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Diagnosis And Accurate Classification of Apple Leaf Diseases Using Vision Transformers

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ABSTRACT

In agriculture, plant pests and diseases are some of the major factors that reduce the fruit and vegetable yields. Early detection of foliar diseases, which cause significant yield losses in apple production, is of great importance for the sustainability of agricultural production. The subjective and inefficient nature of traditional manual and tool-based diagnostic methods is insufficient to provide solutions that meet scientific and production standards. In this context, pattern recognition and deep learning techniques offer more effective alternatives for automatic image analysis and classification. In this study, Vision Transformers are used for disease classification from apple leaf images. The dataset consists of images of healthy apple leaves and apple leaves with different diseases. The results show that Vision Transformers is effective in classifying apple leaf diseases with high accuracy. It is hoped that this study makes an important contribution to increasing the use of digital technologies in agriculture and plant health monitoring.

1. Introduction

Agricultural production plays a critical role in ensuring global food security. However, plants are often threatened by a variety of pathogens and pests, resulting in severe productivity losses. Leaf diseases affect the photosynthetic capacity and overall health of plants, resulting in significant economic losses [1]. In apple production, leaf diseases are among the most important factors directly affecting product quality and quantity. Therefore, early detection and effective management of leaf diseases are essential to ensure the sustainability of apple production [2].

Apple leaf diseases include common pathogens such as apple black spot (Venturia inaequalis), fire blight (Erwinia amylovora) and apple leaf spot (Phyllosticta solitaria). These diseases cause spots, necrotic areas and deformities on the leaves, inhibiting photosynthesis and affecting the overall health of the plant. As a result, fruit yields are reduced, and economic losses increase. These diseases can be largely prevented through early detection, proper crop management and timely implementation of spraying strategies [3, 4].

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Traditional methods of diagnosing plant diseases typically involve vision inspection and manual testing. These methods require expertise and are time consuming. In addition, their applicability to large areas is limited. In recent years, image processing techniques and machine learning algorithms have been used to diagnose plant diseases in agriculture [5,6]. Deep learning-based models, especially convolutional neural networks (CNNs), have shown great success in classifying plant diseases. However, these methods have some limitations due to their large data requirements and computational cost [7].

Recent advances in artificial intelligence have led to the emergence of new approaches such as Vision Transformers (ViT). ViT can capture important features through attentional mechanisms by processing images as sequences. This makes it possible to achieve high accuracy, especially on complex and diverse datasets. ViT is seen as a more flexible and powerful alternative to traditional CNN-based methods [8, 9].

The purpose of this paper is to investigate the effectiveness of ViT in classifying apple leaf diseases. The aim is to use ViT to diagnose apple leaf diseases accurately and quickly. The motivation of this study is to increase the use of digital technologies in agriculture and to optimize plant health monitoring processes. The use of ViT has been chosen due to its superior performance, especially on large and diverse data sets. The results obtained are expected to contribute to the development of disease management strategies and increase productivity in agriculture.

The rest of the paper is divided into the following sections: Section 2 presents the literature review on the diagnosis and classification of apple leaf diseases. Section 3 describes in detail the data set and methods used. Section 4 presents the experimental data and their interpretations. Finally, Section 5 presents the conclusions of the study.

2. Literature Review

Today, the agricultural sector is increasingly recognizing the importance of early detection to maintain the health of economically important plant species, especially apple trees [10]. In this context, deep learning and machine learning algorithms for automatic detection of foliar diseases have made significant progress in recent years. In this paper, we review the recent progress of different deep learning and machine learning methods for the diagnosis of apple leaf diseases. In this section, various studies in the literature on the classification of apple leaf diseases are presented.

The study by Bashir et al. reviewed recent advances in deep learning and machine learning methods for early detection of apple leaf diseases, discussing different techniques, dataset generation methods, and evaluation metrics. It also assessed the current state of the field and highlights future research opportunities [11].

In another study, Perveen et al. addressed the challenges that are important for accurate diagnosis of apple leaf diseases. As a solution to the problems, a unique dual-branch structure apple leaf disease diagnosis system (DBNet) was proposed. It was found that the accuracy of the DBNet model increased by 0.02843, 0.02412, 0.0144, and 0.0125, respectively, compared with previous leaf disease detection models. These results show that the proposed DBNet model has certain advantages over other models in the detection of apple leaf diseases [12].

