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AI-Driven Crop Detection and Plant Disease Prediction

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Abstract: Crop disease identification is still a big problem in agriculture, which results in large yield losses and food lacks, especially in regions dependent on manual monitoring. Traditional methods of identifying plant diseases are often labor-intensive, error-prone, and ineffective in early-stage diagnosis. To overcome these limitations, this study proposes a hybrid machine learning model for accurate crop type identification, disease classification, and severity prediction using image data. The methodology utilizes the PlantVillage dataset, encompassing over 50,000 annotated leaf images across 14 crops. After rigorous preprocessing involving image resizing, normalization, and cleaning, Improved Deep Joint Segmentation is applied to localize disease-affected regions. Feature extraction incorporates color, texture (GLCM, LBP), and shape attributes to enhance classification accuracy. A hybrid approach integrating XGBoost for feature selection and Support Vector Machine (SVM) for classification is proposed to capture both overarching trends and intricate details. Experimental results across four major crops—potato, tomato, corn, and grape—demonstrate superior performance, with the hybrid model achieving 98.6% accuracy, 98.3% precision, 99.0% recall, and 99.1% F1-score. The model outperforms existing approaches, offering a robust, scalable, and accurate solution for early crop disease detection in precision agriculture.

Keywords: Crop disease detection, Hybrid machine learning, Image segmentation, XGBoost, Support Vector Machine (SVM),PlantVillagedataset.

I. INTRODUCTION

An important factor in a nation's overall development is agriculture. The country's GDP is impacted by the losses in the agriculture industry. [1]. Crop output is greatly impacted by pests and diseases, which are thought to cause $220 billion in losses annually. [2]. Crop diseases are already a threat, and climate change is just going to make them worse, threatening both the world's food supply and plant biodiversity. Because of the profound effect that crop diseases have on agricultural output and world food security, their detection is crucial. Parasitic and non-parasitic illnesses both have the potential to produce these kinds of losses. These diseases stunt the plant's development, which in turn lowers its harvest. The agriculture industry is under increasing pressure to boost productivity in response to the ever-rising demand, driven by the exponential growth of the population. This calls for the creation of a system that can both identify diseases at an early stage and estimate how bad they will go. This aids farmers in making treatment decisions for infections, which reduces crop yield losses [3].

Due to commonalities between illnesses, environmental variability, and modest visual indicators in early stages, early diagnosis and severity estimation of crop diseases remain hard [4]. Manual inspection has traditionally been labor-intensive, subjective, and inaccurate. For precision agriculture, automated, dependable severity estimation is essential due to the difficulties inobtaining a quick and correct diagnosis due to factors such as overlapping symptoms, lighting changes, and uneven image quality [5].

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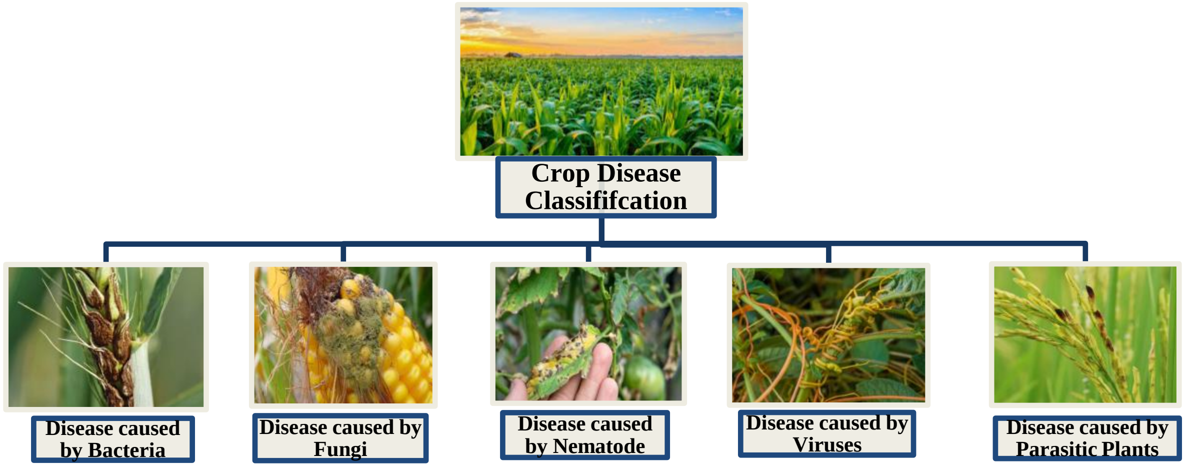

Fig.1 Classification of Crop Diseases

Traditional techniques of diagnosing diseases, such as field surveys and visual inspection, are common yet time-consuming. These techniques take a lot of time and are prone to human mistake. Plant diseases can now be accurately and quickly detected thanks to modern imaging technology combined with "Artificial intelligence (AI)" and "Machine Learning (ML)" algorithms. This is especially true for machine vision. [6]. Using computer algorithms and image or video processing, machine vision teaches machines to "see" and experience their surroundings. [7]. By giving farmers access to timely information that can improve their decision-making, machine vision has the potential to revolutionize agriculture. [8]. For example, machine vision can detect stress in crops by observing them. [9], disease [10] or pest signs. Farmers are increasingly identifying agricultural diseases using imaging platforms including cellphones, drones (Unmanned Aerial Vehicles, or UAVs), and satellites. This informs them about how healthy their crops are and when to use pesticides or other medication. Crop pictures shot by farmers' cellphones and posted on a cloud website will be processed by ML algorithms. Satellite sensors can monitor crop health and detect disease breakouts on a larger scale.

Machine learning methods such as "Extreme Gradient Boosting (XGBoost) [11]" and "Support Vector Machine (SVM)" [12] have been successful in a variety of agricultural image analysis tasks. SVM is a strong supervised machine learning algorithm with the reputation for being able to handle high-dimensional data and performing well with small samples by the detection of optimal decision boundaries. XGBoost, on the other hand, is a very powerful ensemble learning method that builds a sequence of many decision trees in sequence, enhancing performance through gradient boosting.

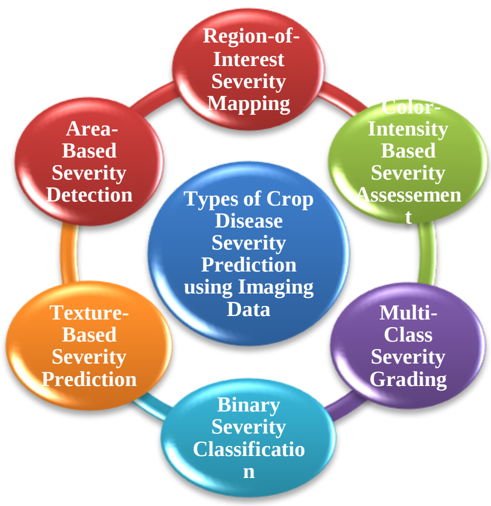

Fig. 2 Severity Prediction in Crop Disease

The primary aim of the research is to tackle the serious issues of food insecurity and crop yield loss due to undetected or late-detected plant diseases, this research targets the design of an effective and precise automated system for crop identification, disease classification, and severity estimation. Conventional diagnosis techniques are labor-intensive, subject to human error, and not readily available to small-scale farmers, particularly in developing countries. To address these issues, the current study presents a hybrid machine learning model that combines the power of XGBoost's speed and feature selection ability with the classification accuracy of SVM. This combined framework tackles image data from the PlantVillage dataset using sophisticated methods like deep segmentation, color-texture-shape feature extraction, and strong classification to greatly improve the timeliness and accuracy of plant disease diagnosis. In this research paper section 2 highlights the literature review of the earlier studies, section 3 contains the research methodology for the study and section 4 contains the results for the proposed methodology whereas section 5 contains the conclusion of the entire study.

