mottling, as shown in Figure 2(a), Figure 2(b), and Figure 2(c), respectively. The bacterial spot is the small black spots of water-soaked on the leaves and gradually browning, coalesce, rugged and cracked. It is mainly due to the pathogen that is known as xanthomonas. The upward curling disease is caused by Begomovirus transmitted by Bemisia whiteflies that caused yellowing of veins and reduced leaf size. The mosaic disease caused the leaves to be yellowed and narrow, which is transmitted mainly by greenfly aphids.

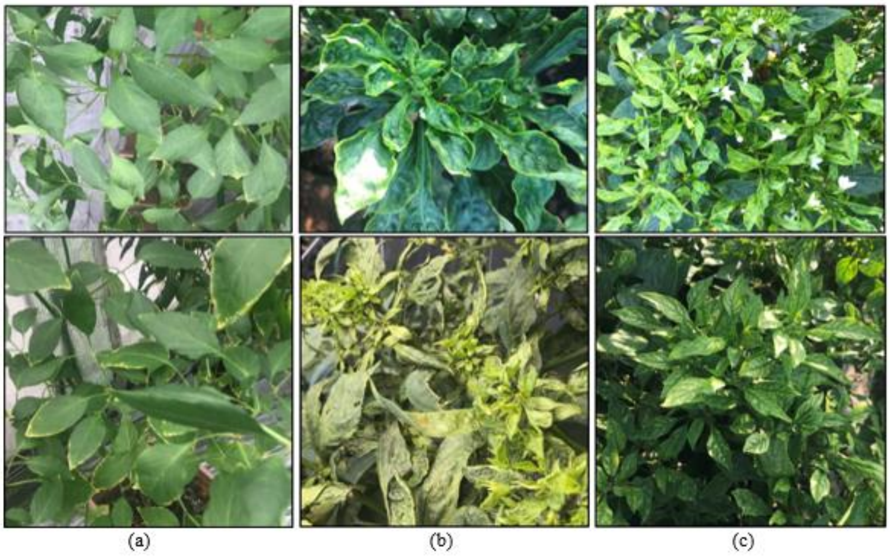


Figure 2. Samples of chili plant diseases image used in the experiments, (a) bacterial spot, (b) upward curling, and (c) mosaic/mottling

3. MATERIAL AND METHODS

3.1. Chili plant disease dataset

The dataset used in this study consists of 3,000 images of capsicum annuum L. plants and annotated into three classes of chilli leaves diseases: namely the upward curling, mosaic/mottling and bacterial spot. The images were self-collected under an uncontrolled environment and various illuminations, views, and distances to reflect the real-life scenarios. The images were collected from three different field environments located at Sijangkang Selangor; Community Urban Farm, Bukit Rimau, Selangor, and a greenhouse at the Faculty of Engineering, Universiti Putra Malaysia (UPM) Selangor. The images were captured using Apple iPhone 7 with the dimension of resolution 3024×4032 and Asus Zenfone 2 with the dimension of resolution 2304×4096. These images were cropped, resized and flipped manually using Microsoft Photos at the initial stage to reduce the background clutter and occlusion issues. Data annotation was done by consulting the experts at the farms and cross-checking with the related published papers. For each disease, 800 and 200 images were used for training and testing, respectively.

3.2. Pretrained DCNN model and parameters

In this study, the performance of VGG16, Inception V3 and EfficientNet B0 in classifying chilli plant diseases from complex images was compared. These models were selected for their outstanding performance when classified the plant disease images from the ImageNet dataset [20]. The VGG16, as illustrated in Figure 3 [21], used a recommended default input image size of 224×224×3 and 13 convolutional layers with a rectified linear unit (ReLU) activation function. The convolutional layers were fed into a max pooling, three fully connected (FC) layers and a Softmax function at the end of the architecture. The last FC layers were replaced by three channels for this study, indicating the three classes of chilli plant diseases understudy.

Meanwhile, InceptionV3 [22] has 42 total deep network layers with a grid size-reduction block between the inception modules blocks and one auxiliary classifier at the third concatenated trunk, as shown in Figure 4. The recommended size of the input image for this model is 299×299×3, and five convolutional layers process the input image with two max-pooling layers at the first stage. Then, a series of inception modules process the input before finally performing classification using a fully connected layer and a Softmax function. EfficientNet [20] is a convolutional neural network architecture with a compound scaling method that uniformly scales all depth, width, and resolution dimensions to pursue better accuracy and efficiency. Currently, there are seven versions of EfficientNet networks, in which each version is the upgraded version of the previous, which is scaled from the EfficientNetB0 baseline using different compound coefficients. The EfficientNetB0 network consists of a convolutional layer, several mobile inverted bottleneck convolutional (MBConv) layersand optimization layers, as shown in Figure 5. The recommended size of the input image for this model is 224×224×3.

