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VGG-DAGSVM FOR MULTI-CLASS APPLE LEAF DISEASE DETECTION: A TRANSFER LEARNING APPROACH

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ABSTRACT

Apple cultivation is essential in world agriculture because of its high nutritional benefits and economic importance. However, increasing pressures from foliar diseases such as apple scab, cedar apple rust, and black rot seriously threaten yield and quality within UK apple orchards. One strategy is to capitalize on advanced technologies such as computer-aided diagnosis systems for improved detection and classification of diseases. To address this challenge, this paper proposes a generic and automatic solution to recognizing and classifying diseases of apple fruit leaves leveraging the VGG-DAGSVM architecture. The workflow begins with bilateral filtering to mitigate image noise without losing core edge information, and Contrast Limited Adaptive Histogram Equalization (CLACHE) for contrast enhancement. SegNet is used to accurately segment diseased regions, and the VGG-19 deep learning model features extraction. Finally, a Directed Acyclic Graph Support Vector Machine (DAGSVM) is used as the classifier for accurate disease classification. Experimental evaluation uses a publicly available dataset comprising 13,124 apple leaf images across four categories. The proposed model achieves a classification accuracy of 96.50%, precision of 96.05%, sensitivity of 95.92%, specificity of 96.43%, and F-score of 96.45%, outperforming several existing models. These results demonstrate the robustness and applicability of the potential of integrating image processing, deep feature extraction, and intelligent classification systems to support early disease detection and promise sustainable apple farming practices.

Keywords: *Apple leaf, Diseases, Deep Learning, Transfer Learning, Support Vector Machine.*

1. INTRODUCTION

Apples, often referred to as the crown jewel of the fruit world, are admired globally for their crisp texture, vibrant appearance, and exceptional nutritional benefits. Apple is one of the most popular and most important fruit trees, but faces a serious challenge in apple cultivation mainly due to the widespread leaf disease. These diseases can have a detrimental impact on both the yield and quality of the crop, resulting in huge economic losses for farmers. Computer-aided diagnosis systems, now evolving technology concerning information and computer technology, have transformed the spectrum of these agricultural attributes, enabling faster, more accurate, and more consistent diagnosis and classification of apple diseases [1]. Renowned not just as a snack that tastes great, but also for their healthy properties, apples are high in many vitamins, including C and K, dietary fiber, and antioxidants. These include staving off chronic diseases, supporting immunity, and aiding heart and bone health, digestion, and more. From an economic standpoint, apples are a fundamental crop in many nations, bolstering local economies, fueling exports, and creating jobs. So, preserving their health with innovative disease management solutions is paramount to contributing to keeping the supply chain alive and thus maintaining global demand [2].

However, apple farmers frequently combat easy diseases like apple scab, fire blight, powdery mildew, and cedar apple rust. These infections diminish plant health and quality, leading to significant economic losses if not treated promptly [3]. Traditional inspection methods are often inadequate — these tend to be time-consuming, heavily dependent on human expertise, and can lack the precision needed for early detection. In this context, AI and image-based computer-aided systems have emerged as an effective alternative

[4]. These systems utilize machine learning or deep learning algorithms to analyze digital images of leaves to quickly detect disease symptoms, thus increasing the speed and accuracy of detection. Pre-trained CNNs, such as VGG and ResNet, have shown remarkable performance in agricultural diagnostics, particularly in conjunction with transfer learning. The ability of these models to learn sophisticated representations of high-dimensional data in one domain and then apply this knowledge to learn new tasks in another domain makes this type of model very good for problems such as the detection of plant diseases [5].

However, many previous apple disease detection methods still directly classify the original pictures without sufficient preprocessing or segmentation. These methods suffer from real-world variability, including noise, low contrast and complex backgrounds, resulting in low accuracy of classification. Moreover, when it comes to the multi-class case, basic classifiers like Softmax or SVM do not deal effectively with many classes and with overlapping feature distributions.

To overcome these challenges, in this work we present an end-to-end multi-stage integrated framework that first utilizes bilateral filtering to remove noise, then performs local contrast enhancement using CLAHE and finally isolates more accurately the diseased region using SegNet based segmentation. Caricature features are extracted with a deep network of VGG-19, and then transferred using transfer learning. In testing, a DAGSVM is applied to enhance the efficiency of multi-class discrimination for classification.

This hybrid VGG-DAGSVM architecture not only improves the robustness of disease detection but also helps adopt early intervention measures in orchards. During the identification of the pests, this system enables automation with high accuracy, enables farmers to give timely treatments, and helps them reduce losses. This supports sustainable apple production. Our model introduces an original fusion of deep learning and classic machine learning units, which in combination presents more superior solution than the traditional models, which has been validated in extensive experimental and comparison analysis [6].

