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AI-Driven Diagnosis of Apple Rust and Scab Using VGG16 Framework

Research Article

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Tayyab Nawaz
School of Computer Science, National College of Business Administration and Economics, Lahore 54000, Pakistan
E-mail: tayyab.nawaz22@yahoo.com
ORCID ID: https://orcid.org/0009-0007-1809-215X

Naila Sammar Naz
School of Computer Science, National College of Business Administration and Economics, Lahore 54000, Pakistan
E-mail: nailanaz@ncbae.edu.pk

Muhammad Saleem
School of Computer Science, National College of Business Administration and Economics, Lahore 54000, Pakistan
E-mail: msaleem@ncbae.edu.pk

Muhammad Mazhar Ali*
School of Computer Science, National College of Business Administration and Economics, Lahore 54000, Pakistan
E-mail: chmazharali@outlook.com
*Corresponding Author

Hafiz Abdul Wahid Khalid
School of Computer Science, National College of Business Administration and Economics, Lahore 54000, Pakistan
E-mail: muhammadwahid4800@gmail.com

Fahad Ahmed
School of Computer Science, National College of Business Administration and Economics, Lahore 54000, Pakistan
E-mail: fahad.ahmed@ncbae.edu.pk

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Abstract: Accurate detection and classification of plant diseases are essential for enabling timely intervention, reducing crop losses, and improving agricultural productivity. Apple scab and apple rust are among the most common diseases affecting apple production worldwide. This study proposes a transfer learning approach based on the Visual Geometry Group 16 (VGG16) convolutional neural network for classifying apple leaf images into three categories: healthy, apple scab, and apple rust. Apple scab is caused by the fungus Venturia inaequalis, whereas apple rust is primarily associated with Gymnosporangium juniperi-virginianae. The proposed method applies image preprocessing and a pretrained VGG16 architecture to extract robust and discriminative visual features from apple leaf images. The dataset was obtained from Kaggle and divided into training and testing sets for model development and performance evaluation. Experimental results show that the proposed model achieved a testing accuracy of 97.28%, corresponding to a misclassification rate of 2.72%. These findings demonstrate that the VGG16-based transfer learning model is effective for automated multiclass classification of apple leaf diseases and has potential for supporting practical plant disease detection applications.

Keywords: Apple leaf disease; Deep learning; Disease classification; Transfer learning; VGG16; Plant pathology.

1. Introduction

In addition to the leaf diseases of apple, other diseases are also important issues in apple production throughout the world. Apple scab and cedar apple rust are two of the most widespread and economically harmful fungal diseases which can substantially reduce fruit yield and quality. Timely diagnosis and subsequent treatment, disease management and economic damage are minimized when these diseases are detected early. The traditional approach to disease diagnosis has been to inspect the plants manually by experienced growers and plant pathologists, or by expert systems. However, these methods are time-consuming, labor-intensive and may not be able to be generalized over a different environmental conditions, requiring high knowledge of experts to make a correct diagnosis [1]. In commercial orchards, severe losses caused by spreading apple scab (VI) and cedar apple rust (GJV) can be experienced if control measures are not taken soon [2]. So, the development of automatic and accurate disease detection systems is a significant research field. In recent years, deep learning (DL) has made significant strides with the emergence of convolutional neural networks (CNNs) which have substantially enhanced the precision and effectiveness of plant disease diagnosis [3]. Visual Geometry Group (VGG) 16 is one of the CNN architectures developed by the Visual Geometry Group at the University of Oxford, which has been proven to perform best in image classification and plant disease recognition. It has a 16-layer deep architecture, which makes it excellent to extract hierarchical image features ranging from low level features like edges and textures to high level features representative of disease-specific features, useful for recognizing apple leaf diseases [4]. Transfer learning has also proven to be very helpful in fine-tuning the pre-trained VGG16 network with the relatively small datasets of apple leaf images for healthy and diseased condition, thus reducing the need for large annotated datasets while retaining high classification accuracy [5]. This is especially useful for agricultural applications where labelled datasets are often scarce.

The disease diagnosis process in VGG16 model consists of several steps as pre-processing of image, feature extraction by convolutional layers, fully connected layers for classification [6]. The network gradually learns more and more complex patterns that are relevant to the diseases from apple leaf images in the feature extraction process [7]. During training, data augmentation techniques like image rotation, flipping, scaling and color jittering are often used to further strengthen the robustness and generalization of the model [8]. Techniques like these make the model highly effective at different lighting conditions, different orientations of leaves, and levels of disease. Moreover, the attention mechanisms have been integrated into the models with VGG16 to highlight the affected areas of leaf images, which leads to a more accurate disease classification and improves the interpretability of the model for plant pathologists and orchard managers [9,10].