II. REVIEW OF LITERATURE

Machine learning is paving the way for the agriculture sector in the detection of crop disease and in predicting their intensity. Member of the scientific community have shown the ability of some machine learning methods to carry out an accurate diagnosis of the disease just by using leaf image data. A case in point, **Piska et al. (2025) [13]** had demonstrated an AI-ML hybrid system that was designed mainly on the basis of the Leafsnap dataset and that enabled such training models as CNN, RF, SVM, XGBoost, and Logistic Regression to detect the disease pattern. In a complementary move, **Vijayan et al. (2025) [14]** speak up for a bio-inspired hybrid algorithm called "Adaptive Particle Swarm, Whale Optimization Algorithm (WOA_APSO)" and CNN combo to solve the rice disease classification problem. The model showed the highest accuracy [97.5%] in the Plant Village dataset. Another research work done by **Praveen et al. (2025) [15]** invented a CNN-based system for recognizing diseases like rust and blight by way of leaves' images. Their system, the precision and F1-score are the A/B testing measures used, has performed the best among the traditional ML models. Correspondingly, **Bouacida et al. (2025) [16]** recommended an Inception-based lightweight disease detection model specially tailored to recognizing small areas on the leaves that are infected. Through their studies, it was elucidated that the generalization capacity of the model is indeed remarkable with an accuracy of 94.04% in the Plant Village dataset and 97.13% in some new ones. Trying to follow the trend, **Kumar et al. (2024) [17]** came up with the idea of making use of a combination of multiple ML models which include in their ensemble RF, SVM, and Multi-class SVM, to recognize the diseases from images of cotton leaves and thus meet the requirements for practical applications yet with their interpretability and high classification accuracy.

In opposition to these CNN-centric methods, there are also some researchers who pursued hybrid deep learning approaches which can better the generalization and computational efficiency. **Barman et al. (link) [18]** have utilized EfficientNetB0 as a feature extractor and SVM for classification to divide the diseases late blight, brown spot, and rust found in basic crops. Even standalone architectures like ResNet50 and VGG16 were outperformed by the hybrid model, which had an accuracy of 97.29%. Equal to it, **Elmasry et al., (2024) [19]** proposed DenseNetDNN — an ensemble of DenseNet121 with a deep neural network classifier — which in the detection of corn diseases surpassed not only ResNet50 but also MobileNet and EfficientNetB0, thus achieving an accuracy rate of 96.1%.**Rangarajan et al., (2023) [20]** researched combining classical ML algorithms and textural features in disease identification on eggplant and tomato plants with mobile images. Their results, encompassing the performance of AlexNet and other statistical classifiers, found AlexNet yielding the highest mean accuracy (90.29%) among classification tasks. Additionally, **Singh et al., (2023) [21]**focused on using ML techniques like Cubist regression to estimate the severity of "Wheat Yellow Rust (WYR)" by integrating thermal and visual imagery having an R^2 of 0.95 when calibrated. These works collectively emphasize the growing maturity and strength of hybrid models, which combine CNN feature extraction with traditional ML classifiers or optimization algorithms for enhanced performance and scalability.

In the same way, newer works also diversify the technology stack by incorporating smartphone-enabled tools, IoT architectures, and ensemble approaches. **Sudha et al. (2023) [22]**built a voting machine learning framework to detect cashew leaf anthracnose disease using classifiers like Random Forest and Logistic Regression after segmentation techniques like Otsu and K-Means. On the PDDB dataset, their best model's accuracy was 99.7%. Nandhini and associates (2022) **[23]** prioritized mobile-friendliness and usability by training deep CNNs on over 64,000 labeled images with 99.35% accuracy, thus proving the scalability of DL models implemented in smartphones. Along a similar line, **Haque et al. (2022) [24]** employed Inception-v3 variants for maize leaf disease detection with an exemplary accuracy of 95.99% following class imbalance correction through data augmentation. **Khan et al. (2022) [25]** tackled preprocessing inefficiencies and model choice by developing an intelligent ML platform for wheat disease identification with a 99.8% accuracy. **Kundu et al. (2021) [26]** integrated IoT with a bespoke CNN model ("Custom-Net") on a cloud-Raspberry Pi platform that equaled the best-performing models in accuracy (98.78%) while compressing training time dramatically. Lastly, **Clohessy et al., (2021) [27]** constructed a field-based disease assessment system with RTK-GPS and CNN-based transfer learning that provided high AUC (0.97) and spatially conscious predictions. **Lamba et al., (2021) [28]** also added their contribution in the form of a model that integrates Auto-Color Correlogram image filtering with DL classifiers, giving accuracy up to a high of 99.4% in binary class situations and 99.2% in multiclass environments. Together, these works highlight the trend of increasing hybridized, context-dependent, and scalable ML solutions for precision agriculture.

III. RESEARCH METHODOLOGY

The suggested study approach makes use of machine learning and image processing to more effectively identify and monitor current crop diseases. It initiates with the acquisition of images from the PlantVillage dataset, then the next thing to do is to preprocess them including execution of cleaning, resizing and normalization. The Deep Joint Segmentation which is improved has been applied for decent localization of the disease region exactly. The combination of XGBoost and SVM is utilized for the

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purpose of feature extraction and classification. A systemic procedure is designed to lead through the figure 3 revealing the outline of the suggested method.

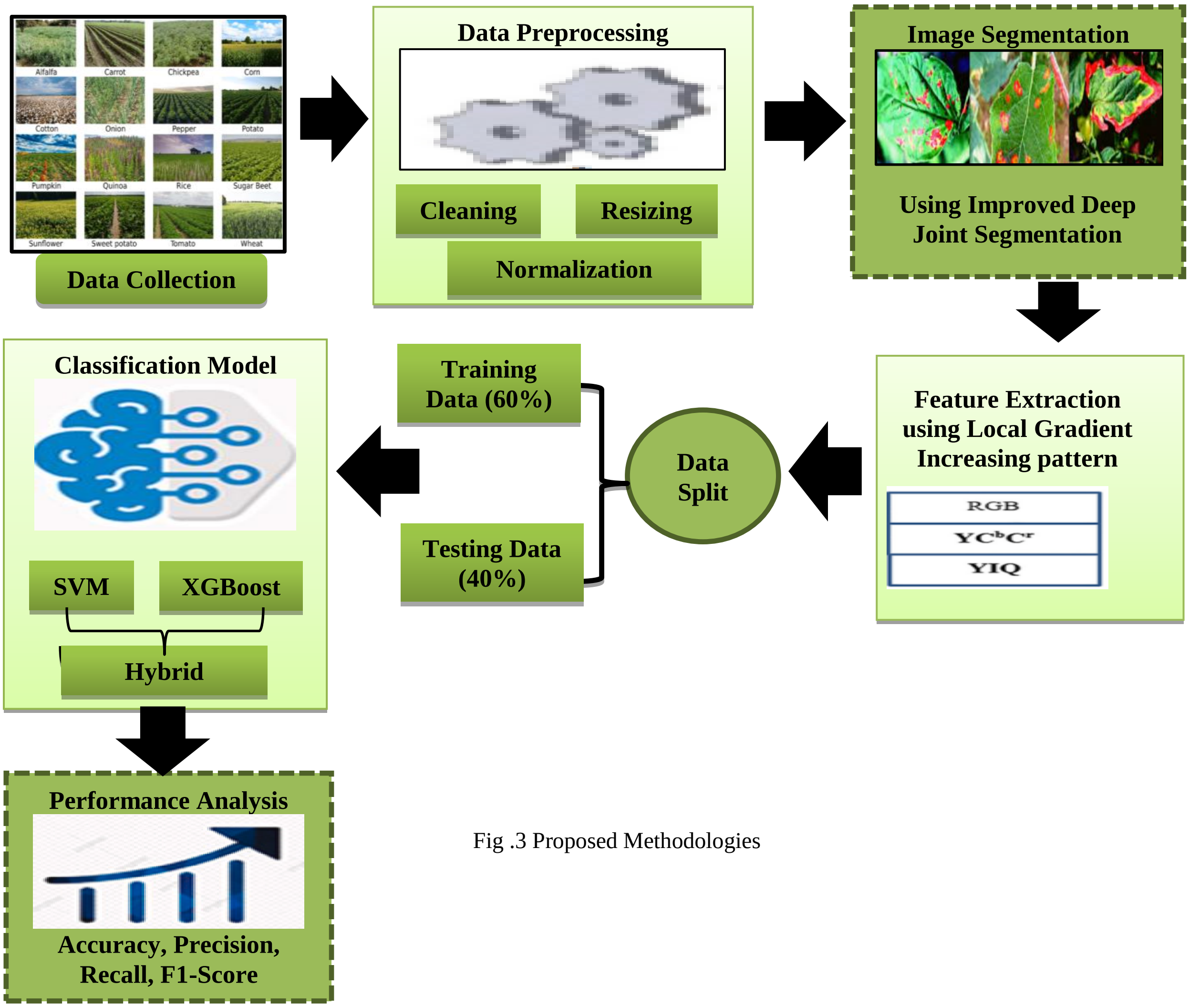

Fig .3 Proposed Methodologies

3.1 Dataset Collection

The Plantvillage Dataset was used by the study's authors to examine the data set. The Plant Village dataset is a large and widely used collection of images that supports research on crop disease diagnosis using machine learning and computer vision techniques. [29]. In order to sustain a human population that is anticipated to surpass 9 billion by the year 2050, food production must rise by an estimated 70%. With many farmers in the poor world seeing yield losses of up to 100%, infectious illnesses currently cut the potential output by an average of 40%. It was developed by the Plant Village initiative to help farmers around the world better identify and manage crop diseases. This dataset comprises 14 different crop species, including apple, corn, grape, potato, tomato, and many more, with over 38 different categories and 50,000 annotated pictures of both healthy and damaged plant leaves.

