



Comparative Analysis of Deep Convolutional Neural Networks for Classification of Fungal Diseases in Guava Leaves

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ABSTRACT

Guava, a nutrient-rich fruit, is severely affected by various fungal leaf diseases, which hinder fruit development, optimal growth, and bud formation. Among the 177 pathogens known to damage guava leaves, 167 are fungal. However, Effective classification of these diseases is crucial to minimizing economic losses in the food industry. This study focuses on classifying six common fungal diseases in guava leaves, including Cercospora leaf spot, Anthracnose, Canker, Rust, Mummification, and Dot. Various Deep Learning models have been used for disease classification but suffer from overfitting and low accuracy on this dataset. To address these limitations, this study evaluates finetuned CNN architectures: EfficientNetB2, EfficientNetB4, and DenseNet201 using both existing and real-world datasets and achieved an accuracy 95.67%, 98.67%, and 98.95% respectively. To assess the effectiveness of finetuned models in classifying fungal diseases in Guava Leaves and improving the agricultural disease management, they are evaluated based on accuracy, recall, precision, and F1 score.



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1. Introduction

Agriculture is a fundamental part that significantly influences the global economy (Khatrri et al., 2024). Horticultural crops, including fruits, vegetables, tuber, roots and medicinal plants, are extensively cultivated in Pakistan due to climatic conditions and diverse topographic. Guava or Psidium guajava is an essential fruit crop in Pakistan, making it the 4th largest global producer, with the production of 1,784,300 metric tons in 2018 (Almadhor et al., 2021; Mostafa et al., 2021). It is cultivated primarily in Punjab (Lahore, Kasur, Sangla Hills), Sindh (Larkana, Hyderabad), and Khyber Pakhtunkhwa (Kohat, Haripur, Bannu) (Khan, 2020). In 2014-15, Guava production touched 489.1 thousand tons over 65.6 thousand hectares (Khan et al., n.d.). Besides its economic importance, Guava plants leaves are highly affected by the several fungal diseases that impact fruit crops and their quality. According to Food Agricultural Organization (FAO), 20-40 percent of food production is lost annually due to plant pests and various diseases (JUNAID & GOKCE, 2024).

Through worldwide analysis, about 19,000 species are known to fungal diseases in plants. Estimated 1/3 of food crops are being ruined annually due to these fungal diseases. In Guava plants leaves, common fungal diseases include Anthracnose, Pseudocercospora Dot, leaf spot, Canker, Mummification, Rust, Guava Wilt (*Fusarium oxysporum*), root rot, mildew, fruit canker, Stem canker gall, and Leaf blight, which reduce both market value and fruit quality (Almadhor et al., 2021; Jain et al., 2019). The dispersion of fungal pathogens is influenced by various environmental factors such as temperature, humidity, and rainfall. Early classification of these fungal diseases is crucial for preventing extensive agricultural losses (Yiallouris et al., 2024).

Traditional methods of diseases detection are relied on manual inspection, which is time-consuming, labor-intensive, and often inaccurate. Recent developments in artificial intelligence (AI), particularly deep learning, have revolutionized plant disease detection and classification (Yao et al., 2023). Convolutional Neural Networks (CNNs) have shown promising results to detect and classify plant and fruit disease image (Shafik et al., 2024). Deep learning is used for image classification and identification. It achieves high accuracy in extracting deep features from images. It has been used in various fields such as Facial Feature Recognition, Object Recognition, and Image Segmentation (Sarwar et al., 2024). Transfer Learning (TL) technique, enables solutions with limited datasets by applying pretrained models that are already trained on similar problems (Sarwar et al., 2025). TL commonly employs two strategies: 'finetuning' and 'deep feature extraction'. In 'feature extraction', pretrained models' learned features train a new output layer. 'Fine-tuning' involves retraining the model with new images and updating the top layer's weights accordingly (Unnisa et al., 2025). The number of classes in the top layer aligns with those in the new dataset (Ullah et al., 2022). Several studies have attempted to classify guava leaf diseases using deep learning models such as DenseNet (169,121) for detection of guava leaves diseases (Canker, Dot, Mummification, Rust) dataset obtain from Kaggle (Thangaraj et al., 2023), EfficientNet (B3) for classification of guava leaves diseases (Canker, Dot, Mummification, Rust) (Doutoum et al., 2023), SqueezeNet, and AlexNet (Gaikwad et al., 2022), for recognize fungal leaves diseases (psedocercospora leaf spot, Rust, Insect eaten leaf). However, these deep models have shown suboptimal accuracy and overfitting in classification and also highlighting the requirements for more robust and accurate architectures.

