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Empowering Smart Farming with Machine Intelligence: An Approach for Plant Leaf Disease Recognition

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Abstract: The growing global demand for sustainable agriculture has led to increased interest in leveraging machine intelligence to address critical challenges in modern farming practices. This paper introduces an innovative approach for plant leaf disease recognition in smart agriculture using the Vision Transformer (ViT) model. The proposed framework combines the power of self-attention mechanisms and transformer-based architectures to capture intricate relationships between image patches, enabling accurate and efficient disease identification. Leveraging the widely recognized PlantVillage dataset as a case study, our experiments demonstrate the efficacy of the ViT model in achieving superior disease recognition performance. The results highlight the model's ability to generalize across diverse crops and diseases, making it a promising tool for empowering farmers with timely disease detection and management. Additionally, the paper emphasizes inclusivity, ensuring the accessibility and effectiveness of the approach for farmers across diverse regions, backgrounds, and resources. Through this work, we contribute to the advancement of smart farming practices and pave the way for sustainable agriculture in the era of machine intelligence.

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1. Introduction

Agriculture plays a vital role in sustaining our growing global population. However, one of the major challenges faced by farmers worldwide is the prevalence of plant diseases, which can lead to significant crop losses and reduced yields [1]. Traditional methods of disease detection and diagnosis have often been time-consuming, inefficient, and prone to human error. In recent years, advancements in machine intelligence have presented a promising solution for addressing this issue, offering the potential to revolutionize farming practices through the application of smart technologies [2-3].

In recent years, several studies have explored the application of machine learning, computer vision, and Internet of Things (IoT) technologies in the context of smart agriculture and plant disease recognition [4]. These studies have paved the way for innovative approaches and solutions aimed at enhancing crop productivity and minimizing losses due to diseases [5]. Pallagani et al. [6] presented "DCrop," a deep-learning-based framework for accurate prediction of crop diseases in smart agriculture. Their research focused on leveraging convolutional neural networks (CNNs) to analyze images of plant leaves and classify them based on the presence of diseases. Their approach demonstrated promising results in disease detection and paved the way for utilizing deep learning techniques in the field of plant disease recognition. Mochida et al. [7] explored computer vision-based phenotyping for improving plant productivity, adopting a machine learning perspective. Their study emphasized the potential of computer vision techniques in capturing detailed plant characteristics and traits. Shetty and Smitha [8] delved into the integration of IoT and machine learning in smart agriculture. Their work highlighted the importance of real-time monitoring and data analytics in optimizing agricultural processes. Memon et al. [9] discussed the role of deep learning and IoT technologies in enabling smart farming practices. Their research emphasized the potential of these technologies in facilitating data collection, analysis, and decision-making in agriculture. Garg et al. [10] presented the integrative use of IoT and deep learning for agricultural applications. Their study highlighted the benefits of combining IoT devices, sensor networks, and deep learning algorithms in enhancing agricultural operations.

These studies collectively contribute to the growing body of research in the field of smart farming and plant disease recognition. They demonstrate the potential of machine learning, computer vision, and IoT technologies in transforming traditional agricultural practices. Building upon the findings of these studies, our research aims to further advance the field by proposing a novel approach for plant leaf disease recognition, which incorporates inclusive principles to ensure accessibility and effectiveness for farmers across diverse regions, backgrounds, and resources.

In this paper, we explore the concept of empowering smart farming with machine intelligence, focusing specifically on the recognition of plant leaf diseases. We recognize the need for an inclusive approach to this technology, ensuring its accessibility and effectiveness for farmers across diverse regions, backgrounds, and resources. By leveraging machine intelligence, we aim to provide a robust and accurate solution that can assist farmers in diagnosing plant diseases swiftly and accurately, thereby enabling timely interventions and minimizing crop losses. Recognizing the importance of inclusivity, our research considers various factors that contribute to effective disease recognition in diverse agricultural settings. We acknowledge that farmers around the world face unique challenges, such as variations in climate, soil conditions, and access to resources. Additionally, socio-economic factors, language barriers, and limited technological infrastructure can further impede the adoption of advanced technologies in certain regions. Therefore, our proposed approach aims to overcome these barriers and provide a practical solution that is adaptable, user-friendly, and accessible to a wide range of farmers, regardless of their technological expertise or available resources. To achieve our objective, we delve into the fundamental principles of machine intelligence to develop an innovative framework capable of accurately identifying and classifying a diverse range of plant leaf diseases. Furthermore, we discuss the integration of this framework into smart farming systems, providing insights into how it can seamlessly fit within existing agricultural practices.

