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MULBERRY LEAF DISEASE DETECTION AND CLASSIFICATION USING HYBRID MACHINE LEARNING

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ABSTRACT

Sericulture plays a vital role in India's agro-industries, with the mulberry plant being essential for cocoon-bearing. The quality and quantity of mulberry leaves are crucial, as they directly impact cocoon production. Therefore, detecting and classifying diseases in mulberry leaves is a necessary process that can assist farmers and boost the economy. To address this need, an innovative Machine Learning (ML) approach is proposed using a Scalable kernel-based Support Vector Machine (S-SVM), which enhances the classification accuracy of traditional Support Vector Machine (SVM) methods. To further optimize the performance of S-SVM, the Al-Biruni Earth Radius Optimization (AERO) technique is introduced, which effectively balances the weight between the majority (healthy) and minority (diseased) classes of the leaves. This approach enables accurate classification of mulberry leaf diseases, such as healthy, leaf spot, and leaf rust. Before classification, image preprocessing is a key step, for which we adopt the K-means clustering algorithm to identify the disease-affected regions on the leaf. Contour tracing is then used to outline these regions for better disease detection. Additionally, Transfer Learning (TL) is applied to extract relevant features from the images, leveraging pre-trained models to improve classification accuracy. The proposed system is simulated using MATLAB software, and its effectiveness is compared with state-of-the-art methods. The results indicated excellent performance, with a training accuracy of 99% and a loss of 0.8%, and a validation accuracy of 98% with a loss of 0.3% over 100 epochs, demonstrating the potential of this approach for real-world application in sericulture.

Keywords: Contour Tracing, K-Means Clustering, Mulberry Leaf Disease, Support Vector Machine, Transfer Learning.

INTRODUCTION

Agricultural output plays a critical role in securing the financial stability of farmers, and for developed nations, strengthening the agricultural sector is crucial for ensuring sustainability and bridging essential gaps in the global economy. Similar to humans, plants are susceptible to diseases at various stages of growth, which can significantly impact crop yields and, consequently, farmers' incomes. With the global population projected to surpass 9 billion by 2050, finding innovative solutions for early plant disease detection and treatment is key to enhance food production while reducing the reliance on harmful pesticides (Sharma *et al*., 2020). The success of the agricultural sector hinges on the timely identification and analysis of plant diseases. Traditionally, this has been done through expert observation, relying solely on human visual inspection, which is often inefficient, labor-intensive, and costly. This method poses a significant challenge for small and medium-sized farmers, especially in developing regions, as it becomes unsustainable and can lead to the rapid spread of disease to healthy plants. To address these challenges, recent studies have turned to cutting-edge autonomous systems powered by Machine Learning (ML) and Deep Learning (DL) to detect plant diseases (Sharma *et al*., 2020). Many of these studies have leveraged real-time data, such as plant and leaf images from datasets like Plant Village, to create more efficient solutions. For instance, Ferentinos (2018) utilized 58 different plant species to categorize plant diseases, providing valuable insights into how machine learning can be applied across various agricultural contexts. One such plant species is mulberry (*Morus spp*.), a fast-growing perennial tree native to the Himalayan foothills of China and a crucial crop in sericulture.

Ferentinos (2018) stated that the major leaf diseases of mulberry include leaf spot, leaf rust, powdery mildew, and bacterial blight. Leaf spot is caused by various fungal pathogens, leading to the formation of lesions that reduce leaf area and quality. Leaf Rust, caused by the fungus *Puccinia mori*, results in yellow-orange pustules that weaken the plant and hinder photosynthesis. Powdery Mildew, caused by *Erysiphe mori*, affects the leaf surface, leading to stunted growth and poor leaf quality. Bacterial Blight, caused by *Xanthomonas mori*, results in water-soaked lesions that can lead to defoliation. These diseases can severely affect the quality and quantity of mulberry leaves, ultimately reducing cocoon production in sericulture. The economic losses due to these diseases can be significant, as they lead to decreased yield, increased production costs for pest management, and overall reduced profitability for farmers, negatively impacting the sericulture industry.

The mulberry foliage reduces insulin levels, lipids, and inflammation, offering promising support in the management of diabetes and cardiovascular diseases as highlighted by Ahilan *et al*. (2019). However, mulberry consumption may also lead to side effects such as indigestion, diarrhea, and abdominal discomfort. While there is limited reliable data on the medicinal properties of white mulberry fruits, the need for effective disease detection in mulberry leaves remains critical. To address this, we propose an advanced AERO-S-SVM approach, designed to accurately classify mulberry leaf diseases, which could significantly enhance the quality and yield of agro-products. This method offers a promising solution for improving disease management in mulberry cultivation, benefiting both farmers and the broader agricultural industry.

This study introduces a hybrid machine learning approach for accurate and efficient detection of mulberry leaf diseases, essential for improving mulberry crop management in sericulture. The key contributions of this work are as follows:

Advanced Image Preprocessing – K-means clustering and contour tracing techniques are employed to preprocess mulberry leaf images, effectively identifying and isolating disease-affected regions. This enhances the feature extraction process by ensuring that the classification model focuses on the most relevant disease patterns.