This paper is structured as follows: Section 1 introduces the topic. Section 2 describes related work. In Section 3, we describe the proposed methodology. Experiments and analysis are provided in Section 4. Section 5 concludes the study and suggests future research directions.

2. RELATED WORKS

In [7], a deep learning-based [VGG16] approach for apple leaf disease detection and classification is presented. This model detects conditions like early symptoms (such as small spots) and widespread lesions that require quick intervention. As proposed in [8], the Enhanced Efficient Deep Learning framework for the detection and classification of five common apple foliar diseases. The second one customizes the Efficient Net B0 model by adding 4 additional layers- an augmentation layer, a dense layer, a dropout layer, and a final output classifier dense layer.

The author in [9] proposes a deep learning-based methodology for apple leaf detection and classification with better accuracy based on an integrated neural architecture for accurate and fast Single Shot MultiBox detector (INAR-SSD) techniques. In [10], the author implements deep learning methods to detect apple leaf disease using VGG-16, which yields a validation accuracy of 97.23%. This is the best model, as it helps farmers in the early diagnosis and treatment of apple leaf disease.

The model achieved an accuracy of 94.09%, which is an accurate image classification for real-time early disease detection with the fastest processing speed compared to existing methods. Faster RCNN, R-SSD, and INAR-SSD. For this research, the author [11] proposed different selections for early detection and classification of apple leaf diseases by using the IFPA-GA approach with MC-SVM and SVI. Author [12] presents an indigenous dataset for the detection and classification of apple leaf diseases using deep learning. It overcomes the challenge of manual detection in a focused manner by providing a widely distributed dataset augmented with techniques to increase the accuracy of the model and the capability to avoid unknown edges. Author [13] proposes a methodology for detecting and classifying apple leaf diseases, specifically black rot, scab, and rust, using Convolutional Neural Networks (CNNs). A classification accuracy of 92.5% is achieved using a customized dataset that includes high-resolution photos of healthy and infected leaves.

Author [14] proposed Transfer Net, a transfer learning model based on RESNET50V2, which detects and classifies apple leaf diseases with achieves an accuracy of 91.63% and F1 score of 91.03%, precision of 94.14%, and recall of 88.12% on the FGCV-8 dataset. The paper [15] introduced E-AppleNet, leveraging EfficientNetV2, attention mechanisms, and dense layers, to bolster apple leaf disease classification. With a 99% accuracy on the PlantVillage dataset, and successfully tackles issues such as image distortion and class imbalance using transfer learning and multi-class focal loss.

3. PROPOSED WORK

The VGG-DAGSVM methodology follows a structural and efficient workflow, illustrated in Fig.1. The process starts with Bilateral Filtering, which effectively removes noise from the leaf images while preserving important edge details, improving the overall image clarity. Following this, CLACHE is applied to improve the local contrast of the images. After that, for segmentation, a SegNet-based model is used to isolate the diseased regions from the healthy parts of the leaf precisely. Following segmentation, deep features are extracted using the VGG-19 model, leveraging its strong representational power through transfer learning. These extracted features are then passed to a Directed Acyclic Graph with Support Vector Machine (DAGSVM) classifier, which efficiently handles multi-class classification to distinguish between different types of apple leaf diseases. Detailed explanations of each step are provided in the upcoming sections.

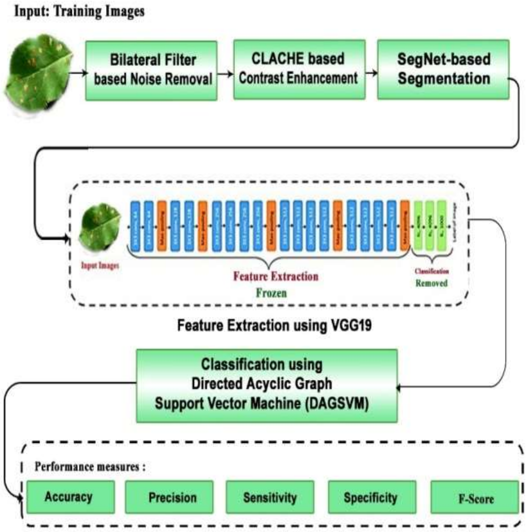

Fig. 1. *Overall Architecture of the proposed VGG-DAGSVM model*

3.1 Bilateral Filter-Based Noise Removal

The Bilateral filter is a widely used technique for noise reduction in image processing. It is particularly beneficial in detecting and classifying diseases in apple leaves. It effectively smooths out noise, preserving important edge details, making it highly suitable for enhancing image quality before disease analysis [16], as illustrated in Fig. 2.