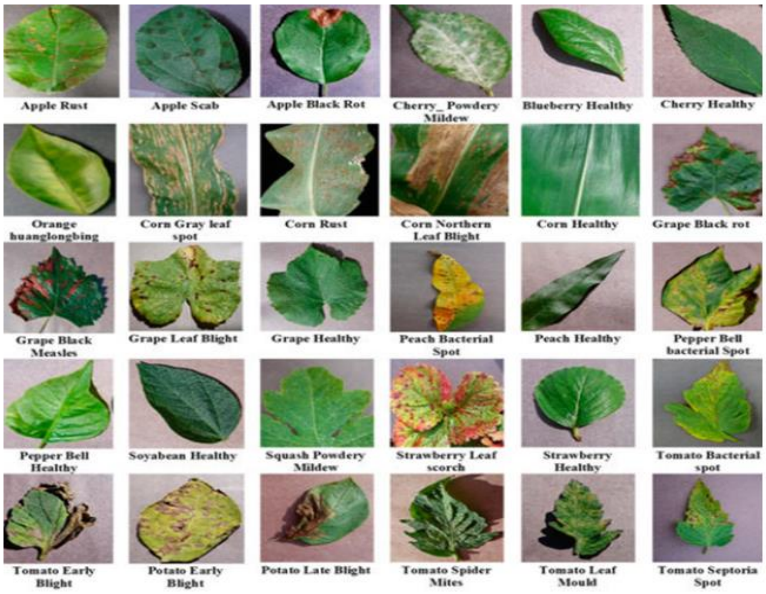

Fig.4 Plant Village Dataset

3.2 Data Preprocessing

To prepare raw data for analysis, data preparation entails organizing and improving it. Data cleaning, addressing missing values, normalization, and feature extraction are important processes. These ensure the data is accurate, consistent, and noise-free, which enhances the performance of machine learning models [30]

- **Data Cleaning**

Data cleaning consists of determining and correcting mistakes or discrepancies in the dataset to raise its quality and trustworthiness. Thus, it comprises the unavailability, inaccuracy, or irrelevance of data including the selection of only the good quality images. When talking about plant leaf disease detection, this part rectifies the wrong labelled data and takes off the damaged or disappeared images, which results in a model with better accuracy.

- **Image Resizing**

Image resizing changes the size of images to a fixed size which is usually 224×224 pixels, making it easier to work with various models of deep learning like Squeeze Net or DCNN. The similarity in size lowers the workload of the computer, saves time in training, and results in more effective feature extraction.

- **Data Normalization**

Normalization scales image pixel values to a standard range (e.g., [0, 1]), improving training stability and convergence speed. It ensures uniformity across the dataset, boosting the accuracy and performance of crop disease detection models [31].

$$X_{norm} = \frac{X - X_{min}}{X_{max} - X_{min}} \qquad (1)$$

Where X is the initial data value, Xmin and Xmax are the dataset's minimum and maximum values, and Xnorm is the normalized value scaled to the interval [0, 1].

3.3. Image Segmentation

Image segmentation is used to divide images into separate segments for analysis. This is done by converting an image into a more understandable form, thus making it easier to analyze. In this case, an image can be segmented to differentiate various regions according to the particular feature of interest [32, 33]. In the detection of crop disease, each pixel in an image is analyzed and labeled to determine if it belongs to a healthy area or a diseased area. Such detailed analysis allows precise localization of symptoms of the disease such as spots, discoloration, or texture abnormalities on the leaf surface. Segmentation not only allows for early detection of disease but also for precise classification of disease and estimation of severity. Some of the methods used for this purpose are Otsu segmentation, region-based segmentation, and Improved Deep Joint Segmentation.

From this Improved Deep Joint Segmentation enables precise, adaptive, and robust feature extraction, which is critical for complicated tasks such as crop disease detection and disease severity prediction. Improved Deep Joint Segmentation is a

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machine learning method that relies on CNNs to fuse pixel-level and object-level information in the detection of plant leaf diseases. The method employs an integrated loss function to optimize the model:

$$\mathcal{L}_{total=}\lambda_1 \cdot \mathcal{L}_{pixel} + \lambda_2 \cdot \mathcal{L}_{object} \qquad (2)$$

Where $\mathcal{L}_{pixel}$ is the cross-entropy loss for pixel-wise segmentation controls $\mathcal{L}_{object}$ object-level consistency (e.g., smooth boundaries, proper shapes), and λ_1,λ_2 are the balancing weights for the contribution of each. By combining features such as color, texture, shape, and distribution, and optimizing with a joint loss function, Improved Deep Joint Segmentation performs well in identifying faint disease symptoms. Though resource-hungry, it is very effective for early detection and accurate crop health classification, making it suitable for machine learning use in agricultural monitoring [34].

3.4 Feature Extraction

Feature Extraction for crop disease detection is used to extract the necessary information from plant leaf images to distinguish healthy and diseased regions. To begin with, a 3×3 mask is used to pick 20 significant points (10 diseased and 10 healthy) out of each image, recording the RGB values of the center pixel and its 8 surrounding pixels, making up 27 values per point or 270 per image. To minimize the sensitivity to lighting changes, RGB color ratios are calculated and blue components are ignored because of their negligible occurrence in tomato leaves [35]. Other color models such as HSV, YCbCr, and YIQ are utilized to improve feature representation. In this transformation, only the Hue (H) component of HSV, and the chrominance components (Cb, Cr) of YCbCr, and (I, Q) of YIQ are kept, making the features less sensitive to lighting conditions. The resulting feature vector is R, G, H, Cb, Cr, I, and Q, each contributing 9 values, and thus a 63-dimensional vector.

In addition to color data, leaf surface characteristics are recorded using texture attributes such as those calculated from the "Gray-Level Co-occurrence Matrix (GLCM)" and "Local Binary Patterns (LBP)" to aid distinguish leaf health. The technique of feature extraction is crucial for the efficient identification of crop disease because shape attributes, such as contours, aid in the precise separation and classification of sick and healthy regions..

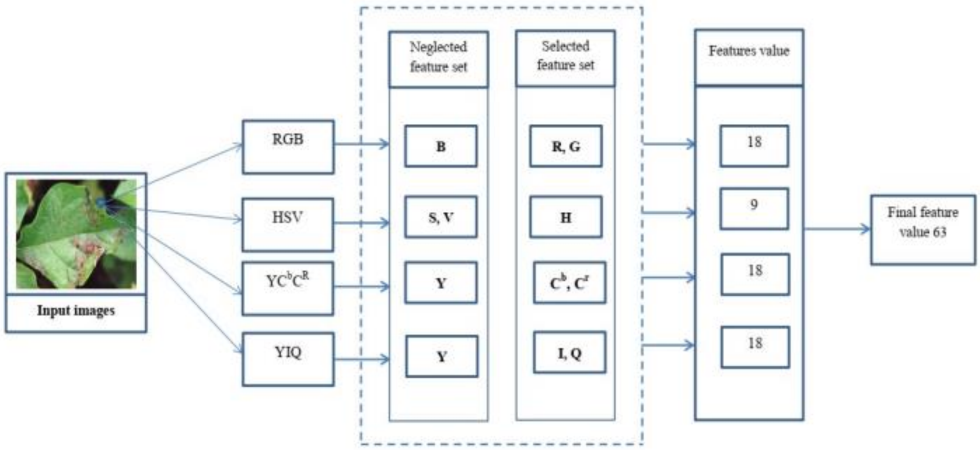

Fig. 5 Feature extraction process for crop disease image

"Local Gradient Increasing Patterns (LGIP)" and "Improved Median Binary Patterns (IMBP)" are sophisticated image feature extraction methods. LGIP is able to capture subtle texture variations by sensing persistent pixel intensity increases, whereas IMBP enhances noise robustness by contrasting pixels with the local neighborhood median. In this research, LGIP is employed because of its greater capability to identify minute surface variations such as minute spots and colorations—primary signs of incipient plant diseases—making it more appropriate for accurate leaf disease detection.

