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Guava Disease Classification Using EfficientNet and Genetic Algorithm-Optimized XGBoost

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Abstract

Guava is an evergreen plant in the Myrtaceae family, is renowned for its adaptability and noteworthy nutritional benefits. However, guava production has experienced a substantial decline in recent years due to various diseases affecting the fruit. Farmers typically employ manual inspection to identify these diseases, a method that is time-consuming, labor-intensive, and susceptible to errors. This underscores the necessity for an automated classification model capable of accurately diagnosing guava fruit diseases. While numerous machine learning and deep learning models have been developed for agricultural disease detection, research on combining deep transfer learning as a feature extractor with machine learning classifiers remains relatively limited. Addressing this research gap, the proposed model integrates the strengths of both approaches, achieving an impressive accuracy of 98.62%, surpassing the performance reported in previous studies. This encouraging outcome underscores the potential of hybrid models in enhancing guava fruit disease classification, paving the way for more efficient and scalable agricultural management solutions.

1. Introduction

Guava (Psidium guajava L.) is an evergreen plant of the Myrtaceae family, known for its adaptability and outstanding nutritional properties, thus being dubbed as the “Tropical Apple” and the “Poor Man's Fruit [1]. Guava production has been declining lately due to several diseases that farmers cannot notice with the naked eye [2]. This highlights the critical challenges faced by guava farmers, emphasizing the need for early detection and intervention to prevent economic losses. Implementing integrated disease management strategies, including the use of resistant cultivars, biological control agents, and precision agriculture technologies, can play a vital role in preventing the spread of guava diseases [3]. Machine learning techniques, such as Support Vector Machine (SVM) and K-Nearest Neighbors (KNN), have been used to detect diseases in guava leaves, with varying degrees of accuracy [4]. Recent advances have led

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to the development of hybrid deep learning models that can identify multiple diseases from a single guava leaf, which significantly improves detection capabilities compared to traditional methods that focus on single disease identification [5].

Guava disease classification has been explored using deep learning and machine learning methods. Al Haque et al. [6] used CNN, achieving 95.61% accuracy. Mostafa et al. [7] applied transfer learning with ResNet-101, reaching 97.74% accuracy on augmented data. Jain et al. [8] combined CNN and LSTM for improved results. Meanwhile, Almutiry et al. [9] used LBP and PCA with traditional classifiers, where Bagging Tree achieved up to 100% accuracy, showing the potential of feature-based machine learning approaches.

From the research mentioned in the paragraph above, there are a few shortcomings in their research, such as a lack of research utilizing hybrid architecture and optimization of the parameters of the deep learning architecture; therefore, this research proposed another Deep Transfer Learning model using EfficientNet and the machine learning algorithm XGBoost as a feature classifier with a Genetic Algorithm to optimize hyperparameters. EfficientNet has been proven to be good enough for feature extraction from the research [10]. While XGBoost is also shown to have exceptional performance when combined with Deep Learning as a feature extractor, such as in the research by [11], [12], [13]. There's also a need to optimize the parameters of the XGBoost, as shown by Mehdary et al. [14], where their research used a Genetic Algorithm to optimize the hyperparameters of XGBoost to detect fraud in smart grid applications. Genetic Algorithm has proven to improve the model performance with increasing accuracy from 82% to 97.8%. Therefore, we proposed a combination method using EfficientNet as a feature extractor and XGBoost with hyperparameters tuned with Genetic Algorithm to classify the guava disease to improve the performance of the guava disease classification model.

2. Literature Review

This study aimed to create accurate models for identifying guava fruit diseases, building on previous research using deep learning methods. One such study was conducted by Al Haque et al. [6], who implemented a Convolutional Neural Network (CNN) to classify three types of guava diseases along with healthy guava fruit. The dataset consisted of 10,000 images, with 2,500 images per class. From each class, 1,800 images were used for training, 200 for validation, and 500 for testing. The CNN model in this study achieved a classification accuracy of 95.61%.

Further research was carried out by Mostafa et al. [7], who utilized deep transfer learning models such as ResNet-50, ResNet-101, AlexNet, SqueezeNet, and GoogleNet. The dataset, initially consisting of 321 images with four classes (including healthy guava), was expanded through augmentation to 2,889 images. All models were trained and tested on the augmented dataset, with ResNet-101 achieving the highest classification accuracy of 97.74%.

In a separate study, Jain et al. [8] proposed a hybrid approach using Convolutional Neural Networks (CNN) and Long Short-Term Memory (LSTM) networks to classify three types of guava diseases and healthy guava. The dataset comprised 6,000 images, of which 70% were allocated for training and the remaining for testing. The CNN layers were used for feature extraction, while the LSTM layers were employed to enhance accuracy, followed by fully connected layers for classification.

