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Intelligent Detection of Tomato Crop Diseases Using Hybrid Transfer Learning with PCA-Enhanced SVM Classifier

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***Abstract*—Tomato crop diseases can be a significant threat to agricultural productivity. We need good ways to find these diseases. This study presents a new method that uses a hybrid transfer learning framework that combines Inception V3 (IV3) features with Principal Component Analysis (PCA) for dimensionality reduction. Then, Support Vector Machine (SVM) classifiers are applied to detect tomato leaf disease. Different kinds of kernels, such as polynomial, Radial Basis Function (RBF), sigmoid and linear are applied to SVM. The proposed approach uses 1,200 tomato leaf images in three disease categories. The proposal study (Reduction of the feature in Inception V3 with PCA (500)) shows that the best model is the SVM with a polynomial kernel. It has the highest AUC of 0.999 and 99% accuracy. The SVN with RBF kernel also performs well. It has an AUC of 0.994 and 98% accuracy. The Sigmoid kernel is the weakest, with an AUC of 0.971 and 88% accuracy. Its superior performance against existing deep learning (DL) methods highlights its robustness, efficiency, and potential for real-world agricultural applications. The aim is to help detect early disease and better crop management.**

***Index Terms*—Leaf Disease, Transfer Learner, Agriculture, PCA, Machine Learning**

I. INTRODUCTION

TOMATO, a nutrient-rich fruit from Solanum lycopersicum. It is famous for its antioxidant properties, which help with heart health, skincare, and many other health benefits. Tomatoes, produced mainly in China, India, Nigeria, Turkey, Egypt, the USA, Iran, Russia, Italy, and Mexico, are essential in various dishes such as sauces, soups, salads, and sandwiches [1]. The tomato sector is essential to the worldwide agricultural economy because it generates revenue and jobs for growers, processors, and distributors. Tomatoes, grown primarily in open fields, face numerous challenges due to their dependence on sunlight and natural pollination. First, pests and diseases such as tomato blight, aphids, and fruit worms can harm plants. Second, climate change affects production due to rising temperatures, unpredictable rainfall, and extreme weather [2]. Lastly, there is an increasing focus on sustainable farming practices to reduce environmental harm and ensure that the industry can thrive in the long run. The continuous success of agriculture is mainly attributed to advances in agricultural technology, breeding methods, and sustainable farming practices [3]. Table I shows the main tomato leaf diseases in the current research. Target Spot Disease (TSD), caused by Corynespora cassicola, causes small, dark spots on tomato leaves to expand into large circles, resembling a target, leading to leaf yellowing, defoliation, and reduced fruit production. The Mosaic Virus, caused by Tomato Mosaic Virus, causes mottled yellow, white, or light green leaves, disrupting plant growth and reducing fruit size and production. The Tomato Yellow Leaf Curl Virus [4], spread by whiteflies, causes leaf curling, stunted growth, and reduced fruit production, significantly affecting the plant's ability to expand.

Inception V3 is a deep-learning method. It uses pre-trained layers to extract image features, making it useful for small datasets. Capture complex patterns and textures to enhance the accuracy of medical and agricultural imaging. The method speeds up model training and applies knowledge to specific tasks. PCA (Principal Component Analysis) reduces the number of dimensions in the data. It transforms original features into uncorrelated components. This process keeps important information while reducing computation time. PCA eliminates redundant features, which helps prevent overfitting in ML models. Removing these redundant features can improve model performance and enhance interpretability. Support Vector Machines (SVMs) are a robust ML technique for classifying diseases in tomato plants. They effectively identify leaf mold, early blight, and late blight by training models on images of tomato leaves. Their user-friendly nature enables timely intervention to reduce crop loss.

We organize the paper as follows: **Section 2** explores progress in detecting tomato crop diseases using machine learning (ML) and DL techniques, focusing on feature selection methods. **Section 3** on Models and Materials describes the dataset used, the steps taken to prepare the data, and how transfer learning with Inception V3 is used to extract features. It also discusses the use of PCA to improve the performance of the SVM classifier. **Section 4** of Results and Comparative Analysis evaluates the performance metrics of the proposed model, comparing its accuracy and effectiveness with those

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TABLE I
COMMON TOMATO LEAF DISEASES AND THEIR MANAGEMENT (CAUSES, PREVENTIONS, AND ACTIONS)

Leaf Disease	Symptoms	Causes	Preventions	Action and Cure
Target Spot Disease	Small, dark brown harms with yellow halos; later stages cause defoliation and fruit rot.	*Corynespora cassiicola* fungus, spread by humid or wet conditions.	Use disease-resistant tomato varieties, ensure good air circulation, and avoid overhead watering.	Apply fungicides like copper-based sprays at early signs. Remove infected leaves and ensure the soil surface dries between watering.
Mosaic Virus	Mottled yellow and green leaves, distorted or curled leaves, stunted growth.	Transmitted through infected tools, insects like aphids, and contaminated seeds.	Control aphids, sanitize tools, and plant certified virus-free seeds.	There is no cure for viral infections. Remove infected plants immediately to prevent spreading.
Yellow Leaf Curl Virus	Yellowing and curling of leaves, stunted plant growth, fewer and smaller fruits.	Spread by the whitefly *Bemisia tabaci*, a virus carrier.	Control whitefly populations with row covers or reflective mulches and plant resistant tomato varieties if available.	Use insecticidal soap or neem oil to control whiteflies. Remove and destroy infected plants. Avoid planting tomatoes near other susceptible plants to reduce virus risk.

of other methods. **Section 5**, on Discussions, describes the findings' significance, potential limitations, and areas for future research to enhance model robustness and adaptability. Finally, **Section 6:** The study concludes by summarizing its contributions, with particular emphasis on the significant improvements in accuracy for detecting tomato crop diseases. This result was achieved using a PCA-enhanced SVM classifier that incorporates transfer learning features.

II. LITERATURE REVIEW

This section discusses recent research works to detect diseases in tomato crops. It focuses on DL and hybrid models. It also mentions TLs and feature selection. CNN-based methods are included. Attallah et al. (2023) [6] proposed a new method for classifying tomato leaf diseases. It uses CCNN networks, TLs, and hybrid feature selection. Ramya et al. (2023) [7] developed a robust deep TL model for identifying and classifying diseases in tomato plants, effectively addressing challenges such as similar colors and variations in leaf characteristics. The model shows outstanding accuracy and reliability across ten conditions. Alzahrani et al. (2023) [8] compared deep learning (DL) models for the early detection of tomato leaf diseases. They found that DenseNet121 outperformed other models in disease detection. The study suggests its potential for timely intervention and improved crop yield. Upadhyay et al. (2023) [9] studied and used transfer learning to detect tomato leaf diseases using the SqueezeNet model. The model classifies ten types, achieving good accuracy (93.1%). The CNN-SVM hybrid model improves precision, with the InceptionV3 model being the most compelling feature extractor. Singh et al. (2023) [10] explored the classification of tomato diseases utilizing Convolutional Neural Networks (CNN) and Transfer Learning (TL). Their research aimed to minimize crop losses caused by diseases and pests. They proposed enhancements to increase the model's reliability and elevate the overall quality of tomato production.

Table II presents recent studies on identifying tomato leaf diseases, employing various datasets and models. The research emphasizes deep learning, transfer learning, and hybrid methodologies. These strategies have effectively achieved high accuracy in the early detection and classification of diseases.

Bora et al. (2023) [20] introduced a novel approach to identifying tomato plant diseases. It utilizes a Multivariate Normal DL-NN classifier. The method includes HSI color transformation, green pixel masking, and ROI-based segmentation to pinpoint unhealthy areas. Afify et al. (2022) [21] developed a DL-based approach for detecting tomato crop diseases in Egypt, enhancing agricultural management. Sakkarvarthi et al. (2022) [22] developed a CNN-based method for detecting and classifying tomato crop diseases, enhancing yield quality and quantity. The model used two convolutional and pooling layers, outperforming pre-trained models. It achieved 98% training and 88.17% testing accuracy. Ullah et al. (2023) [23] developed EffiMob-Net, a hybrid DL model that uses images to detect tomato leaf diseases. The model improves performance and accuracy using regularization, dropout, and batch normalization. This approach demonstrates the potential of hybrid models in agricultural applications. Nawaz et al. (2022) [24] developed a DL framework to find and classify diseases in tomato leaves. They used a model based on ResNet-34 and added a special module to improve feature extraction. This model works well even with changes in images. It provides an efficient and affordable way to detect diseases early.

The literature review focuses on DL and hybrid models. It emphasizes the importance of Transfer Learnings and feature selection techniques. These methods are crucial for the accurate and reliable early detection of tomato leaf diseases.

III. MODELS AND METERIALS

The proposed hybrid model aims to find diseases in tomato plants using Inception V3 to collect key characteristics, PCA to simplify data, and SVM to organize information. The approach includes a thorough preprocessing, careful data set preparation, and experimental setups.

