Vineyard Leaf Disease Prediction: Bridging the Gap between Predictive Accuracy and Interpretability

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Abstract. Balancing the accuracy and interpretability of predictive models has been a persistent challenge in traditional approaches. In this study, we advance this field by integrating cutting-edge artificial intelligence (AI) techniques with Explainable AI (XAI) methodologies to significantly enhance both the accuracy and interpretability of vineyard leaf disease predictions. We employ state-of-the-art convolutional neural networks (CNNs) and introduce a fine-grained model architecture featuring, adept at discerning subtle disease indicators in vineyard leaves. This innovative approach not only boosts the diagnostic performance of the models but also provides clear visualizations of the decision-making processes. This study utilizes a focused dataset strategy, incorporating one specialized grape disease dataset (Esca) and a subset of the general PlantVillage dataset, specifically selecting categories relevant to Apple and Grape diseases. The obtained results have demonstrated our model's exceptional capability in accurately identifying and classifying various leaf diseases, showcasing its practical applicability in real-world vineyard management. Furthermore, our approach addresses the vital need for transparency and trust in AI applications within agriculture, particularly in viticulture.

Keywords: vineyard disease detection, artificial intelligence, deep learning, explainable AI (XAI), fine-grained-classification

1 Introduction

Viticulture, the science and practice of grape cultivation, serves as a cornerstone in the global wine industry, contributing significantly to agricultural economies worldwide [1]. However, the health and yield of vineyards are constantly threatened by various leaf diseases that pose a particularly pervasive challenge. For instance, as reported in [2] one of the oldest disease "Esca" has reached upto 80% in various old vineyards in central Italy and its southern parts. This implies that the presence of these diseases, and lack of effective strategies to mitigate them, could cause a severe loss in production. [3]. Traditional pest and disease detection methods in vineyards exhibit inefficiencies, potentially leading to delayed diagnoses and subsequent yield losses [4]. Figure 1, 2, and 3 show the sample images for both healthy and diseased vineyard leaves. The figures show the different diseases in grape leaves like Esca (Esca dataset), BlackRot (PlantVillage dataset), and for apple leaves like AppleScab, and CedarAppleRust (PlantVillage dataset).

Fig. 1. Sample images from Esca dataset

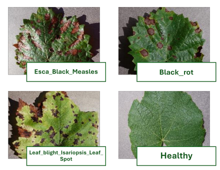

Fig. 2. Sample images from PlantVillage dataset (Grapes)

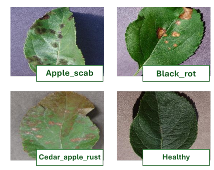

Fig. 3. Sample images from PlantVillage dataset (Apple)

Recognizing these limitations, recent advancements in digital image processing, particularly using AI-based techniques, promise to revolutionize vineyard management practices [5]. These techniques have the potential to expedite anomaly detection within grapevine yields, enabling early intervention strategies to mitigate disease spread and associated financial losses for wine producers [4]. As previously mentioned, the advancements about the use of AI-based techniques in vineyard disease prediction; most of the state-of-the-art (SOTA) studies have recently used deep learning based image analysis techniques such as Convolutional Neural Network (CNN), and its variants like Residual Neural Network (ResNet), and Densely Connected Neural Network (DenseNet) [4]. These techniques will be further discussed later in the paper in section 2. Additionally, transformer-based technique is becoming more popular these days specially for image classification tasks. The most common model in this category is the VisionTransformer (ViT) model [6].

To the best of our knowledge, there exists only single study which used ViT model for leaf disease classification [7]. Hence, in this study we proposed fine-grained model that incorporates a swin-transformer architecture as its backbone to capture detailed image features critical for the accurate classification/predictions of vineyards disease leaf images. Furthermore, this research is distinct in its application, utilizing two public datasets, Esca and PlantVillage as none of the studies have used them together before. Finally, our approach is further enhanced by the integration of XAI techniques, including both Grad-CAM and LIME. Because, we recognize the importance of not only achieving high predictive accuracy but also showing insights against the decision-making procedure of our proposed fine-grained model.

The rest of the paper is organized as follow: Section 2 discusses the relevant SOTA studies and background information; Section 3 shows and explains our proposed methodology; Section 4 discusses the experiments performed with our proposed approach; Section 5 presents our results & findings, and Section 6 shows the conclusion & future work.