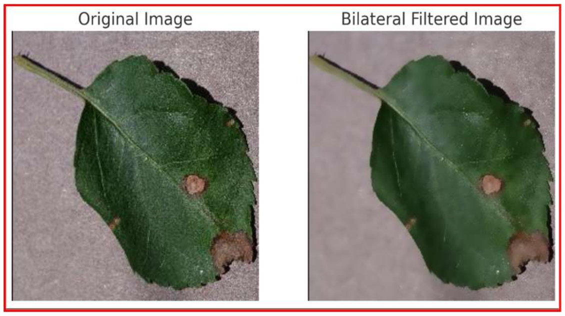

Fig. 2. *Bilateral filter-based noise-removed image*

The Bilateral filter is expressed as shown in Eq. (1):

$$B(I)_p = \frac{1}{W_p} \sum_{q \epsilon \Omega} I_q \cdot g_{\sigma_s}(\| p - q \|) \ . \ \ g_{\sigma_r}(| I_p - I_q |) \qquad (1)$$

In Eq. (1), where:

- The bilateral filter is applied to the input image I to produce a filtered image *B(I)*, where the output value at each pixel location p is determined by combining both spatial and intensity information.
- Specifically, $(I)_p$ and $(I)_q$ represent the intensity values at pixels p and q in the original image.
- The filter operates over a neighborhood Ω around each pixel p.
- A spatial Gaussian function $g_{\sigma_s}(\| p - q \|)$ accounts for the geometric closeness between p and q, while a range Gaussian function $g_{\sigma_r}(| I_p - I_q |)$ evaluates their intensity similarity. This dual consideration ensures that edges are preserved while smoothing regions with similar intensities.
- The normalization *Wp* ensures proper scaling of the filtered result. When applied to apple leaf images, this method effectively reduces noise and retains essential features such as disease indicators and texture details.

3.2 CLACHE-Based Contrast Enhancement

In the proposed disease detection pipeline, contrast enhancement is a crucial stage to enhance the visual contrast between healthy and diseased regions of the apple leaf. In this respect, Contrast Limited Adaptive Histogram Equalization (CLAHE) is used to pre-process the image before applying the Segmentation. It differs from global histogram equalization techniques which adjust contrast of an image uniformly by dividing the image into small and non-overlapping regions and then transforming the intensity value of each of these regions separately and therefore, is particularly suitable for agricultural images that are subjected to different illumination conditions and may have mild characteristics of the diseases [17].

The CLAHE works by splitting the input image into smaller non-overlapping tiles (for each tile) and carrying out histogram equalization for each of those. This increases local contrast and even slightly varying intensity, such as very dark or light disease spots, is more detailed. To avoid excessive noise enhancement of small details, the noise amplitude in CLAHE is restricted by a clip limit to a given constant. The upscale tiles are smoothed by bilinear interpolation, so that there are no artificial boundaries between the two neighboring blocks. CLAHE was used in the present study, where the Luminance (L) channel was used after the image was converted to the LAB color space, which separates luminance from chromatic components. With this method, the enhancement is applied only to the brightness information while the original color composition, an important element for the disease classification, is preserved.

Fig. 3. *Sample Contrast Enhanced Image*

The visibility of disease-affected areas increased significantly after CLAHE application, and texture became more discernible, as well as the boundaries, as depicted in Fig. 3. This directly facilitated the subsequent segmentation, as better extraction of infected regions could be obtained. Improved disease type classification, in turn, benefited from better segmentation results as well as feature extraction presented in the later stages of the processing pipeline. This pre-processing technique helped normalize the contrast of the image under different capture conditions (i.e., outdoor and shadows), leading to the robustness and the trustiness of the automated apple leaf disease detection system.

3.3 SegNet Based Segmentation

SegNet is a deep learning based semantic segmentation architecture that is important for accurately identifying and classifying a region of a diseased apple leaf in an image. It is highly effective in separating the infected part of the leaf by keeping focus on the healthy part of the leaf to analyze and classify properly [18].

SegNet is a convolutional encoder-decoder architecture focused on pixel-wise segmentation tasks. The encoder part is usually based on a pre-trained CNN base (VGG16/VGG19, for instance) that enables the extraction of hierarchical features from the input image. The decoder consists of layers that upsamples these encoded features to restore the spatial resolution and results in a segmented output, classifying each pixel in a desired category (i.e., diseased Vs healthy region).