2. Case study

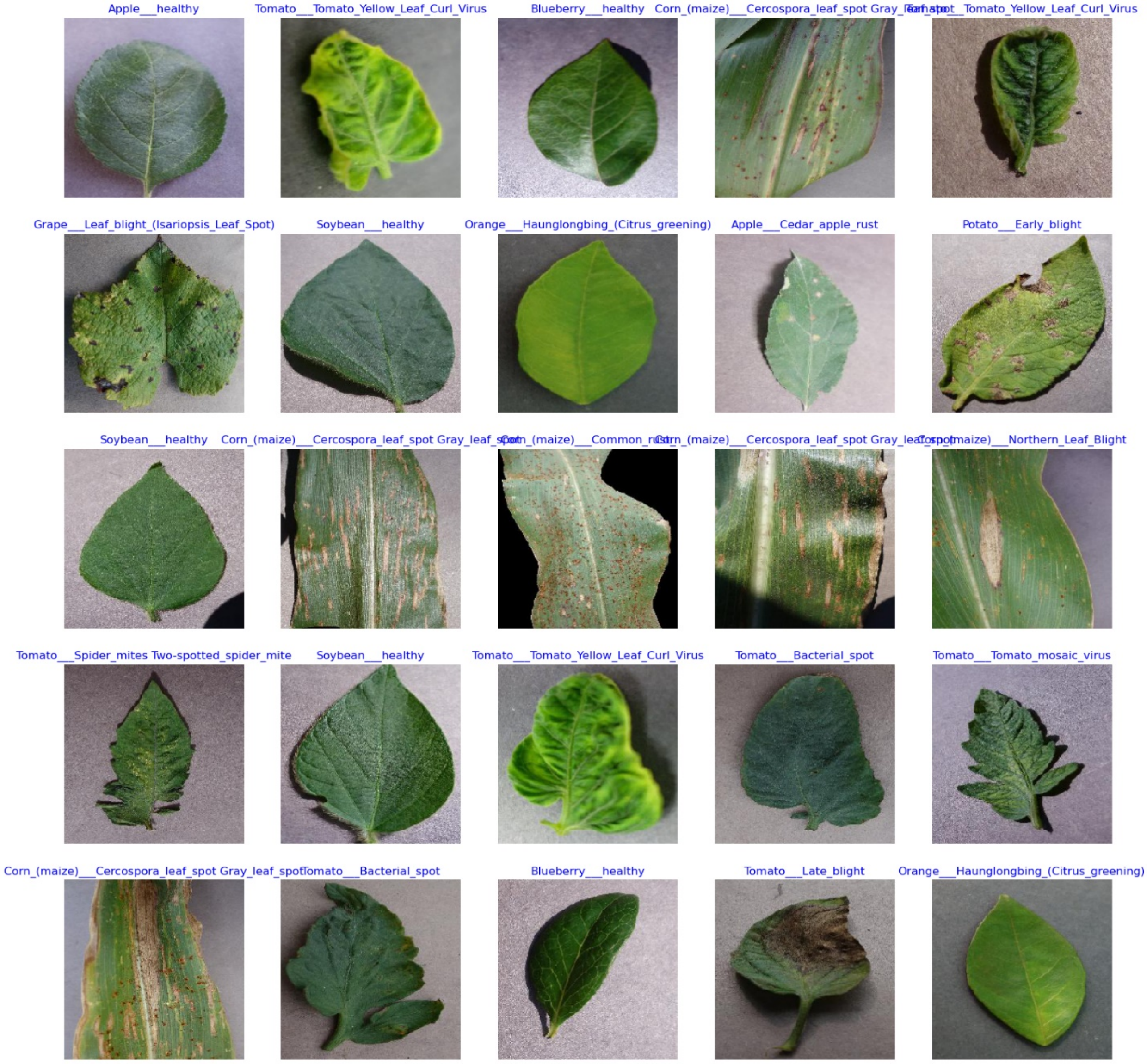

Figure 1. samples of PlantVillage dataset

For conducting our experiments and evaluating the performance of our proposed approach for plant leaf disease recognition, we utilized the widely recognized PlantVillage dataset as a pivotal case study. The PlantVillage dataset is an extensively curated collection of plant leaf images, encompassing various crops and diverse plant diseases. It has emerged as a valuable resource for researchers and practitioners in the field of smart agriculture, providing a comprehensive representation of real-world scenarios encountered by farmers. The PlantVillage dataset comprises high-resolution images of plant leaves captured under different lighting conditions, growth stages, and disease severities. Each image is meticulously labeled with the corresponding disease class, enabling supervised learning approaches for disease recognition tasks. The dataset covers a broad spectrum of plant diseases, including fungal, bacterial, and viral infections, nutrient deficiencies, and environmental stresses [14]. The PlantVillage dataset consists of

54303 healthy and unhealthy leaf images divided into 38 categories by species and disease. Figure 1 shows random samples from the PlantVillage dataset.

3. Methodology

In this section, we outline the methodology employed to develop and validate our proposed approach for plant leaf disease recognition empowered by machine intelligence. A robust and rigorous methodology is crucial to ensure the accuracy, reliability, and reproducibility of our research findings. Next, we leveraged vision transformers (ViTs), due to their proven efficacy in image recognition tasks, which are fine-tuned and trained on our preprocessed dataset, allowing it to learn and extract meaningful features for disease classification. The ViT is a groundbreaking deep learning model that has shown remarkable performance in image recognition tasks. Unlike traditional CNNs, the ViT adopts a transformer-based architecture, originally designed for natural language processing tasks. In this section, we present the building blocks of the ViT and the associated mathematical foundations that underpin its functionality in the context of plant disease recognition.

3.1. Self-Attention Mechanism