Transfer Learning for Feature Extraction – A Transfer Learning (TL)-based approach is utilized to extract critical features from leaf images. Leveraging pre-trained deep learning models improves classification accuracy by capturing robust, high-level feature representations.

AERO-SVM-Based Classification – The Al-Biruni Earth Radius Optimization (AERO)-enhanced Support Vector Machine (SVM) model is applied for precise disease classification. This method optimally balances the weight between majority (healthy) and minority (diseased) classes, ensuring improved classification performance across three categories: healthy leaves, leaf spot, and leaf rust.

By integrating these advanced techniques, the proposed system ensures high accuracy, scalability, and efficiency in disease detection. This research holds significant potential for sericulture, providing a reliable tool for monitoring and managing mulberry crop health, ultimately contributing to enhanced silk production and economic sustainability.

MATERIALS AND METHODS

This section provides a concise overview of the proposed methodology for detecting and classifying mulberry leaf diseases. The techniques employed and their relevance to classifying diseases such as healthy, leaf spot, and leaf rust are outlined. For image preprocessing, we apply two key methods: K-means clustering and contour tracing, which together help isolate and enhance the disease-affected regions of the leaves. Following preprocessing, a Transfer Learning (TL)-based approach is implemented for feature extraction, which significantly aids in the classification process. Finally, the robust AERO-SVM model is used for accurate disease classification, leveraging its ability to handle imbalanced data. An overview of the entire workflow is illustrated in Figure 1, showcasing the seamless integration of these techniques for optimal performance.

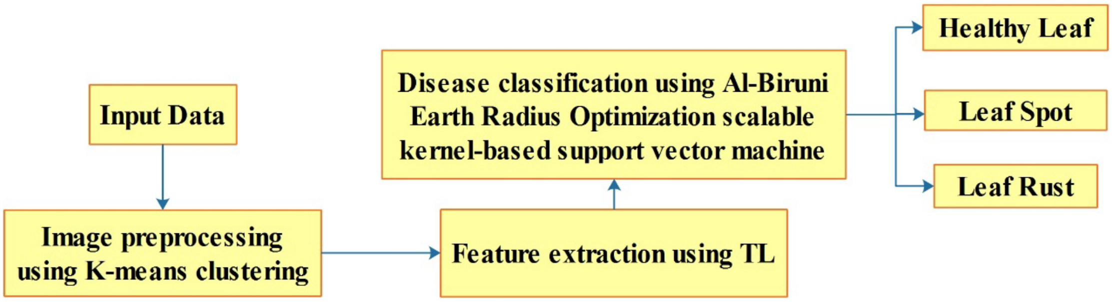

Figure 1. Workflow of the proposed model

Pre-processing: To pre-process the mulberry leaf images, we employ the K-means clustering algorithm (Hartigan, 1979), which is used to identify the affected regions on the leaves. The algorithm clusters the pixels based on their similarity, and the center of each cluster is determined. The distance from the cluster center is then calculated for each cluster to assist in identifying the affected areas. After clustering, contour tracing is applied to outline the shape of the detected regions, providing a clearer representation of the disease-affected areas. The features extracted from the contour tracing process are further analyzed to enhance the classification of the leaf patterns. This two-step pre-processing approach significantly improves the feature extraction process, making it more accurate and reliable.

Feature Extraction: For feature extraction from the mulberry leaf images, we leverage the Transfer Learning (TL) technique (Torrey, 2010). This method utilizes pre-trained models, which have already been exposed to a vast amount of data and have learned relevant features from various tasks. By fine-tuning these models on the mulberry leaf dataset, TL improves the extraction of robust features specific to the diseases present on the leaves. The use of TL allows for efficient learning and enhances the classification performance, as the model benefits from both previously learned tasks and the new tasks at hand. The diseases identified in this work include leaf spot, leaf rust, and healthy leaves, all of which are accurately classified using the features extracted through this approach.

The marginal probability distribution $r(y)$ together with the space related feature J for 2 strictures are $A = \{Y, s(y)\}$. When the 2 strictures are in the dissimilar provinces the feature space is defined as $(Y_s \neq Y_s)$. The formulation of the training data are attained as $\{(n_i, m_i)/i(1,2,3,\ldots,M)\}$ and are imperceptible and its functions are signified as prognostic $h(\cdot)$ in the Z space. The mission of 2 component specified at the particular province are humored as $T\{Z, \mathrm{h}(.)\}$. The probabilistic point is occupied from $s(m_i/n_i)$ and is adapted as $r(n_i)$.

The time T is reassessed for $T = \{Z, S(z/Y)\}$ and according to that conditional probabilities are attained and is specified as $\left(s(Z_s/Y_s) \neq s(Z_s/Y_s)\right)$. The altered deep model of global average pooling layer is employed in the TL to excerpt features.