This study evaluates the performance of various fine-tuned models, DenseNet201, EfficientNetB4, and EfficientNetB2 for the classification of most common fungal diseases in guava leaves. This research uses Kaggle dataset and Realtime data samples collected from Faisalabad guava form, covering the six diseased classes Anthracnose, Cercospora leaf spot and Canker, Dot, Mummification, and Rust along with healthy leaves. These architectures are evaluated based on precision, recall, and F1-score. Some of these architectures are intended to detect and classify the several fungal diseases with higher accuracy and robustness. Previous studies, mainly focused on detecting and classifying these diseases individually by using various deep learning architectures such as EfficientNet (B3), DenseNet (169,121), squeezenet, and Alexnet but show overfitting on this dataset.

For the development of automated fungal diseases classification system for the former, this study evaluates the different CNN architectures on real-time data samples and existing dataset.

2. Materials and Methods

This study using different finetuned deep learning architectures: DenseNet201, EfficientNetB2, and EfficientNetB4 to classify the fungal diseases in guava leaves. **Figure 1** illustrates the framework of this study.

- Collecting guava leaf datasets from real-time and Kaggle.
- Preprocessing the dataset to enhance model performance.
- Splitting the dataset into training, validation, and testing sets.
- Training pretrained models on the guava leaf training dataset and validating them with the validation set.
- Evaluating model performance using the test dataset.

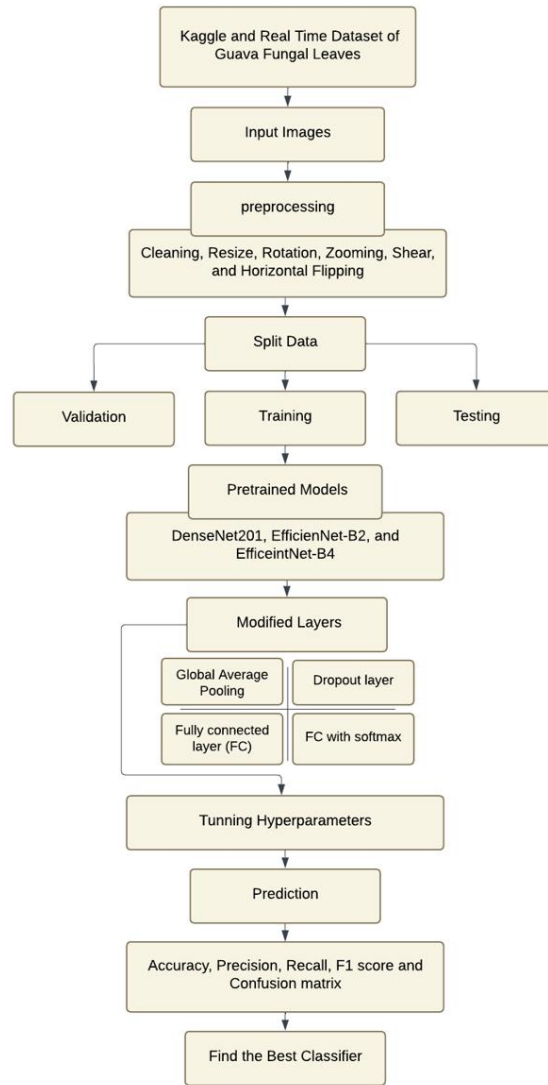


Figure 1. Workflow of Purpose System

A. Dataset Collection

The guava leaf diseased dataset that is used in this study is divided into seven categories: Anthracnose, Cercospora leaf spot, Dot, Mummification, Canker, Rust, and Healthy, as shown in **Figure 2**. The dataset comprises a total of 1,961 samples, which are split into 60% for training, 20% for testing, and 20% for validation sets. Specifically, 1,059 images are used for training, 459 for testing, and 443 for validation. The dataset includes 194 images of Anthracnose, 275 of Mummification, 178 of Dot, 276 of Canker, 279 of Rust, and 605 of Healthy leaves, which were gathered from Kaggle, along with 203 images of Pseudocercospora leaf spot is also called cercospora Leaf Spot collected from guava farms in Faisalabad, Pakistan. The number of each image is detailed in **Table 1**.

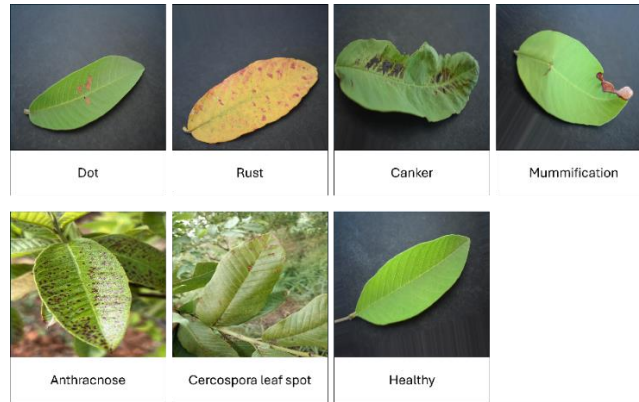


Figure 2. Guava Leaf Diseases

Table 1. Fungal Leaf Disease Dataset

Guava leaf Disease Dataset				
Classes	Training Samples	Testing Samples	Validation Samples	Total Samples
Anthraco	134	32	28	194
Cercospora leaf spot	127	40	36	203
Canker	164	57	55	276
Dot	106	37	35	178
Rust	140	45	45	230
Mummification	165	55	55	275
Healthy	223	193	189	605
Total	1059	459	443	1961

