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Automated detection of rice plant diseases using dual stage thresholding and twin support vector machine

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ABSTRACT

Rice plants are susceptible to various diseases such as brown spot, BLB, and blast, caused by viral, bacterial, or fungal infections, which significantly affect both the quantity and quality of rice production. This study introduces an automated method for detecting these diseases using dual thresholding (DT) in segmentation combined with twin support vector machine (TW-SVM) classification. Early detection and accurate identification of rice leaf diseases are crucial for effective management and optimization of production. The proposed method leverages the strengths of TW-SVM, including its ability to handle high-dimensional data efficiently. The approach is compared with three SVM-based techniques: basic SVM, least-square SVM, and proximal SVM. Simulations are performed using images from both a public dataset and a real-time drone image dataset. Thirteen features, including color, texture, and shape, are extracted for classification. Results show that the proposed dual stage thresholding (DST) TW-SVM achieves superior performance in terms of time complexity and accuracy, with 95% accuracy on the public dataset and 99.3% accuracy on the drone image dataset.

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1. INTRODUCTION

Rice stands as a pivotal grain in addressing global food demands, thus heavily influencing the economies of various nations. However, the production of high-quality rice worldwide is imperilled by a spectrum of diseases categorized broadly as viral, bacterial, or fungal infections [1]. These afflictions detrimentally impact both the quality and quantity of rice yields. Common ailments include rice tungro, ragged stunt, grassy stunt, rice yellow dwarf (mycoplasma) under viral infections; bacterial leaf blight, bacterial leaf streak, pecky rice, foot rot, grain rot, sheath brown rot among bacterial infections; and rice blast, brown spot, downy mildew, false smut, leaf smut, seedling blight, sheath blight, sheath spot, sheath rot, stack burn, leaf scald, root rot, stem rot, and water mold under fungal infections [2].

Traditionally, plant pathologists detect these diseases through invasive means. However, contemporary technologies such as advanced digital data acquisition and image processing offer non-invasive alternatives. Image processing coupled with machine learning injects automation into disease detection. The process typically comprises of four steps i.e., image pre-processing, segmentation, feature extraction, and classification. While current non-invasive techniques are effective, their performance can be further enhanced by integrating efficient automated machine learning algorithms. Pre-processing is crucial, involving effective data transformation to a suitable colour space while eliminating unwanted noise. Segmentation partitions the image into subgroups, reducing complexity. Feature extraction converts raw data into numerical features, preserving essential information in the image. These features, selected for their significance, are arranged into a feature vector for dimension reduction, emphasizing uncorrelation. Key visual features like colour, texture, and shape are pivotal, with techniques such as SIFT, SURF, LBP, gray level co-occurrence matrix (GLCM), and bag of features employed for extraction. The subsequent classification phase categorizes pixels into predefined patterns using methods like artificial neural network (ANN), dual thresholding (DT), support vector machine (SVM), k-nearest neighbours (KNN), fuzzy rule-based classifiers, Naïve Bayes, and MLP.

Table 1 highlights advancements in the automatic detection of leaf diseases across various plants, with a specific focus on machine learning and deep learning-based approaches for rice plant disease detection. Several studies [3]–[6] have utilized machine learning techniques where preprocessing and feature extraction are performed manually. Preprocessing often involves filtering techniques such as rectangular, median, Wiener, and histogram equalization. Feature extraction, based on color, shape, and texture, is tailored to the application. Segmentation plays a critical role in these methods, with algorithms like k-means and fuzzy c-means being commonly applied. Disease detection is then achieved using classifiers such as SVM, KNN, NN, and DT, with some achieving promising results.