Disease classification using S-SVM: The Support Vector Machine (SVM) is used to classify images and data (Ketu and Mishra, 2021). In this study, the SVM is applied to map the input features from mulberry leaves into a higher-dimensional space using kernel functions, ensuring that the different classes of mulberry leaf diseases are distinguishable. The goal is to maximize the margin between the hyperplanes, which serves to optimally separate the disease categories. The formulation for maximizing this margin in SVM is as follows:

$$W.y + c = 0 \qquad (1)$$

The hyperplane employed in SVM used for the separation of categorical classes are illustrated in Figure 2. The optimal pair of the SVM is (W_0, c_0) and decision is made using Eqn. (2).

$$f(y) = \sum_{l \in SVM} \gamma_l z_l \langle y.y_l\rangle + c \qquad (2)$$

For the higher dimensional feature space like mulberry leaves disease classification the value of $\langle y.y_l\rangle$ is substituted with the kernel function such as $Ker\langle y_l.y_k\rangle$ and it is given in Eqn. (3),

$$Ker\langle y_l.y_k\rangle = \langle y_l.y_k\rangle \qquad (3)$$

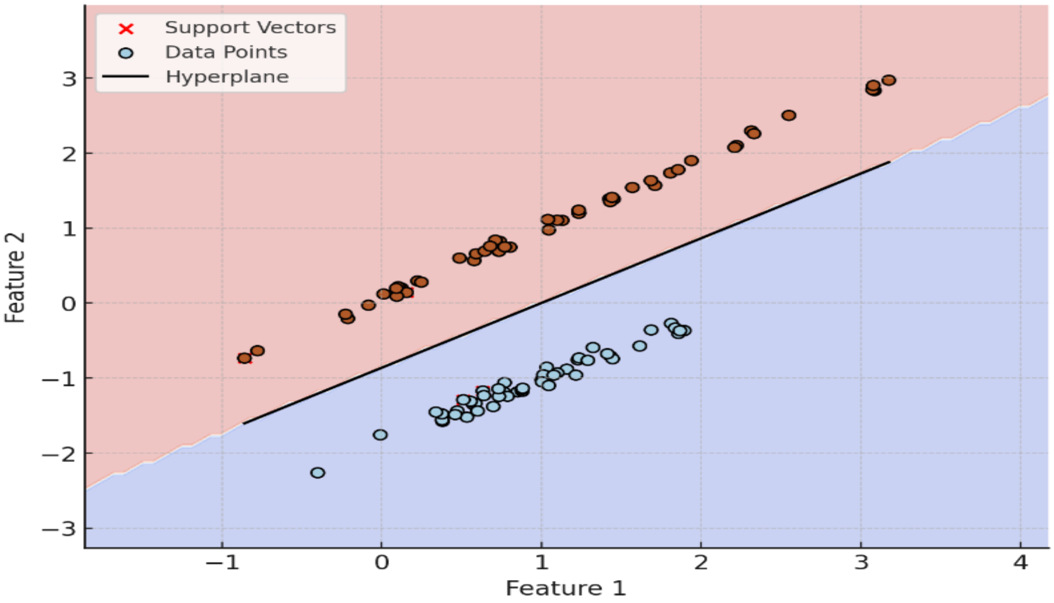

Figure 2. Disease classification using SVM

Choosing Kernel Function: To calculate the boundary position of the diseases of mulberry leaves the kernel function is to be chosen using the conventional SVM. The dataset D comprises the mulberry leaves are alienated into the $D^1, D^2, D^3, \ldots\ldots, D^l$ and after that the application of kernel transformation function as given in Eqn. (4).

$$f(y) = \begin{cases} e^{-x_1 q(y)^2}, if\ y \in D^1 \\ e^{-x_2 q(y)^2}, if\ y \in D^2 \\ \cdot \\ \cdot \\ \cdot \\ e^{-x_B q(y)^2}, if\ y \in D^B \end{cases} \qquad (4)$$

where, $q(y) = \sum_{l \in SVM} \gamma_l z_l \langle y.y_l \rangle + c$ with the support vector factor as γ_l, and the sample for the set of training is D^l and the following step to estimate the parameter value is x_l with the help of Chi-square test (h^2).

Chi-square testing: This test is used to classify different disease categories based on their frequency distribution. It can also be described as assessing the correlation between various groups. The primary goal of this test is to determine the relationship between x_l and the samples from each disease group. Mathematically, this can be represented as follows:

$$\mathrm{h}^2 = \sum \frac{(f_0 - f_e)^2}{f_e} \qquad (5)$$

The frequency of experiential and expected are defined as f_0 and f_e correspondingly.

Optimization-Based Weighting Factor Computation: To address the issue of class imbalance, it is crucial to assign appropriate weights to the factors, which can be a complex and challenging process. To overcome this, we propose a novel optimization algorithm called Al-Biruni Earth Radius Optimization (AERO), which is explained in the following section.

AERO Algorithm: The Al-Biruni Earth Radius Optimization (AERO) algorithm operates within specific constraints to identify the optimal solution (El-kenawy *et al.*, 2023). It defines the vector (*V*) for each member of the population and optimizes the parametric dimensions of the features. The fitness function (*f*) is used to measure various constraints, and the objective is to maximize the fitness vector V^* to search the population space. The algorithm selects random solutions from the population, evaluating solution size maximization and minimization. The fitness function further specifies the parameters involved in the solution.