By deploying VGG16-based disease diagnosis systems on mobile and edge devices, the ability to detect diseases in real-time, in-field, gives farmers and agronomists the opportunity to monitor their orchard health and provide timely disease management strategies. These are intelligent diagnostic systems that can help with precision agriculture, by enabling precise treatment application and minimize pesticide use. In addition, the combination of VGG16 with new technologies like hyperspectral imaging, the Internet of Things (IoT) sensors, and smart agricultural monitoring systems is expected to further enhance the surveillance and management of diseases in orchards for future precision farming applications [11].

2. Related Work

DL techniques have been more popular in recent years as a result of the availability of datasets and the notable advancements in Graphical Processing Unit (GPU) memory and processing capability. Agronomists often carry out this duty by visually observing sick plants; therefore, an automated plant disease detection system would be a useful tool for decision support and help. As a result, a lot of research over the last ten years has concentrated on using DL techniques for the identification of plant diseases.

Ait Nasser and Adnane [12] conducted a study comparing the performance of DL techniques. CNN techniques were used to classify apple leaf images for DL. 3642 pictures of apple leaves are included in this, including ones that show rusty, healthy, and grab leaves, as well as ones that read, "Agriculture is one of the most." We divided the images into important industries within a single country since training and testing groups are essential to the development of a CNN-based model, ResNet34, of raw materials for other industries. The training of the prediction system. Compared to previous studies that required the food, textile, and chemical sectors to train the model, starting with the industry, and so on, our usage of agricultural goods may be different. Beginning with an enormous amount of data. However, farmers still find it challenging to recognize plant diseases, which requires training time and training savings. With plants, we have a 93.765% accuracy record in predicting the likelihood of plant diseases.

Tian, Yunong Li, and En [13] demonstrated how to employ Cycle-GAN to construct realistic anthracnose and ring rot lesions on healthy apple surfaces by capturing the visual features of both healthy and diseased apples. Comparing the diagnostic performance to conventional image augmentation methods, the artificial diseased apple images generated by Cycle-GAN were then added to the training dataset. Multi-scale Dense Inception-V4 and Multi-scale Dense Inception-ResNet-V2 are two more sophisticated models that were created using DenseNet and multi-scale connection techniques. These models made it possible for the classification neural networks to effectively reuse low-level visual characteristics. With accuracy rates of 94.31% and 94.74%, respectively, both models were able to accurately classify 11 distinct image categories, surpassing the DenseNet-121 network and establishing a new standard in the sector.

P. Bansal, R. Kumar, and S. Kumar [14] provide an ensemble model that combines the DenseNet121, EfficientNetB7, and EfficientNet Noisy Student pre-trained architectures. Based on their images, this model aims to categorize apple tree leaves into four groups: healthy, apple scab, apple cedar rust, and various diseases. Several iamge augmentation approaches were used to improve the dataset and the model's performance. Consequently, the suggested ensemble model demonstrated its efficacy in correctly diagnosing apple leaf conditions with a validation accuracy of 96.25%.

T. Sulistyowati [3]. The classification of apple leaf disease by the author. Apple leaf disease data from Plant Pathology-2020, a secondary data set on Kaggle that includes images of specific apple diseases, was used in this experiment. There are 1821 images of apple leaf disease overall. Two experimental situations were conducted to confirm the efficacy of the suggested model: Initially, the VGG16. In order to get the best results, the technique was immediately used for modeling without taking class imbalance into account. To increase the number of balanced datasets, it first oversampled SMOTE and then reduced the number of layers and kernels in each layer. The findings demonstrated that each method's accuracy results were obtained using the confusion matrix, with VGG 16 scoring 85.16% and VGG 16 with SMOTE scoring 92.94%. According to the study's findings, SMOTE increases the precision of apple leaf disease detection.