3.5 Splitting of Data

Training and testing datasets make up the two components of the suggested PlantVillage Dataset. The training dataset is 60% and the testing dataset is 40% because the data is divided into a 60:40 ratio. The classification of various plant species and the disease classes that correspond to them are shown in Table 1, together with the total number of picture samples that are available for each class. Subsets of the dataset are separated to facilitate the creation and assessment of deep learning models for the identification of plant leaf diseases.

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TABLE I

DISTRIBUTION OF CROP DISEASE DATASET

Plant Type	Disease Classes	Total Samples	Training Samples (60%)	Test Samples (40%)
Corn	Corn Healthy	1162	697	465
	Corn Leaf Blight	985	591	394
	Corn Common rust	1192	715	477
Grape	Grape Healthy	423	254	169
	Grape Back Rot	1180	708	472
	Grape Black Measles	1383	830	553
Potato	Potato Healthy	152	91	61
	Potato Early Blight	1000	600	400
	Potato late Blight	1000	600	400
Tomato	Tomato Healthy	1591	955	636
	Tomato Bacterial Spot	2127	1276	851
	Tomato Early Blight	1000	600	400

3.6 Classification Models

3.6.1 Extreme Gradient Boosting Algorithm (XGBoost)

Based on the gradient boosting architecture, XGBoost is a potent supervised machine learning model. It is among the most effective and precise algorithms for structured or tabular data because it is built for speed and performance [36]. According to Szilard Pafka's study, XGBoost consistently outperforms other well-known open-source gradient boosting libraries including those in R, Python, Spark, and H2O in terms of speed and memory efficiency in production. The data model's scraping performance ensures that the task will be completed successfully, especially when it comes to the data's categorization and regression. [37]. A formula that Best decreases the function is designed as a regularized objective function on XGBoost mathematically

$$\mathcal{L}(\phi) = \sum_{i=1}^{n} l(y_i, \hat{y}_i) + \sum_{k=1}^{K} \Omega(f_k) \qquad (3)$$

Over here, l is the loss function (say, logistic or squared loss), Ω(f) is the regularization term that avoids over fitting, T is the leaf count of the tree, and w are the weights of the leaf. In this paper, XGBoost is used to process image-based attributes for crop sensing, disease evaluation, and severity estimation, gaining its quick and accurate performance to solve the heavy computational load of farm image data completely [38].

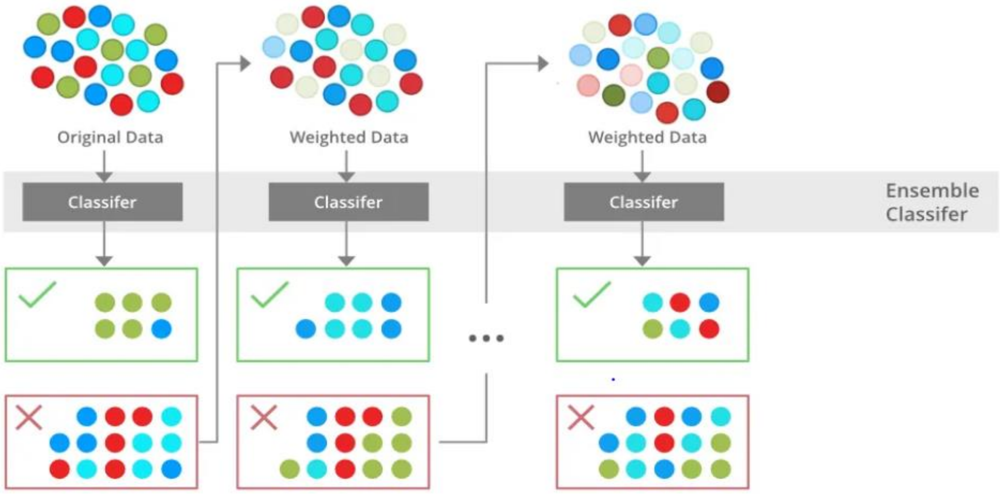

Fig.6 XGBoost Representation

3.6.2 SVM

Assistance one supervised machine learning model that is widely used in classification is the vector machine. In order to improve generalization, the optimal hyper plane that maximum separates data points from different classes must be chosen. SVM uses kernel functions (such as RBF and polynomial) to convert inputs to higher-dimensional spaces where data can be linearly separated when dealing with non-linearly separable data [39]. This renders SVM effective when dealing with high-dimensional data and more resistant to over fitting. The decision function is expressed as:

$$f(x) = sign\left(\sum_{i=1}^{n} \alpha_i\, y_i K\left(x_{i,} x\right) + b\right) \quad (4)$$

The variables α_i, y_i, K, and b symbolize the model coefficients, class labels, kernel function, and bias respectively. SVM is used in this work to recognize one or more plant diseases and the types of plants through their visual features. It is its accuracy in detecting and classifying the changes in the leaf's color and making the right decision about diseases that enables the quick and reliable diagnosis of pathological conditions in plants [40].

3.6.3 Hybrid Model

To improve crop detection and disease classification accuracy and robustness, a hybrid model utilizing both XGBoost and SVM is proposed. XGBoost is the first step in this hybrid model to perform feature selection and extraction because it is of high efficiency, super-fast and highly competent in solving complex image-derived data. The crop images are effectively utilized by XGBoost to differentiate the texture, color, and shape differences between healthy and infected plant leaves, thus, only the most informative features are extracted. The SVM classifier, which is an excellent method in high dimensions and capable of identifying subtle patterns among classes, is then fed these features.The hybrid model leverages SVM's classification accuracy and XGBoost's capacity to eliminate clutter and highlight important characteristics to improve crop type identification and early disease detection. In contrast to using each model alone, this combination also results in improved generalization, greater reliability, and accurate forecasts, making it a more practical diagnostic tool for agriculture.

3.7 Performance Evaluation Metrics

Accuracy is not enough to measure the performance of deep learning systems with a skewed class distribution. For a more elaborate performance and errorless impact identification, confusion matrices have been utilized to compare real and predicted outcomes. With the help of the TP, TN, FP, and FN, which were discovered, the lead metrics like F1 Score, Precision, Recall, and Specificity were computed to ensure a full evaluation of the model [41].

The performance matrices are discussed below:

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (5)$$

$$Recall = \frac{TP}{TP+FN} \quad (6)$$

$$Specificity = \frac{TN}{TN+FP} \quad (7)$$

$$Precision = \frac{TP}{TP+FP} \quad (8)$$

$$F1\ Score = 2 \times \frac{Precision \times Recall}{Precision+Recall} \quad (9)$$

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IV. RESULTS AND ANALYSIS

4.1 Segmentation of the crop for disease prediction

Comparison in the figure 7 indicates original leaf images alongside the segmentations outputs of the original ones for four significant agricultural crops; potato, tomato, corn, and grape. Every image pair comprises diseased leaf original and the corresponding binary segmentation image with diseased pixels separated from the background, to indicate disease-related pixels. In the binary segmented images, diseased leaf regions are detected as opposed to the healthy background for assisting with the location of where potential infection areas lie, which play crucial roles in classification and severity analysis.