B. Data Preprocessing

Data preprocessing is a crucial step in training deep CNN (Convolutional Neural Network) models (Unnisa et al., 2025). The images are resized to 224×224 and the dataset is split into training, testing, and validation sets. To enhance model performance, data augmentation is applied to increase dataset diversity and mitigate overfitting. This process generates new images by using class ‘ImageDataGenerator’ from TensorFlow to apply transformations such as rotation (45°), width shift (0.2), height shift (0.2), zoom (0.2), horizontal flipping, and nearest-fill mode, see the detail in **Table 2**. These augmentations help to improve the model’s generalizability, especially when working with a limited dataset (Tewari et al., 2024). We apply augmentation techniques to increase the number of images so that deep models can perform well on unseen data. Because through the augmentation it generates more images using original image without changing its original appearance. Through this deep model can learn more features from different transmission images.

Table 2. Summary of the Augmentation Methods Employed in the Proposed Study

Methods	Values
Rotation range	45
Width shift	0.2
Hight shift	0.2
Zoom	0.2
Horizontal flip	True
Fill mood	Nearest



Figure 3. Images Before and After Augmentation

System Requirements

A T4 GPU with 15 GB RAM was used for training, along with TensorFlow, Keras, and Scikit-learn libraries in Google Colab, coded in Python 3.11.11. The training was conducted on a system equipped with an Intel Core i7-4600U CPU operating at 2.70 GHz, a 64-bit operating system, and 8.00 GB of RAM.

C. Fine Tuning

Fine-tuning is an essential method for improving our model performance through impactful modifications. Although these modifications may appear minor but they significantly impact on the training outcomes including ‘computation time’, ‘resources requirements’, and convergence speed (Bakr et al., 2022). To optimize our model's precision, we have recognized the ideal training and finetuning parameters, as shown in **Table 3**: learning rate 0.001, 40 epochs, 32 batch size, optimizer (Adam), loss function (categorical cross-entropy), activation function (softmax), and steps per epoch (34).

Table 3. Hyperparameters used in this study for Finetuning

Hyperparameters	Values
Learning Rate	1e-3 (0.001)
Epochs	40
Batch size	32
Optimizer	Adam
Loss Function	Categorical cross-entropy
Activation Function	Softmax
Step per epoch	34

D. Classification Models

Variants of EfficientNet (EfficientNetB2, EfficientNetB4): EfficientNet, proposed by (Tan & Le, 2019), is a neural network architecture designed for improved classification performance while maintaining computational efficiency. It is especially well-known for its simplicity and computational effectiveness, applying compound coefficients to balance depth, width, and resolution. EfficientNet comes in eight variants (B0 to B7) (Ahmadzadeh Sarhangi et al., 2023). In our study, we used pretrained models EfficientNet-B2 and EfficientNet-B4 models for classifying of Fungal diseases in Guava Leaves and finetuned them for optimal performance. We used two variants of EfficientNet, EfficientNet-B2 has 9.2 million parameters, while EfficientNet-B4 has 19.5 million. Both architectures (EfficientNet-B2 and EfficientNet-B4) shared a common structure, beginning with stem, followed by ‘seven’ intermediate blocks and final layer comprising with three modules: Conv2D, Activation, and Batch Normalization. EfficientNet models are optimized to accommodate images with pixel values ranging from 0 to 255 and automatically perform intrinsic normalization (Preetha et al., 2024).

For finetuning, we used various hyperparameters including a batch size of 32, learning rate (0.001), and the ‘Adam’ optimizer. We trained these models for 40 epochs with 224×224×3 input size. EfficientNet variants were selected based on factors like, dataset size, batch size, computational resource requirements, model complexity, and network parameters. EfficientNet offers almost a

reduction of ‘eightfold’ in model size and ‘sixfold’ acceleration for inference compared to deep learning models such as ResNet, Xception, VGG, and GoogleNet (Chollet, 2017).

Fine-tuning involves adjusting the weights of selected layers in pretrained deep architectures, originally trained on ‘ImageNet datasets’, to adapt to new classification tasks (Preetha et al., 2024). In this study, we fine-tuned EfficientNet-B2 and EfficientNet-B4 by unfreezing layers from the 100th onward. As shown in **Figure 4** Additional top layers were incorporated into the base model:

- A Global Average Pooling layer to reduce spatial dimensions
- A Dense layer with (512) neurons and a ReLU activation function
- A Dropout layer with a 0.5 dropout rate to mitigate overfitting
- Final Dense layer with seven classes and a SoftMax activation function for classification.

These additional layers were incorporated into the base model to improve the classification of fungal infections in guava leaves.