(i) Exploration Operation

The exploration phase focuses on identifying the optimal feasible solution by breaking free from local optima. In this phase, the search space is carefully navigated to find new exploration sites. The current location is considered as the starting point for further exploration, and nearby options are evaluated iteratively to identify the most optimal path toward the desired solution. This iterative process ensures that the most promising solution is found by systematically exploring the search space.

$$A = G \frac{cos(y)}{1 - cos(y)} \qquad (6)$$

$$dim = R_1(p(x) - 1) \qquad (7)$$

$$p(x+1) = p(x) + dim(2A_2 - 1) \qquad (8)$$

The limit of [0, 2] picks H number as $0 < y \leq 180$. Equation (6) measures the vector coefficients A_1 and A_2. For promising area, the search agent with the circle diameter is *DA* respect to x^{th} iteration.

(ii) Exploitation Operation

The exploitation phase focuses on refining the current solution. During this phase, each participant is assigned a score based on its performance, and fitness is calculated using the Best-Evolutionary-Ranking (BER) method once the cycle concludes. The primary goal of exploitation is to move towards the optimal solution by leveraging two key BER strategies: first, by directing the search toward the best solution, and second, by exploring the region around this optimal solution for further improvements. This dual approach ensures that the algorithm converges efficiently, focusing its search on the most promising areas while fine-tuning the solution. The movement toward the optimal solution is guided by the following expression, ensuring continuous improvement and refinement.

$$p(x+1) = A^2(p(x) + dim) \qquad (9)$$

$$dim = A_3(l(x) - p(x)) \qquad (10)$$

At iteration *T*, the steps movement to the optimal solution is measured equation (7) and estimate the random vector A_3. The distance vector dimension with the vector solution $(l(x))$ at the x^{th} iteration.

The highest potential is given to the leader by focusing on the region surrounding the optimal solution. This area is prioritized to ensure that the search remains directed toward the most promising and effective solutions, allowing for further refinement and improvement.

$$\grave{p}(x+1) = A(p^*(x) + k) \qquad (11)$$

$$k = 1 + \frac{2 \times L^2}{(iter_{max}()^2)} \qquad (12)$$

From this, $p^*(x)$ signifies the optimal solution with $p(x+1)$ and $\grave{p}(x+1)$ are chosen. When the best fitness unchanged to last 2 iterations, the solution is mutated using Eqn. (13).

$$p(x+1) = k * x^2 - G \frac{cos(y)}{1 - cos(y)} \qquad (13)$$

The number of iterations is denoted as x_l and a random number, also x_l is selected within the range of 0 to 1. In the subsequent cycle, the best solutions are chosen, and the Biruni Earth Radius (BER) method is employed to ensure the selection of high-quality solutions. Multi-modal functions are guided to converge using the most effective techniques available. The BER method delivers advanced exploration capabilities, exploring the region around the optimal solution and adopting a mutational approach to enhance the search process. This approach prevents premature convergence by maintaining robust exploration abilities. The input to the BER consists of iteration counts along with parametric variables such as frequency, mutation rate, and population size. Each individual in the population is assigned an exploration or exploitation task based on the BER method. The best solution is located through an iterative process, with the group size being modified dynamically using BER. The goal is to complete the task by leveraging both exploration and exploitation capabilities across all groups. In each iteration, the exploration and exploitation processes are shuffled to maintain diversity, ensuring that the search space is thoroughly explored. The leader solution is not replaced during the process, preserving its unique role in guiding the algorithm. The AERO algorithm is outlined in Algorithm 1, demonstrating the pseudocode that governs the iterative process and BER-based exploration and exploitation.

Algorithm 1: Pseudocode for AERO algorithm

```
Initialization to fitness function, maximum iteration and population size $p_j (j = 1,2,..,dim)$
Initialize BER parameters
Fix $x=1$
Calculate every outcome fitness $f$
Define the best outcomes
While $x \leq iter_{max}$ do
    For best outcomes
        Move towards best outcomes
        $A = G \frac{cos(y)}{1-cos(y)}$
        $dim = A_1(p(x) - 1)$
        $p(x+1) = p(x) + dim(2A_2 - 1)$
    End For
    For each outcome based on the group do
        Best outcomes elitism
        $p(x+1) = A^2(p(x) + dim)$
        $dim = A_3(l(x) - p(x))$
        Analyze the best outcomes zone
        $p^{`}(x+1) = A(p^{*}(x) + k)$
        $k = 1 + \frac{2 \times L^2}{(iter_{max}()^2)}$
        Divergence $p^{`}(x+1)$ and $p(x+1)$
        Designate the best outcomes s
        if
            The best outcomes remain the same as of prevailing 2 iterations
        then
            Modernise outcome mutation
        End if
    End For
    Modernising the fitness to every outcomes
End While
Back to best outcome.
```

The suggested AERO algorithm offers low weight towards classes with chief and supreme weights to the slight classes with the satisfaction of $x_l \in (0,1)$.