A. Proposed Model

The proposed model (Fig. 1) for detecting diseases in tomato plants uses transfer learning, simplifies the data with Principal Component Analysis (PCA), and employs a Support Vector Machine (SVM) classifier to accurately identify diseases from images of tomato leaves. The study develops a dataset that includes images of tomato leaves that illustrate various diseases. The images undergo pre-processing through augmentation, resizing, and normalization to enhance the model's performance. The Inception V3 model is used

TABLE II
EXISTING RESEARCH ON TOMATO LEAF DISEASE IDENTIFICATION USING DIVERSE DATASETS AND MODELS

Authors	Description	Dataset and Models	Result Analysis
Saeed et al. (2023) [11]	The research aims to improve plant disease detection. Goal: reduce crop losses. Method: use deep learning to diagnose tomato leaf diseases.	Inception V3 and Inception ResNet V2. The models were trained and tested on a dataset of 5225 images.	Inception V3 model: 50% dropout, 0.03 loss. Inception ResNet V2 model: 15% dropout, same performance.
Djimeli-Tsajio et al. (2022) [12]	Research aims to improve tomato leaf disease detection using DL techniques. Incorporates Transfer Learning models.	Used PlantVillage Dataset and Field-Recorded Videos. Utilized ResNet101 and ResNet152 models.	Proposed method achieves 98.3% accuracy using five-fold cross-validation and concatenates two mean deviation features from pre-trained models.
Sanida et al. (2023) [13]	Novel network identifies tomato leaf disease.	VGGNet and Inception blocks on PlantVillage Dataset.	The model achieved a high accuracy on the test set.
Al-Gaashani et al. (2022) [14]	Hybrid tomato leaf disease classification method combines traditional ML and Transfer Learning techniques. Utilizes pre-trained models for input.	PlantVillage dataset and Transfer Learning models.	Proposed method achieved an average accuracy of 97% using multinomial logistic regression.
Bhosale et al. (2024) [15]	The research presents a new method for detecting and assessing tomato leaf disease. It improves accuracy by using image preprocessing, feature extraction, and DL techniques.	The WUDHOA training method enhanced the CNN model's performance on the Tomato Plant image dataset.	Proposed method showed a high specificity of 0.9384, outperforming traditional techniques.
Javidan et al. (2024) [16]	The research focuses on improving the diagnosis of fungal diseases in tomatoes using microscopic image processing and ML techniques.	Models like CNN and EfficientNet with BOA optimizer. The dataset consists of 100 microscopic images per disease.	Proposed method, utilizing RF and BOA, achieved 98% accuracy, outperforming DL models like CNN and EfficientNet, which were less accurate and time-consuming.
Chowdhury et al. (2021) [17]	The study explores the effectiveness of various DL models in classifying tomato leaf diseases for automated disease detection and improved crop health.	ResNet18, MobileNet, DenseNet201, and InceptionV3 on 18,162 tomato leaf images dataset.	DenseNet201 outperformed other models in six-class and ten-class classifications, with accuracies of 97.99% and 98.05%, respectively.
Trivedi et al. (2021) [18]	The research utilizes a CNN to detect and classify tomato leaf diseases, aiming to assist farmers in early disease identification and appropriate action.	CNN model on 3000 tomato leaf image datasets.	CNN model classified nine tomato leaf diseases and achieved an accuracy of 98.49%.
Nagamani et al. (2022) [19]	The study uses ML methods to identify tomato leaf diseases, aiming to improve early detection and reduce crop losses.	Fuzzy SVM, CNN, and R-CNN models used on tomato leaf images with six diseases and healthy samples.	R-CNN classifier achieved the best accuracy of 96.735%, outperforming both Fuzzy SVM and CNN.

for feature extraction, generating a comprehensive 2048-dimensional feature vector for each image. Subsequently, these vectors are simplified using PCA, reducing them to 500 components while preserving essential information. This approach improves the robustness and efficiency of the model, allowing it to perform better in various situations. The data set of 500 component vectors is divided into training and testing sets in an 80:20 ratio for evaluating the model. The study uses SVM kernels such as RBF, polynomial, sigmoid, and linear to find the best setup to classify tomato diseases. To assess the performance of each SVM model, we calculate metrics such as precision, precision, recall, F1 score, and AUC, which help in selecting the most effective model. We evaluated the SVM model using new data to determine its ability to predict tomato leaf diseases. Reports are generated to showcase the accuracy and reliability of the model. These findings support the application of the model in agriculture and inform potential enhancements for practical implementation.

B. Datset Description

The Tomato Leaf Disease dataset (Table III) consists of 1,200 images, with 240 designated for testing. These images are categorized into three types of disease: target spot disease, mosaic virus, and yellow leaf curl virus, each category containing 400 images. All images are in JPG format and feature a 24-bit RGB color depth. They are square images with a resolution of 96 pixels per inch (bpi) and dimensions of 256x256 pixels (width x height), making them suitable for image processing and ML applications. The resolution of 96 bpi is ideal for display and analytical tasks. Each pixel is represented by 24 bits, with 8 bits allocated to each color channel (red, green, and blue). This high-fidelity color representation allows for 16.7 million color combinations, enhancing their utility in image recognition and pattern analysis tasks.

Fig. 2 shows the images of Tomato Leaf Disease. Fig. 2(A) describes how target spot disease affects tomato plants, causing dark circular spots on the leaves that grow into concentric patterns. The condition often results in yellowing and damage to the leaves. Fig. 2(B) explains that the mosaic virus leads to mottled yellow, white, or light green patches on tomato leaves. It also causes distortions in the shape of the leaves and affects the overall growth of the plant. Fig. 2(C) displays how the Yellow Leaf Curl Virus causes tomato leaves to turn yellow, curl, and stunt the plant's growth. This condition significantly harms the plant's health and productivity.

C. Inception V3 (IV3) Transfer Learner

Transfer learning uses pre-trained weights from a large dataset like ImageNet to avoid scratch training. IV3's (**Fig. 3**) lower layers capture general features, while higher layers adapt to specific features relevant to the target dataset, like tomato leaf diseases [20] [21].

1. Convolution Layers use different filter sizes (1x1, 3x3, and 5x5) in parallel in its modules, allowing it to capture features at multiple scales. It is represented in eq.

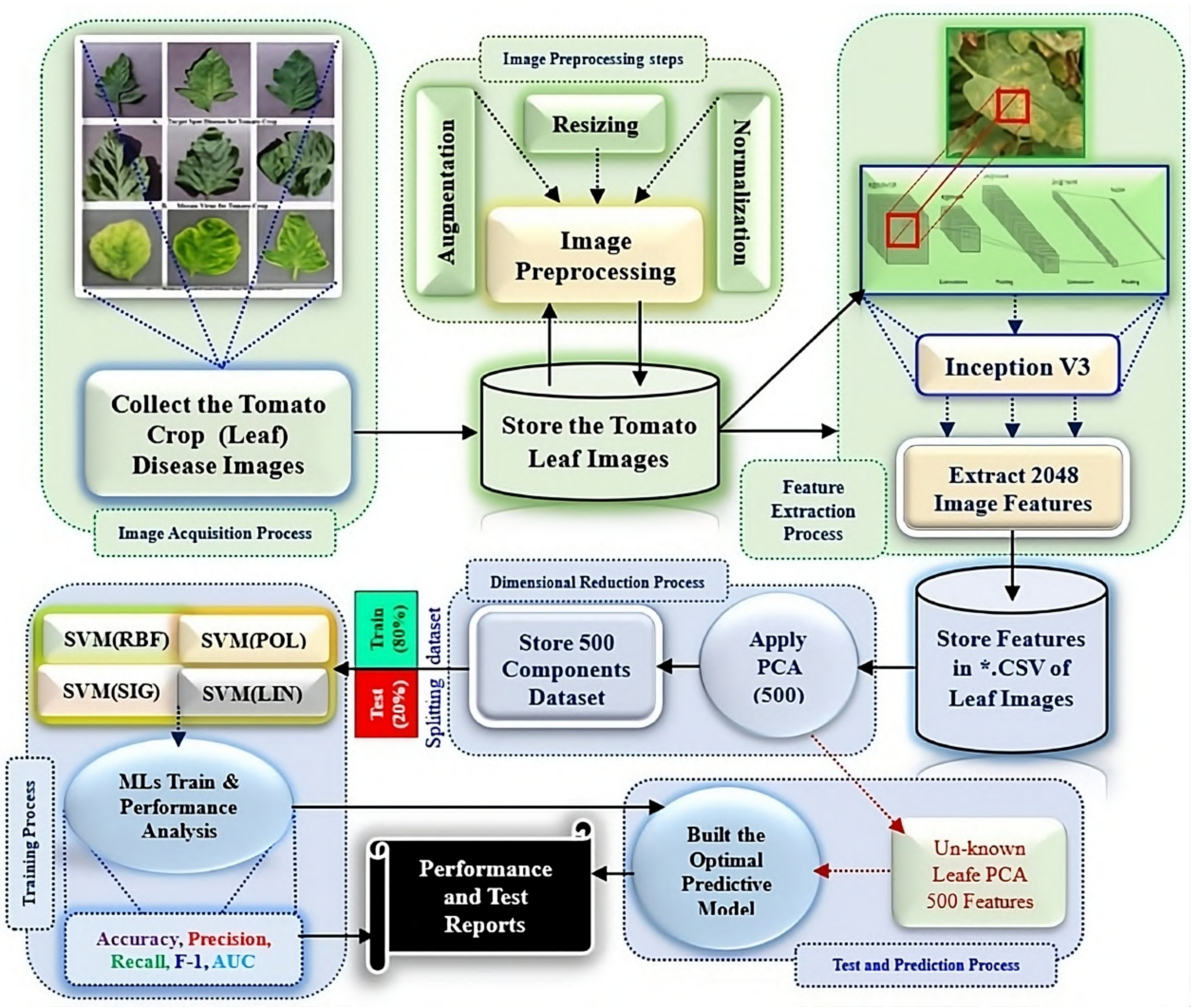


Fig. 1. Proposed Model for Detecting Tomato Crop Diseases Using IV3 Features PCA Enhanced SVM Classifier

TABLE III
SUMMARY OF TOMATO LEAF DISEASE DATASET CHARACTERISTICS

Tomato-Leaf Disease	Files Type	Images Count	Test Images Count	Image Features
Target Spot Disease	Image (*.jpg)	400	87	Size (256x256), resolution (96 bpi, 24-bit RGB)
Mosaic Virus	Image (*.jpg)	400	73	Size (256x256), resolution (96 bpi, 24-bit RGB)
Yellow Leaf Curl Virus	Image (*.jpg)	400	80	Size (256x256), resolution (96 bpi, 24-bit RGB)

(1).

$$f_{i,j}^{(l)} = \sum_{k} \sum_{p,q} W_{p,q,k}^{(l)} \cdot f_{i+p,j+q,k}^{(l-1)} + b^{(l)} \tag{1}$$

$f_{i,j}^{(l)}$ is the output feature at layer l for position (i, j) and filter weights $W_{p,q,k}^{(l)}$. $f_{i+p,j+q,k}^{(l-1)}$ is the previous layer input feature map and $b^{(l)}$ is the bias.