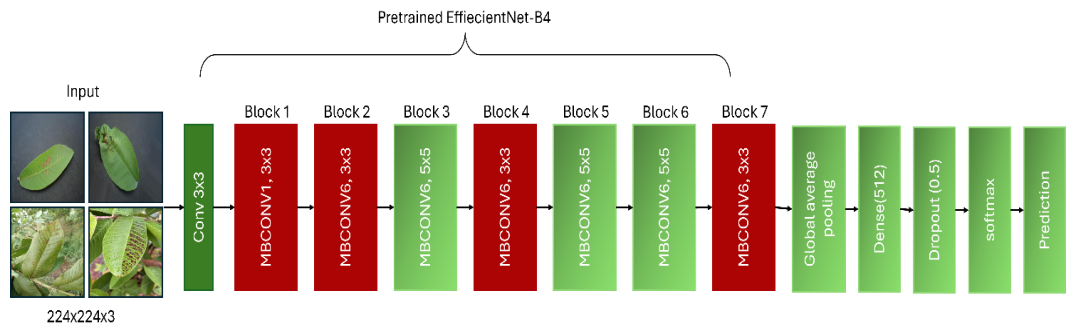


Figure 4. Architecture of Fine-Tuned EfficientNetB4

DenseNet201: DenseNet (Dense Convolutional Neural Network) offers several advantages, including enhanced feature propagation, efficient feature reuse, mitigation of vanishing gradients, and a significant reduction in parameter requirements. Due to its ability to accelerate processing with fewer feature maps, DenseNet is well-suited for image classification tasks. Each layer directly accesses gradients from the loss function and input image. DenseNet exists in four versions: DenseNet169, DenseNet121 (Huang et al., 2017), DenseNet264 and DenseNet201(Steen et al., 2018). In this work, we employed the pretrained model DenseNet201 to classify fungal diseases in guava leaves. DenseNet's architecture uses feedforward manner to exchange the information between layers $L*(L+1)/2$. Each layer connected to the preceding layers and uses feature maps to ensure that minimizing the problem of vanishing gradient and reuse the features efficiently. (Huang et al., 2017).

Main stages of classification process shown in **Figure 5**.

Data Preprocessing: Preparing the dataset and applying augmentation techniques.

Feature Extraction: to extract the relevant features by using fine-tuning technique on pretrained DenseNet201 architecture.

Classification: classify the guava leaf diseases using extracted features: Anthracnose, Mummification, Cercospora Leaf Spot, Canker, Rust, Dot, and Healthy.

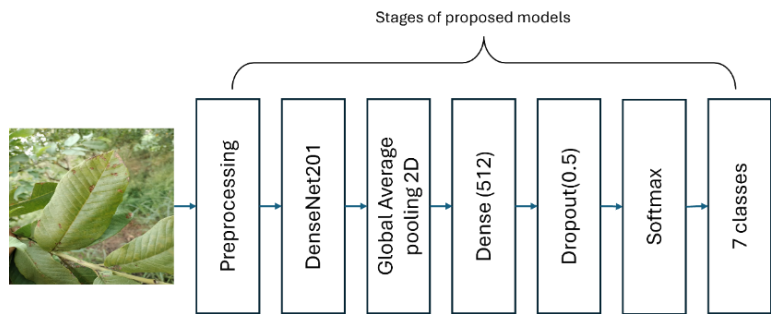


Figure 5. Finetuned DenseNet201 Classifier

DenseNet201 enhances performance by incorporating bottleneck design and pooling layers, reducing model complexity and computational requirements (Bakr et al., 2022). Each layer applies nonlinear transformations, including Convolutional layer (Conv), Batch Normalization (BN) and Rectified Linear Unit Activation (ReLU) (Steen et al., 2018).

In this study, used pretrained DenseNet201 model of TensorFlow Keras library. We use input dimensions 224×224×3 ('width', 'height', and 'RGB color channels'). We employed the ~19 million parameters to reduce the computational complexity of our model. DenseNet originally trained model on ImageNet, so remove its fully connected (top=False) layers and integrating its custom classification layers. In previous study, DenseNet169 and 121 used 25 and 23 million parameters respectively (Thangaraj et al., 2023).

New classification layers shown in **Figure 6**. These layers are:

Global Average Pooling Layer: used to reduce the parameter and computational load.

Dense Layer: 512 Enhances feature extraction by using 512 Neurons and ReLU Activation.

Dropout Layer: Prevents overfitting using effective rate 0.5.

Final Dense Layer with 7 Units and Softmax Activation to performs multi-class classification.

By adding these layers in this model, we improve the classification accuracy to classify the fungal diseases.