***Approximation of x_l*:** For estimation, we define the dataset as *D*, consisting of samples *G* and classes *B*. The value of x_l is evaluated, and the updated Chi-square value is calculated during the process of optimal distribution. This method ensures that the distribution of values is fine-tuned to achieve the most accurate representation of the dataset's structure, as described in the following formulation

$$h^2 = \sum_{l=1}^{B} \frac{(g_l - G/B)^2}{G/B} \tag{14}$$

The no. of samples in the l^{th} category is g_l
where, $l = 1,2,3,\ldots.,B$

Let, $Y_l = \frac{(g_l - G/B)^2}{G/B}$

It suggests,

$$h^2 = \sum_{l=1}^{B} Y_l \tag{15}$$

From this the x_l is assessed as,

$$x_l = W_l \times \frac{Y_l}{h^2} \tag{16}$$

From eqn. (15), eqn. (16) it is revised as,

$$x_l = W_l \times \frac{Y_l}{\sum_{l=1}^{B} Y_j} \tag{17}$$

The comprehensive flow diagram illustrating the proposed AERO-based S-SVM methodology for classifying mulberry leaf diseases is presented in Figure 3. This diagram outlines the entire process, highlighting the key steps involved in the classification system.

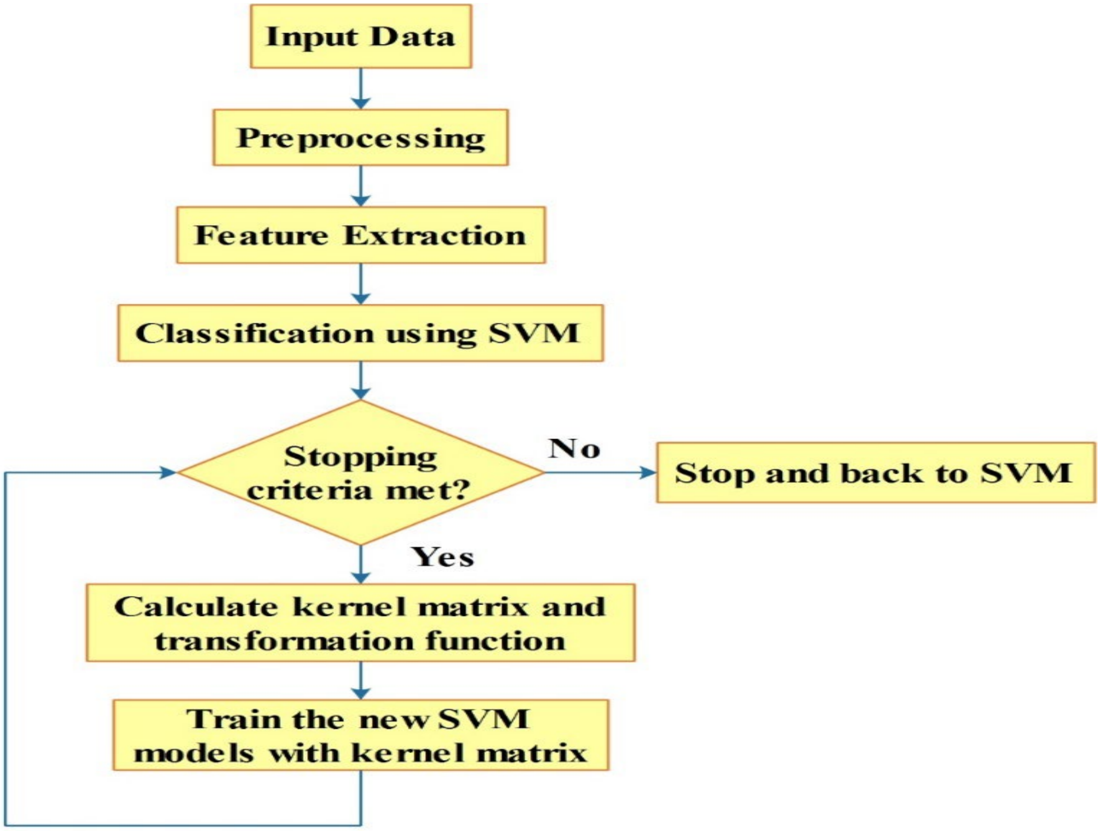

Figure 3. Flow diagram for Mulberry leaf disease classification using of AERO-S-SVM

RESULTS

During each epoch, several performance indicators, including training and validation loss, as well as training and validation accuracy, are monitored to assess the effectiveness of the proposed S-SVM model in classifying mulberry leaf diseases. Throughout the training phase, the model's accuracy is evaluated based on its training performance, while its ability to classify test data is measured through validation accuracy. The performance of the classifier is continuously refined by comparing training and validation results. The image dataset is split into two groups: 70% for training and 30% for validation. The model's performance is evaluated using the validation set, ensuring sufficient data is available for effective training. Hyperparameter tuning for the S-SVM model is carried out with the AERO algorithm, utilizing 5-fold cross-validation to optimize the model’s parameters. As the number of iterations increases, detection accuracy typically improves, though in some cases, further iterations may not lead to significant gains. This indicates a plateau where additional epochs do not contribute to improved mulberry leaf disease detection accuracy. Ultimately, the S-SVM model achieves the best detection accuracy when the optimal number of epochs is selected. Table 1 summarizes the simulation parameters used in this work.

Table 1. Simulation strictures.