Li et al. proposed the DeepLabV3+ semantic segmentation network model to accurately identify apple leaf diseases and determine disease severity. This model aims to extract apple leaf lesion features more effectively compared to classical semantic segmentation network models such as

PSPNet and GCNet. The research showed that the model achieves an average pixel accuracy of 97.26% and an average mean intersection on unity (MIoU) value of 83.85% [13].

Liu et al. proposed a deep convolutional neural network-based method for identifying apple leaf diseases. The newly designed model was trained with 13,689 diseased apple leaf images, achieving 97.62% accuracy and saving 51,206,928% parameters compared to the standard AlexNet model. Furthermore, a 10.83% accuracy improvement was achieved by generating diseased leaf images, which increases the robustness of the model [14].

Zhong et al. proposed three methods (regression, multi-label classification, and focus loss function) based on DenseNet-121 deep convolutional network to detect apple leaf diseases. The proposed methods achieved accuracies of 93.51%, 93.31% and 93.71%, respectively, on the test set, outperforming the traditional multi-class classification method based on cross-entropy loss function [15].

Khan et al. created an apple disease dataset containing 9000 high quality RGB images and proposed a deep learning-based apple disease detection system. This two-step system first performed classification into diseased, healthy, or damaged categories, and then, if the disease was detected, identification and localization processes were performed. The system achieved successful results with about 88% classification accuracy and 42% mAP and can be applied to other fruits and vegetables in the future [16].

In their study, Kunduracioglu et al. focused on diagnosing grape leaf diseases using deep learning models. In experiments using PlantVillage and Grapevine datasets, four models achieved 100% accuracy. The Swinv2-Base model was found to be particularly successful, indicating that this approach holds promise for improving crop productivity [17].

In their study, Zhang et al. proposed a novel deep learning-based detection algorithm for accurate and fast detection of multi-scale apple leaf spots. BCTNet, integrated with the proposed Bole Convolution Module (BCM), Cross Attention Module (CAM), and Bidirectional Transposition Feature Pyramid Network (BTFPN), provides high accuracy and speed in detecting apple leaf spots in natural environments [18].

3. Methodology

This section details the dataset, data processing steps, model and evaluation metrics used for the classification of apple leaf diseases. The research process consists of three main stages: preparation of the dataset, use of the ViT model and evaluation of the model's performance.

3.1 Vision Transformer Approach

In the field of image processing, inputs are broken into multiple patches that resemble words, which are then used as input elements. Vit is the pioneering attempt to implement a pure transducer architecture for processing images. While the original transducer model included both encoder and decoder components, the ViT model includes only an encoder. The operating principles of image transducers closely parallel those observed in natural language processing. In the ViT architecture, the input image I is represented in the dimensions $\mathrm{R}^{\mathrm{HxWxC}}$.

This image is then divided into N patches of size PxPxC. The value of N is expressed mathematically as shown in Equation 1 [20].

$$N = \frac{HW}{P^2} \tag{1}$$

Flattening and Embedding Process: Here, H stands for the image's height, W for its width, P for its patch size, and C for its channel count. After splitting the broken image patches into N pieces, they are flattened and put through a linear embedding procedure. To preserve the positioning information of the patches, a positional embedding procedure is then used. Vision transformers operate in a manner similar to natural language processing. Three layers typically make up the ViT architecture: the classifier, encoder, and embedding layers. Figure 1 provides an illustration of this construction.

Embedding Layer: A learnable linear projection is used to map each patch to embedding dimensions E and D. Each patch is handled as a single token in this layer. To complete the classification process, the learnable class token U_{class}, which also functions as a trainable token is paired with the embedding projections. E_{pos}, or positional embedding, keeps track of each patch's placement and maintains it so that the real image may be recognized more easily. Equation 2 below provides the mathematical expression for the patch-encoded series, known as Z_0 [20].

$$Z_0 = \left[U_{class}; X_p^1 E;\ X_p^2 E; \dots \dots X_p^N E\right] + E_{pos} \tag{2}$$

Encoder Layer: The previously acquired set of embedded patches Z_0is processed using the transformer encoder. The encoder unit in vision transformers consists of L identical layers. A fully connected feed-forward dense block (MLP) structure and a multi-head self-attention (MSA) block comprise each identical layer (Equations 3 and 4) [20]. The core part of the transformer encoder is the MSA block, which combines layers and self-attention. These blocks consist of the GeLU activation function after two dense layers. Skip connections are used in the encoder, and layer normalization (LN) is used prior to the output layer.