Table 1. Summary of techniques used for automatic detection of plant leaf diseases

S. No.	Ref.	Diseases	Segmentation	Pre-processing	Feature extraction and classifier
1	[2]	Rice blast, brown spot, and leaf smut	Otsu's model and Centroid k-mean	HSV plane conversion and histogram equalization	GLCM and SVM
2	[6]	Rice blast	K-mean	Weiner filter and contrast enhancement using histogram equalization	Mean and standard deviation
3	[3]	Bacterial leaf blight, rice blast, and sheath blast	Otsu's model	Resolution reduction and noise reduction by median filtering	Area, perimeter, contrast uniformity, entropy, inverse, difference, linearity correlation, rectangularity, compactness, elongation, and roundness
4	[7]	Brown spot, leaf blast, leaf smut, tungro, and bacterial leaf blight	Spatial fuzzy clustering	histogram equalization and Kuwahara filtering	LeNet-5 as feature extraction and LS-SVM as classifier
5	[8]	Bacterial leaf blight, leaf smut, brown spot, and leaf blast	K-mean clustering	Otsu’s thresholding and median filtering	SVM and LS-SVM

Deep learning approaches [9], [10] have also gained traction, offering the advantage of automatic feature learning. CNN-based models, such as VGG16, ResNet50, and DenseNet, have demonstrated high accuracy, outperforming traditional machine learning methods. It has been observed that median filtering is effective for preprocessing large patches but less suitable for small spots. Additionally, SVM-based classification consistently outperforms other machine learning techniques. Building on these insights, this study proposes a non-invasive, machine learning-based classifier for disease detection using various SVM variants. The contributions include a comprehensive study of SVM as a classifier, a detailed performance analysis of existing learning-based classifiers across diverse datasets, and a performance comparison of SVM variants for three-class disease classification.

2. MATERIALS AND METHODS

The block diagram illustrating the proposed methodology is shown in Figure 1. The algorithm comprises four major steps. The first step is image pre-processing, where transformations are applied to improve the visual quality of the image or enhance the analysis process. This may involve converting the image to a different color space, resizing, or applying filtering techniques tailored to the specific application. The second step is segmentation of the disease-affected image, which isolates the region of interest (ROI) by classifying the image based on relevant features. This is followed by feature extraction, where key attributes such as color, shape, and texture are extracted, aiding in dimensionality reduction. The final step is classification, which focuses on accurately identifying different diseases using traditional methods alongside advanced machine learning, deep learning, and transfer learning techniques. Two datasets, DS1 and DS2, were used for validating the proposed methodology. DS1, sourced from Kaggle [2], comprises 120 images divided into three disease classes, with 40 images per class. Sample images are displayed in Figure 2. DS2 contains 4,432 drone-captured images of rice leaves affected by bacterial leaf blight, blast, and brown spot diseases [11]. Sample images are shown in Figure 3. The images in DS1 were captured using standard cameras, while those in DS2 were obtained using drones, ensuring the proposed algorithm's robustness under varying image capture conditions. Figure 2 shows examples of images taken with a standard camera, including leaves affected by leaf smut (Figure 2(a)), bacterial leaf blight (Figure 2(b)), and brown spot disease (Figure 2(c)). Similarly, Figure 3 provides examples of drone-captured images, illustrating rice blast disease (Figure 3(a)), brown spot disease (Figure 3(b)), and bacterial leaf blight (Figure 3(c)). These datasets validate the algorithm's ability to handle diverse scenarios effectively.