Strictures	Values
Population size	50
No. of epochs	100
Mutation probability	0.5
Exploration (%)	70
No. of runs	30
Kernel type	Scalable
Kernel degree	2
Penalty parameter rate	100

Dataset Description: During the training process, we closely monitor both the loss function and accuracy of the model. The total number of epochs is set to 100, with the most optimal results observed between 20 and 75 epochs. Within this range, the loss function and validation accuracy stabilize, making 100 epochs sufficient for achieving the best performance. The trained algorithm successfully classifies all validation samples, and the time required for computation is measured accordingly.

The mulberry leaf images used in this study were collected from two different regions, each representing distinct disease conditions. These images were labeled by an experienced sericulture researcher (Nahiduzzaman *et al.*, 2023), categorizing them into healthy leaves and disease-affected leaves, including leaf spot and leaf rust. A total of 1,091 mulberry leaf images were gathered, consisting of 162 images of leaf spot, 489 of leaf rust, and 440 of healthy leaves. The images have a resolution of 6,000 pixels. A sample of the mulberry leaf dataset is shown in Figure 4.

(i) (ii) (iii)

Figure 4. Sample mulberry leaf, (i) Healthy Leaf, (ii) Leaf spot and (iii) Leaf rust

Performance Measure: The training and validation performances are depicted in Figures 5 and 6. These figures illustrate the effectiveness of the proposed approach in detecting mulberry leaf diseases during both the training and validation phases, allowing for an evaluation of accuracy and loss over time. Figure 5 shows the training and validation accuracy, while Figure 6 represents the corresponding training and validation loss. As the number of epochs increases from 20 to 100, both the training and validation accuracy fluctuate accordingly. Notably, the system's accuracy plateaus at certain points, ultimately reaching a peak of 99% for training accuracy and 98% for validation accuracy by the 100th epoch. In terms of loss, the system demonstrates significant improvement, with training loss reducing to 0.8% and validation loss to 0.3% by the 100th epoch, as determined by the loss function.