$$Z_1' = \mathrm{MSA}(\mathrm{LN})(Z_1 - 1) + (Z_1 - 1), 1 = 1 \dots . L \tag{3}$$

$$Z_1' = \mathrm{MLP}(\mathrm{LN})(Z_1') + Z_1', 1 = 1 \dots . L \tag{4}$$

Multiple self-attention heads are aggregated within the transformer encoder to produce the MSA output. Equation 5 provides a mathematical representation of self-attention [20].

$$H = \mathrm{Atten}(Q, K, V) = \mathrm{softmax}\left(\frac{QK^T}{\sqrt{D_K}}\right)V \tag{5}$$

Equation 5 shows that Q is the query received following matrix multiplications, K is the key, and V is the value matrix. Concatenating all self-attention heads through a linear layer yields the final output of the MSA in vision transformers. Equation 6 provides a mathematical expression for this linear layer [20].

$$\mathrm{MSA}(Q, K, V) = [H_1, H_2, \dots \dots . . H_h]W_0 \tag{6}$$

where H is the number of self-attention heads and W_0 is the learnable output transformation matrix.

To predict the last layer of the encoder for classification, the entity Z_l^0 is first extracted and then fed into an external auxiliary head classifier within this unit that is devoted to the classification process. This process is explicitly expressed in Equation 7, where y is the output of the model and Z_l^0 is the first variable used in the decision-making process [20].

$$y = \text{layer\_normalization}\ (Z_l^0) \quad (7)$$

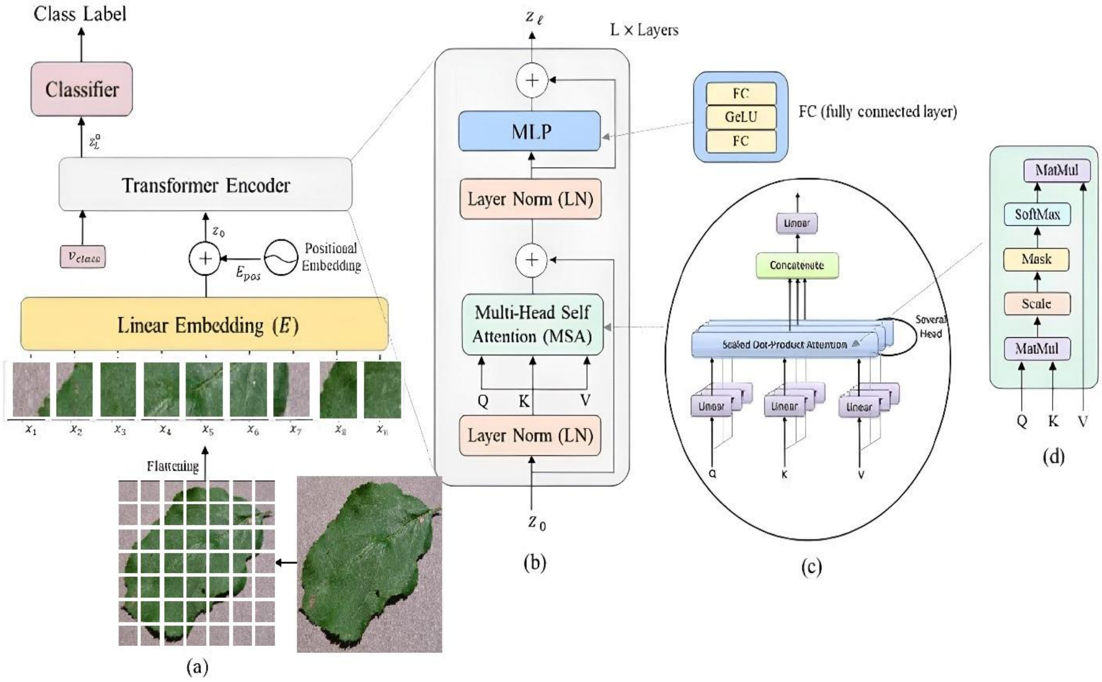


Fig. 1. Working principle of ViT

ViT method is a useful tool for natural language processing (NLP) tasks. ViT provides a pure transformer model without any convolutional blocks in the field of computer vision. Historically, image recognition attempts have been dominated by CNN. However, CNNs have a number of shortcomings. Most notably, they process information more slowly due to processes like max pooling, and big datasets are needed for effective processing and neural network training. The proposed model applies the ViT method to classify apple disease from a dataset of Plant Village Dataset. Notably, the Vision Transformer has recently acquired favor over CNNs when it comes to managing large computer vision datasets. ViT uses a transformer architecture with self-attention to enable data integration over the entire image. Figure 1 illustrates the ViT's working principle.