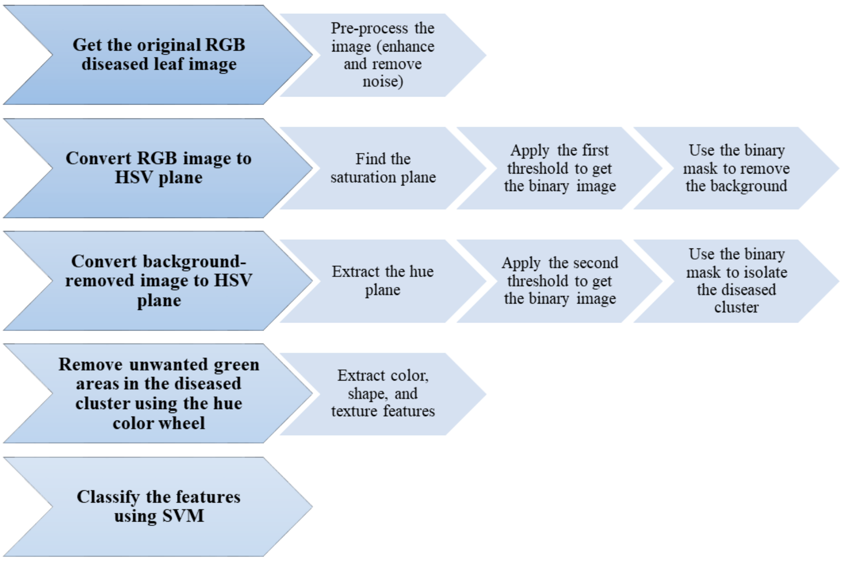

Figure 1. Workflow of the algorithm for diseased leaf image processing


(a) (b) (c)

Figure 2. Images of diseased rice leaves; (a) bacterial leaf blight, (b) brown spot, and (c) leaf smut


(a) (b) (c)

Figure 3. Images of diseased rice leaves; (a) bacterial leaf blight, (b) leaf blast, and (c) brown spot

3. PROPOSED WORK

This section describes the image classification process, focusing on segmenting diseased areas of leaves and classifying specific diseases. RGB images are first transformed into the HSV color space, which simplifies thresholding operations. The saturation plane (S-plane) is extracted as it contains valuable information for disease detection, even though it may appear predominantly white. To enhance the quality of the extracted plane, residual noise is removed using a median filter. Segmentation, a critical step, isolates the diseased regions or ROI within the leaf images, enabling a focus on features most relevant to disease classification. The segmentation method was evaluated using the DS1 rice dataset [2], which includes 120 images equally distributed among three diseases: brown spot, bacterial leaf blight, and leaf smut. Comparisons were made between the segmentation performance in LAB and HSV color spaces to identify the most effective approach. The LAB color space posed challenges: diseased regions often appeared scattered across different clusters, complicating isolation, and healthy green areas sometimes overlapped with diseased clusters, potentially causing misidentification. Based on these observations, the HSV color space was selected for segmentation due to its superior performance in isolating diseased regions.

To address segmentation challenges, the HSV color space was utilized due to its effectiveness in handling color information. DT with Otsu's method was employed for optimal threshold selection, achieving segmentation through two thresholds. The first threshold (th1) was applied to the saturation plane (S-plane) to create a mask (mask1) that isolated potential diseased areas. The second threshold (th2) was applied to the hue plane (H-plane) of the background-removed image (using mask1) to generate a refined mask (mask2), further isolating the diseased regions. Optimal threshold values (th1 and th2) for different diseases were determined based on their color characteristics: for bacterial blight and blast disease, th1=0.28 and th2=0.15; for brown spot and leaf smut, th1=0.28 and th2=0.12. These thresholds were selected after analyzing their impact on detection accuracy using a set of 10 sample images. During segmentation, some diseased clusters contained green pixels, which could affect detection accuracy. To mitigate this, the hue color wheel properties [2] were utilized. Green, corresponding to a hue range of 17.2° to 45°, translates to 0.048 to 0.125 in the H-plane. A binary map was created based on this range to remove unwanted green pixels, resulting in improved segmentation of the diseased areas.

The next step, feature extraction, identifies key aspects of the images, including color, shape, and texture. Thirteen features were extracted to represent each image. Color features were obtained using techniques like color histogram descriptors and color moments, which include mean, standard deviation, kurtosis, and skewness. Shape features, such as the area, percentage of diseased area, eccentricity, circularity ratio, and convexity, were calculated to characterize the visual information of the image. Texture features, derived from the GLCM, included contrast, energy, variance, correlation, homogeneity, and inverse difference moment. GLCM, based on second-order statistics, is computed using a displacement vector $d(\delta,\theta)$, where δ represents the radius and θ the angle of rotation (0°, 45°, 90°, and 135°). These features help capture the spatial variation of brightness, contributing to accurate image representation.