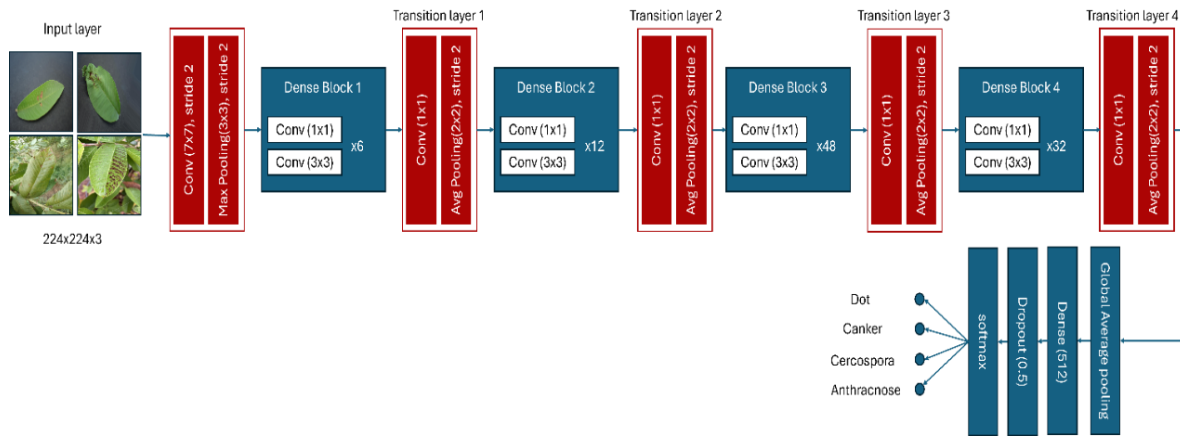


Figure 6. Finetuned Architecture of DenseNet201

3. Results

This study evaluated the effectiveness of three deep learning architectures: EfficientNetB2, EfficientNetB4, and DenseNet201 for fungal disease classification in guava plant leaves. To achieve optimal results, each model was trained for 40 epochs with a batch size of 32. Given the multiclass nature of the problem, the Adam optimizer was used with a learning rate of 0.001. A dropout layer (0.5) was incorporated to enhance model robustness and prevent overfitting. To enhance the generalizability, we apply augmentation techniques so that deep models can perform well on unseen data. In **Figure 11**, Model performance was assessed using key metrics, including accuracy, precision, recall (sensitivity), and F1-score. In this work, the performance of the classifier is evaluated by using the following metrics with formulas: The accuracy, F1 score (Doutoum et al., 2023), precision, and recall (Preetha et al., 2024) formulas are defined using False Positives (FP), False Negatives (FN), True Positives (TP), and True Negatives (TN). **Table 4**, shows the Comparative Performance of each Finetuned Architecture

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad \dots (1.1)$$

$$Precision = \frac{TP}{TP + FP} \quad \dots (1.2)$$

$$Recall = \frac{TP}{TP + FN} \quad \dots (1.3)$$

$$F1 \text{ score} = \frac{2(Precision * Recall)}{Precision + Recall} \quad \dots (1.4)$$

Table 4. Fine-Tuned Architectures Performance

Finetuned Models	Parameters (M)	Training Accuracy	Validation Accuracy	Test Accuracy	Training Loss	Validation Loss
EfficientNetB2	08	0.9658	0.9497	0.9567	0.1338	0.1976
EfficientNetB4	18	1.0000	0.9746	0.9867	9.8060e ⁻⁰⁴	0.0638
DenseNet201	19	1.0000	0.9900	0.9895	4.4127e ⁻⁰⁵	0.0804

EfficientNetB2: This study, employed EfficientNet-B2 for classifying the fungal diseases. In categorization of several diseases, this pretrained classifier demonstrate an excellent discrimination. In **Figure 7** orange learning curves represents the cross validation and blue curve to the training accuracy on different epochs. After evaluation, EfficientNet-B2 achieved 96.58%, 95.67%, and 94.97% training accuracy, test accuracy, and validation accuracy respectively. The detailed predictions of this classifier shown in

Figure 10 (a), where confusion matrix indicates true labels on y-axis and predicted labels on x-axis. EfficientNet-B2 performs well but showing some negatives false for canker class, with recall of 0.80 and precision of 1.00. Chart bar in **Figure 11 (a)** demonstrates the evaluation as metrics where blue bar for precision, green bar for recall, and red bar indicate F1-score. This classifier achieved accuracy (97%), precision (97.08%), recall (96.87%), and F1-score (96.75%).