3.2 Dataset

In this study, the dataset named "Plant Village Dataset Updated" available on Kaggle is used. This dataset contains leaf images of 9 different plant species and each image is labeled with the corresponding plant disease or health status. The dataset consists of 70,000 images and is categorized into 38 different classes. Apple leaf images and diseases were selected from this dataset and analyzed.

This dataset is ideal for machine learning researchers and practitioners working on plant disease detection and classification, as well as agronomists aiming to improve plant health and crop yields. The data is split 80%-20% for the training and testing phases. The dataset contains a total of 7771 samples for apple leaf. There are four different classes for apple leaf in the dataset. These are named as Apple Scab, Black Rot, Cedar Apple Rust and Healthy. Figure 2 shows the number of images belonging to the classes in the dataset [19]. Figure 3 shows a sample image for each class in the dataset.

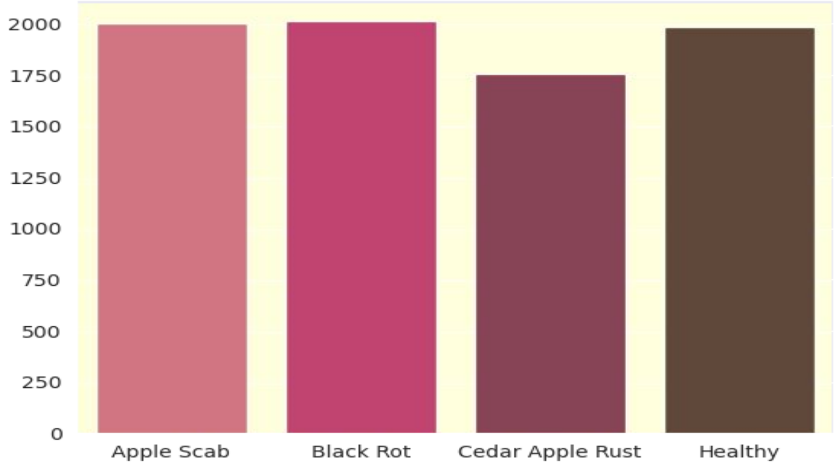


Fig. 2. Number of samples for each class in the dataset

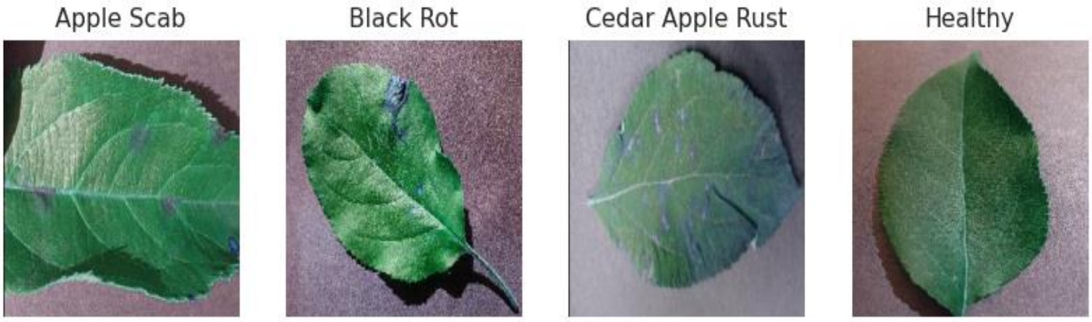


Fig. 3. Example image for each class in the dataset

3.3 Proposed Method

In this study, we employ ViT for the classification of apple leaf diseases using the Plant Village Dataset. The dataset consists of high-resolution images of healthy and diseased leaves, categorized into multiple classes. Our approach begins with data preprocessing, where images are resized to 224x224 pixels and normalized. We utilize data augmentation techniques such as rotation, zoom, and flipping to increase the diversity of the training data and improve model generalization **[21].**