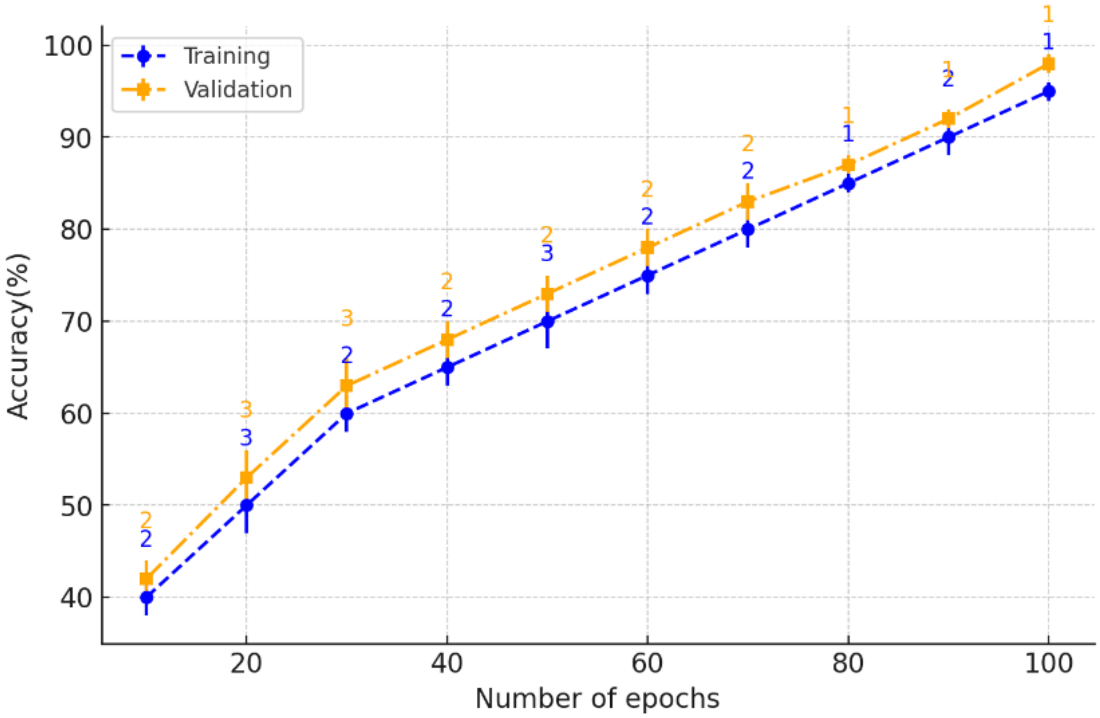

Figure 5. Accuracy plot to measure training and validation performances

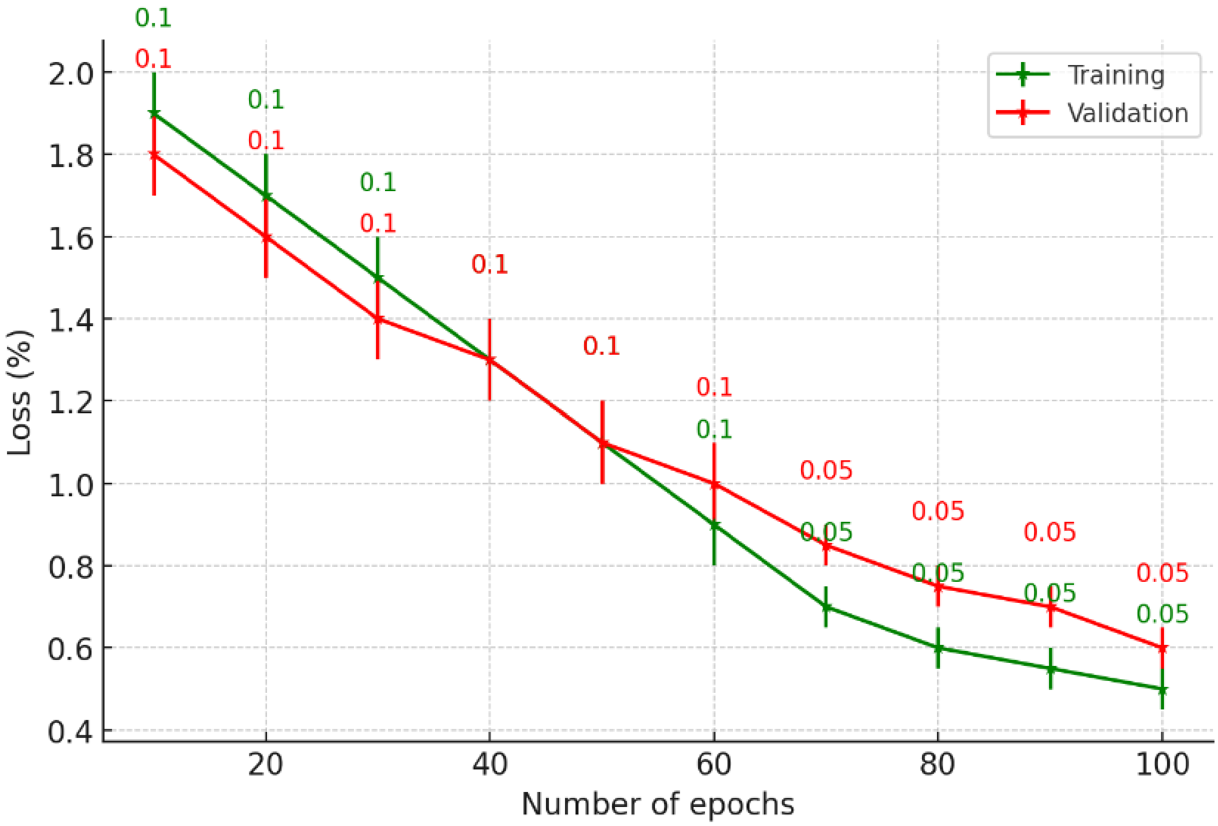

Figure 6. Loss plot to measure training and validation performances

DISCUSSION

The classification performances based on 5-fold validation in terms of accuracy are outlined in Table 2. The folds from 1 to 5 for the accuracy vary from 0.90%, 0.92%, 0.94%, 0.95%, and 0.96% for the proposed method. The fold results proposed are superior when compared to the CNN, K-means, LIBS, and KELM approaches. In matrix format, the mulberry leaf prediction summary defines the method of confusion matrix. Based on the classes, the mulberry leaf class, with its correct and incorrect accuracy, is effectively denoted. Figure 7 depicts the confusion matrix results. The proposed system's accuracy is higher when compared with the previous methods. The illustration of comparative outcomes of accuracy, specificity, and sensitivity is shown in Figure 7. The state-of-the-art methodologies, namely CNN, K-means, LIBS, KELM, and proposed, are carried out to compute the overall performances. The measures like accuracy, sensitivity, and specificity validate the performance of each state-of-the-art. Based on the proposed work, we get an accuracy of 96%, 95%, and 95.8%, respectively. The proposed work performance is higher than that of previous techniques like CNN, K-means, LIBS, and KELM.

Table 2. Comparative analysis for accuracy of mulberry leaf disease classification.

No. of folds	Convolutional Neural Networks (Ashtiani *et al.* 2021)	K-means (Luo 2023)	Laser-Induced Breakdown Spectroscopy (Yang *et al.* 2021)	Kernel Extreme Learning Machine (Ji *et al.* 2022)	Proposed
1	0.80	0.82	0.83	0.85	0.90
2	0.83	0.83	0.84	0.86	0.92
3	0.84	0.85	0.86	0.88	0.94
4	0.86	0.88	0.88	0.90	0.95
5	0.87	0.89	0.90	0.92	0.96