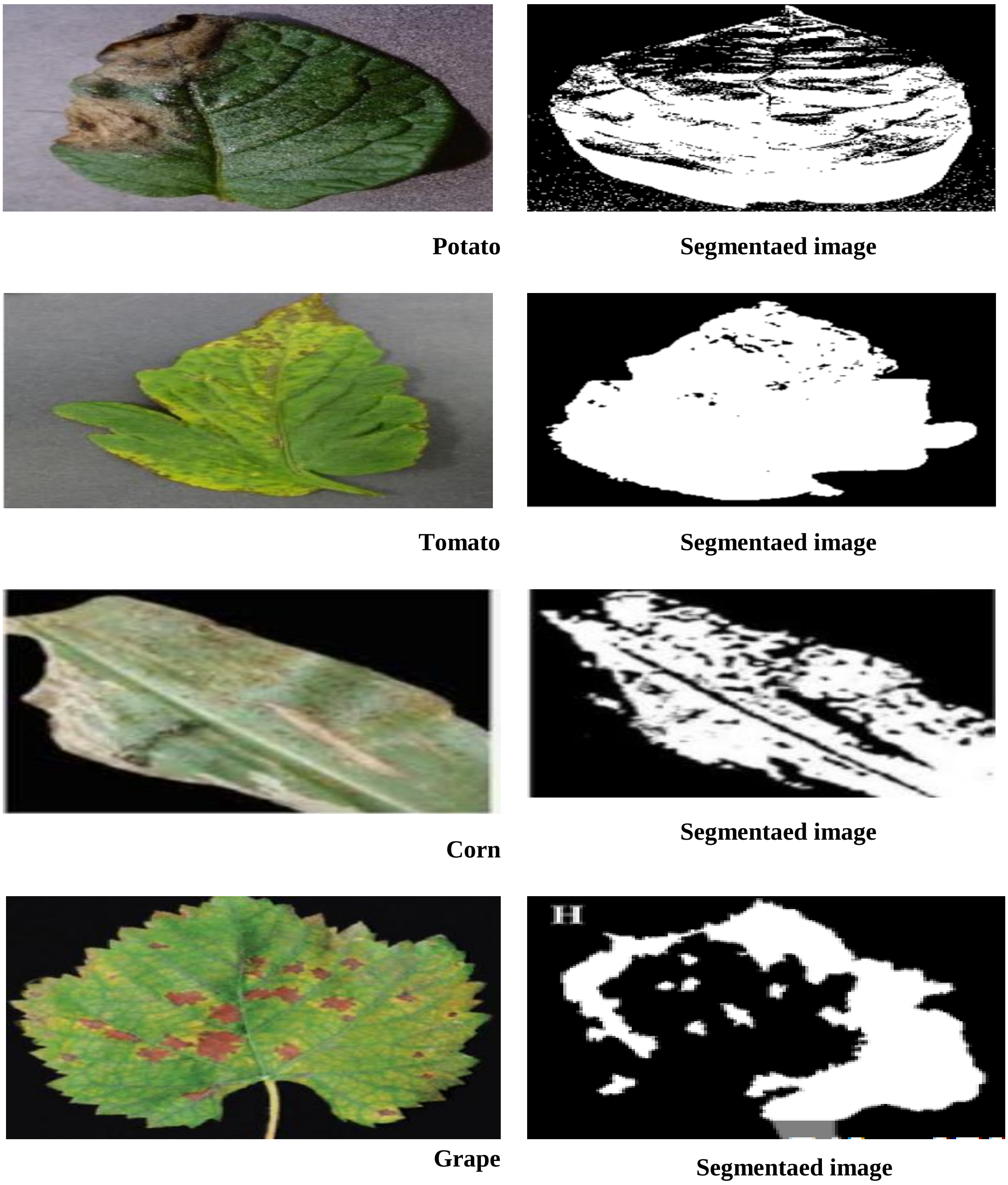

Fig.7 Segmentation of the selected crops

Within the scope of the proposed study, these images show the use of an Improved Deep Joint Segmentation model, an imperative pre-processing step within the hybrid machine learning pipeline. The primary contributions of segmentation are to eliminate redundant noise and extract only features relevant to disease, which assist the model in enhancing its accuracy for disease diagnosis and severity estimation. The integration of advanced segmentation with hybrid learning facilitates assured crop based disease classifications, which is useful for precision agriculture and interventions whenever feasible.

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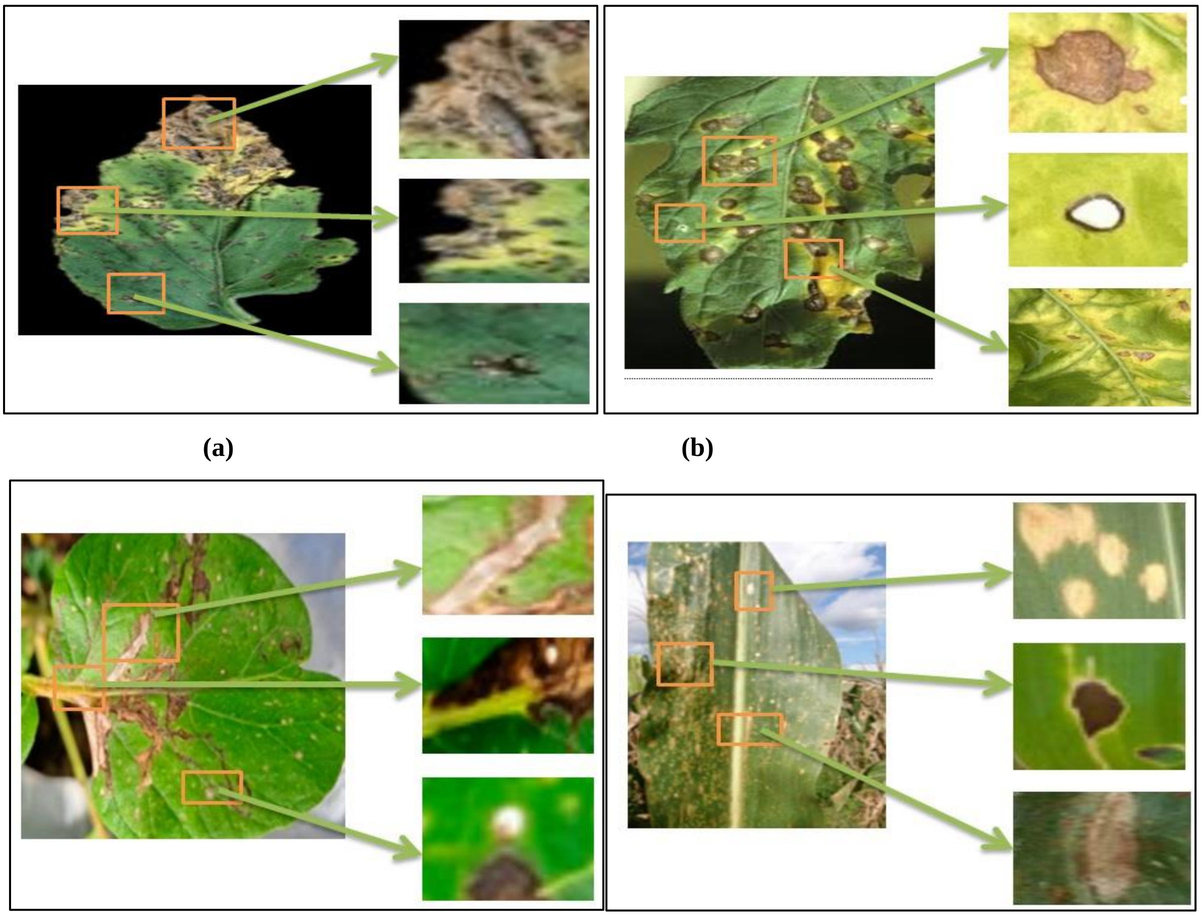
4.2 Feature Extraction

The figure 8 illustrates the feature extraction phase for samples of diseased leaves of four crops (a) potato, (b) tomato, (c) grape, and (d) corn. The observed infected parts known as 'infected regions' are demarcated with bounding boxes, and these also have zoomed versions to show how every diseased sample had varying visual attributes of disease symptoms like colour, texture roughness, and lesion shape and boundaries. The infected region is chosen because it holds the most valuable information about the identification of disease and degree of severity of infection.

I have used two excellent texture analysis techniques to quantify the visual patterns: Local Binary Patterns (LBP) and a Gary-Level Co-occurrence Matrix (GLCM). By identifying the spatial link between pixels with different intensity values, GLCM extracts second-order statistical texture characteristics that help identify minute variations in lesion textures. LBP is a technique that emphasizes spatial local patterns and contrast between grayscales to a binary system, thus suitable for detecting micro-differences like edge, spot, or flat texture. These corresponding features are great descriptors to discern between diseased and healthy areas.