SegNet is a deep learning framework as depicted in Fig. 4, designed for semantic segmentation, focusing on learning class boundaries through the encoding and decoding of feature maps. By performing a series of convolutional and pooling layers, the input image is compressed spatially to the encoder network, forming abstract and discriminative features. The decoder receives these feature maps, and with the pooling indices from the encoder, it performs non-linear upsampling to keep spatial accuracy in the segmentation outputs. The final output for segmentation is a probability distribution over the classes for each pixel, obtained using a SoftMax activation function in the last layer and assigning a class label to each pixel. This ability allows even small or subtle diseased areas on apple leaves to be recognized accurately.

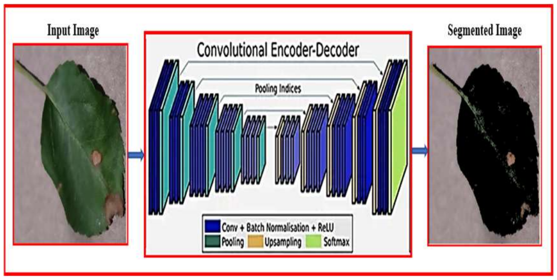

Fig. 4. *SegNet Architecture*

Let the encoder be represented as a function E, and the decoder as D, then the segmented output $S(x, y)$ at pixel coordinates (x, y) can be represented as:

$$S\,(x,y) = D\,(E\,(\,Image\,(x,y))) \tag{2}$$

In Eq. (2), where:

- $Image\,(x,y)$ represents the input apple leaf image.
- E encodes features from the image using convolution and pooling.
- D decodes those features using upsampling guided by pooling indices.
- $S\,(x,y)$ is the segmented output, labeling each pixel as either diseased or healthy.

3.4 Feature Extraction Using VGG-19

VGG-19 is a deep convolutional neural network architecture that includes a configuration of convolutional, Max-Pooling, and fully connected layers. As a foundational model, VGG-19 was originally trained on large-scale images (for example, ImageNet as a benchmark) renowned for their capability to extract complex visual features, including edges, textures, patterns, and shapes, relevant to high-level image classification tasks. Its simplicity and depth make it not only a powerful and competitive candidate for tasks with rich feature representation but also a strong candidate for tasks such as apple leaf disease detection.

In this study, a pre-trained VGG-19 network is used as a feature extractor for apple leaf image sensing. When feeding an apple leaf image through the network, VGG-19 extracts deep feature activations from various parts of its intermediate layers, usually the fully connected layer or convolutional block before the final flatten stage. The activations from this are combined as feature vectors characterizing the visual properties of the leaf as it relates to the disease, which may consist of complex patterns (e.g., spots, discoloration, texture changes). Since VGG-19 is already trained on a wide range of data, it has a very good knowledge of generalized visual features. But transfer learning is employed to tailor it in greater detail to the task of classifying apple leaf diseases. By freezing the top layers of the model–that is, those that learn general features–training the last layers with a specific dataset of labeled images [19] of apple leaves as depicted in Fig. 5. Such a learning process improves the model's attention on global features related to a disease and is unique to apple leaves. By leveraging the powerful generalization ability of VGG-19 and adapting it through transfer learning, this methodology ensures a more precise, robust, and scalable solution for real-time apple leaf disease detection and classification.

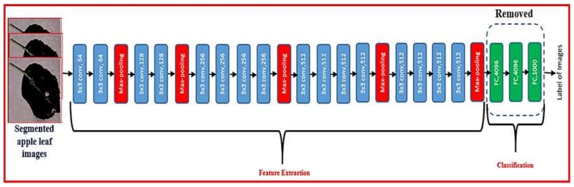

Fig. 5. *Architecture of VGG-19 for feature extraction*

3.5 Classification Using DAGSVM

The DAGSVM, or Directed Acyclic Graph Support Vector Machine, is a powerful multi-class classification approach based on the rationale behind Support Vector Machines (SVMs). As an extension of standard SVM, DAGSVM can construct a multi-class classifier more efficiently by building binary classifiers on top of a Directed Acyclic Graph (DAG), as standard SVM can only separate two classes [20]. So, DAGSVM ensures a superior classification mechanism in the apple leaf disease detection and classification application domain, especially while classifying the multiple-class disease (in this case, whether the leaf is affected by apple scab, rust, black rot, etc.), as well as for healthy leaf detection as depicted in Fig. 6. Once the features are extracted through a deep learning model (VGG-19), the resulting feature vectors are fed into the DAGSVM to get the final classification.