Table 1. Observations in the literature review

Ref.	Model Used	Accuracy (%)	Dataset Type	Key Observations
[3]	VGG16	92.42	Plant Pathology-2020 (Kaggle), 1,821 Images	Baseline experiment without addressing class imbalance. Lower accuracy due to imbalanced dataset
[12]	CNN	93.73	Apple Leaf Images (3,642 images)	CNN-based classification of apple leaf diseases. Reduced training time while maintaining high accuracy. Limited details on class distribution.
[13]	Multi-scale Dense Inception-V4	94.31	Apple Disease Image Dataset	Cycle-GAN generated synthetic diseased images to augment data. Improved performance compared to traditional augmentation methods.
[14]	Ensemble Model	96.25	Apple Leaf Images with Data Augmentation	Ensemble learning significantly improved classification performance. Increased computational complexity
[15]	UNet + VGG Backbone	96.41	Apple Leaf Dataset (5,382 samples)	Effective in identifying disease-affected regions. Used for disease severity estimation.

Liu, Bo YuanFan, and Ke Jun [15]. The 5,382 samples in the dataset were randomly divided into four subsets: 74% (4,004 samples) for model training, 8% (444 samples) for testing, 9% (494 samples) for validation, and an extra 8% (440 samples) for overall testing. To prepare the data, deep learning techniques with distinct backbones were first used to isolate Apple leaves from their complex backgrounds. Following that, the segmented leaves were inspected to identify the disease-affected areas. In terms of leaf segmentation, the PSPNet with a MobileNetV2 backbone fared better than the other models, achieving precision, recall, and MIoU scores of 99.15%, 99.26%, and 98.42%, respectively. For disease-area prediction, the UNet model with a VGG backbone performed better than the others, with a precision of 95.84%, recall of 95.54%, and MIoU of 92.05%. To determine the severity of the disease, the ratio of the affected area to the total leaf area was calculated the average classification accuracy was 96.41%.

2.1. Limitations of the Literature Review

Although previous studies have reported promising results in apple leaf disease classification, several methodological and practical limitations remain. These limitations mainly concern model complexity, dependence on augmented data, and the need for a simpler yet reliable classification framework. The main limitations identified in the existing literature are summarized as follows:

1. Advanced deep learning architectures, such as ResNet34, Dense Inception-ResNet-V2, ensemble models, and U-Net-based frameworks, have been employed in previous studies to achieve high classification performance. However, these architectures often involve greater model complexity, higher computational costs, and increased processing requirements [12]–[15].
2. To address class imbalance and improve classification accuracy, several studies rely on data augmentation and oversampling techniques, such as the Synthetic Minority Oversampling Technique (SMOTE). This indicates a considerable dependence on artificially supplemented datasets to achieve robust classification performance [3], [13].
3. Although previous studies have demonstrated encouraging classification results, there remains an opportunity to improve disease detection accuracy using a straightforward and computationally efficient transfer learning approach while maintaining reliable multiclass classification performance for healthy, rust, and scab apple leaf images [3], [12]–[15].

2.2. Contributions of the Proposed Model

To address the limitations identified in previous studies, this research develops a practical transfer learning framework for automated apple leaf disease classification. The main contributions of the proposed model are summarized as follows:

1. This study proposes a VGG16-based transfer learning model for the multiclass classification of apple leaf images into three categories: rust, scab, and healthy leaves.
2. The proposed framework integrates image preprocessing with a pretrained VGG16 network to extract discriminative visual features for accurate apple leaf disease classification.
3. The experimental results demonstrate that the proposed model achieves an accuracy of 97.28%, with a misclassification rate of 2.72%. The model also outperforms the previously published methods considered in this study, demonstrating its effectiveness for automated apple leaf disease identification.

3. Methodology

The general architecture of the suggested VGG16-based apple leaf disease classification system, which was put into practice using google colab and the tensorflow deep learning library, is shown in figure 2. the 516 healthy, 622 rust, and 592 scab leaf photos in the picture collection were gathered via kaggle. preprocessing involved resizing each image to 224 × 224 pixels, normalizing the pixel values by scaling them to the range [0,1], and labeling each image based on the disease class [16-17]. the dataset was split into 20% testing and 80% training subsets at random. for transfer learning, a pretrained vgg16 model with imagenet weights was used; the convolutional base was frozen, and the final classification layers were adjusted for the three class classification work.