The core of our method is the ViT architecture, which leverages self-attention mechanisms to process image patches instead of traditional convolutional layers. This model is pre-trained on large-scale datasets and fine-tuned on our specific dataset. The ViT architecture divides each image into a sequence of fixed-size patches, linearly embeds them, and adds positional embeddings. These embeddings are then passed through multiple transformer layers, allowing the model to capture global contextual information. Training is conducted with early stopping and learning rate reduction callbacks to prevent overfitting and ensure optimal performance. Post-training, the model's performance is evaluated using standard metrics such as accuracy, precision, recall, and F1-score. Confusion matrices are generated to visualize classification results and identify misclassified instances. Our method demonstrates the efficacy of ViTs in handling plant disease classification tasks, showcasing improved accuracy and robustness compared to traditional convolutional neural networks. This approach not only advances the state-of-the-art in automated plant disease detection but also provides a scalable solution for precision agriculture.

3.4 Evaluation Metrics

Important measures including accuracy, F1 score, precision, and recall are used to evaluate the suggested model. Four parameters are used in the calculation of these metrics: true positive (TP), false negative (FN), false positive (FP), and true negative (TN). The following definitions apply to the parameters in these equations: Examples of data that the model correctly categorized as positive are called~~)~~ TP. Examples of negative outcomes that the model correctly detects are called TN. FP are instances in which something was mistakenly categorized as positive by the model. Examples of negative numbers that the model misinterpreted are called FN. Figure 4 shows the Confusion Matrix for the Evaluation Metrics [22].

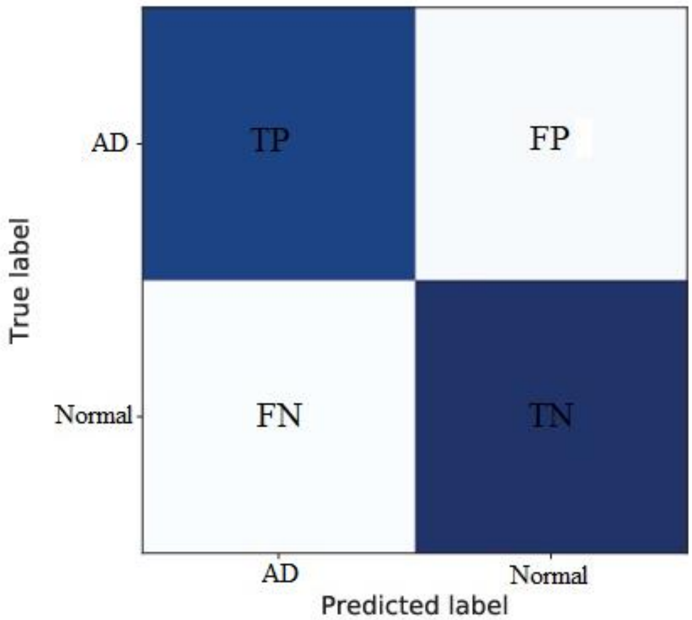


Fig. 4. Confusion Matrix for Evaluation Metrics

By taking into consideration both positive and negative classifications, these indicators offer a thorough assessment of the model's effectiveness. Although recall and accuracy provide information on the model's ability to correctly identify positive and negative samples, respectively, the F1-score strikes a balance between the two. An overall assessment of the model's prediction accuracy is provided by the accuracy metric.

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{(\text{TP} + \text{TN} + \text{FP} + \text{FN})} \tag{8}$$

$$\text{Recall} = \frac{\text{TP}}{(\text{TP} + \text{FN})} \tag{9}$$

$$\text{Precision} = \frac{\text{TP}}{(\text{TP} + \text{FP})} \tag{10}$$

$$\text{F}_1 = 2 * \frac{\text{Precision} * \text{Recall}}{(\text{Precision} + \text{Recall})} \tag{11}$$

4. Results and Discussion

In this study, a classification for apple scab, black rot, cedar apple rust and healthy leaf classes was performed for the diagnosis of apple leaf diseases. This classification process was trained on the Plant Village dataset using the Python programming language and the ViT method. The performance of the model was evaluated using metrics such as accuracy, precision, recall and F1 score and the results were found to be quite successful.

The evaluation results show that the model can accurately classify diseases with high accuracy and consistency. The results are presented in Table 1. These results show that the ViT model can be used as an effective tool for diagnosing plant foliar diseases.