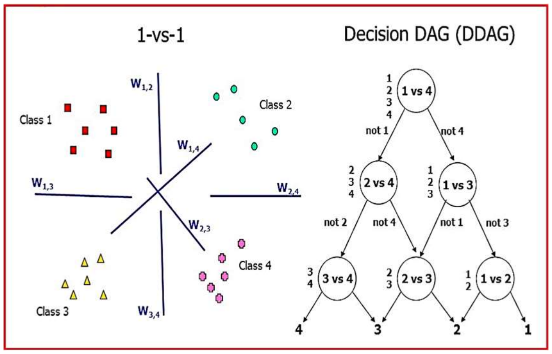

Fig. 6. *Structure of Directed Acyclic Graph Support Vector Machine (DAGSVM)*

DAGSVM builds $\frac{N(N-1)}{2}$ Binary Support Vector Machine (SVM) classifiers for a classification task of N classes. Each of these is trained to distinguish between a unique pair of classes i and j, as shown in Eq. (3):

$$f_{ij}(x) = sign\big(\omega_{ij}^{T}x + b_{ij}\big) \tag{3}$$

In Eq. (3), $f_{ij}(x)$ denotes the Decision Support, ω_{ij} refers to the Weight vector, x refers to the Input features, and T stands for transpose. b_{ij} stands for Bias term, and $sign(.)$ refers to the class decision (+1/-1). If $f_{ij}(x) > 0$, then class i *"wins"*, and class j is eliminated. If $f_{ij}(x) < 0$, then class j *"wins"*, and class i is eliminated.

DAGSVM arranges all classifiers in the form of a Directed Acyclic Graph instead of utilizing all classifiers at once. This makes each node in the DAG a binary classifier, while edges determine the path based on whether a classifier at a node hits positive or negative. Inference starts at the root node of a DAG during the process of prediction. At each node, a decision is made between two classes, with the class that loses the comparison being eliminated as shown in Eq. (4):

$$\begin{bmatrix} If\, f_{ij}(x) > 0 \;\rightarrow\; \text{Eliminate class } j \\ Else \;\rightarrow\; \text{Eliminate class } i \end{bmatrix} \tag{4}$$

The classifier then forwards the process to the next relevant node and continues the elimination round by round. Eventually, only one class remains, and it is set as the predicted label. This graph-oriented structure not only lowers the number of classifiers evaluated during inference time but also makes DAGSVM computationally efficient and scalable for multiclass-target problems, such as the classification of apple-leaf-disease categories.

3.6. Comparison With Prior Work

To differentiate our methodology from existing studies, we include a direct comparison with other leading models [22], such as MobileNet, ResNet152, and INAR-SSD, etc. which are depicted in Table 3. Unlike earlier works that relied solely on image classification, our model integrates bilateral filtering, CLACHE–based enhancement, SegNet-based segmentation, and a hybrid deep learning- classical classification strategy. Most prior work neglected the importance of robust segmentation and multi-stage preprocessing. By incorporating DAGSVM, our model further optimizes classification efficiency and decision flow in a multiclass environment.

4. EXPERIMENTAL RESULTS

4.1 Implementation Setup

To assess the performance of the VGG-DAGSVM model in detecting and categorizing apple leaf disease, a series of validation experiments were performed using healthy and diseased leaf images. The evaluation was conducted in a computing environment configured with Python version 3.6.5, running on a system equipped with an Intel i5-8600K processor, 16GB of RAM, a 250GB SSD, a 1TB HDD, and a GeForce 1050 Ti graphics card with 4GB of memory. The performance evaluation of the VGG-DAGSVM analyzes key metrics like accuracy, sensitivity, specificity, precision, and F-score. The apple fruit leaves dataset from the Kaggle repository is used (PlantifyDr Database) for experimental validation [21]. The dataset contains 3105 apple black rot-infected leaf images, 4234 healthy leaf images, 3232 apple scab-infected images, and 2553 Cedar apple rust-infected images. Sample images for each classification are depicted in Fig. 7, along with the corresponding samples are shown in Table 1.