The final stage involved disease classification using three SVM variants: least squares SVM (LS-SVM) [12], proximal SVM (PSVM) [13], and twin SVM (TWSVM) [14]. SVMs are widely used due to their ability to separate classes with wide margins, making them effective for high-dimensional data while being memory-efficient [15]. However, SVMs face limitations, such as slower performance on large datasets and difficulties with overlapping class boundaries. Additionally, SVMs do not provide probabilistic outputs and may underperform when there are more features than training samples. To overcome these issues, advanced variants like LS-SVM, PSVM, and TWSVM were employed, which enhance SVM efficiency in terms of speed and accuracy, making them suitable for disease classification tasks.

The performance and accuracy of SVM depend on tuning certain training parameters, which can result in longer training times. However, proximal SVM for binary classification assigns a class to the nearest of two parallel planes that are driven apart as far as possible [16]. Here, the training time is very fast, but the accuracy degrades due to the presence of slack variables. Hence, class assignment is done by measuring proximity to the two parallel hyper-planes. TWSVM is another important machine learning classifier, nearly four times faster than SVM [17]. TWSVM is a nonparallel extension of multiclass classification. In comparison to SVM, TWSVM solves two small quadratic programming problems (QPP) rather than one larger one.

4. RESULTS

The proposed model is compared and analyzed with several established supervised classification methods, including SVMs [18], KNN [19], and ANNs [20]. Due to its sensitivity to parameter selection, a dedicated subsection details the process of optimizing SVM parameters for the best performance. The performance of these SVM variants is evaluated against the proposed dual stage thresholding (DST) with TWSVM method. This comparison focused on both accuracy and time complexity. For training and testing, both datasets were split into 80% training and 20% testing sets. The trained models were then evaluated on the testing data to assess their classification accuracy. The simulations were conducted in a MATLAB-2018 environment on a system with an Intel Core i5 processor running at 2.4 GHz, a 64-bit operating system, and 6 GB of RAM.

4.1. Pre-processing of sample image

The pre-processing operation is first performed on the images. In this step the images are resized to (3×3) pixels and are converted to HSV colour space. The saturation plane (S-plane) is extracted from the HSV colour images and passed through a median filter of size (3×3) to remove the noise [21]. Figure 4 shows the original sample frame (Figure 4(a)), the HSV image (Figure 4(b)), and the extracted S-plane after the application of median filter. In leaf disease detection, diseases often cause changes in the intensity value of the pixels in the image. Hence, S-plane is extracted to indicate any colour variation in the diseased part of the image. It is observed from Figure 4(c) that there exists a colour variation at the beginning and towards the end portion of the S-plane image. This colour variation shows the possibility of diseased region on the rice leaf. These regions are extracted through the segmentation operation which is narrated in section 4.2.

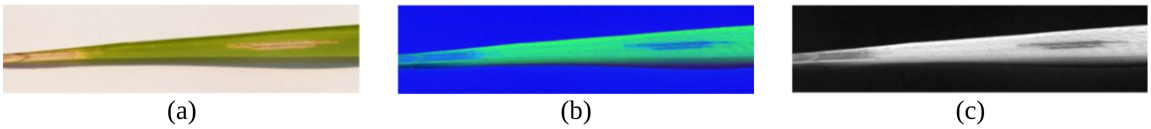

Figure 4. Pre-processed images; (a) original image, (b) HSV plane image, and (c) S-plane median filtered image

4.2. Segmentation of sample image

The step-by-step process for segmenting diseased areas in a sample image is illustrated in Figures 5(a) to (e), using a sample image from the bacterial blight dataset. Figure 5(a) shows the S-plane thresholded image, marking the first stage of segmentation. In Figure 5(b), the background is removed, isolating the ROI in the image. Figure 5(c) displays the Hue-plane thresholded image, highlighting specific color ranges that potentially correspond to the disease. Figure 5(d) represents the non-diseased portion, showing the healthy areas of the rice leaf, while Figure 5(e) presents the segmented diseased area, illustrating the final result of the segmentation process for the bacterial blight sample.