While the above studies predominantly rely on deep learning and transfer learning methods, there are also efforts to utilize traditional machine learning techniques through feature extraction. Almutiry et al. [9] for instance, employed Local Binary Pattern (LBP) for feature extraction and Principal Component Analysis (PCA) for dimensionality reduction. Their self-collected dataset contained 400 images spanning four disease classes and healthy guava. They used machine learning models such as K-Nearest Neighbors (KNN), Support Vector Machine (SVM), and Bagging Tree. Among these, Bagging Tree achieved the highest classification accuracy, reaching up to 100% on certain disease classes, such as fruit flies, and consistently over 94% on others. This demonstrates the potential of combining hand-crafted feature extraction with traditional machine learning algorithms for guava disease classification.

Based on the results of previous studies, there is still an opportunity to develop a model using alternative approaches such as enhanced traditional machine learning or hybrid architectures to improve classification performance and efficiency.

3. Method

This study will be focused on building a Guava Fruit Disease using EfficientNet and XGBoost-HGS. The flow of the research starts with collecting a dataset from Kaggle. After that, pre-processing is needed to image from the dataset using ImageDataGenerator and preprocess_input from the keras library. Later, EfficientNetB3 will be employed as a feature extractor, extracting features from training and testing images to a feature map that later will be classified by XGBClassifier from the XGBoost library, with the hyperparameter of the XGBClassifier being tuned using Genetic Algorithm. The model will be evaluated using a confusion matrix and a few metrics such as accuracy, precision, recall, and F1-score. Figure 1 explains in short the flow of this research.

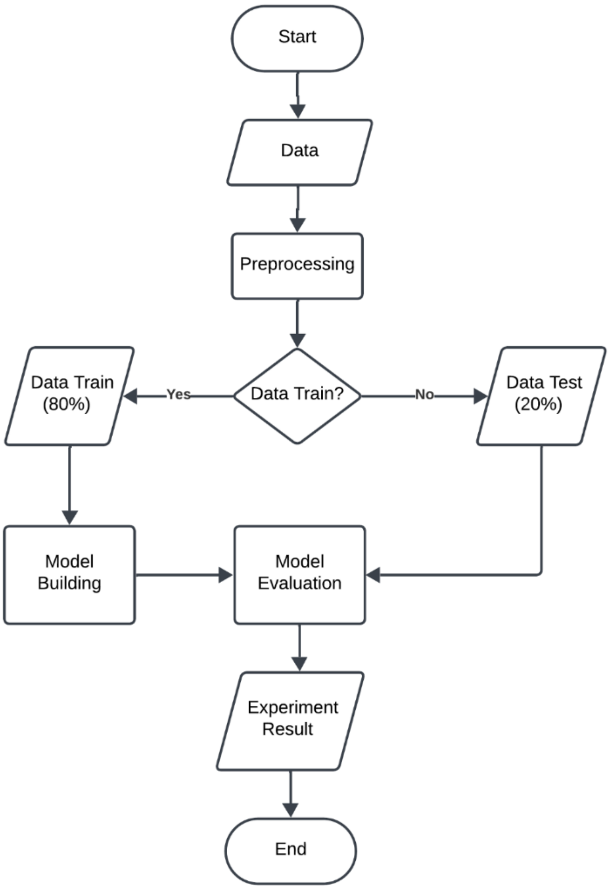

Figure 1. Flow of this research

3.1. Dataset

The dataset collected from Kaggle is named the Guava Fruit Disease Dataset. Original Data was sourced from Mendeley Data [15]. The data consists of 3804 image data. The data was split by the original author into 2647 image data for training, 775 image data for validation, and 382 image data for test. However, this study only uses the training and test data to create a classification model to classify Guava Fruit Disease. Figure 1 shows an example of the image from the dataset.

Figure 2. Example image from the dataset

3.2. Pre-processing

Preprocessing was carried out using ImageDataGenerator from the keras library. The pre-processing method consists of Batching and adding the preprocess input. Another process in this section is adding the preprocess_input function for EfficientNet from the keras library to the image. This process ensured the image's pixels are in the range of 0 to 255, as EfficientNet requires the image to have a pixel range of 0 to 255.

3.3. Classification Model

EfficientNetB3, a convolutional neural network architecture, was developed specifically for the purpose of performing image classification tasks in an efficient manner [16]. This is accomplished by increasing the network's depth, width, and resolution in a manner that is balanced [17]. A compound scaling method is utilized in this architecture. This method optimizes not only the size of the model but also the resources that are available for computation within the system [18]. EfficientNet scales all 3 dimensions simultaneously using the formula below [19]:

$$depth: d = \alpha^{\theta} \quad (1)$$

$$width: w = \beta^{\theta} \quad (2)$$

$$resulution: r = \gamma^{\theta} \quad (3)$$

Subject to: $\alpha \cdot \beta^2 \cdot \gamma^2 \approx 2$ and $\alpha \geq 1, \beta \geq 1, \gamma \geq 1$

Where α, β, γ are constants that can be determined using a small grid search, and θ are user-specific coefficients to control model scaling of the architecture. EfficientNetB3 is a variant of EfficientNet with the same depth as EfficientNetB0 but having 1.3 times the width and 1.2 times the resolution due to $\theta = 3$ [20].