2. *Inception modules* are an important part of the Inception architecture. They use several parallel convolutions (CNs) with different sizes and concatenate the results (big dot(**.**)). It helps the network to recognize various spatial features effectively. It defines Eq. (2)

$$f^{Inception} = concat\left(f^{(1\times1)}, f^{(3\times3)}, f^{(5\times5)}, f^{pool}\right) \tag{2}$$

$f^{(1\times1)}, f^{(3\times3)}, f^{(5\times5)}, f^{pool}$ feature maps are created through various convolutional operations (CNs) and pooling operations. This concatenation combines features from various scales. It enables the model to attention to both coarse and fine details.

3. Batch (BN) Normalization is a technique used to reduce internal covariate shift, accelerate training, and enhance stability by transforming a given activation in a layer. These are represented in Eq. (3) and Eq. (4).

$$\hat{x} = \frac{x - \mu}{\sqrt{\sigma^2 + \epsilon}} \tag{3}$$

$$y = \gamma \cdot \hat{x} + \beta \tag{4}$$

The mean μ has been calculated for the mini-batch. The variance σ^2 has also been calculated for the mini-batch.

4. Pooling layers decrease the size of feature maps. Inception-V3 (IV3) employs both MAX pooling and AVG pooling techniques. MAX pooling focuses on selecting the

A. Target Spot Disease for Tomato Crop

B. Mosaic Virus for Tomato Crop

C. Yellow Leaf Curl Virus for Tomato Crop

Fig. 2. Sample Images of Tomato Crop Diseases

maximum value from a specific region R, as shown in Equations (5) and (6).

$$f^{max} = \max_{(i,j)\in R} f_{i,j} \tag{5}$$

$$f^{avg} = \frac{1}{|R|} \sum_{(i,j)\in R} f_{i,j} \tag{6}$$

Average pooling calculates the mean of values in a region. Pooling layers reduce the size of feature maps, making the model more computationally efficient.

5. Auxiliary Classifiers (During Training): Inception V3 uses auxiliary classifiers during Training. These classifiers are small sub-networks that help with feature learning at earlier stages. Each auxiliary classifier has its loss function, which guides the weights before reaching the final classifier (Eq. (7)).

$$\chi_{aux} = -\sum_{c} y_c \cdot \log \hat{y}_c \tag{7}$$

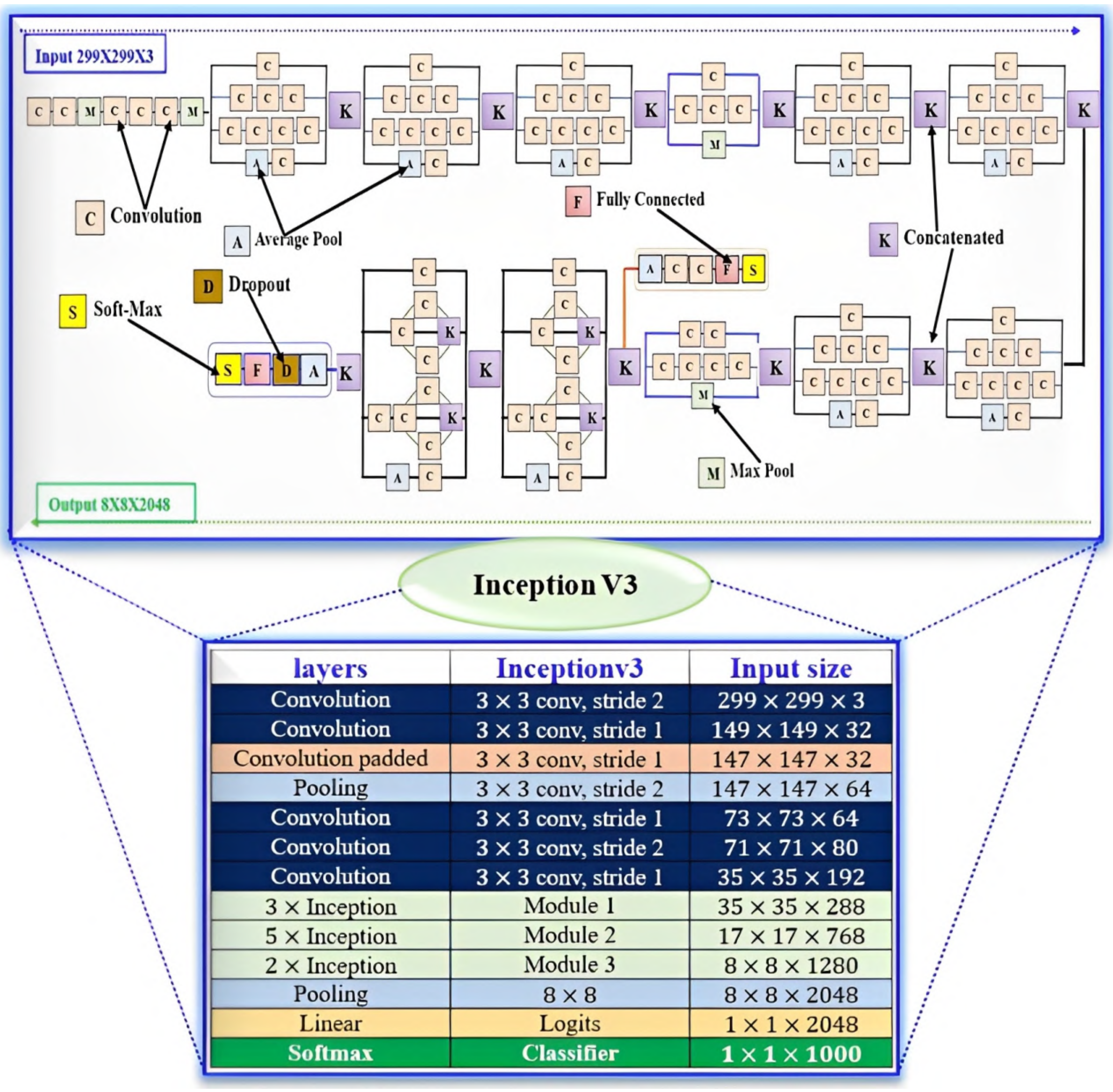
y_c is the ground truth, c is the class, and $\hat{y}_c$ is the predicted probability for c.

6. Fully Connected Layers and Softmax: The model processes feature maps after the Inception modules. It then flattens these maps and inputs them into FCLs. Finally, a softmax layer produces a probability distribution for the classes. This shows in the equation (8).

$$\hat{y}_c = \frac{\exp(z_c)}{\sum_k \exp(z_k)} \tag{8}$$

where z_c is the output of the final layer for the c class.

The IV3 transfer learning model is enhanced with PCA and SVM. This combination effectively extracts deep fea-



layers	Inceptionv3	Input size
Convolution	3×3 conv, stride 2	$299 \times 299 \times 3$
Convolution	3×3 conv, stride 1	$149 \times 149 \times 32$
Convolution padded	3×3 conv, stride 1	$147 \times 147 \times 32$
Pooling	3×3 conv, stride 2	$147 \times 147 \times 64$
Convolution	3×3 conv, stride 1	$73 \times 73 \times 64$
Convolution	3×3 conv, stride 2	$71 \times 71 \times 80$
Convolution	3×3 conv, stride 1	$35 \times 35 \times 192$
$3 \times$ Inception	Module 1	$35 \times 35 \times 288$
$5 \times$ Inception	Module 2	$17 \times 17 \times 768$
$2 \times$ Inception	Module 3	$8 \times 8 \times 1280$
Pooling	8×8	$8 \times 8 \times 2048$
Linear	Logits	$1 \times 1 \times 2048$
Softmax	Classifier	$1 \times 1 \times 1000$

Fig. 3. Detailed Architecture and Workflow of Inception V3 Transfer Learner

tures and classifies them efficiently. It achieves robust performance in detecting tomato crop diseases.

D. PCA Algorithm

PCA is a popular technique for reducing the dimensions of a dataset. It finds the directions, known as Principal Components, where the information or data varies most significantly in certain areas. This transformation simplifies the data while retaining essential information. PCA is beneficial for noise reduction, data visualization, and improving the speed of ML models [22].

1. Standardize the Dataset: We standardize the data, which helps each part of the data contribute equally. It involves centering the data around the scaling and mean it to unit variance. We first calculate the mean for each feature for dataset X with n samples and d dimensions or features (Eq (9)).

$$\mu_j = \frac{1}{n}\sum_{i=1}^{n} X_{ij} \quad for j = 1, 2, \ldots, d(features) \tag{9}$$

The standardized data matrix Z (Eq. (10)) is created by subtracting each feature's mean.

$$Z_{ij} = X_{ij} - \mu_j \tag{10}$$

2. Covariance Matrix Computation: The covariance matrix $M(\Sigma)$ captures relationships between features. It is a $(d \times d)$ matrix, where each element represents the covariance between two features. These computations are shown in Eq. (11) and Eq. (12).

$$M(\Sigma) = \frac{1}{n-1} Z^T Z \tag{11}$$

$$M\left(\sum_{jk} m\right) = \frac{1}{n-1}\sum_{i=1}^{n} Z_{ij} Z_{ik} \tag{12}$$

Z^T is the standardized data transpose matrix. $\left(\sum_{jk} m\right)$ represents the covariance matrix.

3. Eigenvalues and Eigenvectors Computations: To find the Principal Components (PCs), we compute the eigenvalues and eigenvectors of the covariance matrix Σ. The eigenvalue equation for the matrix $M(\Sigma)$ is Eq. (13).

$$\Sigma v = \lambda v \tag{13}$$

λ is an eigenvalue of Σ, and $\mathbf{v}$ is the corresponding eigenvector. Eigenvectors show the directions of PCs. Eigenvalues indicate the dimension of variance in each direction.