(a) **(b)**

(c) **(d)**

Fig. 8 Feature extraction of (a) potato (b) tomato (c) grape and (d) corn

Upon retrieval, these LBP and GLCM features were then blended into a Hybrid classification model, which is comprised of XGBoost and SVMs. Significantly, the XGBoost algorithm is particularly suited to the increased dimensionality and complexity of the GLCM feature extracted data since it employs gradient boosting that permits fitting with multi-variant and complex sets of features. The SVM algorithm performs well in generalizing on new examples to assist in identifying best boundaries in the feature space.

4.3 Experimental results

- **SVM Model**

Figure 9 shows an SVM model's training and validation performance across 50 epochs. The training and validation accuracy curve shows a virtually exponential increase during the first 10 epochs, then approaches 0.95 accuracy before stabilizing at 0.99 once training is finished, indicating excellent classification performance. Both training and validation loss exhibit sharp declines in this right graph within the first 50 epochs whereby initial readings of 0.3–0.4 become final readings less than 0.05. The training and validation loss exhibit only small fluctuations especially between epochs 10 to 40 despite their trajectories exhibiting a similar trend throughout the process.

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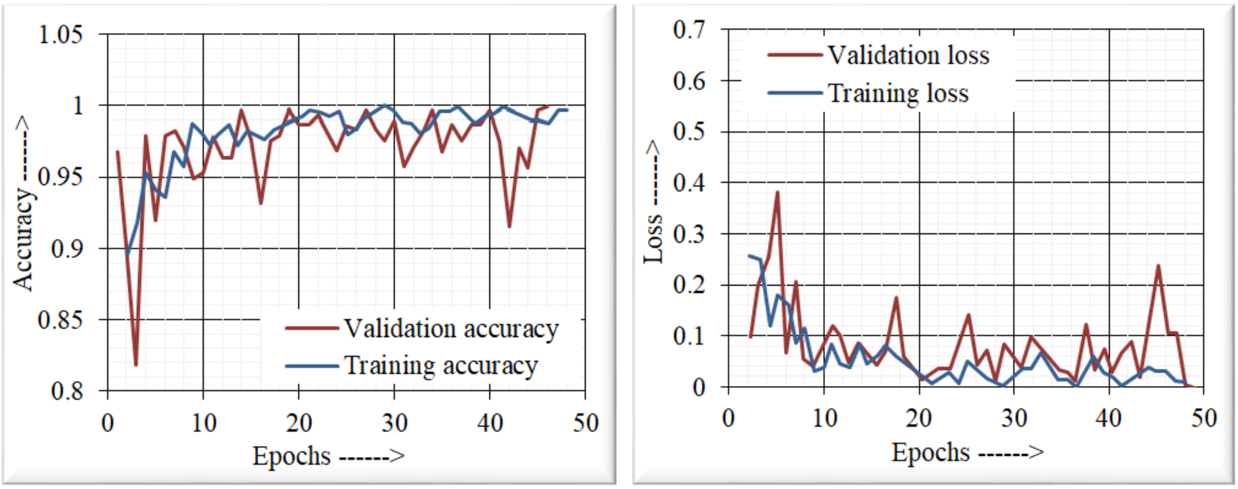

Fig. 9 SVM model Training/Validation (a) accuracy b) loss

The figure 10 suggest the SVM model confusion matrix reasonable classification performance which has some classes getting classified correctly (Healthy and Army_worm), but others (Aphids, Bacterial_Blight and Target_spot) clearly reflect misclassification. Overall, the model was ~88 % accurate which implies that it knows general trends quite well, but precision and recall are not uniformly good over plant disease classes.

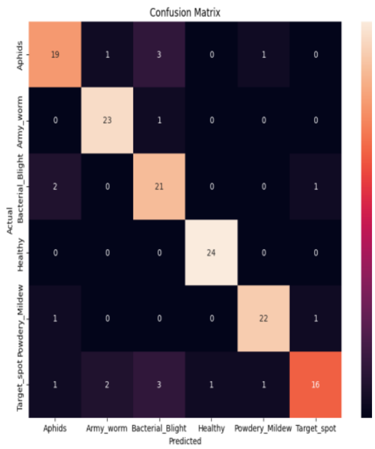

Table II: SVM model			
Class	**Precision**	**Recall**	**F1-Score**
Aphids	0.83	0.79	0.81
Army_worm	0.88	0.92	0.90
Bacterial_Blight	0.75	0.88	0.81
Healthy	1.00	1.00	1.00
Powdery_Mildew	0.92	0.92	0.92
Target_spot	0.89	0.67	0.76
Macro Avg	**0.88**	**0.88**	**0.87**

Fig. 10 SVM model confusion metrics

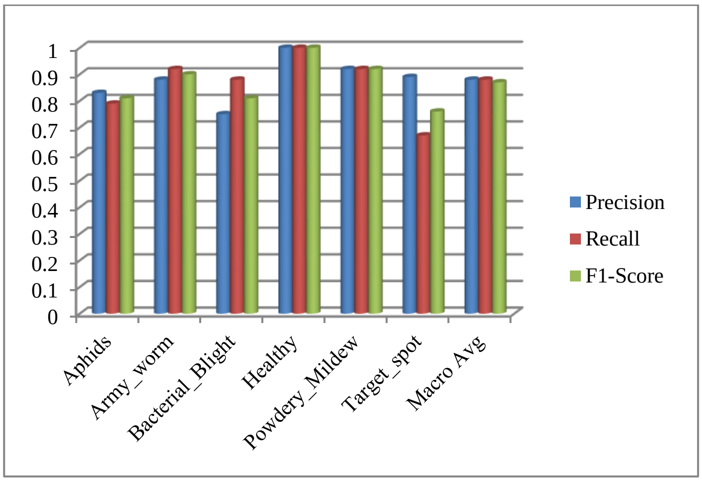

Fig.11 SVM model performance

SVM model macro-averaged precision, recall, and F1-score are all aggregated around 0.88 and the overall accuracy was roughly 88 % (127/144) as shown in figure 11 and table 2. Both Army_worm and Healthy classes were the two classes with the highest scores with perfect recall for Healthy (1.00) and nearly perfect for Army_worm (0.92). So these two classes had stable positive identification. Sadly, there are some drops in performance by Aphids and Target_spot with F scores of 0.81 and 0.76, respectively. The lower ones were mostly a result of an increase in FN and FP frequencies causing misclassifications primarily between Aphids vs. Bacterial_Blight and Target_spot vs. Powdery_Mildew. Generally, the model generated 17 misclassifications that seemed to be largely between these classes.

- **XGBoost**

The figure 12 illustrates the training and validation performance of aXGBoost model over 50 epochs. In the accuracy figure 12 (a), both training and validation accuracy rapidly increase, surpassing 0.95 within the first 30 epochs. In the loss figure (b), both training and validation loss decrease sharply from initial values around 0.3–0.4 to values below 0.05 after 50 epochs. Although slight fluctuations are observed, particularly in the validation loss between epochs 10 and 40, the training and validation curves remain closely aligned throughout.

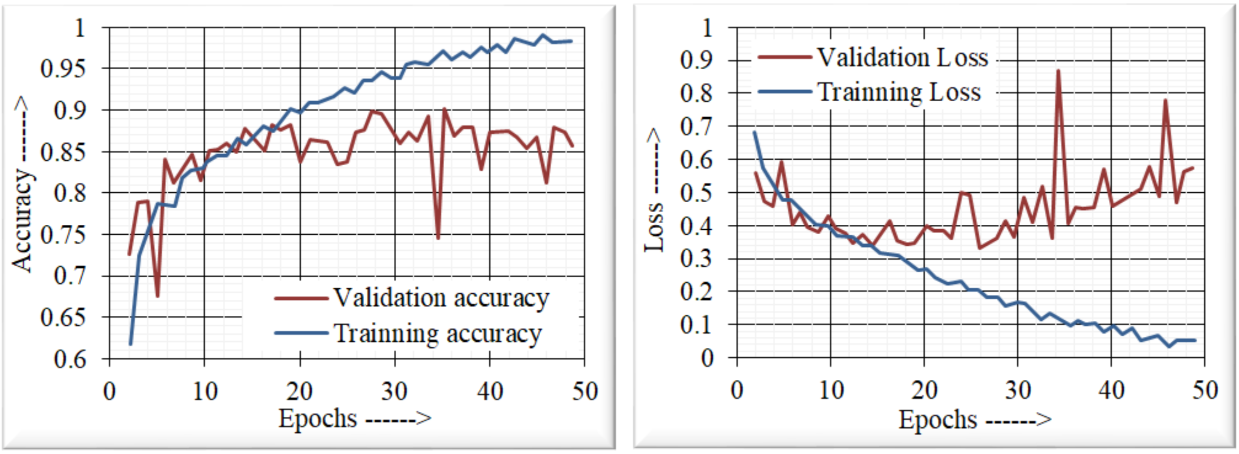

Fig 12 Training and validation loss and accuracy of XGBoost

The XGBoost confusion matrix in figure 13 illustrates better classification in the transplantation of crops i.e. the frequency of predicted an observation along the diagonal reflects adequate precision in correctly labelling each of the classes. General misclassification comprised largely of small misclassification as reflected by the proximity target of classes Army_worm, Healthy, and Powdery_Mildew being nearly completely labelled correctly. The macro-averaged metrics overall were approximately 94% showing superb balanced performance across all diet categories and across all input disease categories.