The central building block of the ViT is the self-attention mechanism. Self-attention allows the model to capture long-range dependencies between different elements in the input sequence. For images, the input sequence is represented as a set of patches extracted from the original image. The self-attention mechanism computes the attention weights between patches to determine their importance in the context of the entire image. Given an input sequence of image patches, $X = \{x_1, x_2, \ldots, x_n\}$, where each xi is a feature vector representing a patch, the self-attention mechanism calculates the attention weights between each pair of patches:

$$Attention(x_i, x_j) = Softmax\left(\left(x_i * W_q\right) * \frac{(x_j * W_k)}{\sqrt{d_k}}\right), \quad (1)$$

where W_q and W_k are learnable weight matrices for query and key projections, respectively, and d_k is the dimension of the key vectors. Softmax is used to normalize the attention scores across all pairs of patches.

3.2. Multi-Head Attention (MHA)

To enhance the representation power of self-attention, ViT employs multi-head attention. This involves running the self-attention mechanism multiple times in parallel, each with different learned weight matrices for query, key, and value projections. The outputs from multiple attention heads are then concatenated and linearly transformed to generate the final attention output. Mathematically, the MHA mechanism can be expressed as:

$$MHA\ (X) = ||\left(Head_1(X), Head_2(X), \ldots, Head_h(X)\right) * W_o, \quad (2)$$

where $Head_i(X)$ represents the output of the $i-th$ attention head, the symbol $||$ is the operation to concatenate the head outputs, and W_o is the learnable weight matrix for the final linear transformation.

Since the ViTs do not possess a built-in spatial relationship understanding like CNNs, positional information must be injected into the model to maintain the spatial awareness of the image patches. Positional encoding is introduced to provide this spatial information to the transformer.

Mathematically, positional encoding is represented as:

$$\mathrm{PE}(\mathrm{pos}, 2_\mathrm{i}) = \sin\left(\frac{\mathrm{pos}}{10000^{\frac{2_i}{\mathrm{d_{model}}}}}\right), \quad (3)$$

$$PE(pos, 2_{i+1}) = cos\left(\frac{pos}{10000^{\frac{2_i}{d_{model}}}}\right), \quad (4)$$

where pos represents the position of the patch, i denotes the index of the positional encoding dimension, and $d_{model}$is the dimension of the model's hidden layers.