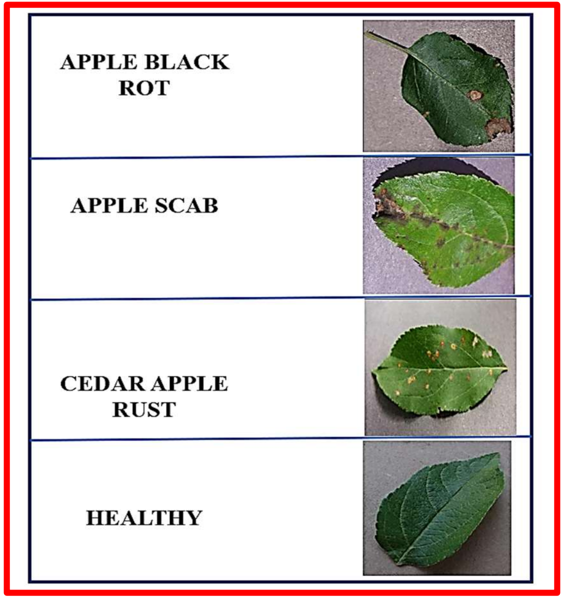

Fig. 7. *Sample Images*

Table 1. *Dataset Description*

Class	**No. Of. Samples**
Apple black rot	3105
Healthy	4234
Apple scab	3232
Cedar apple rust	2553
Total	**13124**

4.2 Discussions and Observations

Fig. 8 presents the confusion matrix, highlighting the classification challenges encountered by the VGG-DAGSVM model across various apple leaf disease categories. The evaluations of the VGG-DAGSVM model, as seen in Table 2, highlight its effects in diagnosing Apple Leaf diseases within training and testing datasets. The research used a 70% and 30% split between training and testing data. The proposed model shows exceptional performance in identifying and classifying diseases in Apple Leaf images, by achieving high metrics such as an accuracy of 96.50%, a Precision value of 96.05%, a Sensitivity of 96.93%, an F-score of 96.45%, and a Specificity of 96.43%.

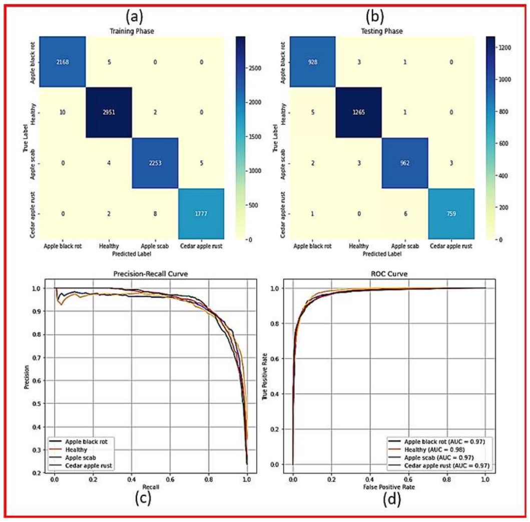

Fig. 8*. (a) Confusion Matrix based on TR set, (b) Confusion Matrix based on TS set, (c) Precision-Recall Curve, (d) ROC Curve*

In Fig. 9, the comprehensive disease detection results of the VGG-DAGSVM model are studied in terms of Accuracy, Precision, Sensitivity, Specificity, and F-score based on training data. In the Apple black rot class, the VGG-DAGSVM model obtains Accuracy, Precision, Specificity, Sensitivity, and F-score of 94.80%, 94.30%, 95.10%, 95.00%, and 94.60%, respectively. Concurrently, for the Healthy class, the model gains 96.10% of accuracy, 95.10% of precision, 95.50% of specificity, 95.50% of sensitivity, and 95.80% of F-score values, respectively. Similarly, for the Apple scab class, the VGG-DAGSVM model obtains 95.30%, 94.80%, 95.30%, 94.60%, and 95.20% of Accuracy, Precision, Specificity, Sensitivity, and F-score values, respectively. For the Cedar apple rust class, the VGG-DAGSVM model achieves Accuracy, Precision, Specificity, Sensitivity, and F-score of 95.80%, 95.30%, 95.40%, 95.10%, and 95.70%, respectively.