Table1.
Metrics showing the performance of the trained model on the test data

Classification Report				
	Precision	**Recall**	**F1-Score**	**Support**
Apple Scab	1.00	1.00	1.00	51
Black Rot	0.99	1.00	0.98	50
Cedar Apple Rust	1.00	0.98	0.99	44
Healthy	0.98	0.98	0.99	51
accuracy			0.99	196
macro avg	0.99	0.99	0.99	196
weighted avg	0.99	0.99	0.99	196

The results obtained regarding the performance of the model are quite remarkable. The precision, recall and F1-score values obtained for Apple Scab disease were all recorded as 1.00. This shows that the model classifies Apple Scab cases completely correctly. For Black Rot, precision was 0.99, recall 1.00 and F1-score 0.98. These values reveal that the model performed almost perfectly, but with a margin of error in a few cases. For Cedar Apple Rust, precision was 1.00, recall was 0.98 and F1-score was 0.99. This shows that the model can classify Cedar Apple Rust cases with great accuracy. For healthy leaves, the precision and recall values are 0.98 and the F1-score is 0.99. This indicates that the model also detects healthy leaves with high accuracy.

The overall accuracy was recorded as 0.99. This high accuracy rate indicates that the model is able to correctly classify apple plant leaf diseases in general. The macro mean and weighted mean values were similarly 0.99. This shows that the model performs consistently across classes and does not discriminate against any class.

These results confirm that the ViT model is an effective and reliable tool for diagnosing apple leaf diseases. This model can make an important contribution for early diagnosis and management of diseases in agriculture. The confusion matrix of the proposed model is shown in Figure 5. On the horizontal axis are predicted values and on the vertical axis are actual values.

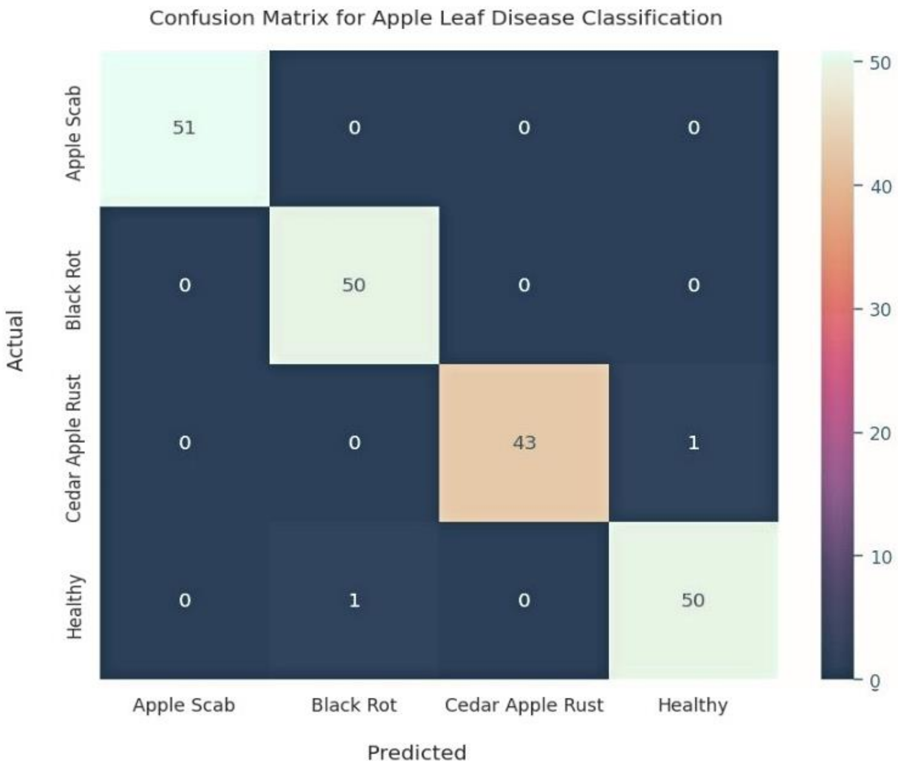
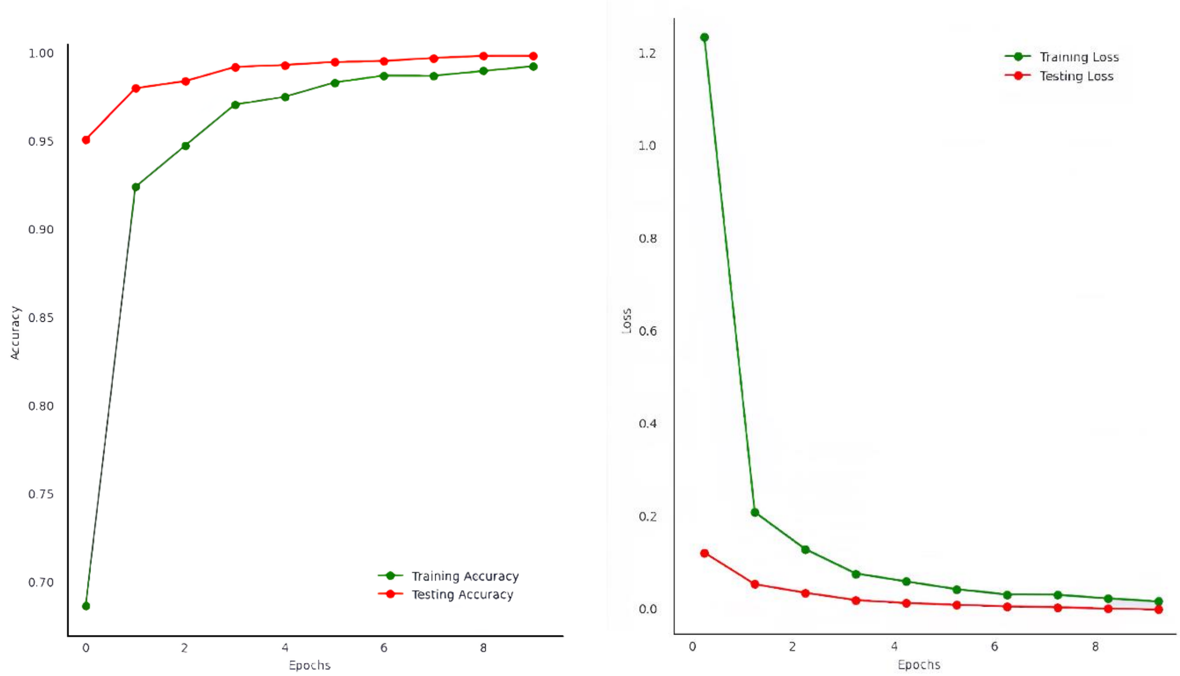