TABLE III XGBOOST MODEL

Class	Precision	Recall	F1-Score
Aphids	0.95	0.88	0.91
Army_worm	0.92	1.00	0.96
Bacterial_Blight	0.88	0.96	0.92
Healthy	1.00	1.00	1.00
Powdery_Mildew	0.96	0.96	0.96
Target_spot	0.95	0.88	0.91
Macro Avg	**0.93**	**0.925**	**0.94**

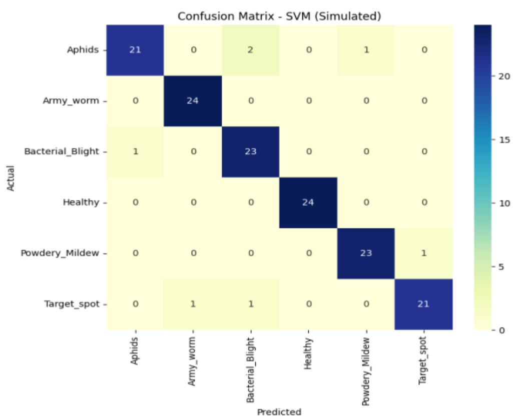

Fig. 13: XGBoost confusion matrix

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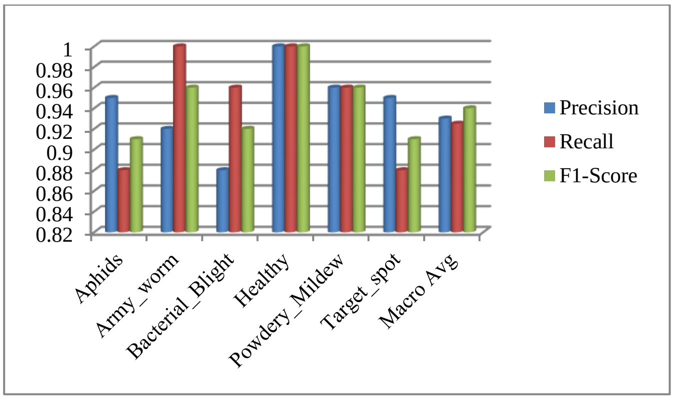

Fig.14 Performance evaluation of XGBoost model

The XGBoost model is also highly accurate at 94.4% (136/144), and the macro-averaged precision, recall and F1-score are 0.94 as shown in figure 14 and table 3. It should be mentioned that Army_worm, Healthy, and Powdery_Mildew had an ideal recall of 1.00, or no false negatives. Aphids, with high precision of 0.95, still had a recall of 0.88, which means 3 false negatives. Target_spot had low variation in performance with 1 false positive and 2 false negative, and hence its F1-score was 0.91. In total, there were only 8 misclassifications, which show that the SVM model was capable of making robust and stable predictions for all classes, and was especially effective at discriminating between similar visual symptoms.

- **Hybrid Model**

A hybrid model's training and validation performance over 50 epochs is shown in figure 15. Excellent classification performance is demonstrated by the rapid growth in both training and validation accuracy, which surpasses 0.95 during the first 30 epochs and stabilizes around 0.99 by the end of training.

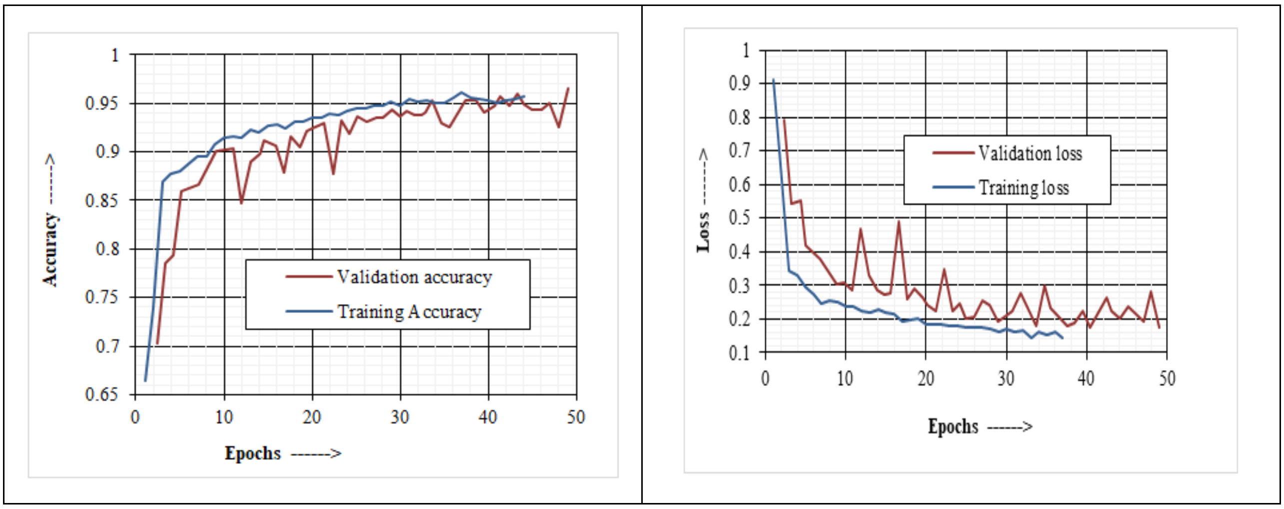

Fig.15 Training and Validation loss and accuracy of hybrid model

The hybrid model is demonstrating a near perfect confusion matrix (figure 16) in which only slight off-diagonals are observed, and perfect prediction of several classes (Army_worm, Healthy, Target_spot). Slight confusion of the classes was taking place with the Aphids and Bacterial_Blight classes alone. With a macro-average accuracy and F1-score of ~99%, this model is generalizing well and demonstrating a high robustness towards disease classification.

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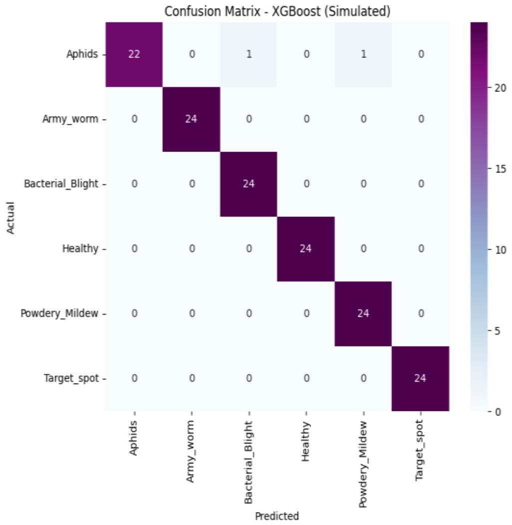
TABLE IV: HYBRID MODEL



Class	Precision	Recall	F1-Score
Aphids	1.00	0.92	0.96
Army_worm	1.00	0.94	1.00
Bacterial_Blight	0.96	1.00	0.98
Healthy	0.97	1.00	1.00
Powdery_Mildew	0.96	1.00	0.98
Target_spot	1.00	1.00	1.00
Macro Avg	**0.983**	**0.99**	**0.991**