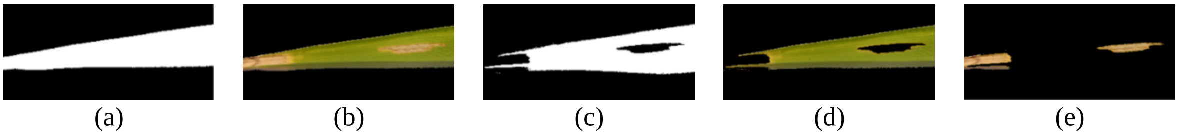

Figure 5. Segmentation result; (a) S-plane image after applying threshold, (b) image after background removal, (c) hue-plane image after applying threshold, (d) segmented image showing non-diseased areas, and (e) segmented image highlighting diseased areas affected by bacterial blight

Figure 6 provides a visual analysis of the segmentation process for brown spot disease, demonstrating the refinement achieved using the hue color wheel. Figure 6(a) depicts initial segmentation, where diseased spots are identified along with extraneous green portions, indicating inaccuracies. In Figure 6(b), the segmentation is improved by applying the hue color wheel, which eliminates irrelevant green areas, resulting in a more precise representation of the diseased cluster. This highlights the effectiveness of the hue color wheel in enhancing segmentation accuracy by excluding non-diseased regions. For blast disease, segmentation results are shown in Figure 7. Figure 7(a) depicts the segmented diseased area in the sample image, while Figure 7(b) illustrates the disease cluster after background removal. The percentage of the leaf affected by blast disease is quantified and visualized in Figure 8, providing a clear representation of disease impact on the sample rice leaf.

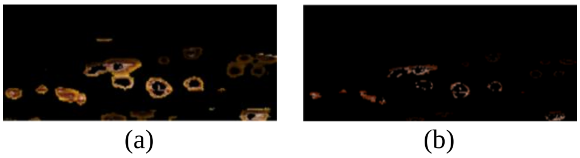

Figure 6. Sample segmented image for brown spot disease; (a) diseased cluster with unnecessary green portion and (b) diseased cluster after applying hue colour wheel

Figure 7. Sample segmented image for blast disease; (a) diseased cluster and (b) background removed image

The performance of SVM classifiers depends significantly on parameter selection. To ensure a fair comparison with other state-of-the-art methods, the effects of kernel function variation and regularization are analyzed. The optimal kernel function and regularization parameter obtained from this study are then used for the performance evaluation of the proposed algorithm. To examine the impact of kernel function variation, accuracies for different kernel functions are plotted in Figure 9. Training accuracies for all kernel functions range between 91% and 95%. However, the selection of the optimal kernel function requires validation using cross-validation and testing accuracy. From Figure 9, the RBF kernel is found to outperform other kernel functions and is thus used for the performance analysis of all SVM variants.

Figure 8. Feature extraction of sample image

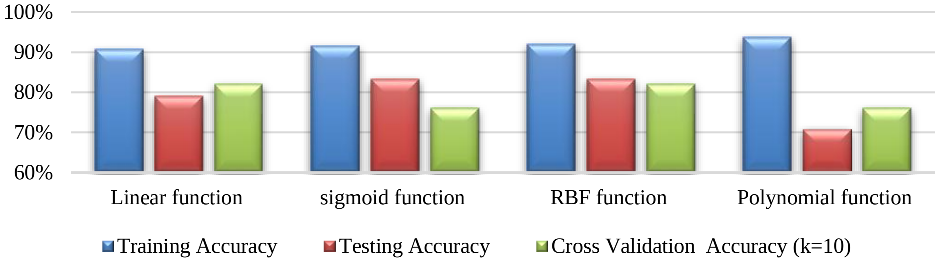

Figure 9. Accuracies for different kernel function for K=10

The different cost function parameters of RBF kernel are box constraint or regularization parameter or penalty factor denoted as ‘C’ and kernel scale parameter denoted as ‘γ’. ‘C’ controls the influence of test data. The higher the ‘C’ value higher is the cost of misclassified points [22]. Now γ controls the similarity of data. When γ is zero, all points are treated as same class and if it is high, overfitting condition may occur where all the training data behave as support vector. But it should not be too high as well [22]. To study the effect of variation of (C) at constant γ on the performance of the RBF kernel, the value of ‘C’ is varied from 1e-3 to 1e3 and corresponding training accuracy, testing accuracy and cross validation accuracy are reported in Table 2. Moreover, cross validation with 5 and 10 fold cross validation are applied to predict lowest classification error. It is observed from Table 2 that a C value of 1e-3 provides the best result among all other values of ‘C’ and 10 fold cross validation produced better result than 5 fold cross validation. Hence 10 fold validation is used for all our simulation analysis.