4. Sort Eigenvalues and Eigenvectors: Eigenvalues are sorted from largest to smallest, and corresponding eigenvectors are arranged in the same order. The eigenvector with the largest eigenvalue indicates the direction of maximum variance. Subsequent eigenvectors show directions of decreasing variance. The eigenvalues in descending order are denoted by $\lambda_1, \lambda_2, \ldots, \lambda_d$, while the corresponding eigenvectors are denoted by $\mathbf{v}_1, \mathbf{v}_2, \ldots, \mathbf{v}_d$.

5. Select k PCs: To minimize dimensionality, we choose the top k eigenvectors with the highest eigenvalues, which form the data's PCs. The number k is determined by the cumulative explained variance, indicating the proportion of variance explained by these components.

$$ExplainedVariance = \frac{\sum_{i=1}^{k} \lambda_i}{\sum_{j=1}^{d} \lambda_j} \tag{14}$$

This value is usually picked to keep a specific percentage of the total variance.

6. Project Data onto PCs: The original data, called $\mathbf{Z}$, is transformed to fit into fewer dimensions using the selected k PCs. The lower-dimensional representation, $\mathbf{Y}$, is expressed as shown in Eq. (15).

$$Y = ZW \tag{15}$$

$\mathbf{W}$ is a matrix containing the top k eigenvectors as its columns. Its size is $d \times k$. $\mathbf{Y}$ is another matrix representing the transformed data in the new dimensions, with size $n \times k$.

E. SVM Classifier

SVMs are supervised learning algorithms designed for categorization problems. They optimize hyperplanes by increasing the gap between data points in each class, which improves generalization as well as efficiency on training and unknown test data. SVMs are flexible tools for classification. They can handle data that is not easily separable. This is done using kernel functions. Kernels change the input data into a higher-dimensional space [23].

1. Linear Kernel: The linear kernel is a basic type of kernel function. It is calculated by taking the dot product of two vectors. We can also add a constant term if needed. The equation is

$$K(x, x') = x \cdot x' \tag{16}$$

The linear kernel is used for data that can be separated in a straight line. It works well with high-dimensional data, such as text classification. It is also efficient in terms of computation.

2. The RBF Kernel , also known as the Gaussian kernel, is defined as:

$$K(x, x') = \exp\left(-\gamma \|x - x'\|^2\right) \tag{17}$$

3. Polynomial Kernel is a non-linear kernel representing the similarity between vectors as a polynomial function of their dot product. It defined as

$$K(x, x') = (\alpha \cdot x \cdot x' + c)^d \tag{18}$$

4. Sigmoid Kernel, derived from the sigmoid function in neural networks, is defined as:

$$K(x, x') = (\alpha \cdot x \cdot x' + c)^d \tag{19}$$

where α and c are parameters that control the slope and intercept, respectively. SVM classifiers can use different kernel functions, which makes them flexible for various types of data. Each kernel has its own benefits, allowing the SVM model to be customized for the data it works with. This helps improve classification results in many different situations.

F. Performance Metrics and Confusion Matrix

The Confusion Matrix (CM) (Fig. 4) provides insights into how well a model predicts different classes. In this analysis, we focus on three types of tomato leaf diseases: 1. **C-1:** Target Spot Disease (**TSD**) 2. **C-2:** Mosaic Virus (**MV**) 3. **C-3:** Yellow Leaf Curl Virus (**YLCV**). The matrix evaluates the model's performance by examining precision and recall metrics. It identifies misclassifications, allowing us to pinpoint areas for improvement. The CM is used to assess a model's effectiveness in multi-class classification by calculating key metrics like the F1 score, recall, precision, and accuracy. These metrics help determine the ratio of correctly predicted instances, positive predictions, and the model's ability to identify instances accurately. The specific calculations for these performance metrics are detailed in equations Eq. (20) to Eq. (30).

$$Acc = \frac{TP(1,1) + TP(2,2) + TP(3,3)}{T} \tag{20}$$

$$Precision(C_1) = \frac{TP(1,1)}{T_4} \tag{21}$$

$$Precision(C_2) = \frac{TP(2,2)}{T_5} \tag{22}$$

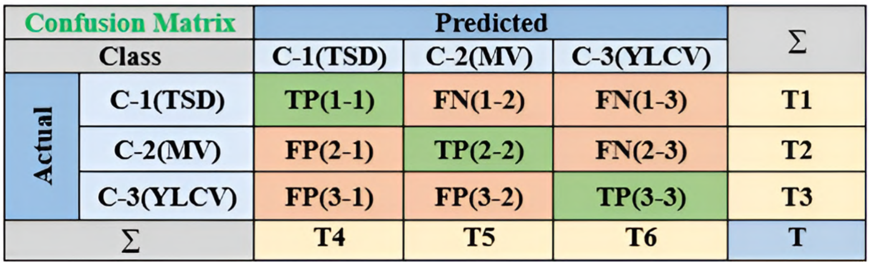
$$Precision(C_3) = \frac{TP(3,3)}{T_6} \tag{23}$$

$$Recall(C_1) = \frac{TP(1,1)}{T_1} \tag{24}$$

$$Recall(C_2) = \frac{TP(2,2)}{T_2} \tag{25}$$

$$Recall(C_3) = \frac{TP(3,3)}{T_3} \tag{26}$$

$$F1Score(C_1) = \frac{2 \times (Precision(C_1) \times Recall(C_1))}{Precision(C_1) + Recall(C_1)} \tag{27}$$



Confusion Matrix		Predicted			Σ
	Class	C-1(TSD)	C-2(MV)	C-3(YLCV)	
Actual	C-1(TSD)	TP(1-1)	FN(1-2)	FN(1-3)	T1
	C-2(MV)	FP(2-1)	TP(2-2)	FN(2-3)	T2
	C-3(YLCV)	FP(3-1)	FP(3-2)	TP(3-3)	T3
Σ		T4	T5	T6	T

Fig. 4. Confusion Matrix for Three Classes

$$F1Score(C_2) = \frac{2 \times (Precision(C_2) \times Recall(C_2))}{Precision(C_2) + Recall(C_2)} \tag{28}$$

$$F1Score(C_3) = \frac{2 \times (Precision(C_3) \times Recall(C_3))}{Precision(C_3) + Recall(C_3)} \tag{29}$$

$$TPR = \frac{TP}{TP + FN} \tag{30}$$

$$FPR = \frac{FP}{FP + TN} \tag{31}$$

$$AUC = \int_0^1 TPR(FPR)\, d(FPR) \tag{32}$$

IV. RESULT ANALYSIS

The analysis assesses the efficacy of SVM kernel models on PCA-reduced features from Inception V3. The goal is to classify tomato crop diseases accurately. The performance is measured using AUC, accuracy, precision, recall, and F1-score.

A. *Inception V3+PCA(500) +SVM (Linear) Model Analysis*

Fig. 5 (A) shows the performance values of each class. The Inception V3 + PCA (500) + SVM (Linear) model works well for classifying tomato diseases. It has a high accuracy of 96.69% for each disease class. The model shows precision, recall, and F1 scores above 0.93. Target Spot and Mosaic Virus have almost perfect recall and precision. Leaf Curl Virus has a perfect precision score of 1.00. The average metrics score is 0.97, showing that the model is a balanced and reliable classification across classes. Fig. 5(B) shows the Confusion matrix for each class. The model's classification performance across Target Spot, Leaf Curl Virus, and Mosaic Virus is evaluated. Of 87 instances, 86 were correctly classified, with only one misclassified as Mosaic Virus. Leaf Curl Virus had 68 cases correctly identified, but four were misclassified as Target Spot and one as Mosaic Virus. Mosaic Virus showed strong performance with 78 correct classifications out of 80.

ig. 5 (C) shows the ROC curves analysis of each class. The blue curve represents the model's ability to detect Target Spot Disease. The orange curve demonstrates its accuracy in identifying the Yellow Leaf Curl Virus, while the green curve illustrates its performance in detecting the Tomato Mosaic Virus.

The model's high accuracy is evident from the low misclassification rates across all classes, with minor confusion, particularly between the Leaf Curl Virus and Target Spot. The model performed exceptionally well in identifying different disease types, achieving high AUC values for all classes.

The Mosaic Virus class recorded the highest AUC score of 0.9983, followed by the Target Spot class with a score of 0.996. The Leaf Curl Virus class achieved an AUC score of 0.9845.

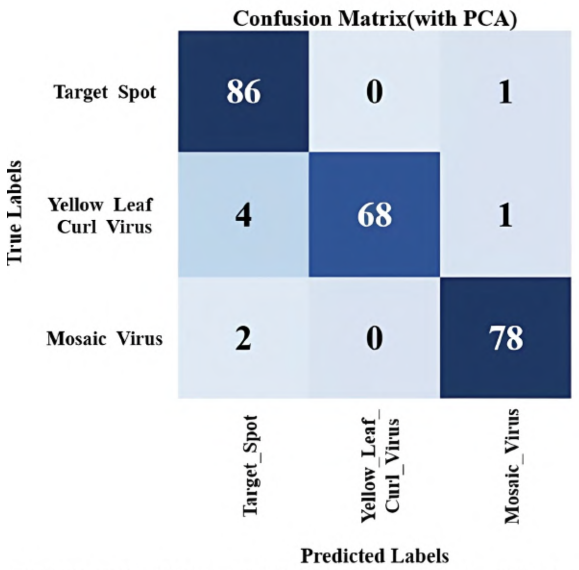
B. *Inception V3+PCA(500) +SVM (Polynomial) Model Analysis*

The Inception V3 + PCA (500) + SVM (POLY) (Fig. 6 (A)) model has shown exceptional accuracy in classifying various disease categories in a dataset. It achieved a high accuracy of 98.75% for Target Spot, with a precision of 0.99 and recall of 0.99. Leaf Curl Virus achieved a perfect precision of 1.00 with no false positives and a recall of 0.97. The model also performed exceptionally well in detecting Mosaic Virus, with a recall of 1.00 and a precision of 0.98. The overall macro average for accuracy, precision, recall, and F1-Score is approximately 0.99, indicating high consistency across all classes. The confusion matrix (Fig. 6 (B)) shows the model's effectiveness with minimal misclassifications across the classes. The model accurately classified three disease categories: Target Spot, Leaf Curl Virus, and Mosaic Virus. Out of 87 cases, 86 were correctly classified, with one misclassification. Leaf Curl Virus was identified 71 out of 73, with one misclassification each. Mosaic Virus was correctly classified for all 80 cases, indicating high specificity and reliability.