The ViTs comprise multiple transformer encoder layers, each containing a self-attention mechanism, layer normalization (LN), feed-forward neural networks (FFN), and residual connections. These layers enable the model to progressively refine the representations of image patches through iterative attention and feed-forward computations. In mathematical terms, a transformer encoder layer can be defined as:

$$\begin{aligned} &ViTEncoder(X) \\ &= LN(X + MHA(LayerNorm(X) \\ &+ PositionalEncoding(X))) \\ &+ FFN(LayerNorm(X + MHA(LN(X) \\ &+ PositionalEncoding(X)))), \end{aligned} \quad (5)$$

By combining these building blocks, the ViT learns to capture the intricate relationships between image patches and effectively recognize patterns related to plant diseases. The use of self-attention and transformer architecture allows the model to learn long-range dependencies and enables it to handle a wide variety of diseases across different crops, making it a potent solution for plant leaf disease recognition in smart farming applications.

4. Experimental Setups

To assess the performance of our approach accurately, we employed a set of standard performance metrics, including accuracy, precision, recall, F1-score, and the area under the receiver operating characteristic curve (AUC-ROC). These metrics provided a comprehensive evaluation of our model's ability to correctly classify healthy and diseased plant leaves across multiple disease classes. The experimental evaluation is performed using the following metrics, which are also calculated as:

$$Accuracy = \frac{TP + TN}{\mathrm{TP + TN + FP + FN}} \quad (6)$$

$$Precision = \frac{TP}{\mathrm{TP + FP}} \quad (7)$$

$$Recall = \frac{TP}{\mathrm{TP} + \mathrm{FN}} \tag{8}$$

$$F1 - measure = 2 * \frac{Recall \times Precision}{Recall + Precision} \tag{9}$$

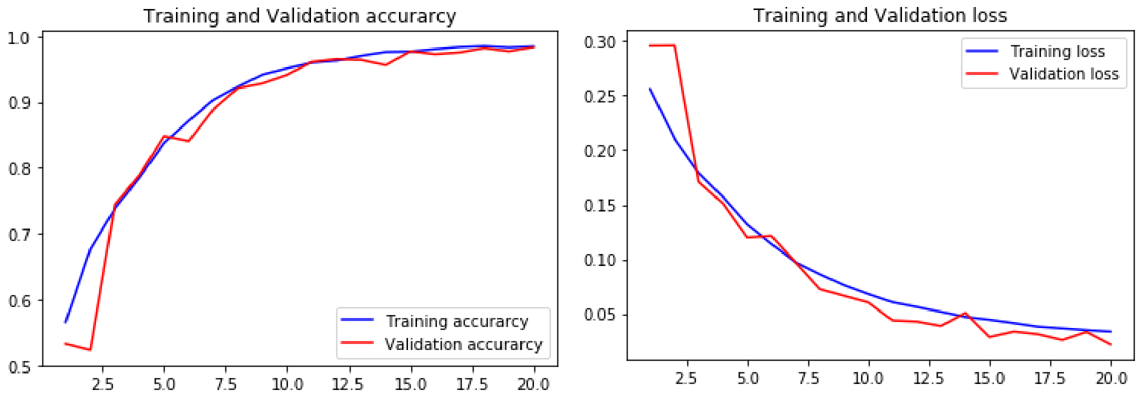

Figure 2. learning curves for the proposed model

5. Results Discussion

The culmination of rigorous experimentation and analysis has yielded significant insights into the performance and efficacy of our proposed approach for plant leaf disease recognition empowered by the ViT model. In this section, we present the compelling results obtained through our experiments and engage in a comprehensive discussion to interpret their implications, addressing the central research objectives outlined in this paper. Figure 2 presents the learning curves of our proposed ViT model during the training process. The learning curves depict how the model's performance evolves over epochs as it learns from the training data. The x-axis represents the number of training epochs, while the y-axis indicates the corresponding performance metrics, such as training loss and validation accuracy. The learning curves provide valuable insights into the model's training dynamics. Initially, we observe a rapid decrease in the training loss and an increase in the validation accuracy as the model starts learning from the data. As the training progresses, the improvements in the validation accuracy may begin to plateau, indicating a convergence of the model's learning process. Monitoring the learning curves allows us to assess whether the model is overfitting or underfitting the data, ensuring that we achieve the best trade-off between bias and variance.