Table 2. Performance comparison of different classifiers on DS1 & DS2

Classifier	Cross validation accuracy (%)		Test accuracy (%)		Elapsed time (sec)	
	DS1	DS2	DS1	DS2	DS1	DS2
ANN	59.4	45	66.6	61	**3**	**12**
KNN	80	87.3	83	**99.24**	136	711
SVM	**82**	**98.3**	**83.3**	98.75	128	640

The performance of SVM was analyzed and compared with two widely used algorithms, ANN and KNN, based on cross-validation and testing accuracy for both datasets, DS1 and DS2, as shown in Table 3. The data was split into an 80:20 ratio for training and testing in all simulations. The ANN model used for classification consisted of one hidden layer with 13 inputs and 3 outputs. KNN classified data points based on the KNN using a specific distance metric. KNN is known for its effectiveness in low-dimensional spaces, making it suitable for this application [23]. The results for KNN were reported using the optimal distance metric and the best value of k for each observation. SVM performance was evaluated using the RBF kernel. As shown in Table 3, SVM achieved the highest testing accuracy of 83.3% for DS1, while KNN outperformed other methods for DS2 with a testing accuracy of 99.24%.

For DS1, SVM outperformed other classifiers, while for DS2, KNN showed better performance as the data size increased, as detailed in Table 3. The performance of SVM variants, including LS-SVM, PSVM, and twin support vector machine (TW-SVM), was evaluated for leaf image-based disease classification using a multi-class framework. The results in Figure 10 and Table 3 indicate that TW-SVM achieved the highest accuracy of 95% for DS1 and 99.3% for DS2, followed by LS-SVM, while PSVM had the lowest accuracy at 77.6% and 70.6%, respectively. ANN showed the lowest performance among classical classifiers. These findings highlight the superior accuracy and efficiency of TW-SVM compared to other classifiers and SVM variants in this study.

Table 3. Performance comparison of DS1 and DS2 with different classifiers

Diseases classes	Dataset	ANN (%)	KNN (%)	SVM (%)	LS-SVM (%)	P-SVM (%)	TW-SVM (%)
BLB, BS, and LS	DS1	66.25	83	83.3	91	77.6	95.2
BLB, BS, and BLST	DS2	61	99.24	98.84	98.87	70.6	99.24