The ROC curves in Fig. 6 (C) show that the model performs very well in classifying three plant diseases. The blue curve for Target Spot Disease has an AUC of 0.9997, which means it classifies almost perfectly. The orange curve for the Yellow Leaf Curl Virus has an AUC of 0.983, indicating it also performs well, but not as perfectly. The green curve for the Tomato Mosaic Virus has a perfect AUC of 1.0, meaning it can separate this disease. It has an average AUC score of 0.9942, showing its accuracy across different types of diseases.

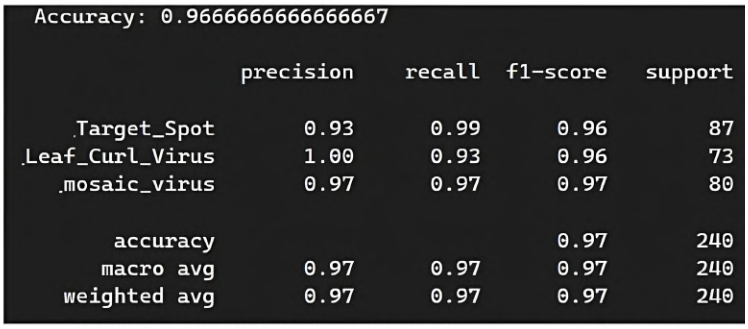
C. *Inception V3+PCA(500)SVM(RBF) Model Analysis*

The Inception V3 model combined with PCA and SVM with kernel RBF Fig. 7 (A)) performs well in classifying three plant diseases. It achieves an accuracy of 0.9791 for the Target Spot, 0.9791 for the Leaf Curl Virus, and 0.98 for the Mosaic Virus. The model also achieves an F1-score of 0.98 and an AUC of 0.9960 for Leaf Curl Virus. The macro and weighted averages across all classes also show consistent and



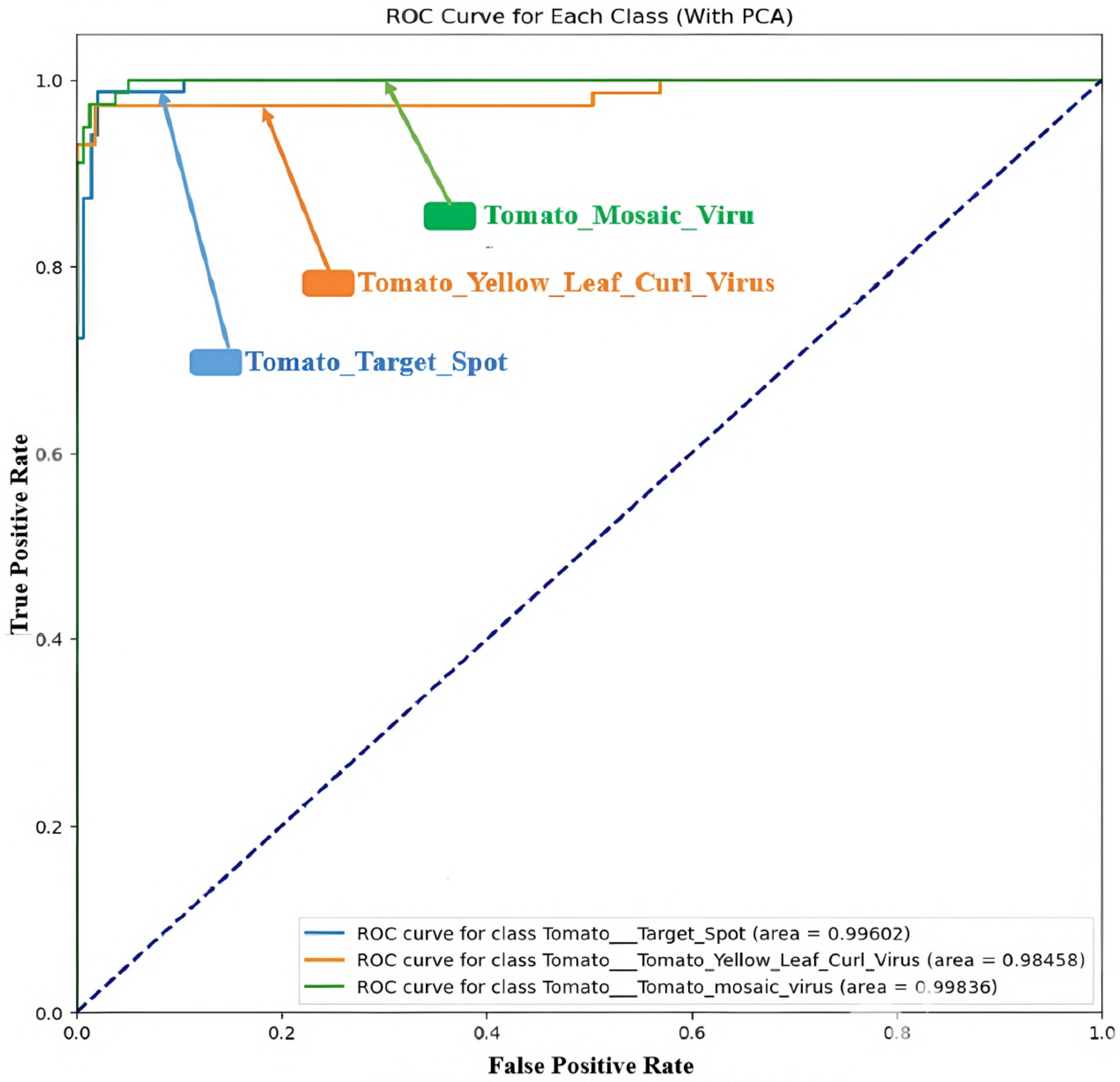
	Target_Spot	Yellow_Leaf_Curl_Virus	Mosaic_Virus
Target Spot	86	0	1
Yellow Leaf Curl Virus	4	68	1
Mosaic Virus	2	0	78

(B) IV3+PCA(500) + SVM (Linear) Confusion Matrix



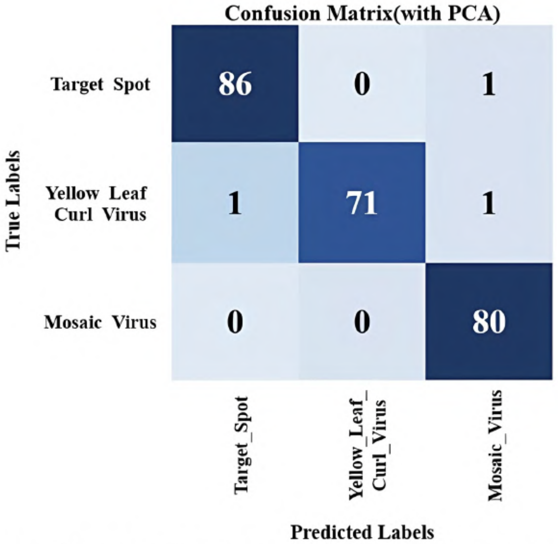
```
Accuracy: 0.9666666666666667

                  precision    recall  f1-score   support

      Target_Spot       0.93      0.99      0.96        87
 Leaf_Curl_Virus       1.00      0.93      0.96        73
    mosaic_virus       0.97      0.97      0.97        80

        accuracy                           0.97       240
       macro avg       0.97      0.97      0.97       240
    weighted avg       0.97      0.97      0.97       240
```

(A) IV3+PCA(500) + SVM (Linear) Performance Analysis

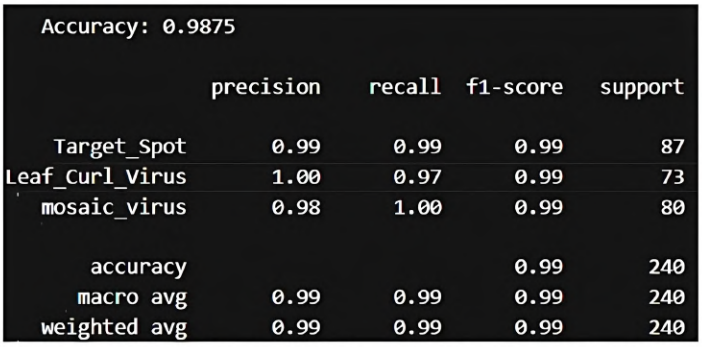


(C) IV3+PCA(500) + SVM (Linear) ROC Curves

Fig. 5. IV3+PCA(500) + SVM (Linear) Model Performance Analysis about Tomato Disease Dataset