2 Related Work

There has been an increasing interest in recent years toward the application of machine learning and deep learning techniques for the early detection and classification of grapevine diseases. In general, there are some new achievements in the early detection and classification of diseases in vineyards. However, most of these studies have focused on broad classifications or have been limited to specific types of diseases without a deeper, fine-grained analysis or robust interpretability mechanisms that are crucial for practical applications. For example, few advancements particularly in the application of CNNs, have facilitated significant progress in the analysis of grape leaf diseases. Alessandrini et al. in [8] proposed a new grapevine image dataset to classify between two classes: healthy and unhealthy grape images affected by Esca disease. The dataset is suitable for various machine-learning tasks, including image segmentation and synthesis. Furthermore, Carraro et al. address the significant challenges of detecting the Esca disease complex in asymptomatic grapevine leaves using CNNs [9]. In their exploration of grapevine diseases, they employ hyperspectral imaging combined with CNNs to differentiate between symptomatic and asymptomatic leaves. While this approach marks a significant step forward, it lacks the deep granularity provided by our proposed model in this study.

Additionally, Zia et al. in [10] further contribute to the enhancement of prediction accuracy and performance in disease diagnosis. They performed using the AlexNet model on the publicly available PlantVillage dataset. As they demonstrated high accuracy using CNNs on the PlantVillage dataset, their approach did not incorporate the critical element of explainability, which is a core component of our proposed approach in our study. The integration of XAI into agricultural AI systems has been in focus of several studies [7, 11, 12]. Bandi et al. utilized the YOLOv5 model to train two different datasets, PlantDoc and PlantVillage, for disease detection and employed ViT for disease stage classification. Expanding upon previous research on disease detection in grapevine leaves, another study introduced by Mamba et al [5] discusses the effectiveness of federated learning in crop disease detection using CNN models and those based on attention mechanisms. In general, the experiments have shown that the performance of federated learning is highly affected by factors such as the number of learners involved, communication rounds, total iterations, and data quality. Among the models tested, ResNet 50 demonstrated the highest performance, while ViTB16 and ViTB32 were found to be less suitable for federated learning due to their computational time and cost implications. Hence, while extensive work has been done on explainable AI, research on interpretable methods in the agricultural field remains limited. The authors in [11] focuses on enhancing the interpretability of deep learning models used in classifying leaf diseases across various fruit leaf datasets. By utilizing models such as ResNet, VGG, and GoogLeNet augmented with attention mechanisms, they demonstrate an improvement in the models' ability to focus on relevant features of leaf images.

In contrast to these studies, our research adopts a unique dual-dataset approach, utilizing both the Esca dataset and specifically the Apple and Grape classes from the PlantVillage dataset. This method is innovative and fills several gaps in the current research by offering a technique that not only improves the accuracy of disease diagnostics but also enhances the interpretability of results across different types of data. By combining the proposed fine-grained model with advanced XAI techniques, our model meets the high-accuracy demands of modern agriculture while also providing deeper insights into the decision making processes. This facilitates greater trust and adaptability in real-world vineyard management. Table 1 shows the SOTA summary of several AI techniques applied for vineyard leaf disease detection together with the gap in the techniques which is covered in our research study.

Table 1. SOTA summary of AI models for vineyard disease prediction

Ref.	**CNN**	**Dense Net**	**Res Net**	**Mobile Net**	**Efficient Net**	**VIT**	**Alex Net**	**YOLO v5**	**VGG**	**Fine Grained**
Paper [8]	✓									
Paper [9]	✓						✓			
Paper [10]	✓			✓			✓			
Paper [7]		✓				✓		✓		
Paper [11]			✓		✓				✓	
Paper [12]			✓	✓	✓			✓	✓	
Our study	✓	✓	✓	✓						✓

3 Proposed Methodology

Figure 4 shows the proposed methodology involving a sequence of steps for processing leaf images for healthy vs disease classification and analysis. Initially, the leaf image undergoes preprocessing steps including resizing, normalization, and augmentation to enhance the dataset and improve the model's robustness. Following this, the fine-grained model combined with Swin-Transformer (Swin T) is employed for the detailed and accurate classification of the leaf images. Finally, the methodology uses Grad-CAM (Gradient-weighted Class Activation Mapping) and LIME (Local Interpretable Model-agnostic Explanations) to interpret and visualize the model's predictions, highlighting important regions of the leaf that contribute to the models' decisions. This approach aims to enhance both the performance and interpretability of the model.