Extraction of features is accomplished through the utilization of EfficientNetB3 during this investigation. The model in this research is developed with the assistance of the Keras library is accountable for the processing of input images to generate feature maps. These feature maps are used to extract significant features from the images, which are then provided to the XGBoost classifier so that it can carry out additional classification tasks. To enhance the classification accuracy of the XGBoost model, this strategy makes use of high-quality features that were extracted by EfficientNetB3.

XGBoost is a well-known and high-performance machine learning algorithm used for classification and regression tasks. It was developed to handle missing values and prevent overfitting while simultaneously optimizing speed and performance through its design [21]. XGBoost is responsible for building an ensemble of decision trees. The errors made by the previous trees are corrected by each new tree added to the ensemble, leading to an overall improvement in the model's accuracy [22]. Another feature of XGBoost is the regularization techniques incorporated into the algorithm to reduce overfitting [12]. XGBClassifier, which comes from the XGBoost library, is used in this research for feature classification purposes. To facilitate the improvement of the XGBoost model's performance, adjustments were made to the model's parameters using a Genetic Algorithm [23]. This strategy is carried out by investigating various combinations of hyperparameters and finding the optimal settings to produce the best classification results.

Genetic Algorithm is a search optimization algorithm inspired by natural selection and genetics [14]. The search process using the Genetic Algorithm operated based on selection, mutation, and crossover to produce a better solution [24]. This study used a Genetic Algorithm to select the best parameter for XGBoost, as the Genetic Algorithm for XGBoost has a lot of parameters, and different combinations may affect the performance of the model [25]. Figure 3 shows the flow of hyperparameter tuning using the Genetic Algorithm.

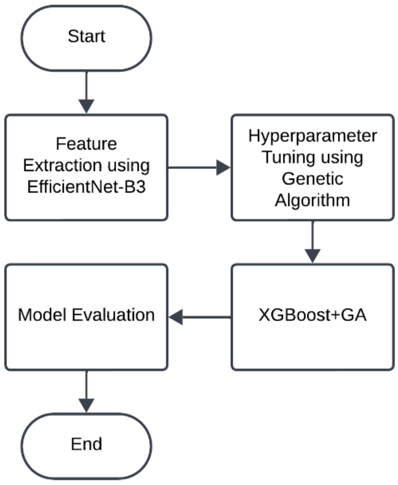

Figure 3. Flow of Classification Model Building

3.4. Evaluation Method

Model is evaluated using the following metrics: accuracy, precision, recall, and F1-score. Formulas (1), (2), (3), (4) calculate these.

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

$$precision = \frac{TP}{TP + FP} \quad (2)$$

$$recall = \frac{TP}{TP + FN} \quad (3)$$

$$F1 - score = 2 \times \frac{precision \times recall}{precision + recall} \quad (4)$$

True Positive (TP) is where the model correctly predicts the positive class, where the disease guava correctly classified as diseased, while True Negative (TN) is where the model correctly predicts the negative class, where healthy guava is correctly classified as healthy guava. False Positive (FP) is when the model incorrectly classifies negative cases as positive, and False Negative (FN) is when positive cases are incorrectly classified as negative.

4. Results and Discussion

4.1. Result

The Guava Fruit Disease Dataset contains 2,647 training images and 382 test images. The preprocessing steps involve batching the data into batches of 32 and applying the preprocess_input function to ensure that image pixel values fall within the 0 to 255 range, as required by EfficientNet.

EfficientNetB3 serves as the feature extractor, generating feature maps that will be classified using XGBoost.

To make the extracted features compatible with the classifier, a GlobalAveragePooling2D layer is added after the last layer of EfficientNetB3. After extracting features from both the training and test images, the feature maps are classified using the XGBoostClassifier. This study evaluates two models: one with default XGBoost hyperparameters and another with optimized hyperparameters. A comparison of the two models is presented in Table 1.

Table 1. Comparison between default and optimized hyperparameters

Parameters Name	Value List	Default	Optimized
n_estimators	(50, 500)	100	229
max_depth	(3, 10)	6	10
learning_rate	(0.01, 0.3)	0.3	0.29928590588358195
lambda	(0, 10)	1	8.996140846429455
alpha	(0, 1)	0	0.36028138060830606
min_child_weight	(1, 10)	1	1.8952111330699568

After training the model using default and optimized parameters for XGBoostClassifier, both models will be tested using the testing feature map extracted from EfficientNetB3. Both models will be compared as shown in Table 2, while the confusion matrix of both models can be seen in Figure 4.