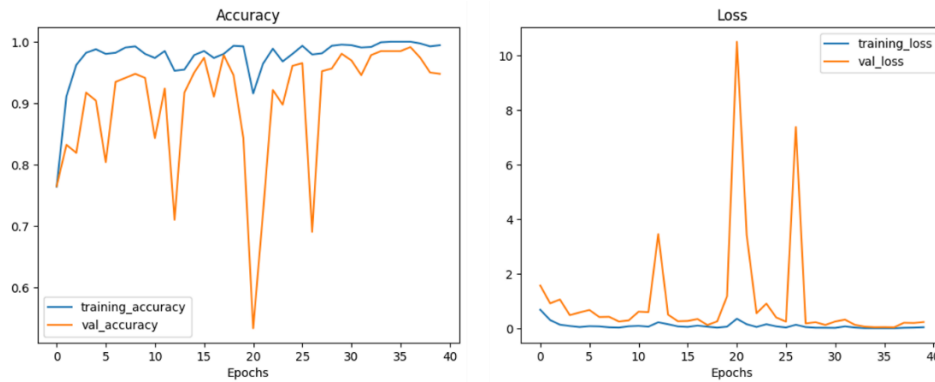


Figure 7. Training and Validation Performance of EfficientNetB2

EfficientNetB4: For the classification of fungal diseases, we used deep CNN architectures and finetuned them. On several epoch EfficientNetB4 showed significant performance as shown in **Figure 8**, it achieved '0.9498' training accuracy and validation accuracy 0.8976 with '0.1889' and 0.9870 loss respectively on five epochs. After ten epochs, accuracy gradually improved with training 0.9842 and 0.9390 validation accuracy. At fifteen epochs, validation accuracy improved as 0.9695 but training accuracy remain same. By thirty, its highest training accuracy 1.0 with 2.4194e-04 minimal loss and validation accuracy 0.9826 that represent the robustness of our model. After forty epochs, it attained the 'training accuracy' 1.00 and 'validation accuracy' 0.9847 with 0.0379 loss. Prediction performance of our model across all classes is shown in

Figure 10 (b). Highest classes of cercopora disease are correctly identified by EfficientNetB4. For this architecture metrics bar chat with precision (blue bar), F1-score (red bar) and recall (green) is plotted against all diseased classes in **Figure 11 (b)**. Classification accuracy on training data is 1.00 percent, on testing data is 98.67% and on validation dataset shows 97.46%.

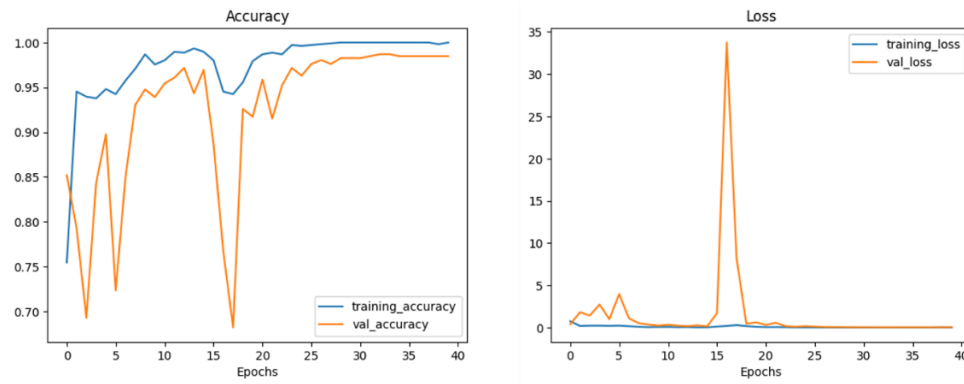


Figure 8. Training and Validation Performance of EfficientNetB4

DenseNet201: We employed trained model on ImageNet dataset for classification of fungal diseases. The performance of DenseNet201 was evaluated by validation and test accuracy. Unlike the previous employed models, DenseNet201 also achieved highest classification accuracy (1.00) on the training dataset and test accuracy (98.85%) and 99% on validation dataset. In **Figure 9** show the continuous improvement in classification performance across all classes through training and validation accuracy on each epoch. Proposed model achieved classification accuracy (0.8368) at fifth epoch with loss of (0.4791) as well as validation accuracy (0.3834) and loss of (11.1747). After tenth epoch, increased the training accuracy (0.9545) and reduced the validation loss (2.4681). At fifteen epochs, the validation loss dropped further to 0.0861, with the model reaching perfect training accuracy (1.0) and a training loss of 0.0049. It maintained the training accuracy (1.0) with training loss to 1.1115×10^{-4} , and its validation accuracy of 0.9869 with loss of 0.514 at thirty epochs. After fifteen epochs, this model showed convergence and refinement. DenseNet201 achieved final accuracy (1.00) with minimal loss ($.0116 \times 10^{-4}$) after forty epochs. Similarly, validation accuracy (0.9847) with loss (0.0533) that indicating the minimal overfitting. Confusion matrix for this model in **Figure 10 (c)** indicates the predictions for all classes with 1.00 percent classification accuracy. In **Figure 11 (c)** bar chart for our proposed model is plotted with precision, recall and F1-score with 1.0 prediction score against all fungal diseased classes.