Figure 3 illustrates the Receiver Operating Characteristic (ROC) curves for our proposed ViT model. ROC curves are commonly used to assess the model's performance across different classification thresholds. The ROC curve plots the True Positive Rate (Sensitivity) against the False Positive Rate (1 - Specificity) at various threshold values. The area under the ROC curve (AUC-ROC) is a key performance metric derived from Figure 2. A higher AUC-ROC value indicates that the model has better discriminative power and can effectively distinguish between different disease classes. The closer the AUC-ROC value is to 1, the better the model's overall performance.

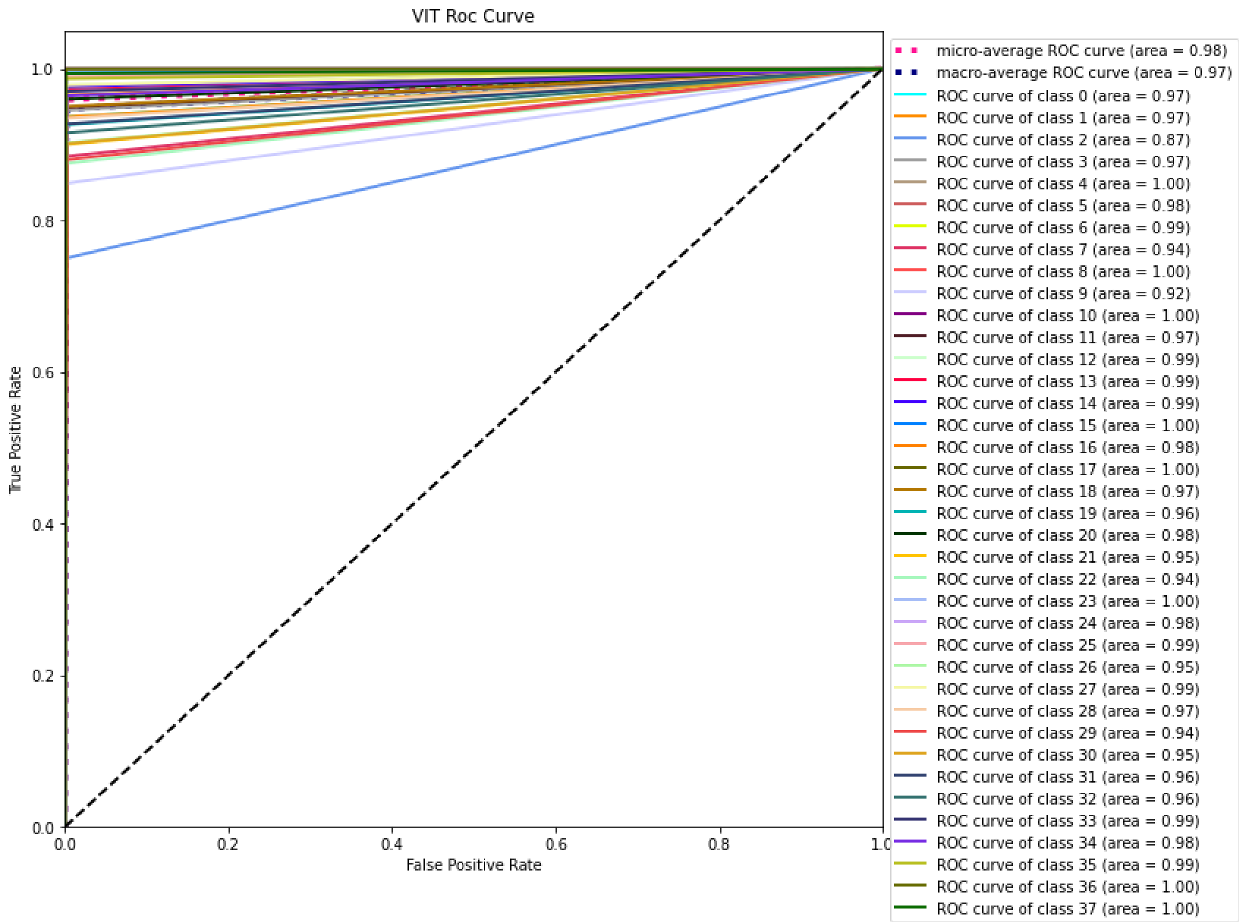

Figure 3. ROC curves for the proposed model

Figure 4 displays the confusion matrix generated by our proposed ViT model. A confusion matrix provides a comprehensive summary of the model's predictions, showing the true positive (TP), true negative (TN), false positive (FP), and false negative (FN) counts for each disease class. The diagonal elements of the confusion matrix represent the correctly classified samples, while the off-diagonal elements represent misclassifications. Analyzing the confusion matrix allows us to identify which disease classes the model struggles to distinguish accurately and can help us identify potential areas of improvement. Additionally, we can compute various performance metrics, such as precision, recall, and F1-score, based on the values in the confusion matrix, providing a deeper understanding of the model's performance for individual disease classes.