Table 2. Performance comparison between default and optimized XGBoost

Model Name	Accuracy	Precision		Recall		F1-Score	
		Macro	Weighted	Macro	Weighted	Macro	Weighted
XGBoost	98.42	98.27	98.44	98.36	98.43	98.31	98.43
XGBoost + GA	98.95	98.83	98.96	98.97	98.95	98.90	98.95

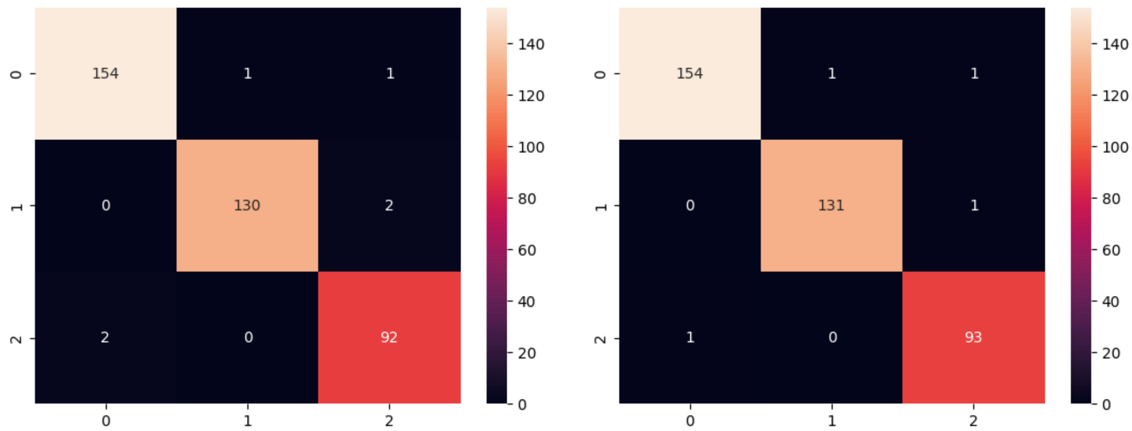

Figure 4. Confusion Matrix of XGBoost (Left) and XGBoost+GA (Right)

Based on the comparison shown in Table 2 and the confusion matrix in Figure 4, the XGBoost model combined with Genetic Algorithm (GA) receives a slight performance improvement when compared to the Standard XGBoost model on all evaluation metrics. The accuracy of XGBoost improves from 98.42% to 98.95% with GA, indicating that the optimization process improves the model's ability to correctly classify samples. Similarly, precision also improves, with macro precision increasing from 98.27% to 98.83% and weighted precision increasing from 98.44% to 98.96%, reflecting better consistency in predicting positive cases across all classes. Recall, which measures the model's sensitivity, also benefits from GA integration, with macro recall increasing from 98.36% to 98.97% and weighted recall rising from 98.43% to 98.95%. This demonstrates an improved ability to detect true instances, particularly for minority classes. Furthermore, the F1-score, which balances precision and recall, shows improvement, with the macro F1-score rising from 98.31% to 98.90% and the weighted F1-score increasing from 98.43% to 98.95%.

The confusion matrix provided additional insights into the improvements. For Class 0, the number of correctly classified samples remains at 154, but there are fewer misclassifications. Class 1 sees an increase in correctly classified samples, from 130 to 131, with fewer errors. Similarly, Class 2 improves from 92 to 93 correctly classified instances, again with reduced misclassifications. These results demonstrate that the integration of the Genetic Algorithm successfully optimizes the model, leading to enhanced classification outcomes. Overall, the combination of XGBoost with Genetic Algorithm achieves better performance increase, as evidenced by the improvements in all metrics and the reduction in classification errors.

4.2. Discussion

From the results before, the model will be compared with past research. Table 3 shows the comparison between past research and our proposed model.

Table 3. Comparison between past research

Author	Method	Result
Al Haque et al.	CNN	95.61%
Mostafa et al.	ResNet-101	97.74%
Jain et al.	CNN+LSTM	95.90%
Proposed Method	**EfficientNetB3+XGBoost+GA**	**98.95%**

The model showed exceptional accuracy of 98.95%, outperforming traditional Deep Learning and Deep Transfer learning methods; therefore, it can be said that the model effectively improves the performance of past research.

5. Conclusion

Guava, an evergreen plant from the Myrtaceae family, is highly valued for its adaptability and exceptional nutritional qualities. However, recent declines in guava production caused by fruit diseases have underscored the need for an effective classification model to identify and manage these diseases. In this study, the proposed model achieved an impressive accuracy of 98.95%, surpassing previous research results. Future improvements could involve using a more comprehensive guava fruit dataset or combining various deep learning and machine learning algorithms to enhance the model's performance further.

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