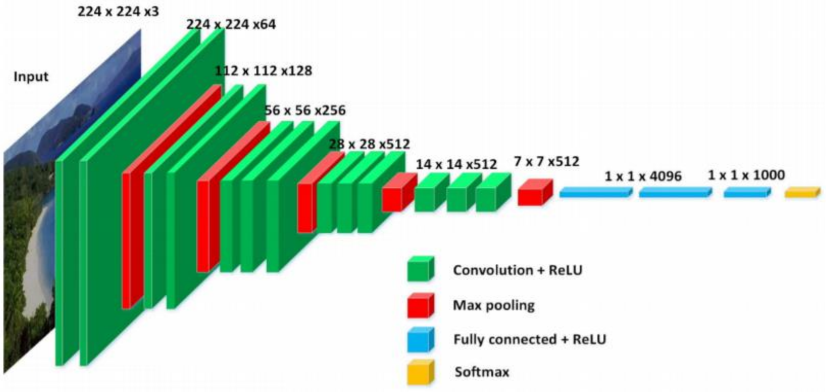


Figure 3. The architecture of the VGG16 network [21]

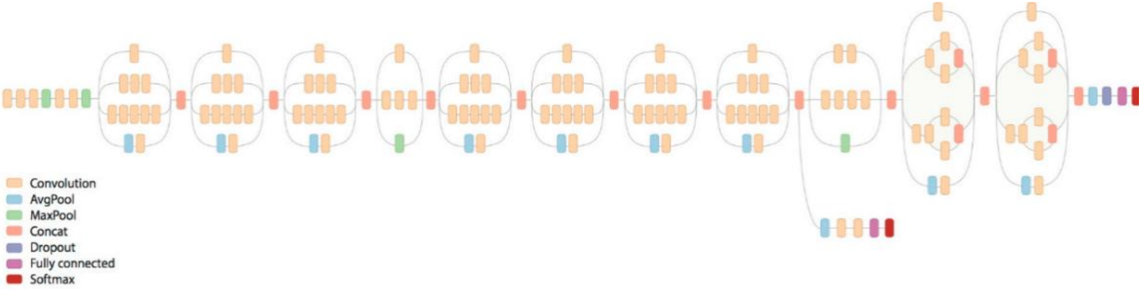


Figure 4. The architecture of InceptionV3 network [23]

Figure 5. The architecture of EfficientNetB0 network [23]

3.3. Experimental setup

The experiment was conducted on a 64-bit operating system, an x64-based processor running on Intel(R) Core (TM) i5-10200H CPU @2.40 GHz with NVIDIA GeForce GTX 1650 and 8 GB RAM. All deep learning models were compiled with GPU support. The proposed chilli plant disease classification is shown in Figure 6. The filters, feature maps, pooling layers and hyperparameters of the VGG16, InceptionV3 and EfficientNetB0 models remain the same structure, as obtained from Keras Applications API with ImageNet [24]. Nevertheless, a combination of fully connected layers and Softmax activation was applied. This part has been converted into three outputs representing the chilli plant disease classes (upward curling, bacterial spot and mosaic/mottling). All pre-trained models were set to frozen layers to avoid Keras from updating their weights during the training. Other settings include batch normalization and batch size. Based on [25], each pixel value of the images was divided by 255 for batch normalization, and the selected batch size was 32. Batch normalization could overcome the problem of internal covariate shift, which can impede the training of deep neural networks. Stochastic gradient descent (SGD) was used as the optimizer due to its high performance [26], while the learning rate of 0.0001 was adopted based on [16]. The epoch is set to 50, and the selectionis based on several trials, such as 10, 30, 50 and 100 epochs. The resultshave shown that 50 epochs have produced high accuracy and better processing stability.

The input images were divided into two sets, 80% for training and 20% for testing, as recommended by [27]. The images were resized according to the model's default size, 224×224 pixels for VGG16 and EfficientNetB0, and 299×299 pixels for Inception V3. The methods were trained with two training sets, where the first set consists of original images and the second setconsists of augmented images. Both sets consist of the same amount of images that is 2400 images. In the second training set, the images were sheared at an angle of 0.2 degrees, zoomed at 0.2 magnification and horizontal flipped using Imagedatagenerator in Kerasapplication. Image data generator works randomly in real-time, with the number of images remaining the same. The augmentation parameters selection was decided based on the observation from a few trials, where the features of the disease can be visualized using these parameters.