Fig. 5. Confusion matrix of the proposed model

The accuracy of the model after testing and training is shown in Figure 6.a. and the losses of the model are shown in Figure 6.b. Some examples showing the actual values in the dataset and the values predicted by the model are shown in Figure 7. Table 2 presents a comparison of the proposed model with the literature review.



(a) (b)

Fig. 6. Training and validation accuracy and loss results

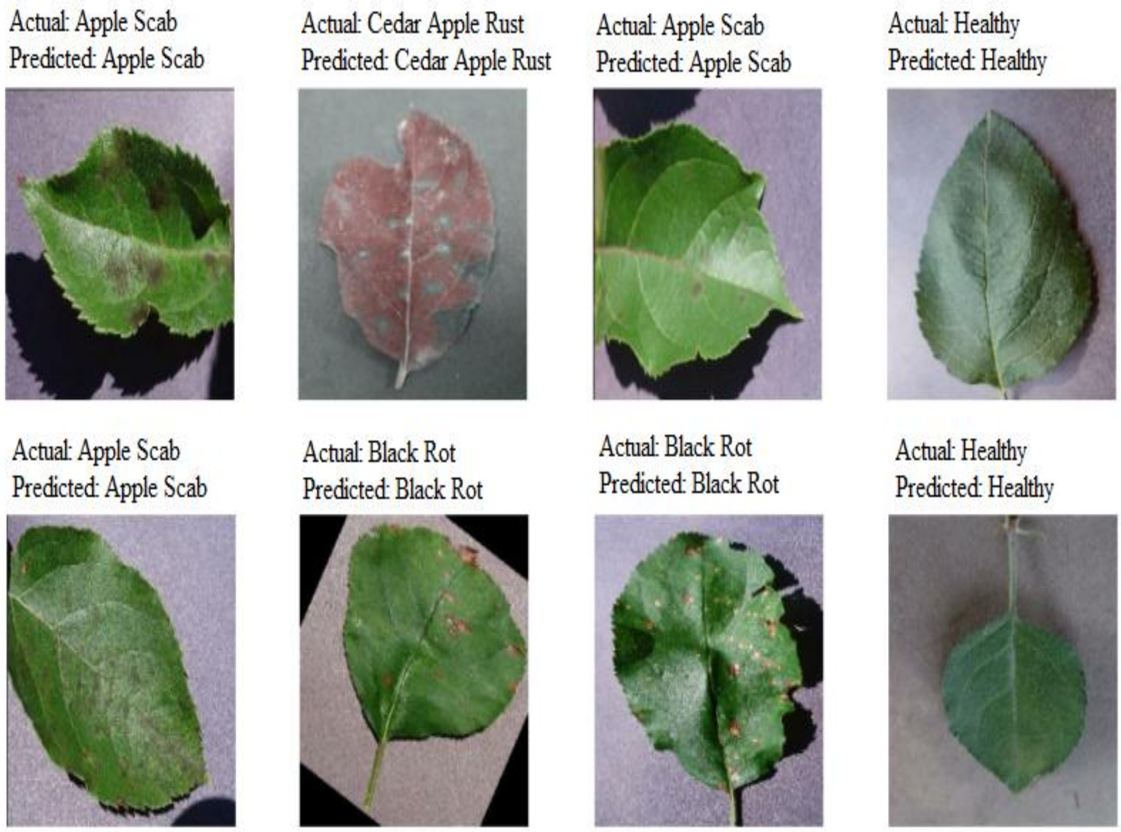


Fig. 7. Some examples showing actual and predicted values

Table 2
Comparison of the proposed model with the literature

Model	$Accuracy$(%)
[13]	97.26
[14]	97.62
[15]	93.71
[16]	88.00
Proposed Model	**99.00**

Table 2 compares the accuracy of different models used to diagnose and classify apple leaf diseases. The accuracy rates of existing studies in the literature provide an important benchmark for evaluating the performance of the models. Study [13] showed a high performance with an accuracy rate of 97.26%. Similarly, [14] stands out as the most accurate model with an accuracy rate of 97.62%. However, studies [15] and [16] show relatively lower performance with accuracy rates of 93.71% and 88.00%, respectively. With an accuracy of 99.00%, our proposed model outperformed all the models in the existing literature. This result shows that our model provides superior performance in diagnosing and classifying apple leaf diseases. The high accuracy rate means that the model can make more accurate and reliable predictions. This success of the proposed model is the result of advanced deep learning techniques and careful data preprocessing. In this context, our model can make an important contribution to the early detection and management of apple leaf diseases. These results provide valuable insights for optimizing agricultural production processes and improving phytosanitary monitoring systems.

5. Conclusions

This paper presents an investigation using ViT for early detection and classification of apple leaf diseases, which cause significant losses in agricultural production. It has been shown that automatic image analysis methods such as deep learning and pattern recognition techniques provide more effective and accurate results when traditional apple leaf disease diagnosis methods are insufficient. By analyzing the accuracy rates of the existing studies in the literature, it is understood that our proposed model provides better results. In this context, our proposed model outperforms all the models in the literature with an accuracy rate of 99.00%. The high accuracy rate of the proposed model shows that it can make more accurate and reliable predictions in the diagnosis of apple leaf diseases. This achievement is a result of advanced deep learning techniques as well as careful data preprocessing methods. This superior performance of our model makes an important contribution to the early diagnosis and management of apple leaf diseases in agricultural production. Thus, valuable insights are provided for increasing the use of digital technologies in agriculture and improving phytosanitary monitoring systems. In conclusion, this study makes a significant contribution to supporting sustainable production processes in agriculture by demonstrating the effectiveness of ViT for early detection and classification of apple leaf diseases. These findings provide guidance for future research and applications, and provide an important foundation for the development of digital agricultural technologies.

Author Contributions

Methodology, Emrah ASLAN, Yıldırım OZUPAK.; software, Emrah ASLAN, Yıldırım OZUPAK.; validation, Emrah ASLAN, Yıldırım OZUPAK. resources, Emrah ASLAN, Yıldırım OZUPAK.; writing—original draft preparation, Emrah ASLAN, Yıldırım OZUPAK.;All authors have read and agreed to the published version of the manuscript.

Conflicts of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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