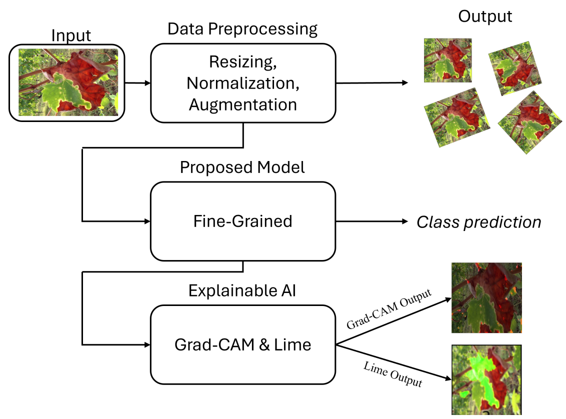

Fig. 4. Proposed Methodology

3.1 Dataset

In this study, we used two SOTA datasets; 1) Esca dataset, and 2) PlantVillage (PV) dataset. From the PV dataset, we selected only two categories grapes and apples. The datasets comprises of healthy and various disease images related to vineyards leaves. The overall distribution as well as train, validation, and test set split is shown in the Table 2.

Table 2. Overall, train, valid, and test set distribution of the datasets

Esca Dataset					PlantVillage (Grapes) Dataset					PlantVillage (Apple) Dataset				
	Train set	Valid set	Test set	Total		Train set	Valid set	Test set	Total		Train set	Valid set	Test set	Total
Healthy	529	132	221	882	**Healthy**	254	423	106	783	**Healthy**	987	1645	411	3043
Esca	533	133	222	888	**Black Rot**	708	1180	295	2183	**Apple Scab**	378	630	158	1166
					Black Measles	830	1383	346	2559	**Black Rot**	373	621	155	1149
					Leaf Blight	646	1076	269	1991	**Cedar Apple Rust**	165	275	69	509
Total	1062	265	443	1770	**Total**	2438	4062	1016	7516	**Total**	1903	3171	793	5867

3.2 Preprocessing

This section outlines the preprocessing steps essential for preparing the data for subsequent model training and analysis. 1) **Image Resizing**: In the preprocessing stage, all images from both datasets were initially resized to 1280×720 pixels. This standardization was crucial for ensuring consistency across all instances, particularly for the SOTA models such as CNN, DenseNet, and ResNet. For the fine-grained implementation, however, the images were resized to 384×384 pixels. The reason for choosing this size was to facilitate feature extraction without compromising consistent information across images.

2) **Data Normalization**: Before feeding the data to the model, we have normalized the data with the mean values 0.4762, 0.3054, 0.2368, and standard deviation values 0.3345, 0.2407, 0.2164. This normalization process helped center the data around zero and scale it to a comparable range, facilitating stable and efficient model training. 3) **Data Augmentation**: We implemented data augmentation techniques to increase the diversity and improve the robustness of the training dataset. The techniques opted for augmenting images include horizontal and vertical flips, rotation of up to 90 degrees, and scaling.

3.3 Fine-Grained Model

Figure 5 illustrates the basic architecture of fine-grained model used as a part of the proposed methodology. The proposed model utilizes the Swin-Transformer as its backbone, due to its effectiveness in capturing fine details through its hierarchical architecture. The Swin-Transformer is composed of four integral components, Patch Partitioning, Swin Transformer Blocks, Shifted Window, and Feature Hierarchy. It first segments the image into non-overlapping patches. Further, these patches are processed through a series of Swin-Transformer Blocks with a shifted window framework, which enhances the model to capture local features with the global context in a flexible and efficient fashion. [13]. This approach will be very good in complex tasks of image classification for tasks like vineyard leaf disease prediction.

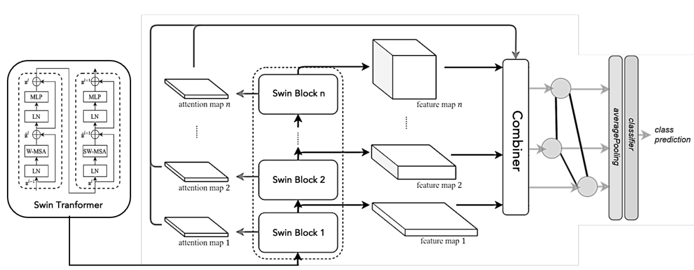

Fig. 5. Model Architecture for fine-grained model with Swin Transformer as a backend.

3.4 Explainable AI (XAI)

In fact, the increased use of AI in the treatment of healthcare and agricultural management is leading to increased demand for transparency and understandability in such systems [14]. The subsequent section discusses ways in which we have implemented XAI techniques, such as Grad-CAM and LIME, in order to increase the transparency and trustworthiness of our predictive models. 1) **Grad-CAM**: In our experiments, we have used the Grad-CAM model to visualize the explanation of the decisions and predictions from our models. The ability to show us the points of focus in an image makes it a great tool for providing such information [15]. Thus, this serves to highlight parts of the input that most affect the model's decision—valuable interpretability [16].