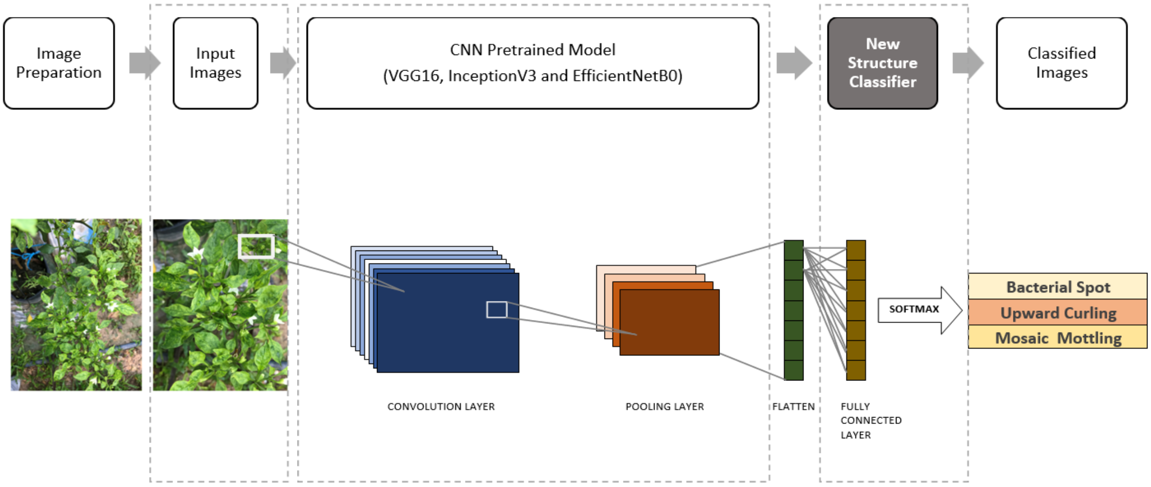
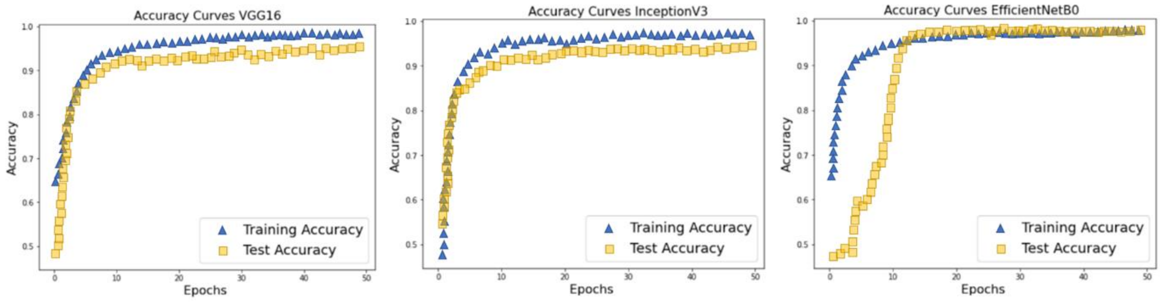


Figure 6. The proposed chili plant disease classification framework

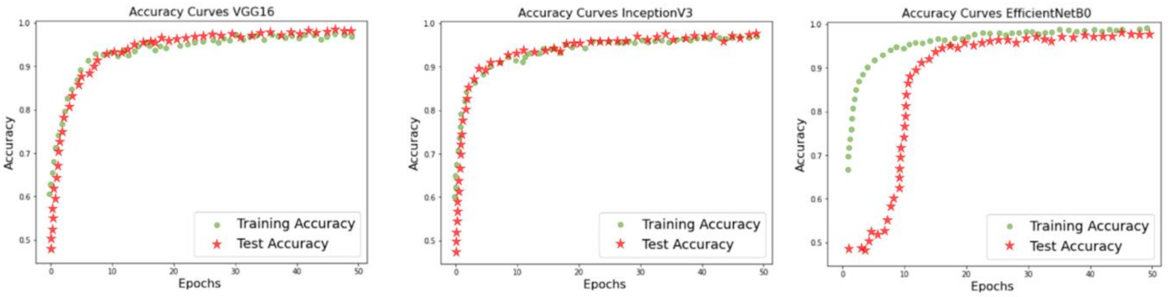
4. RESULTS AND DISCUSSION

The performance of the selected deep learning algorithms was evaluated based on accuracy, recall, precision, and F1-score. Accuracy is the number of correctly identified samples, and recall is the number of positive samples that are accurately identified. Meanwhile, precision is the measurement of accurately identified samples among all the true samples, andthe F1-scorerepresents a harmonic mean between sensitivity and precision. The experiments were conducted on two datasets, where the first dataset consist of original images and augmented images in the second dataset. The results in Figure 7(a), Figure 7(b) and Figure 7(c) show that EfficientNetB0 outperformed VGG16 and InceptionV3, but in Figure 8(a), Figure 8(b) and Figure 8(c), it is shown that InceptionV3 outperformed VGG16 and EfficientNetB0. It is also observed that for both cases, VGG16 and InceptionV3 required less computation time compared to EfficientNetB0 to reach above 90%.