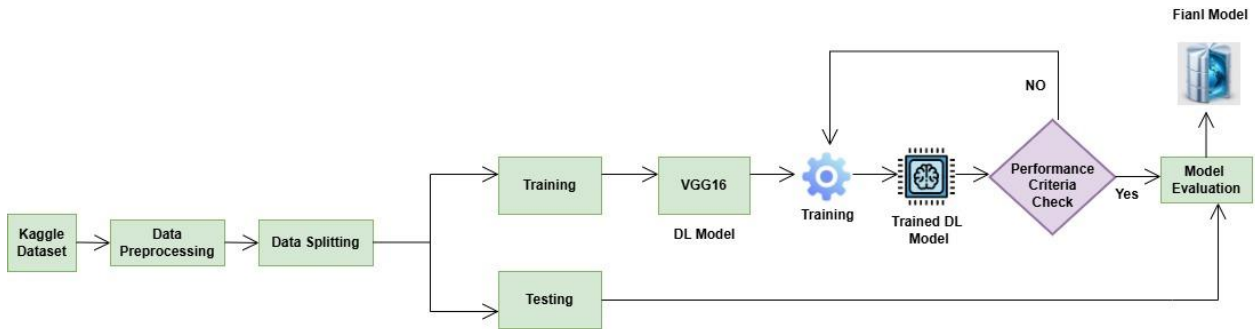

Figure 1. Architecture of the proposed model

3.1. Proposed VGG16 Model

The DL architectures in the VGG series was the VGG16. Figure 3 shows the VGG16 architecture. Its 16 layers were borrowed from the University of Oxford and combine 3 x 3 convolutional filters with carefully positioned pooling layers. 224 × 224 RGB images can be handled by the input layer of the VGG16. After using a 3 x 3 kernel for each of its 13 convolutional layers, ReLU activation functions are used. Five max-pooling layers systematically lower spatial dimensions while maintaining critical information [18]. This design substitutes feature extraction for image analysis. Its hierarchical feature learning is the key to its adaptability. In addition to picture classification, VGG16 excels at tasks like content-based image retrieval and object location. Three fully interconnected layers are used for classification. In the first two levels, 4096 channels have ReLU activations. The last layer creates an output vector with 1000 dimensions, which corresponds to ImageNet's 1000 classes, and produces a softmax activation for class probabilities. Dropout regularization was necessary after the first two fully linked layers in order to avoid over-fitting. This randomization increases the network's resistance to real-world input by avoiding an over-reliance on certain neurons. As a result, VGG16 is an extremely powerful and sophisticated tool for a variety of applications. We can see the strength of deep neural networks because of its simplicity [19].

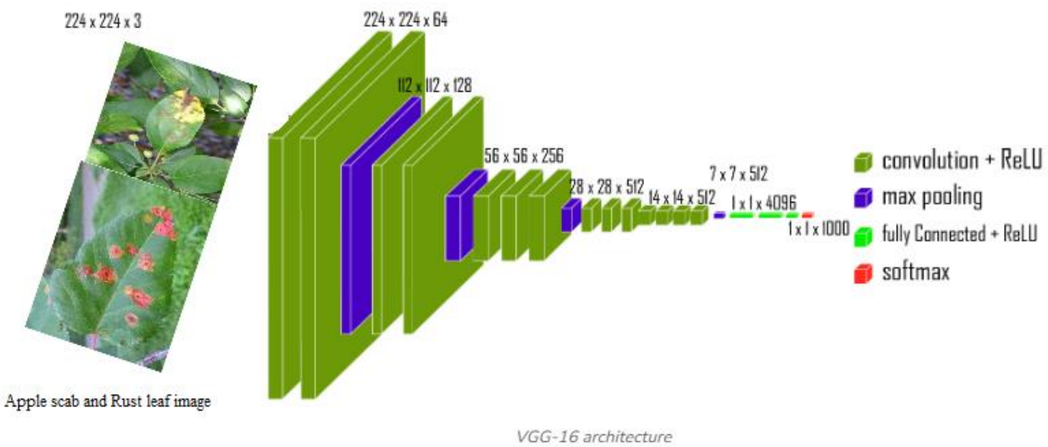

Figure 2. Modified VGG 16 architecture for the proposed model

4. Experiments

The proposed paradigm was put into practice for analysis and simulation using Google Colab, a cloud-based platform that enables Python code execution in a group setting. The confusion matrix served as the basis for a number of performance criteria that were used to evaluate the model's efficacy. Analyzing the model's accuracy in detecting apple leaf diseases requires knowledge of the assessment metrics, which are expressed by particular equations. Together, these measures assess the model's ability to accurately categorize cases, minimize mistakes, and preserve a balance between true positive and true negative predictions, making it a dependable resource for plant pathologists. In order to ensure the model's efficacy in precision agriculture or digital plant pathology contexts, they jointly assess how well the model classifies events, reduces misclassifications, and balances true positive (TP) and true negative (TN) predictions, both positive and negative

4.1. Dataset and Preprocessing

A dataset of 1730 images from the Kaggle platform was used in this investigation. Based on predetermined leaf Diseases conditions, the dataset was divided into three different classes healthy (516), Rust (622), Scab (592).