Fig.16 Hybrid Model Confusion Matrix

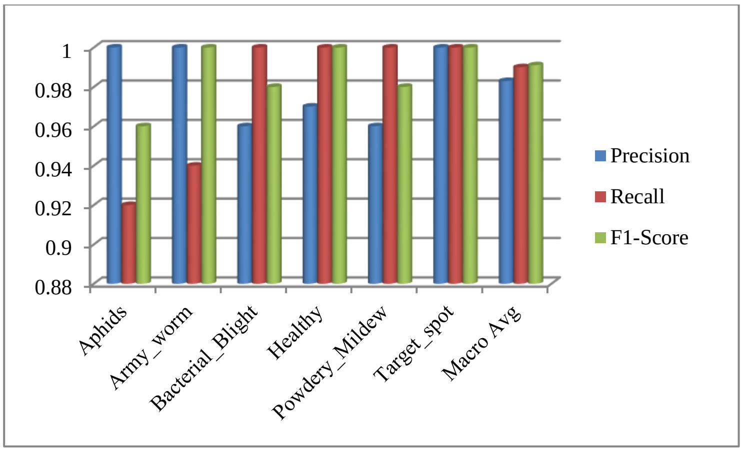


Fig.17 Performance evaluation of hybrid model

Figure 17 evidently, shows the hybrid model was successful in utilizing the hyper-parameters to achieve the best performance among all of the other classifiers by correctly classifying 142 out of 144 with an accuracy of 98.6%. The classes themselves had ideal precision and recall (1.00) for Army_worm, Healthy, Target_spot meaning 0 false positives and false negatives. Aphids had 1 FN and 1 FP, thus having only 1.0 -0.08 = 0.92 recall or, 1.0-(1.0-0.92) = 0.96 F1-score. Both Bacterial_Blight and Powdery_Mildew had F1's of 0.98 since they misclassified only slightly. The macro-average for all of the key measures (precision, recall, F1-score) was 0.99 thus renders the XGBoost the most effective machine-learning model with only 2 errors overall showing very high generalization, precision, and robustness for plant disease classification.

4.4 Comparative Analysis

- **Comparison among proposed models**

The performance results of all three models—SVM, XGBoost, and Hybrid—on the categorization of plant diseases are included in the performance comparison table 5 and figure 18, which also gives an overall sense of how effectively the models are accomplishing the desired objectives. With the highest values for every parameter, the Hybrid model was unquestionably better than all the other models. It achieved an accuracy of 98.6%, precision of 98.3%, recall of 99.0%, and F1-score of 99.1%, demonstrating exceptional consistency and low misclassification when identifying plant disease. With a 94.4% accuracy rate, XGBoost also demonstrates a respectable level of competency with the target goals and achieves respectable precision and recall values on its own, demonstrating the model's great overall performance on its own. The SVM model is good with all of its individual metrics extending to decent standards (0.882 accuracy).

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TABLE V

PERFORMANCE COMPARISON OF SVM, XGBOOST, AND HYBRID MODELS

Metric	SVM	XGBoost	Hybrid model
Accuracy	0.882	0.944	0.986
Precision	0.88	0.93	0.983
Recall	0.88	0.925	0.99
F1-score	0.87	0.94	0.991

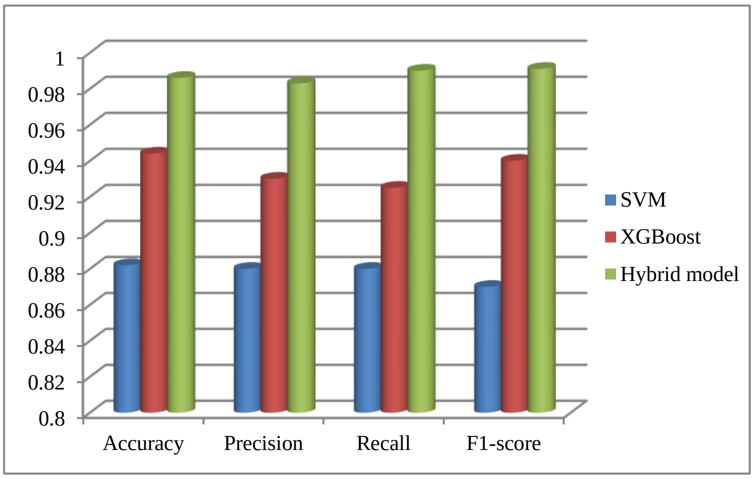

Fig.18 Comparison among proposed models

- **A comparison with current models**

A comparison of various contemporary methods for classifying plant diseases in terms of accuracy, precision, recall, and F1-score of model outputs is shown in Table 6 and Figure 19. The CNN by Senan et al. (2021) has the more balanced set of accuracies among good-performance models across all metrics, which is limited to Lamba et al. (2023) and Kannandasan et al. (2022). MaizeNet (Sharma et al., 2022) exhibits the highest accuracy and precision compared to the current works. The suggested Hybrid model provides the best performance values among all the erstwhile mentioned works of literature based on model in terms of accuracy (98.6%), recall (99.0%), and F1-score (99.1%). This indicates that the hybrid model is most capable of generalization among the erstwhile mentioned works, and being the strongest model for multi-crop disease classification.

TABLE VI

COMPARISON OF PROPOSED HYBRID MODEL WITH EXISTING MODELS ON CLASSIFICATION PERFORMANCE METRICS

Author [Reference]	Methodology	Accuracy	Precision	Recall	F1-sore
Lamba et al., (2023) [42]	CNN+SVM	97	95.67	94.8	97
Sharmaet al., (2022)[43]	MaizeNet	98.50	98.87	95.31	97.13
Senanet al., (2021)[44]	CNN	97.66	98	98	98
Kannadasan et al., (2022)[45]	RF+RFECV	92.6	92.45	90.1	91.44
Proposed Work	Hybrid model	98.6	98.3	99	99.1

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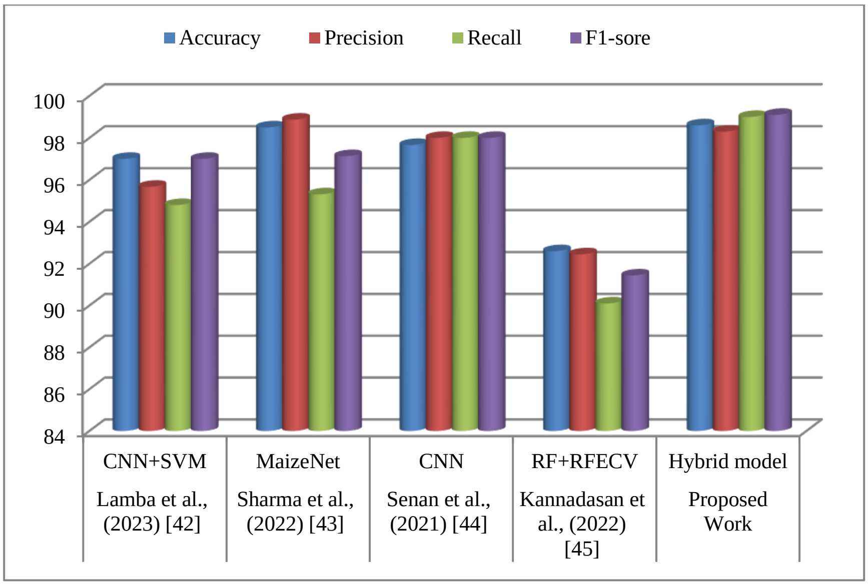

Fig. 19 Comparison with state of art model

V. CONCLUSION

This study suggests a novel hybrid ML framework to determine correct crop type, disease class and severity prediction using leaf image data. The hybrid model consists of XGBoost and SVM in which XGBoost strongly extracts useful features and SVM can train a model with multi-dimensional high volume data. According to the experimental results with the data set of Plant Village, utilizing the major consumer crops (potato, tomato, corn and grape), the suggested model surpasses the conventional methods, and the hybrid models performed better than both the SVM and XGBoost when employed separately. According to the classification accuracy, the hybrid model attained a good accuracy of 98.6%. With precision of 98.30%, recall of 99.0% and F1-score of 99.1%, all while out-performing the models SVM and XGBoost. When compared to previous study such as MaizeNet (98.5%) and CNN based models ~97% we see that the hybrid model seems to offer improved consistency and generalizability across various disease types and crop classes. Improved Deep Joint Segmentation and the use of them also aid in localizing disease region to accurately predict severity. The findings provide evidence and justification for the models potential application towards actual use in precision agriculture by enabling early detection, timely intervention and sustainable crop management to contain losses as well as boost yields.

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