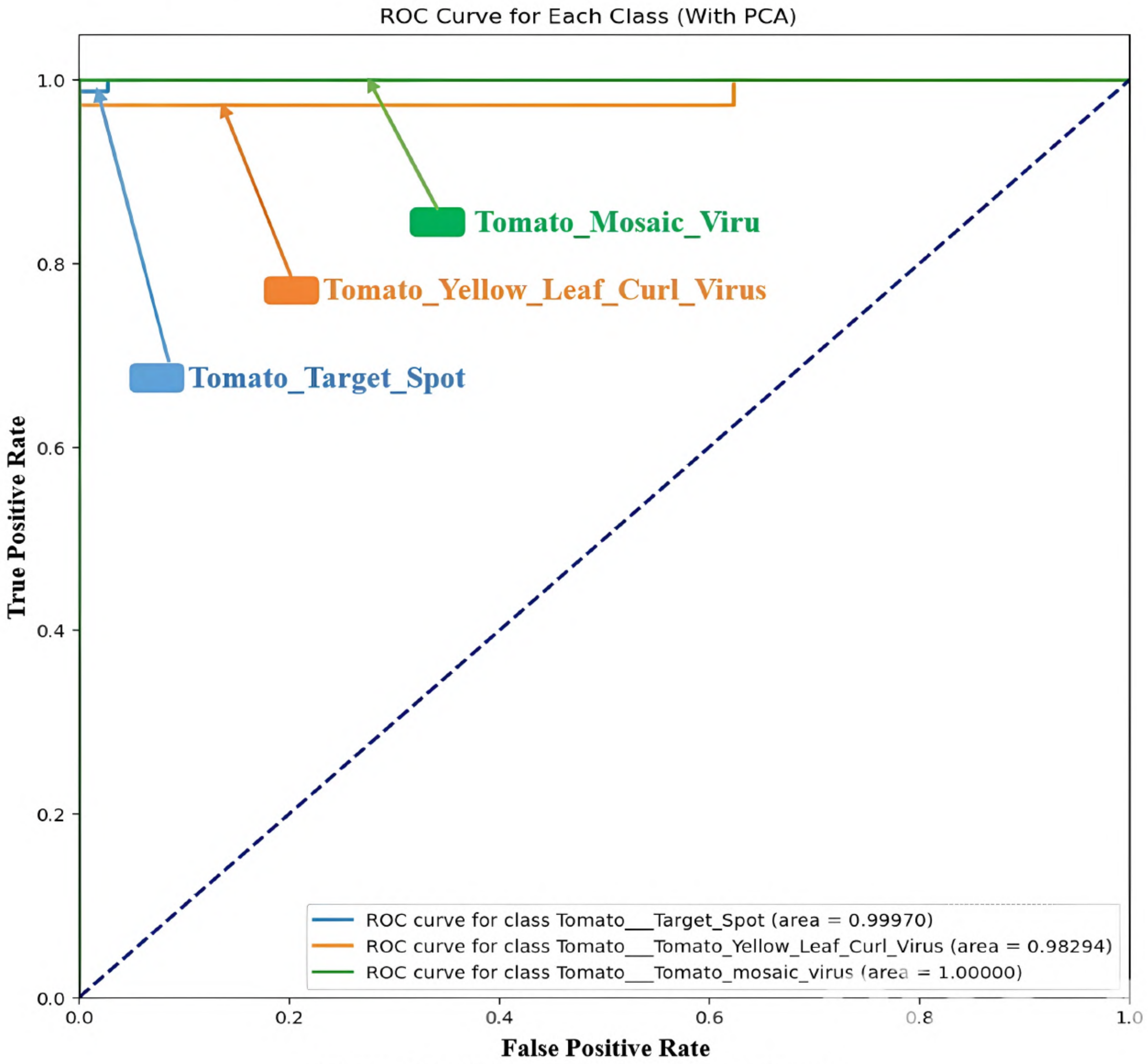


(B) IV3+PCA(500) + SVM (Polynomial) Confusion Matrix



```
  Accuracy: 0.9875

                  precision    recall  f1-score   support

    Target_Spot        0.99      0.99      0.99        87
Leaf_Curl_Virus        1.00      0.97      0.99        73
  mosaic_virus         0.98      1.00      0.99        80

       accuracy                            0.99       240
      macro avg        0.99      0.99      0.99       240
  weighted avg         0.99      0.99      0.99       240
```

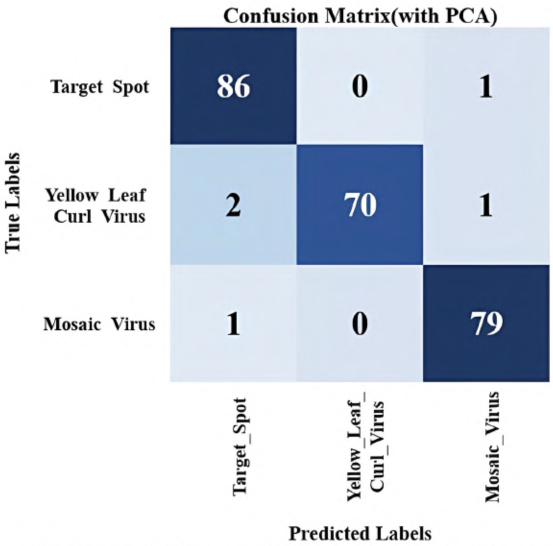
(A) IV3+PCA(500) + SVM (Polynomial) Performance Analysis



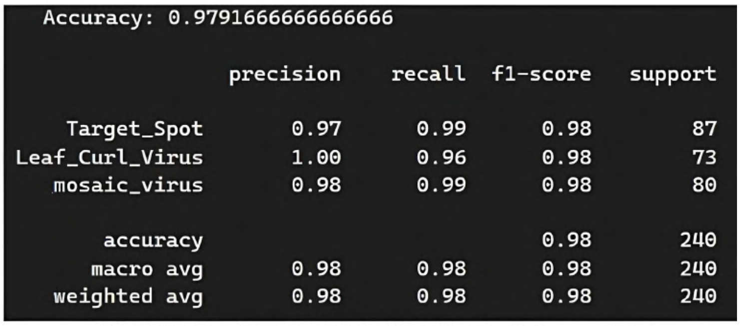
(C) IV3+PCA(500) + SVM (Polynomial) ROC Curves

Fig. 6. IV3+PCA(500) + SVM (Polynomial) Model Performance Analysis about Tomato Disease Dataset

effective classification performance, with an AUC of 0.9929. The model (confusion matrix, Fig. 7 (B)) was tested on 240 samples to classify three diseases: Target Spot, Leaf Curl Virus, and Mosaic Virus. It correctly identified 86 out of

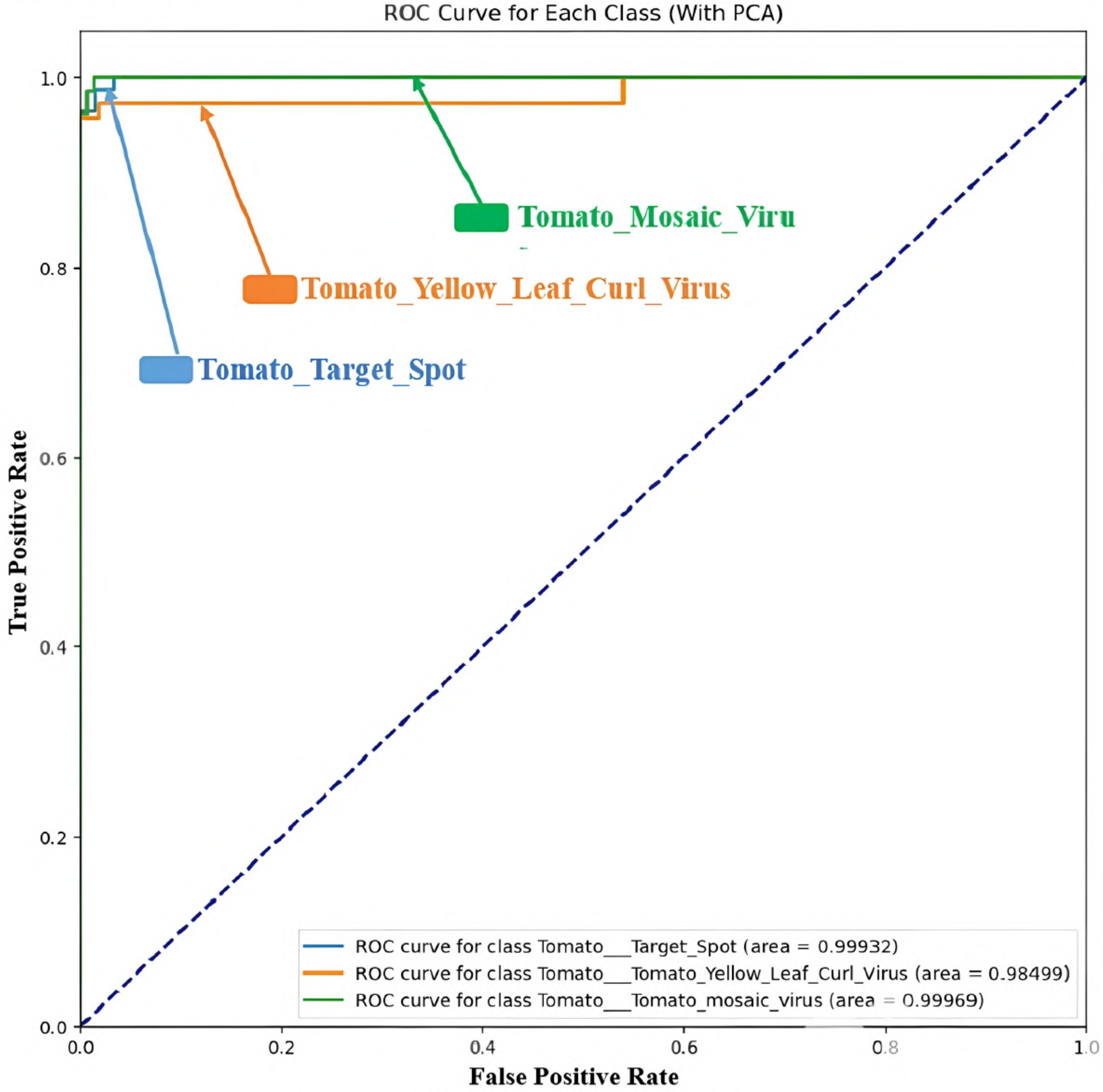


(B) IV3+PCA(500) + SVM (RBF) Confusion Matrix



```
 Accuracy: 0.9791666666666666

                precision    recall  f1-score   support

   Target_Spot       0.97      0.99      0.98        87
Leaf_Curl_Virus       1.00      0.96      0.98        73
  mosaic_virus       0.98      0.99      0.98        80

      accuracy                           0.98       240
     macro avg       0.98      0.98      0.98       240
  weighted avg       0.98      0.98      0.98       240
```