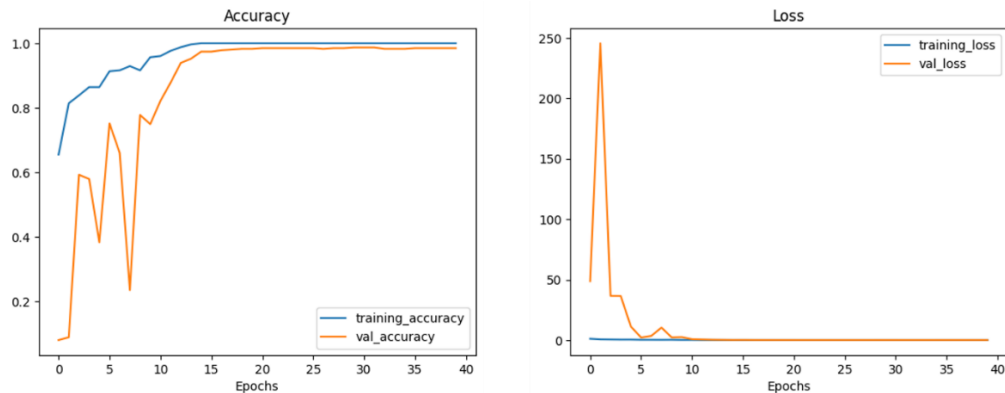


Figure 9. Training and Validation Performance of DenseNet201

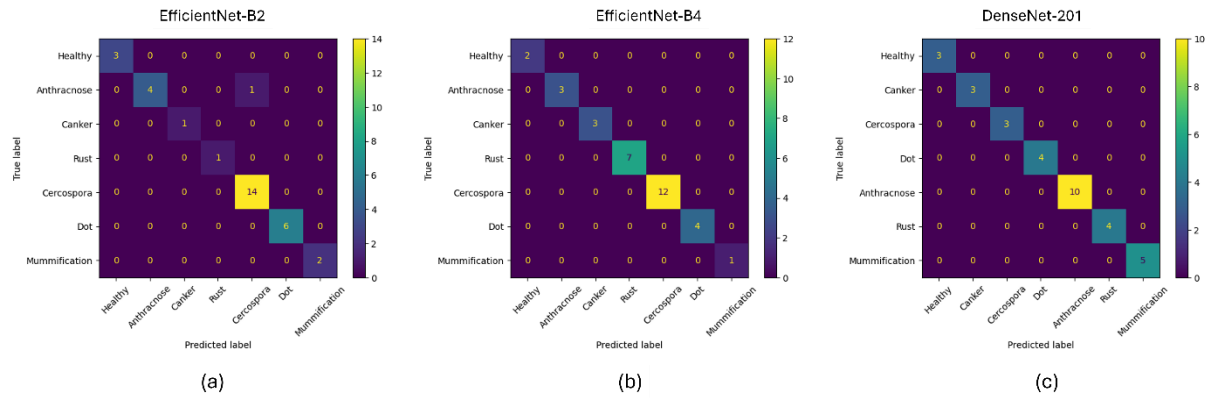


Figure 10. Comparative Performance of Proposed Architectures in the Confusion Matrix