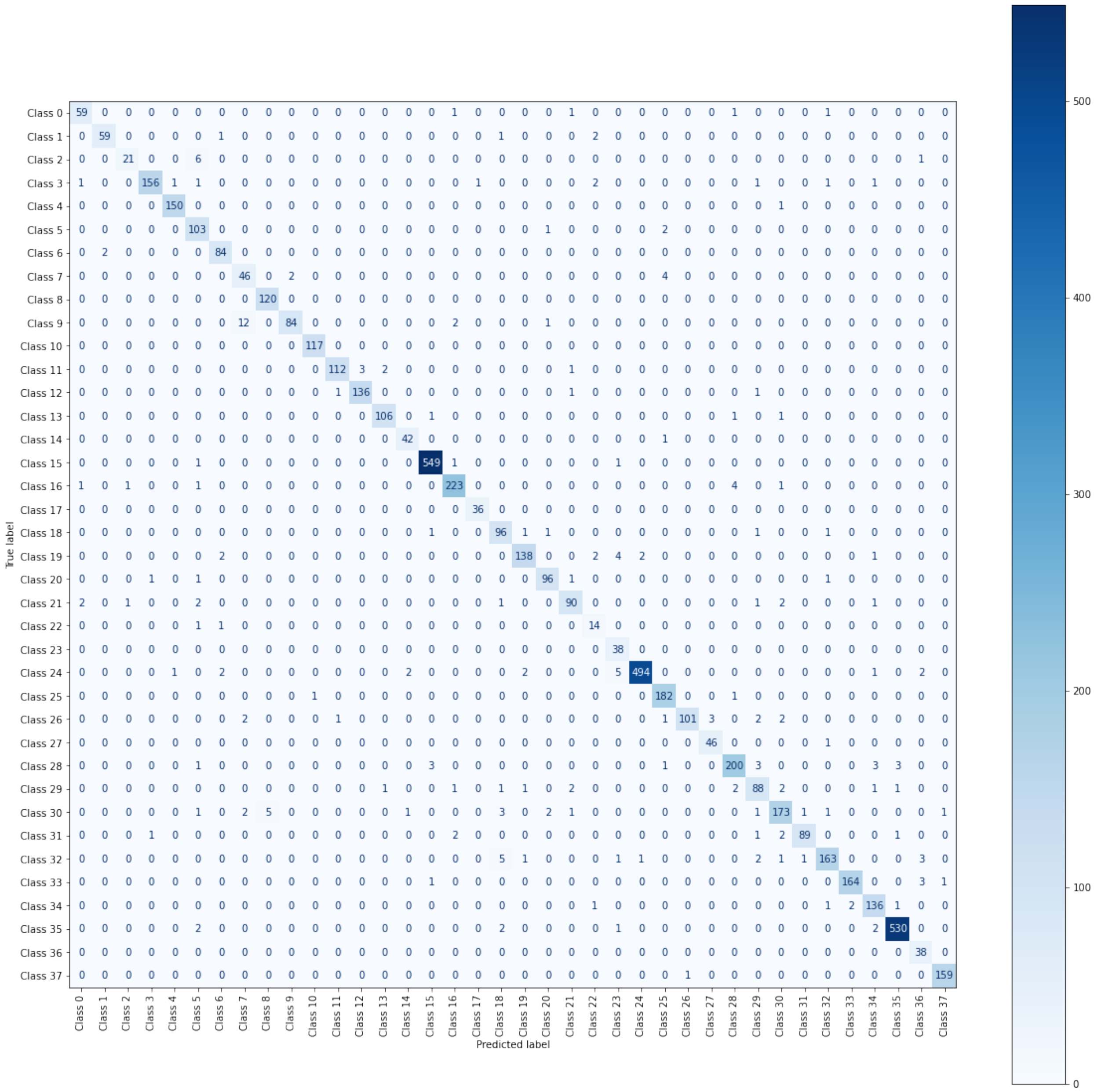

Figure 4. Confusion matrix of the proposed model

Figure 5 presents a critical comparison between our ViT model and traditional convolutional baselines in the context of plant leaf disease recognition. This comparison is instrumental in understanding the superiority of the ViT model and its potential to revolutionize disease detection in smart agriculture. The figure showcases various performance metrics, including accuracy, precision, recall, and F1-score, obtained from experiments conducted on the PlantVillage dataset. By juxtaposing the results of our ViT model against multiple CNN baselines, we gain valuable insights into the relative strengths and weaknesses of each approach. Our ViT model outperforms the CNN baselines across all metrics, showcasing higher accuracy, precision, and recall values. This significant improvement in disease recognition performance can be attributed to ViT's unique architecture, which effectively captures long-range dependencies and intricate relationships between image patches. The self-attention mechanisms in the ViT enable it to discern subtle

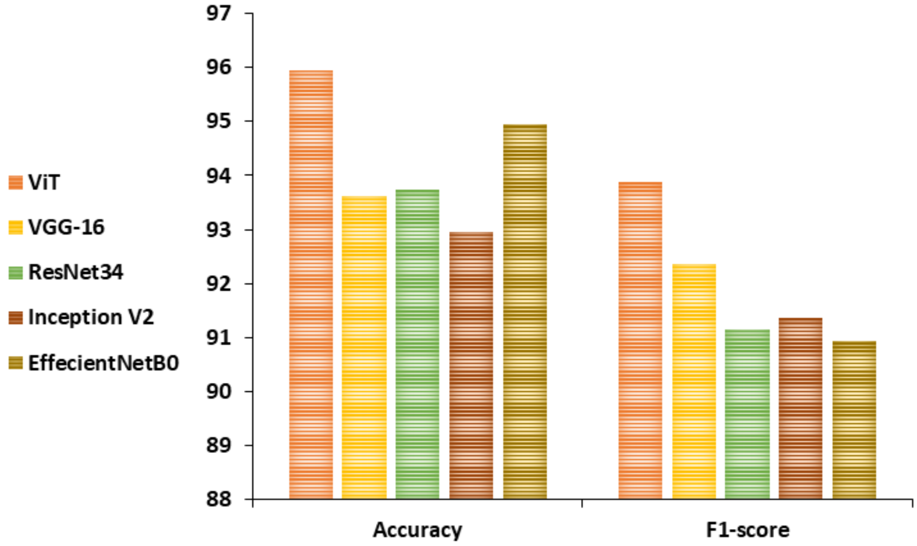

Figure 5. comparison of our model against convolutional baselines

patterns and features indicative of various plant diseases, contributing to its superior discriminative ability.

6. Conclusions

This research presents a novel and effective approach for plant leaf disease recognition in smart agriculture, leveraging the power of the ViT model. Through rigorous experimentation and analysis, we have demonstrated the superiority of the ViT model over traditional CNNs and its ability to generalize across diverse crops and diseases. The integration of self-attention mechanisms and transformer-based architectures enables the model to capture long-range dependencies in image patches, facilitating accurate and efficient disease identification. Leveraging the widely recognized PlantVillage dataset as a case study, our results showcase the potential of the proposed framework to empower farmers with timely disease detection and management, contributing to enhanced crop productivity and reduced losses. The ViT model's ability to revolutionize disease detection offers a transformative solution to meet the ever-increasing demands of the agricultural industry. As we advance toward a future characterized by precision agriculture and data-driven decision-making, our research serves as a stepping stone, unlocking the potential of machine intelligence to empower farmers and sustainably feed a growing global population.

Supplementary Materials

Not applicable.

Author Contributions

For research articles with several authors, a short paragraph specifying their individual contributions must be provided. The following statements should be used "Conceptualization, B.A. and I.A.; methodology, A.S.; software, A.S.; validation, A.S.; formal analysis, A.S.; investigation, A.S.; resources, A.S.; data curation, A.S.; writing—original draft preparation, A.S.; writing—review and editing, A.S.; visualization, A.S.; supervision, A.S.; project administration, A.S. All authors have read and agreed to the published version of the manuscript.

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Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

Conflicts of Interest

The authors declare that there is no conflict of interest in the research.

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Not applicable.

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