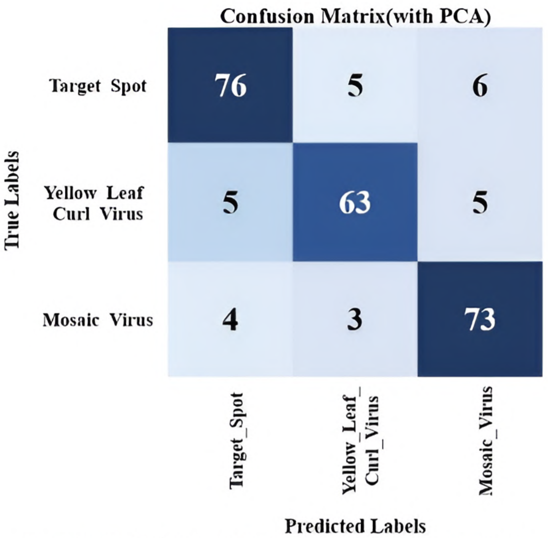
(A) IV3+PCA(500) + SVM (RBF) Performance Analysis



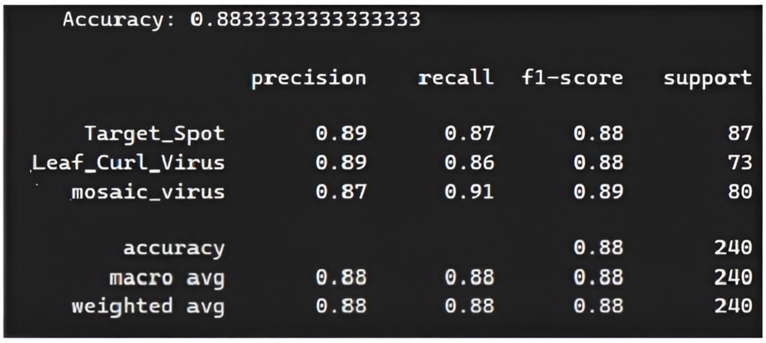
(C) IV3+PCA(500) + SVM (RBF) ROC Curves

Fig. 7. IV3+PCA(500) + SVM (RBF) Model Performance Analysis

87 cases for Target Spot, with only one mistake, which was misclassified as Mosaic Virus. For Leaf Curl Virus, the model recognized 71 cases but made two errors. Despite this, it still performed well, indicating some challenges in distinguishing

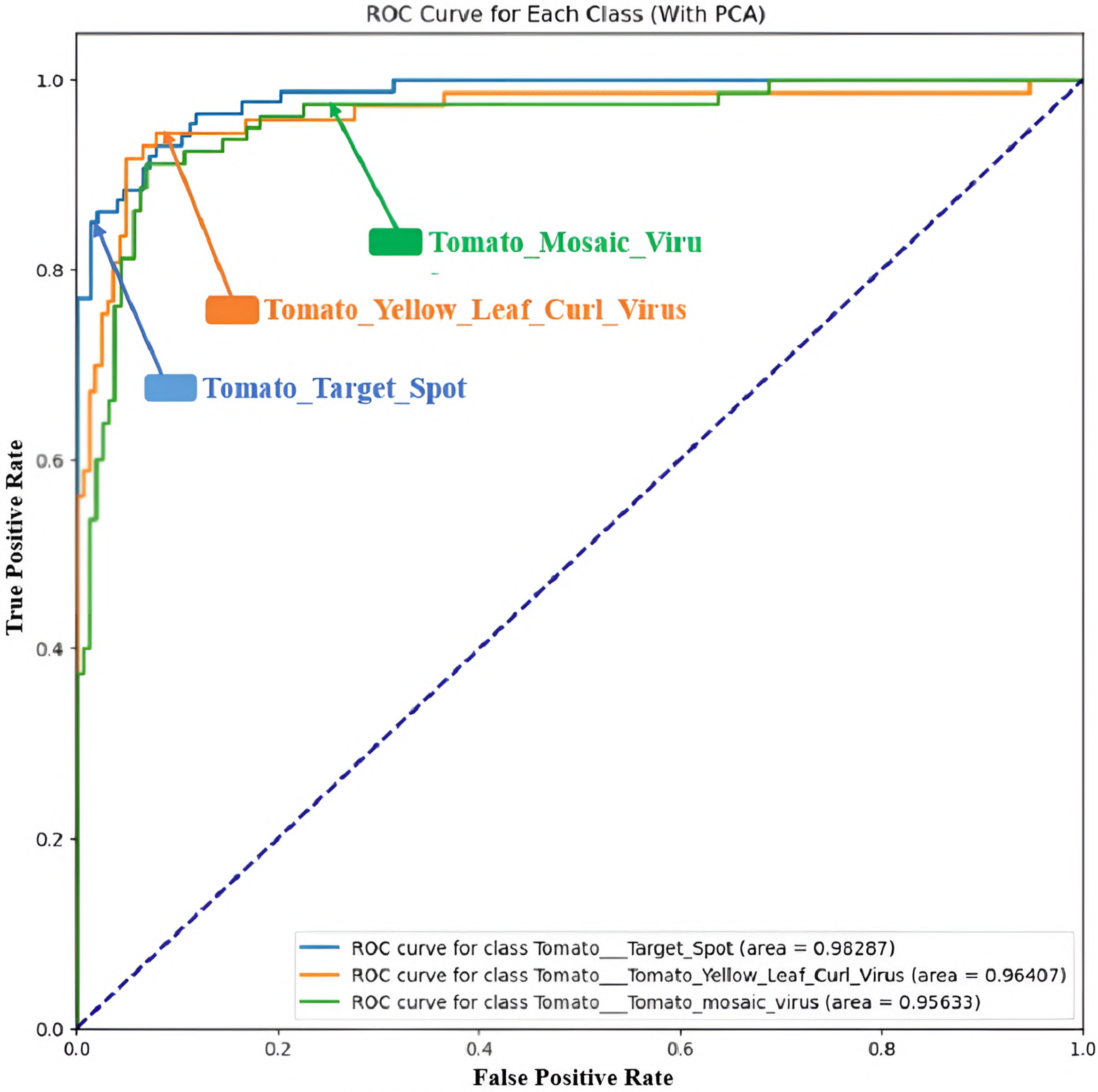


(B) IV3+PCA(500) + SVM (SIG) Confusion Matrix



```
    Accuracy: 0.8833333333333333

                      precision    recall  f1-score   support

        Target_Spot       0.89      0.87      0.88        87
    Leaf_Curl_Virus       0.89      0.86      0.88        73
       mosaic_virus       0.87      0.91      0.89        80

           accuracy                           0.88       240
          macro avg       0.88      0.88      0.88       240
       weighted avg       0.88      0.88      0.88       240
```

(A) IV3+PCA(500) + SVM (SIG) Performance Analysis



C) IV3+PCA(500) + SVM (SIG) ROC Curves

Fig. 8. IV3+PCA(500) + SVM (Sigmoid) Model Performance Analysis

this disease. The model accurately classified all 80 cases of Mosaic Virus, showing its strong performance.

The ROC curve analysis in Fig. 7 (C) shows the high discriminative power of the model for each disease. Target