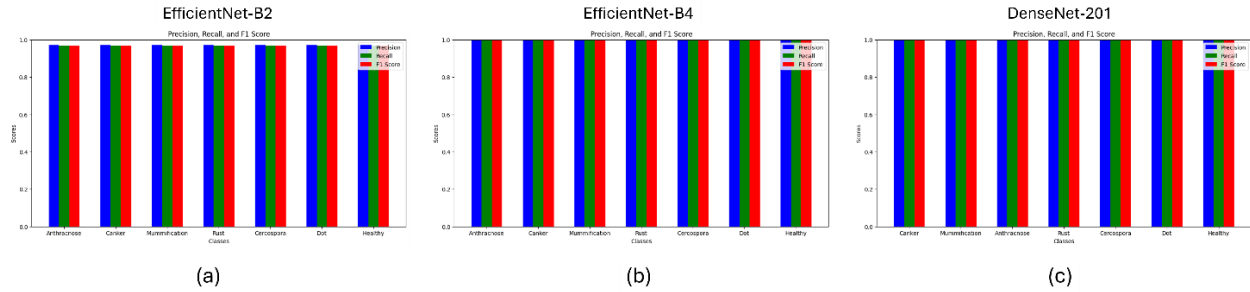


Figure 11. Proposed finetuned models' performance for each class

4. Discussion

These proposed architectures “EfficientNetB2, EfficientNetB4, and DenseNet201” used in this study. Evaluation of these classifiers based on accuracy, precision, recall or sensitivity and F1-Score for fungal diseases in guava leaves. For this evaluation, dataset is collected from Kaggle and real world include Cercospora leaf spot, Anthracnose, Mummification, Canker, Rust, Dot, and Healthy. In **Table 3**, outlined all the hyperparameters that is used for finetuned our deep models, including 0.001 learning rate, 32 batch size and Adam optimizer to optimize the models’ classification performance. The DenseNet201 finetuned model performed well as compared to other deep models by achieving the highest accuracy in training, validation and testing. This proposed model achieved 98.95 percent testing accuracy with 4.4127e-05 training loss as compared to EfficientNetB4 with 98.67 percent testing accuracy and minimal 9.8060e-04 training loss. On the other hand, EfficientNetB2 achieved 95.67 percent test accuracy to classify these diseases. While its overall classification accuracy was 97%, it struggled with the Canker class, achieving a recall of only 80%. Compared to the other models, EfficientNetB2 demonstrated lower performance, with a precision of 97.08%, a recall of 96.87%, and an F1-score of 96.74%. However, all the proposed models outperformed previously used models, achieving the highest accuracy for disease detection and classification, as shown in **Table 5**. However, among all models, DenseNet201 performed the best, achieving high accuracy, minimizing overfitting, and correctly classifying each disease. Various hyperparameters were utilized to enhance the suitability of proposed models for practical applications. Overfitting was mitigated using dropout layers, while model complexity was managed through Global Average Pooling and an optimized batch size. As a result, these models accurately classify fungal diseases, “Anthracnose, Cercospora leaf spot, Mummification, Canker, Rust, and Dot”. As shown in **Figure 12**, DenseNet201 achieves the highest test accuracy of 98.95%, which is greater than other models and performs well for prediction of each class and gets 1.00 accuracy. We used pretrained models from the Keras/TensorFlow library and finetuned them. For other models EfficientNetB2 and EfficientNetB4, we attain test accuracies of 95.67% and 98.67% respectively. Predictions of EfficientNetB4's is 1.00 percent and 97 percent achieved by EfficientNetB2 for each class.

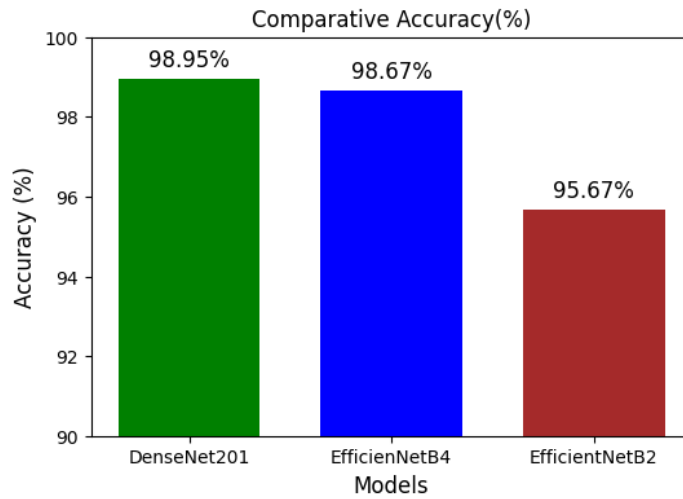


Figure 12. Comparative classification Accuracy of our proposed Models

Table 5. Benchmark Analysis of Guava Disease Detection

Author	Plants	Diseases						Algorithms	Accuracy
		Canker	Dot	Mummifi- cation	Rust	Cercopora leaf spot	Anthracnos e		
(Doutoum et al., 2023)	Guava leaves	✓	✓	✓	✓	✗	✗	EfficientNetB3, InceptionV3 Vgg16 and Resnet50	94.93%
(Thangaraj et al., 2023)	Guava leaf	✓	✓	✓	✓	✗	✗	DenseNet121, DenseNet169, InceptionV3, and Xception	96.12%
(Mostafa et al., 2021)	Guava Fruit	✓	✓	✓	✓	✗	✗	ResNet101 AlexNet, SqueezeNet, GoogLeNet, ResNet50,	97.74%
(Gaikwad, 2021)	Guava leaf	✗	✗	✗	✓	✓	✗	Alexnet, Squeeznet	75.9%
(Gaikwad et al., 2022)	Apple, Custard apple, Guava	✗	✗	✗	✓	✓	✗	Alexnet, Squeeznet	86.8% 86.6%
(Tewari et al., 2024)	Guava	✗	✗	✗	✓	✗	✗	DenseNet169	99.62%

(Perumal et al., 2021)	Guava leaves	✗	✗	✗	✗	✗	✓	SVM	98.17 %
(Rashid et al., 2022)	Guava leaf	✗	✗	✗	✗	✗	✓	MobilenetV2 & U-Net and GLSM for segmentation , YOLOv5 for detection	92.41%
Our Methodology	Guava leaves	✓	✓	✓	✓	✓	✓	EfficientNetB2 EfficientNetB4 DenseNet201	98.95%

5. Conclusion

In conclusion, our study demonstrates the effectiveness of proposed finetuned architectures used for classifying the fungal diseases in guava plant leaves with 98.67 percent classification accuracy by finetuned EfficientNetB4 and 98.95 percent accuracy by DenseNet201. These architectures demonstrate the remarkable performance for classification of guava leave diseases. Various hyperparameters include batch size, dropout layers and Global Average pooling to reduce the overfitting and model complexity as well as to enhance the accuracy. These proposed models provide advanced classification techniques that decrease the manual detection and help the farmers in timely diseases detection which reduce the economic losses as well as chemical treatment cost. For further, we can improve these finetuned models for detection and classification of viral and bacterial infection in guava fruit.

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