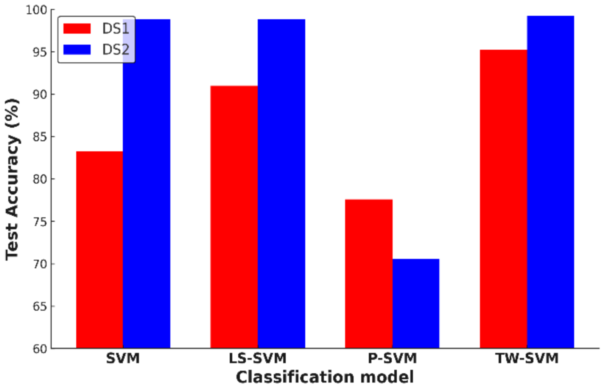

Figure 10. Performance comparison of SVM Variants for DS1 and DS2

The proposed DST TW-SVM method is compared with state-of-the-art methods, including those by Prajapati *et al.* [2], Azim *et al.* [24], Chen *et al.* [25] for DS1 dataset and Sethy *et al.* [11] for DS2 dataset with results summarized in Table 4. Prajapati *et al.* [2] reported a testing accuracy of 73.3%. Azim *et al.* [24] utilized LBP and GLCM-based feature extraction followed by SVM and XGBoost classifiers, achieving accuracies of 81.6% with SVM and 86.58% with XGBoost. Chen *et al.* [25] employed a DenseNet-201 pre-trained network with an SVM classifier, achieving a test accuracy of 94.07%, enhanced by fully connected layers and a focal loss function. For the DS1 dataset, the proposed TW-SVM method achieved the highest accuracy of 95%, outperforming these approaches. For the DS2 dataset, Sethy *et al.* [11] evaluated transfer learning models with SVM for rice leaf disease detection, achieving a test accuracy of 98.3% using ResNet50 features. However, the proposed TW-SVM method achieved the highest accuracy of 99.3%, demonstrating superior performance for rice leaf disease classification.

Table 4. Comparison of performance of the suggested technique with existing best performing methods

Author's name	Dataset	Methods	Testing accuracy (%)
Prajapati *et al.* [2]	DS1	K-mean segmentation+SVM	73.3
Azim *et al.*[24]	DS1	LBP and GLCM feature+XGBoost	86.58
Chen *et al.* [25]	DS1	DenseNet-201+SVM	94.07
Sethy *et al.* [11]	DS2	ResNet50+SVM	98.3
Proposed method	DS1	DST+P-SVM	76
		DST+LS-SVM	91
		DST+SVM	83.3
		DST+TW-SVM	95
Proposed method	DS2	DST+P-SVM	70.6
		DST+LS-SVM	98.84
		DST+SVM	98.4
		DST+TW-SVM	99.3

4.3. Computational complexity of support vector machine and its variants

Big 'O' notation is commonly used for evaluating time and space complexity. This study analyzes the time complexity of SVM and its variants. The time complexity of standard SVM ranges between $O(n^2)$ and $O(n^3)$, depending on the number of loops in the algorithm, where n is the total number of training instances. LS-SVM improves computational efficiency by replacing inequality constraints with equality constraints and using a squared error term. It solves a set of linear equations instead of quadratic equations, resulting in a time complexity less than $O(n^3)$. PSVM, interpreted as regularized least squares, generates two parallel planes, each closer to one class and as far apart as possible. Its complexity is approximately $O(m^3)$, where m is the input space dimension, making it faster than standard SVM. TW-SVM uses a non-parallel plane classification strategy, where each plane is closer to one class and farther from the other. It solves two smaller QPPs instead of one larger one. If both classes have equal numbers of instances (n/2 each), the time complexity is $O(2\times(n/2)^3)$, which is nearly four times faster than the $O(n^3)$ complexity of standard SVM. This makes TW-SVM significantly more efficient for classification tasks [14].

5. CONCLUSION

This work introduces a DST technique combined with TW-SVM for the automatic detection of rice leaf diseases and evaluates the performance of various SVM variants. Machine learning-based approaches are increasingly favored for their non-invasive, fast, and accurate detection capabilities, making them suitable for agricultural applications. The proposed method involves detecting diseased areas in leaf images, extracting relevant features, and classifying them using four SVM variants: SVM, LS-SVM, PSVM, and TW-SVM. Among these, TW-SVM achieved the highest detection accuracy of 95.2% and 99.3% on datasets DS1 and DS2, respectively, with training-testing times of 0.27 seconds for DS1 and 0.47 seconds for DS2. These results highlight the robustness of TW-SVM across varying conditions and its lower time complexity compared to other methods. This study contributes to precision agriculture by providing an efficient and accurate system for detecting common rice leaf diseases. Future work will focus on expanding the dataset, enabling real-time field applications, and developing a hybrid model integrating machine learning and deep learning for multi-disease detection. Addressing challenges such as dataset quality, availability, and environmental variability will be crucial for enhancing the system's practicality and effectiveness. This research underscores the potential of integrating image processing, machine learning, and remote sensing techniques for scalable plant disease detection.

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Prince Jain		✓		✓		✓				✓				

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are available from the corresponding author, [PKS], upon reasonable request.

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