2) **LIME**: LIME helps in understanding complex model decisions by changing the input data and looking at how those changes affect the output. This approach adds another perspective by showing what features contribute to bringing about a prediction. In disease detection from vineyards, for example, LIME can show how features of the image of leaves, such as spots or color gradations, lead to the identification of a specific disease. Thus, with LIME, we can embellish the interpretability of our model, ensuring that the decisions are precise and comprehensible at a granular level.

4 Experiments

This section discusses the experimental detail which we performed to evaluate the performance of SOTA models vs our proposed fine-grained model on the task of leaf disease prediction. Our approach employed a series of pre-trained models that includes DenseNet121, DenseNet169, ResNet50, MobileNetV2, and the proposed FineGrained model across two distinct datasets: Esca, which is specific to grapevine leaves, and selected classes from the PlantVillage dataset, namely Apple and Grapes.

We selected several SOTA models such as DenseNet121, DenseNet169, ResNet50, MobileNetV2 to compare their performance with our proposed fine-grained model using swin-transformer. We trained, validated, and tested all the SOTA as well as our proposed model on the respective selected datasets' using the distribution shown in the Table 2 with the following hyperparameters shown in the Table 3.

Table 3. Hyperparameters for models' training

Batch size	8 to 32
Learning rate	0.0001
Epochs	30

To evaluate the performance of our predictive models, we used a comprehensive set of key metrics that include accuracy, precision, recall, and f1-score. The below four equations show how all of these metrics are calculated.

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

$$\text{Precision} = \frac{TP}{TP + FP} \tag{2}$$

$$\text{Recall} = \frac{TP}{TP + FN} \tag{3}$$

$$\text{F1-Score} = 2 \times \frac{\mathrm{P} \times \mathrm{R}}{\mathrm{P} + \mathrm{R}} \tag{4}$$

*TP = True Positive; TN = True Negative; FP = False Positive;

*FN = False Negative; P = Precision; R = Recall

5 Results and Discussion

This section discusses the results obtained using the experiments performed based on experimental settings explained in the section 4.

5.1 Fine-Grained model results

The results shown in Tables 4, and 5 clearly show the proposed fine-grained models' improved performance compared to other SOTA models. The proposed model in this study achieved 100% scores for all the evaluation metrics discussed in the section 4. The use of the fine-grained model with swin-transformer backbone significantly enhanced its capability to discriminate between closely related disease states, providing high precision and recall.

Table 4. Performance Metrics for Esca Dataset

Model	Accuracy	Precision	Recall	F1 Score	Support
DenseNet121	1.00	1.00	1.00	1.00	444
ResNet50	0.99	0.99	0.99	0.99	443
DenseNet169	1.00	1.00	1.00	1.00	444
MobileNetV2	0.99	0.99	0.99	0.99	443
FineGrained	1.00	1.00	1.00	1.00	444

Table 5. Performance Metrics for PlantVillage Dataset

Model	Apples				Grapes			
	Acc.	Prec.	Recall	F1	Acc.	Prec.	Recall	F1
DenseNet121	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
ResNet50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
DenseNet169	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
MobileNetV2	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99
FineGrained	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Furthermore, Figure 6, 7, and 8 shows the confusion matrices of the proposed fine-grained models' performance on the test set of the datasets shown in the Table 2. Figure 6 shows the performance of fine-grained model for predicting the test dataset images either as "Healthy" or affected by "Esca". The confusion matrix shows perfect classification performance, with no false positives or false negatives. The fine-grained model correctly identified all 221 healthy samples and all 222 Esca-affected samples. This indicates a highly accurate model for this dataset, as every prediction made was correct.

Figure 7 shows the performance of fine-grained model, specifically for predicting various diseases of grapes leaves from PlantVillage dataset. The diseases being predicted are "Black rot," "Esca black measles, "Leaf blight isariopsis leaf spot", and "Healthy". The confusion matrix indicates that the model has perfectly classified all samples across all the target classes. The model demonstrates perfect accuracy for the given dataset, correctly classifying all samples into their respective classes without any errors. This suggests highly effective performance of the model for predicting these specific grapes leaves diseases from the PlantVillage dataset. Figure 8 shows the fine-grained models' performance specifically for predicting various diseases of apple leaves from PlantVillage dataset. The diseases being predicted are "Apple scab", "Black rot", and "Cedar apple rust". The confusion matrix indicates that the model has perfectly classified all samples across all the target disease classes together with "Healthy" class. This demonstrates the model's high effectiveness and accuracy in distinguishing between Apple scab, Black rot, Cedar apple rust, and Healthy classes.