Figure 3. Sample images of apple leaf

In order to ensure a fair yet varied distribution for model training and evaluation, these categories represent several stages of the situation under research. The goal of the dataset selection process was to enable the building of a robust DL approach and model VGG16 by offering a thorough representation of the target classification problem [20].

4.2. Evaluation Metrics

Evaluation metrics to measure the performance of the proposed method are outlined in the given equations 1-6.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \times 100 \tag{1}$$

$$\text{Misclassification Rate } = \frac{FP+FN}{TP+TN+FP+FN} \times 100 \tag{2}$$

$$\text{Precision } = \frac{TP}{TP+FP} \times 100 \tag{3}$$

$$\text{Sensitivity } = \frac{TP}{TP+FN} \times 100 \tag{4}$$

$$\text{Specificity } = \frac{TN}{TN+FP} \times 100 \tag{5}$$

$$\text{F1 Score } = 2 \times \frac{\text{Precision}\times\text{Sensitivity}}{\text{Precision}+\text{Sensitiovity}} \times 100 \tag{6}$$

1. Results and Discussion

True positive, false positive, false negative, and true negative are represented by the abbreviations TP, FP, FN, and TN, respectively. True positive, false positive, false negative, and true negative are represented by the letters TP, FP, FN, and TN in this context, respectively. Figure 4 shows the training and testing progress plot. It shows the development of training loss versus testing loss and the development of training accuracy versus testing accuracy. Figure 4 shows the training and testing progress plot. It shows the development of training loss versus testing loss and the development of training accuracy versus testing accuracy.

The proposed VGG16 model is used for multiclass classification of healthy, rust and scab apple leaf images and the testing confusion matrix is shown in Figure X. This model succeeded in correctly identifying 120 healthy, 124 rust and 114 scab samples, and only made 10 misidentification errors out of 368 test samples. The classification errors were mainly in the healthy class misclassification, in which six healthy leaves were misclassified as scab and three leaves that were scab were misclassified as healthy. Only one sample of rust was misclassified as healthy. There was no confusion among the rust and scab classes, which suggests a good learning of the discriminative features of rust disease in the model.