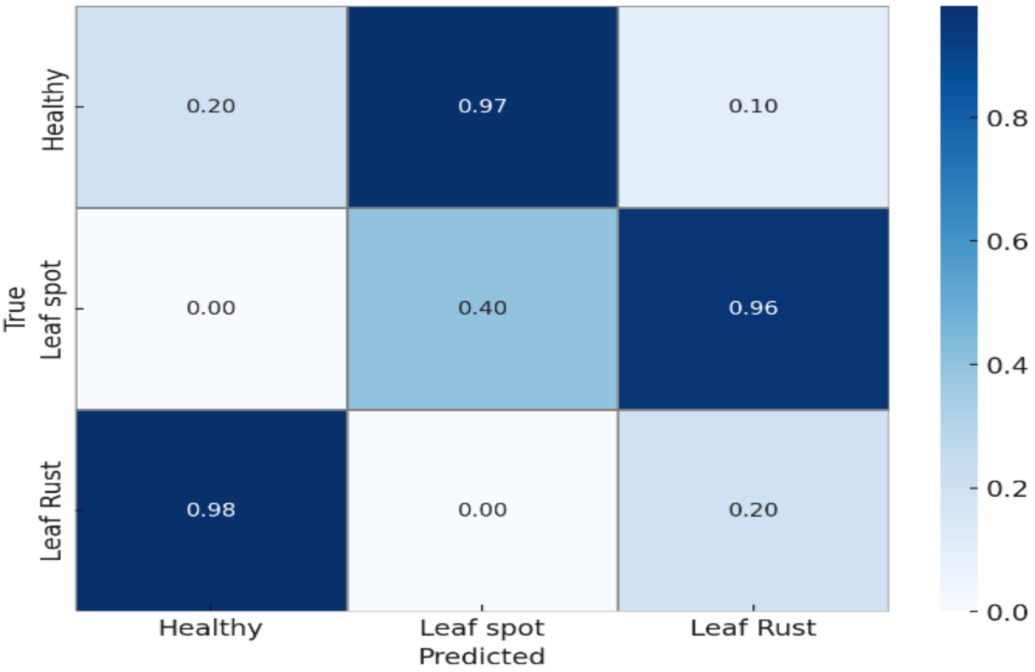

Figure 7. Confusion matrix of proposed model for mulberry leaf disease classification

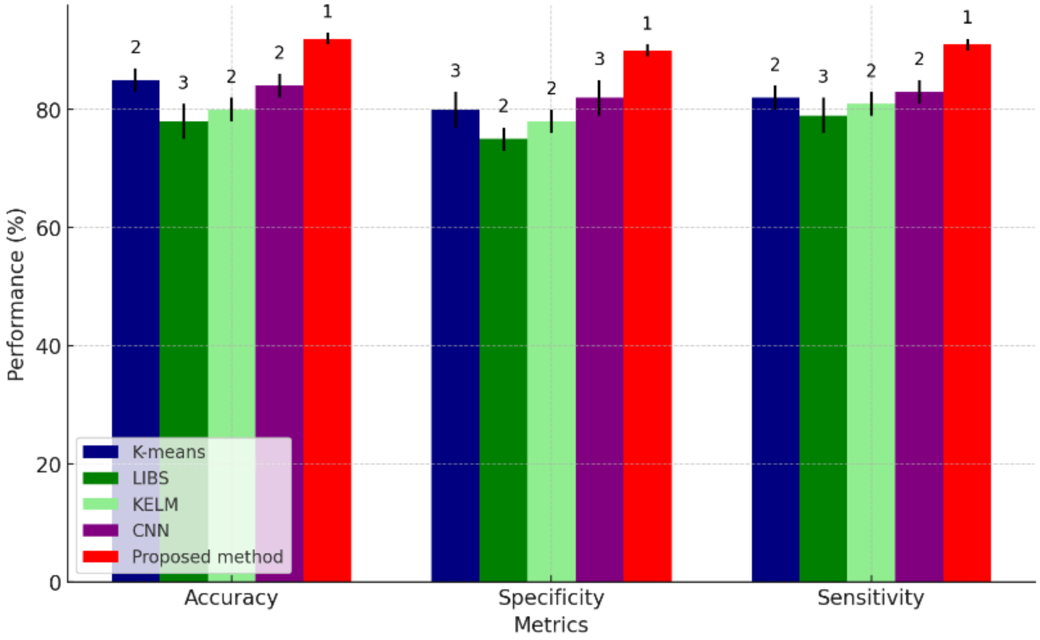

Figure 8. Comparative analysis of performance of various models for mulberry leaf disease classification

Conclusion: This study presents an S-SVM model combined with the AERO algorithm for detecting and classifying mulberry leaf diseases (healthy leaves, leaf rust, and leaf spot). Using MATLAB for simulation, the proposed model was compared to advanced methods like CNN, K-means, LIBS, and KELM. The dataset consisted of 1,091 mulberry leaf images with a resolution of 6000 pixels each. The model achieved a training accuracy of 99%, with a low training loss of 0.8%, and a validation accuracy of 98% with a validation loss of 0.3% over 100 epochs. Cross-fold-5 validation confirmed its robustness with 96% accuracy. In disease detection, it demonstrated high performance with 96% accuracy, 95% specificity, and 95.8% sensitivity. The results highlight the model's superiority over traditional methods and its strong potential for practical use in precision agriculture.

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Ethics approval statement: Not Applicable.

Permission to reproduce material from other sources: Not Applicable.

Authors' Contribution: PK and RR conceived of the presented idea. VK developed the theory and performed the computations. PK verified the analytical methods. PK and RR discussed the results and contributed to the final manuscript.

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