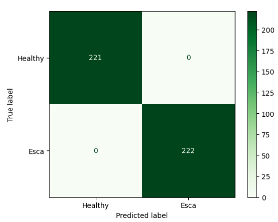

Fig. 6. Confusion matrix for Esca dataset using fine-grained model

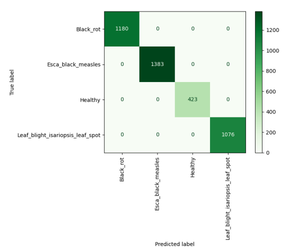

Fig. 7. Confusion matrix for grape leaves from PlantVillage dataset using fine-grained model

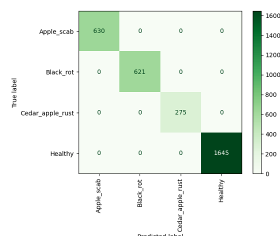

Fig. 8. Confusion matrix for apple leaves from PlantVillage dataset using fine-grained model

5.2 XAI results

Figure 9 illustrates the application of XAI techniques, specifically LIME and Grad-CAM, to various datasets of leaf images affected by different diseases. The image is structured in a tabular format with three main columns: "Original Image", "LIME", and "Grad-CAM". In this visual representation, we observe how two prominent XAI techniques, LIME and Grad-CAM, explain the decision-making process of the proposed fine-grained model tasked with classifying vineyard leaf diseases. The Original Image column shows the raw images of leaves, each exhibiting distinct disease symptoms. In the LIME column, the model's predictions are explained by highlighting regions of the leaves that significantly influence its decision. LIME, on the other hand, uses a colorised overlay, with light green areas highlighting the sections that agree with the result and dark red areas highlighting those which disagree with it, making it easier to trace out which parts of a leaf contributed most towards predicting whether or not it was disease.

The Grad-CAM column, on the other hand, is a more comprehensive one which involves overlaying heatmaps on the images. These heatmaps typically show the areas where the model pays more attention, with the warmer colors implying that something is far much important than the others. For the ESCA dataset, both LIME and Grad-CAM point out discolored parts that are affected by disease on the leaf, thereby affirming these areas as essential for predicting by the model. Like LIME, Grad-CAM emphasizes the spotted areas in the images in line with the exhibited symptoms. Both methods clearly show the damage patterns in the images which the model is interested in when diagnosing a disease. This side-by-side visualization is centered on the potential uses of LIME and Grad-CAM in the process of understanding and verifying the outcomes of models as well as shedding light on what the model takes into account and why it makes decisions. In this regard, implementing these XAI techniques helps make AI models that aid in agricultural diagnostics more understandable and trustworthy because their main focus can be broken down into simple words while showing how some regions in the pictures contribute towards identifying diseases.

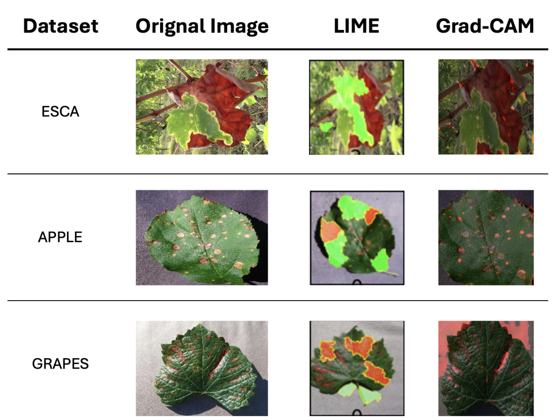

Fig. 9. XAI results for fine-grained model performance

6 Conclusion & Future Work

The study has managed to bridge the gap between high prediction accuracy attainment and model interpretation within vineyard leaf disease prediction. The detection of leaf disease has been greatly improved through the application of fine-grained models as well as interpretability techniques like LIME and Grad-CAM. We did not only improve the accuracy of detection but also conveyed actionable knowledge to vineyard owners through our findings, who can use it for disease management strategies that form basis for decision making. Our research progress is of great significance for AI application in farming especially in connection with growing grapes. Users grasp and rely on system predictions better hence increasing their use in vineyard operations. This research helps in developing AI models that are beneficial in cultivating vineyards sustainably through provision of in-depth interpretations for model predictions, important in ascertaining onset symptoms of diseases for prompt remediation.

In future work, we are planning to further improve the proposed approach by applying it to real-world dataset by collecting leaf images directly from vineyards. Further, we would also like to use federated learning to retain data privacy and security. This method can be used to train federated models across a good number of decentralized devices or servers, holding local data samples, without the need for data sharing—thereby keeping sensitive information at source. This approach will enhance not only the strength and generalization of our model but also meet regulations and industry standards for data privacy, making it more suitable for field practice within agricultural settings.

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