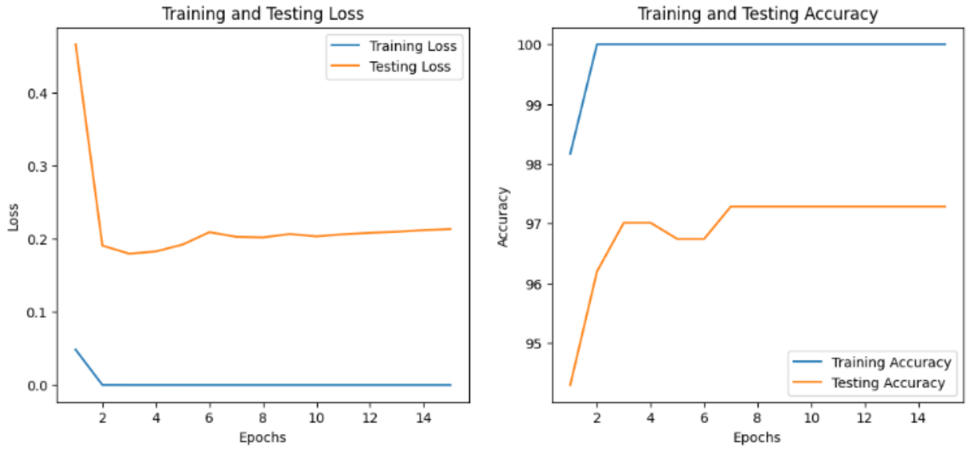

Figure 4. Training and Testing Evolution Plot

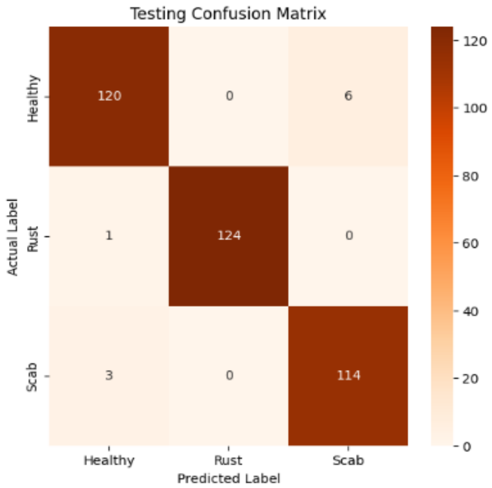

Figure 5. Testing confusion matrix of the VGG16 model

The overall model accuracy of the proposed model was 97.28%, accuracy precision was 97.26%, accuracy sensitivity was 97.29%, accuracy specificity was 98.65%, and accuracy F1-Score was 97.27% with a low misclassification rate of 2.72%. The results indicate that the VGG16 model gave a very reliable and balanced result for all types of diseases of apple leaves, which will help in the diagnosis of apple leaf diseases with high accuracy and automation in practical conditions.

Table 2. Evaluation matrix performance

Evaluation matrices	**Macro Average Values**
Accuracy	99.28%
Misclassification rate	2.72%
Precision	97.26%
Sensitivity	97.29%
Specificity	98.65%
F1 Score	97.27%

The low misclassification rate of 2.72% and an accuracy of 97.28%, the suggested VGG16 model showed outstanding classification performance. Furthermore, the model achieved an F1score of 0.9727, a precision of 97.26%, a sensitivity of 97.29%, and a specificity of 98.65%, demonstrating a balanced and dependable categorization of images of healthy, rust, and scab apple leaves with few false predictions.

In Table 3 presents a comparison between the proposed model and existing plant disease classification approaches. The results show that the proposed VGG-16-based deep learning model achieved the highest accuracy of 97.28% and the lowest misclassification rate of 2.72%, outperforming previously reported methods. While earlier studies achieved accuracies ranging from 92.94% to 96.41%, the proposed approach demonstrates improved classification performance and greater reliability in distinguishing plant disease conditions. These findings indicate that the proposed model provides a more accurate and robust solution for automated plant disease detection.

Table 3. Comparison of proposed model

Reference	Model Name	Accuracy (%)	Misclassification (%)
[3]	VGG16 + SMOTE	92.42	7.58
[12]	ResNet34	93.73	6.27
[13]	Dense Inception-ResNet-V2	94.31	5.59
[14]	Ensemble Mode	96.25	3.75
[15]	Severity Classification Framework	96.41	3.59
Proposed Model	**DL Algorithm VGG-16**	**97.28**	**2.72**

6. Conclusion and Future Work

This study evaluated the effectiveness of a VGG16-based transfer learning model for the multiclass classification of apple leaf images into healthy, apple scab, and apple rust categories. By utilizing a pretrained VGG16 network and fine-tuning it on the selected dataset, the proposed model was able to extract relevant visual features and achieve reliable classification performance. Global average pooling was employed to transform the extracted feature maps into a fixed-length feature vector before the final classification layer. Based on the experimental results, the model achieved a testing accuracy of 97.28% at epoch 15, with a misclassification rate of 2.72%. The confusion matrix further demonstrated the model's ability to distinguish among the three apple leaf categories. These findings indicate that VGG16-based transfer learning can provide an effective approach for automated apple leaf disease classification. Future research may investigate more advanced architectures, such as ResNet and EfficientNet, to further improve classification performance. The framework may also be extended by incorporating attention mechanisms, explainable artificial intelligence techniques, larger and more diverse datasets, and real-time mobile applications for practical disease detection.

Declarations

Not applicable.

Supplementary Materials

Not applicable.

Author Contributions Statement

Tayyab Nawaz: Conceptualization, Methodology, Software, Writing – original draft, Writing – review and editing. **Fahad Ahmed:** Conceptualization, Methodology, Software, Validation, Formal analysis, Investigation, Data curation, Writing – original draft, Writing – review and editing, Visualization. **Naila Samar Naz:** Conceptualization, Validation, Writing – review and editing, Visualization, Supervision. **Muhammad Saleem:** Conceptualization, Formal analysis, Investigation, Data curation, Writing – review and editing, Supervision. **Hafiz Abdul Wahid Khalid:** Methodology, Investigation, Supervision. **Muhammad Mazhar Ali:** Validation, Data curation, Visualization. All authors have read and approved the final version of the manuscript.

Conflict of Interest Statement

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Funding Declaration

The authors received no specific funding for this study.

Data Availability Statement

The data and materials used in this study is publicly available at Kaggle repository https://www.kaggle.com/datasets/nirmalsankalana/apple-leaf-disease-dataset.

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Not applicable.

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