(a) (b) (c)

Figure 7. The accuracy produced by (a) VGG16, (b) InceptionV3, and (c) EfficientNetB0 using original images for training



(a) (b) (c)

Figure 8. The accuracy produced by (a) VGG16, (b) InceptionV3, and (c) EfficientNetB0 using augmented images for training

Nevertheless, the accuracy of models trained by original images did not differ much when trained on augmented images. At the 50 epochs, it is shown that the InceptionV3 has produced the highest accuracy of 98.83% on augmented images while EfficientNetB0 highest accuracy of 97.67% on original images, respectively. The obtained accuracy, precision, recall, and F1-score for the VGG16, InceptionV3 and EfficientNetB0 are shown in Table 1. It is shown that the performance of EfficientNetB0 and InceptionV3 is approximately similar for both cases, that is, when original or augmented images train the models. However, EfficientNetB0 has better performance when trained by original images, but opposite to InceptionV3, the model performed better when trained by augmented images.

The summary of the classification results for each disease, namely upward curling (UC), mosaic/mottling (M) and bacterial spot (BS) diseases, are shown in the confusion matrix in Table 2. It is demonstrated that InceptionV3 has produced the highest true positivevalue when classifyingbacterial spots for both cases but the mosaic/mottling, the InceptionV3 model, has the highest true positive value when trained by augmented images. Nevertheless, the true positive value of the InceptionV3 model is lower than the true positive value of EfficientNetB0 when trained by original images. All three methods have equivalent performance when classifying the upward curling disease. It is also shown that the models have difficulty classifying the mosaic/mottling disease, as the produced true positive value is the lowest compared to other diseases. The complex features of the mosaic/mottling disease are approximately similar to the upward curling disease that caused the methods to misclassify.

Table 1. The VGG16, InceptionV3 and EfficientNetB0 testing performance

Training Set	Models	Accuracy (%)	Precision (%)	Recall (%)	F1 Score
First set (original images)	VGG16	95.17	95.00	95.00	0.95
	InceptionV3	97.50	97.00	97.00	0.97
	EfficientNetB0	**97.67**	**98.00**	**98.00**	**0.98**
Second set (augmented images)	VGG16	95.83	96.00	96.00	0.96
	InceptionV3	**98.83**	**99.00**	**99.00**	**0.99**
	EfficientNetB0	96.83	97.00	97.00	0.97

Table 2. Confusion Matrix of the methods that were trained using original and augmented images

		First Training Set (Original Images)									Second Training Set (Augmented Images)								
		VGG16			InceptionV3			EfficientNetB0			VGG16			InceptionV3			EfficientNetB0		
True	BS	0.97	0.02	0.01	0.99	0.0	0.1	0.98	0.0	0.02	0.98	0.02	0.0	1.0	0.0	0.0	0.98	0.0	0.02
Label	M	0.01	0.91	0.08	0.02	0.96	0.02	0.0	0.98	0.02	0.02	0.90	0.08	0.0	0.98	0.02	0.0	0.94	0.06
	UC	0.0	0.02	0.98	0.0	0.03	0.97	0.0	0.02	0.98	0.0	0.02	0.98	0.0	0.02	0.98	0.0	0.02	0.98
		BS	M	UC	BS	M	UC	BS	M	UC	BS	M	UC	BS	M	UC	BS	M	UC
		Predicted Label																	

5. CONCLUSION AND FUTURE WORKS

The efficacy of deep learning algorithms, namely VGG16, Inception V3 and EfficientNet B0, methods in classifying three types of chilli plant diseases, namely upward curling, mosaic/mottling and bacterial spot from a dataset that consists of 3,000 images in an uncontrolled condition and under various imaging conditions is demonstrated. The experiment results showed that InceptionV3 has better performance than the VGG16 and EfficientNetB0 in classifying bacterial spot images. Still, all the models have difficulty classifyingthe mosaic/mottling disease due to the complex features of the mosaic/mottling disease that are approximately similar to the upward curling disease. All three methods have equivalent performance when classifying the upward curling disease. In conclusion, deep learning algorithms have shown a great potential for classifying chilli plant diseases. The performance algorithms can be further improved by exposing them to high-complexity images and several other types of diseases, which will create more opportunities for developing more advanced classifiers.

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