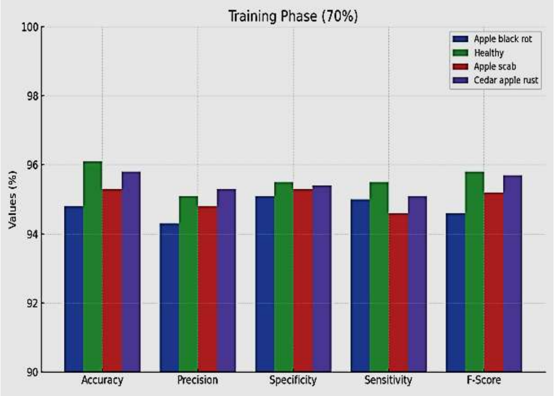

Fig. 9. *Outcomes of the VGG-DAGSVM model on 70% of the training dataset*

In Fig. 10, the comprehensive disease detection results of the VGG-DAGSVM model are studied in terms of Accuracy, Precision, Sensitivity, Specificity, and F-score based on testing data. In the Apple black rot class, the VGG-DAGSVM model obtains Accuracy, Precision, Specificity, Sensitivity, and F-score of 95.90%, 95.40%, 95.80%, 95.10%, and 95.70%, respectively. Concurrently, for the Healthy class, the model gains 97.30% accuracy, 96.60% of precision, 96.70% of specificity, 96.80% of sensitivity, and 97.20% of F-score values, respectively. Similarly, for the Apple scab class, the VGG-DAGSVM model obtains 96.40%, 96.00%, 96.40%, 95.70%, and 96.30% of Accuracy, Precision, Specificity, Sensitivity, and F-score values, respectively. For the Cedar apple rust class, the VGG-DAGSVM model achieves Accuracy, Precision, Specificity, Sensitivity, and F-score of 96.40%, 96.20%, 96.80%, 96.10%, and 96.60%, respectively.

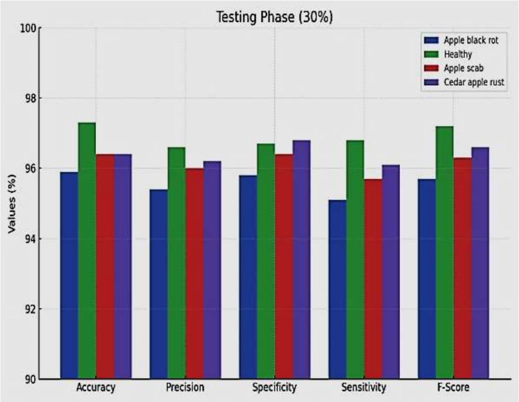

Fig. 10. *Outcomes of the VGG-DAGSVM model on 30% of the testing dataset*

***Table 2.** Outcomes of the VGG-DAGSVM model for Apple Leaf disease Detection and Classification*

Class	Accuracy (%)	Precision (%)	Specificity (%)	Sensitivity (%)	F-Score (%)
Training Phase (70%)					
Apple black rot	94.80	94.30	95.10	95.00	94.60
Healthy	96.10	95.10	95.50	95.50	95.80
Apple scab	95.30	94.80	95.30	94.60	95.20
Cedar apple rust	95.80	95.30	95.40	95.10	95.70
Average	**95.50**	**94.88**	**95.32**	**95.05**	**95.33**
Testing Phase (30%)					
Apple black rot	95.90	95.40	95.80	95.10	95.70
Healthy	97.30	96.60	96.70	96.80	97.20
Apple scab	96.40	96.00	96.40	95.70	96.30
Cedar apple rust	96.40	96.20	96.80	96.10	96.60
Average	**96.50**	**96.05**	**96.43**	**95.92**	**96.45**

Table 3 highlights the improved performance of the new VGG-DAGSVM model using an in-depth comparative analysis. The table provides an evaluation of the VGG-DAGSVM model's Accuracy compared to Table 3; the accuracy figures for the models cited as [22] were noted as being the lowest, recorded at 73.05%, 75.99%, 77.65%, 78.80%, 93.51%, and 93.58%, respectively. On the other hand, sensitivity measurements for the [22] models showed lower rates, ranging from 73.00% to 93.03%. The proposed VGG-DAGSVM model outperformed these with a sensitivity rate standing at 95.92%. When it comes to precision metrics for those models marked as [22], results were also significantly lower, stretching from 73.00% to 93.00%. The proposed VGG-DAGSVM model, however, demonstrated better precision, hitting a mark of 96.05%. Additionally, the F-score evaluation reveals that F-score metrics for the [22] models were lower too, spanning from 72.99% to 93.02%. The VGG-DAGSVM model achieved an F-score of 96.45%, which strongly reflects its robust classification performance. Fig. 13 provides a graphical comparison of the newly proposed model with existing ones.

The TACY value of the VGG-DAGSVM model is examined on apple leaf disease detection accomplishment in Fig. 11. The figure shows that the VGG-DAGSVM model has illustrated an enhancement accomplishment with the highest TACY values and VACY values. The VGG-DAGSVM model has reached enhanced TACY outputs.