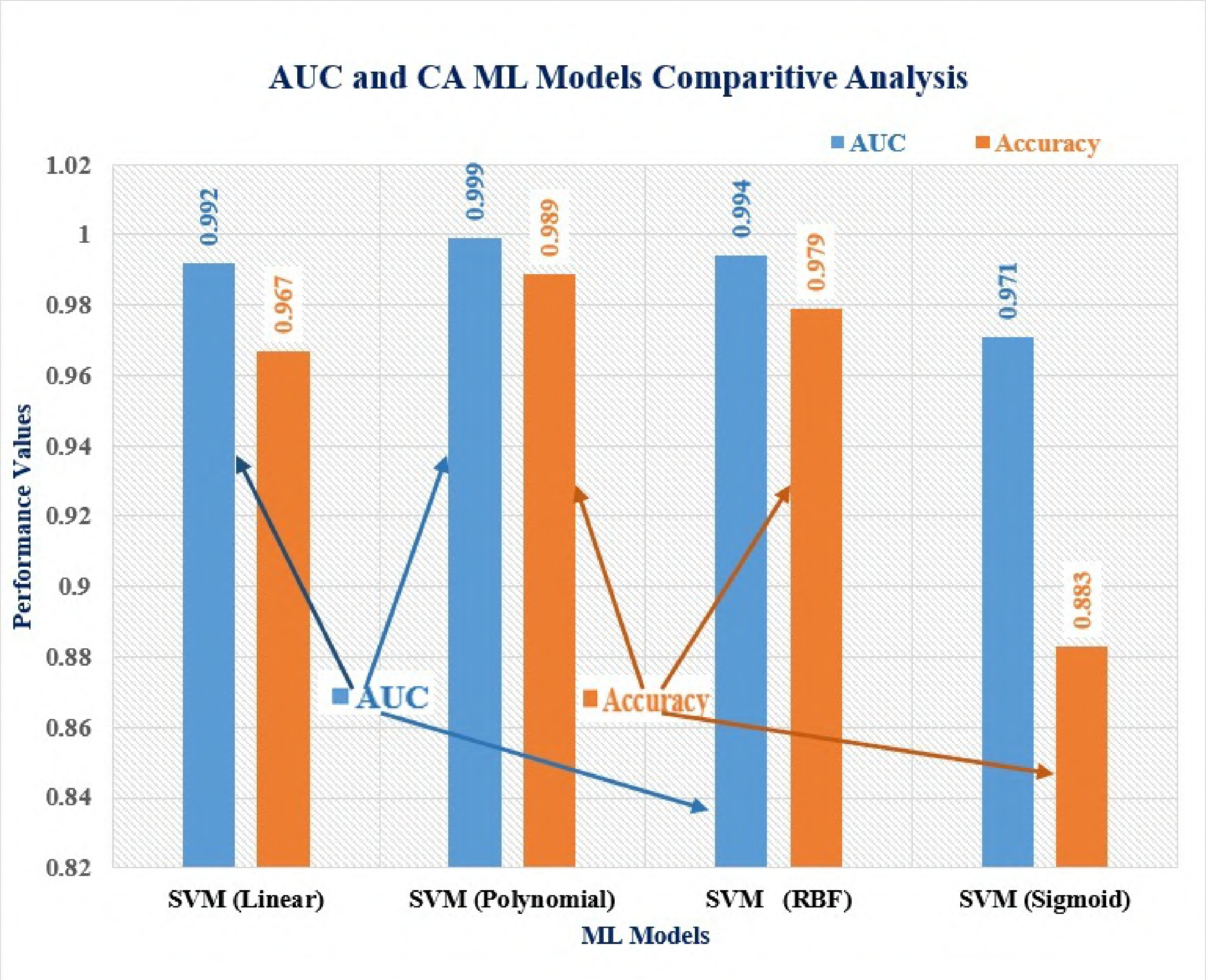


Fig. 9. Compartive Analysis for IV3+PCA(500) Features SVM (Kernels) Model

TABLE IV
COMPARATIVE ANALYSIS FOR EXPERIMENTAL IV3+PCA(500)+SVM MODELS

ML Models	AUC	Accuracy	Precision	Recall	F1-Score
SVM (Linear)	0.992	0.967 (97%)	0.967 (97%)	0.967 (97%)	0.967 (97%)
SVM (Polynomial)	**0.999**	**0.989 (99%)**	**0.989 (99%)**	**0.987 (99%)**	**0.989 (99%)**
SVM (RBF)	0.994	0.979 (98%)	0.983 (98%)	0.980 (98%)	0.980 (98%)
SVM (Sigmoid)	0.971	0.883 (88%)	0.883 (88%)	0.880 (88%)	0.883 (88%)

Spot disease achieves an AUC of 0.9960, indicating near-perfect sensitivity and specificity. Leaf Curl Virus has an AUC of 0.9845, while Mosaic Virus has an AUC of 0.9983, indicating excellent detection capability. The weighted average AUC across all classes is 0.9929, highlighting the model's effectiveness in multiclass disease classification.

D. Inception V3+PCA(500)+SVM(SIG) :

The Inception V3 model uses SVM (Fig. 8(A)), a sigmoid kernel, and PCA to organize 500 components, and it consistently shows high accuracy for different target classes. The Target Spot class has an accuracy of 88.33%, while the Leaf Curl Virus class also performs well. The Mosaic Virus class has better recall and F1 scores, indicating strong classification. The Target Spot class achieves an accuracy of 88.33%, while the Leaf Curl Virus class exhibits solid predictive capability. The Mosaic Virus class shows slightly higher recall and F1-score, suggesting robust classification. Macro and weighted averages indicate consistent model performance, with all metrics stable at 0.88 and an impressive AUC of 0.9677.

Fig. 8(B) presents the confusion matrix, illustrating the performance of the Inception V3 + PCA (500) + SVM (SIG) model in classifying various classes. The model accurately identified 76 out of 87 instances for the Target Spot class, 63 out of 68 for the Leaf Curl Virus class, and 73 out of 80 for the Mosaic Virus class, with only a few errors. This reliability is evidenced by the diagonal dominance in the matrix, which reflects the model's consistency. The few misclassifications can be attributed to similarities between the classes.

The Inception V3 + PCA (500) + SVM (SIG) model (Fig.

TABLE V
Comparative Analysis for Existing Research Works with Proposed Model

Authors	Description	Dataset and Models	Result Analysis
Paymode et al. (2022) [24]	The study uses deep learning to identify diseases in tomato and grape leaves. It aims to enhance crop health and boost agricultural productivity.	A dataset of tomato and grape leaf images. The proposed model is based on the VGG16 architecture.	The VGG16 architecture achieved an accuracy of **98.40%** for grapes and **95.71%** for tomatoes.
Zhang et al. (2023) [25]	Introduces a new network architecture, IBSA_Net, to identify tomato leaf diseases.	Used PDDA and PlantVillage datasets with the IBSA_Net model.	The IBSA_Net model performed well with high precision, recall, and F1-score. Test accuracy: **94.6%.**
Shafik et al. (2024) [26]	The research introduces two DL models for early detection and classification of plant diseases, enhancing accuracy and efficiency through transfer learning with nine pre-trained CNNs.	PDDNet-AE and PDDNet-LVE models used on the PlantVillage dataset.	The proposed model, PDDNet-LVE, achieved a high accuracy rate of **97.79%**, outperforming individual CNN models and other advanced methods.
Mputu et al. (2024) [27]	Proposes a hybrid method for tomato quality classification, combining pre-trained CNNs with traditional ML algorithms to automate the grading process.	The CNN-SVM hybrid model used on custom and public datasets.	The CNN-SVM hybrid model reached an accuracy of **97.50%** in binary and **97.54%** in multi-class classification. Additionally, the InceptionV3 model proved to be the most effective feature extractor.
Kaur et al. (2023) [28]	Introduces a novel DL model, Modified InceptionResNet-V2, which classifies tomato leaf diseases using transfer learning for enhanced performance.	Used Modified InceptionResNet-V2 (MIR-V2) on public and self-collected datasets.	The MIR-V2 model classified seven tomato leaf diseases, achieving an accuracy of **98%** and an F1-score of **97.94%.**
Chouchane et al. (2024) [29]	Suggests a hybrid DL method for detecting and classifying tomato leaf diseases, combining transfer learning with EDA for improved accuracy.	Used hybrid DL and transfer learning models on Taiwan and PlantVillage datasets.	The proposed method achieved mean accuracies of **98.29%** and **98.09%** on the datasets.
Wang & Liu (2024) [30]	Introduces TomatoDet, a new DL model for accurate and efficient detection of tomato diseases.	Swin-DDETR on a custom dataset of tomato images with intricate backgrounds.	Achieved a mean average precision (mAP) of **92.3%**, an improvement of 8.7% over the baseline model. It has a high detection speed of 46.6 FPS in real-time applications.
Present Study	**Proposes a hybrid transfer learning method utilizing PCA-enhanced SVM for detecting tomato leaf diseases.**	**Inception V3 features reduced with PCA (500) + SVM classifiers (POL, RBF, LIN, SIG).**	**SVM (Polynomial): AUC-0.999, Accuracy-99%; SVM (RBF): AUC-0.99, Accuracy-98%; SVM (Linear): AUC-0.992, Accuracy-97%; SVM (Sigmoid): AUC-0.971, Accuracy-88%.**

8(C)) demonstrates strong discriminative performance across all three plant disease categories. The blue ROC curve for the Target Spot class achieves the highest AUC value of 0.9829, indicating near-perfect classification with minimal false positives. The orange ROC curve for the Leaf Curl Virus class shows slightly lower separability compared to the Target Spot class. The green ROC curve for the Mosaic Virus class records the lowest AUC of 0.9563.

E. SVM Models Comparative Analysis for IV3+PCA(500) Features Classification

Table IV compares different SVM kernel models used to classify features from Inception V3 combined with PCA (500). The SVM with a Polynomial kernel stands out as the best performer, achieving an impressive AUC of 0.999 and an accuracy of 99%. This indicates that it is highly effective at classifying data. The SVM with an RBF kernel also performs well, with an AUC of 0.994 and an accuracy of 98%, making it a strong contender. The Linear SVM model shows reliable results, with an AUC of 0.992 and an accuracy of 97%. However, the SVM using the Sigmoid kernel shows comparatively lower performance, with an AUC of 0.971 and an accuracy of 88%. As per the study, the polynomial kernel demonstrates superior capability in furnishing the dataset's complex features.

V. DISCUSSIONS

The study (Fig. 9) evaluates the performance metrics of various SVM kernels used in classification tasks. The polynomial model demonstrates superior performance, achieving the highest AUC of **0.999** and an accuracy of **99%**. The RBF kernel closely follows, showcasing strong predictive capabilities. The linear model performs slightly less, suggesting a less flexible feature representation. In contrast, the sigmoid kernel underperforms, with an AUC of 0.971 and an accuracy of 88.3%, indicating limitations in capturing complex data relationships.

Table V presents a comparison of various methods for detecting tomato leaf diseases. Previous studies utilized advanced models such as VGG16 and IBSA_Net, demonstrating high accuracy. However, the proposed model outperformed these approaches. It employed a polynomial SVM kernel, achieving an accuracy of 99% and an AUC of 0.999. Additionally, the model incorporated PCA to reduce data size and enhance classification. This study highlights increased efficiency and reliability, making it a promising solution for agricultural disease management.

VI. CONCLUSION

Identifying diseases in tomato leaves is vital for maintaining crop yields. It helps prevent losses and enables timely intervention to reduce disease spread and enhance productivity. This study introduces a hybrid transfer learning framework for detecting diseases in tomato crops. It combines Inception V3 features with PCA to reduce dimensions. The approach uses SVM classifiers with different kernels. The method showed strong performance across various disease categories. The polynomial kernel SVM achieved the best results, with an AUC of 0.999 and 99% accuracy. The findings indicate that hybrid transfer learning approaches can improve classification accuracy. They also reduce computational complexity when combined with dimensionality reduction techniques. This research covers a scalable and efficient solution for early disease detection. It has potential applications in agriculture, enhancing crop management and productivity. Future studies will aim to expand the dataset, explore more feature extraction methods, and adapt the model for different crops and environments.

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