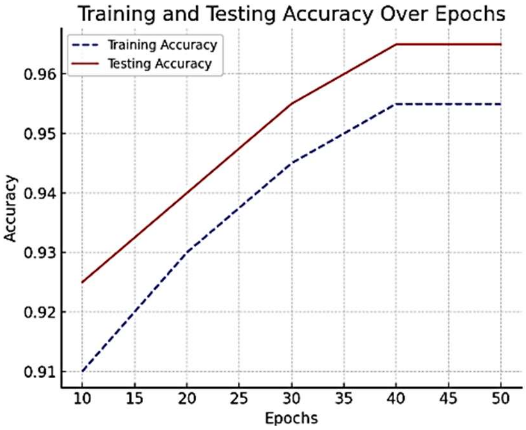

***Fig. 11.** Accuracy graph based on the training and testing data*

The TLOS value and VLOS value of the VGG-DAGSVM model are examined on apple leaf disease detection accomplishment in Fig. 12. The figure shows that the VGG-DAGSVM model has depicted the highest accomplishment with reduced TLOS values and VLOS values. The VGG-DAGSVM model has given a result in minimized VLOS outputs.

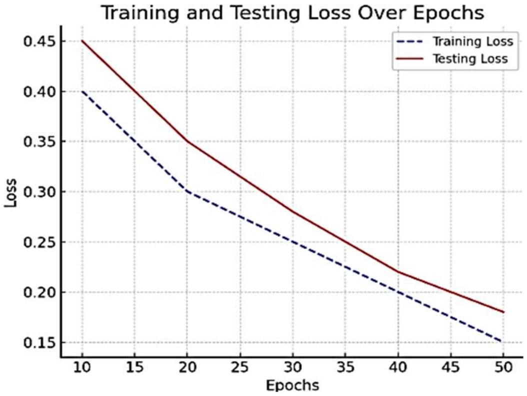

***Fig. 12.** Loss graph based on the training and testing data*

***Table 3.** Assessment of the proposed model in comparison to existing models*

Model	Accuracy (%)	Sensitivity (%)	Precision (%)	F-Score (%)
MobileNet [22]	73.50	73.00	73.00	72.99
InceptionV3 [22]	75.99	74.65	74.64	74.60
ResNet152 [22]	77.65	76.98	76.92	76.89
INAR-SSD [22]	78.80	77.97	77.95	77.95
DenseNet-121 [22]	93.51	93.15	93.05	93.00
BLSENet [22]	93.58	93.03	93.00	93.02
Proposed VGG-DAGSVM	**96.50**	**95.92**	**96.05**	**96.45**

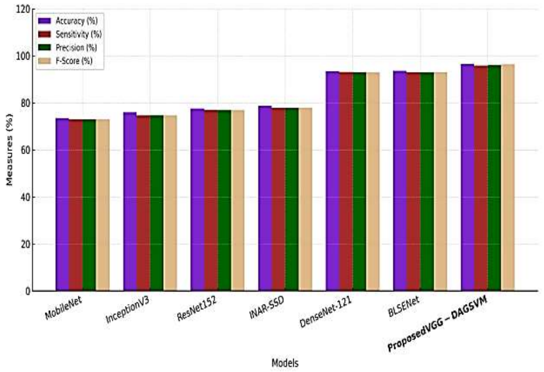

Fig. 13. *Overall Analysis of the Existing Models with the Proposed VGG-DAGSVM Model*

4.3. Critique and Limitations

Although the VGG-DAGSVM model achieves high performance, some limitations are acknowledged. The model may experience performance drops under severely inconsistent lighting or when applied to unseen cultivars. Future versions could benefit from augmentation techniques, broader multi-seasonal datasets, and additional channels such as hyperspectral data. Furthermore, the current setup assumes labeled data: transitioning to semi-supervised learning may improve scalability.

5. CONCLUSION

The proposed VGG-DAGSVM model introduces a hybrid architecture that fuses image enhancement, semantic segmentation, deep feature extraction, and DAG-based multi-class classification into a single pipeline for robust apple leaf disease detection. The model's experiments demonstrate improved metrics across all categories, validating the model's applicability for real-world agricultural environments. This study contributes to the literature by demonstrating that combining classical SVM structures with deep Convolutional Neural Network (CNN) representations leads to improved interpretability, classification efficiency, and robustness in challenging scenarios. Future expansions toward real-time integration and broader disease coverage will further elevate the practical value of this system.

5.1. Open Challenges and Future Directions

While this study presents a comprehensive pipeline, challenges remain in translating it into field-deployable tools. These include optimizing real-time inference speed for edge devices, adapting the model to environmental variability, and automating dataset labeling. Integration with drones, IoT-enabled sensors, and edge-AI architectures holds great promise for continuous orchard surveillance and precision spraying systems. Collaboration with agricultural scientists and agronomists is essential to validate and generalize these models in practical settings.

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