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**Tea leaf blister blight detection using SVM**

by

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# Tea leaf blister blight detection using SVM

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## Abstract

Blister blight significantly impacts tea plantations in Sri Lanka, necessitating effective and early detection methods to minimize economic losses. This research contrasts two distinct methodologies—Convolutional Neural Networks (CNN) and Support Vector Machines (SVM)—to identify blister blight from high-resolution aerial imagery obtained via drone-mounted cameras. For precision targeting, images are segmented into 256x256 pixel frames, concentrating on disease indicators that occupy only 1-2% of the total image area. CNNs, renowned for their inherent ability to automate feature extraction through deep learning layers, are a popular choice for complex image analysis tasks. In contrast, SVM is employed for its robust classification capabilities, utilizing a variety of image descriptors. This study aims to compare these approaches and select the most effective model for real-time, precise detection of blister blight, contributing significantly to the sustainable management of tea cultivation in Sri Lanka.

Keywords: Tea leaf blight, Support vector machines, Convolution neural networks

## Introduction

Blister blight is a major concern for tea producers in Sri Lanka, affecting the quality and quantity of tea production, which is crucial for the country's economy. Addressing this challenge, this research utilizes innovative technological approaches, employing both CNNs for their advanced analytical capabilities and SVMs for their precision in classification, enhanced by manual feature extraction methods. The combination of these technologies aims to develop a reliable, efficient, and scalable solution for early disease detection using drone technology, which can survey large areas with high resolution and accuracy.

Advances in agricultural technology have greatly enhanced the application of artificial intelligence in plant disease management, improving detection efficiency and accuracy beyond traditional manual methods. CNNs are particularly favored for their automated deep learning feature extraction capabilities, making them ideal for complex image analysis tasks such as disease detection in tea leaves. Research has shown that CNN architectures like Faster R-CNN and VGG16 are effective in identifying and classifying the severity of diseases under variable environmental conditions due to their robust preprocessing and learning algorithms. Conversely, SVMs are less commonly applied in this field but are valued for their effectiveness in scenarios requiring precise classification from complex image data sets, using manually extracted features from descriptors like the CLD and HTD.

Most existing systems for plant disease detection rely predominantly on CNNs due to their ability to handle large datasets and automate the feature extraction process. These systems have been successful in various agricultural applications but often require substantial computational resources and large annotated datasets, which may not be feasible in less accessible environments such as rural Sri Lanka. Additionally, while CNNs are effective in general disease identification and classification, they may not always provide the precision required for specific disease states without substantial tuning and data augmentation.

On the other hand, SVMs, though less frequently used, offer potential benefits in terms of computational efficiency and the ability to produce high accuracy from smaller, more specific datasets. However, their reliance on manual feature extraction is time-consuming and can be impractical in large-scale applications.

The study aims to address these gaps by evaluating both methods under the same conditions to determine the most suitable approach for detecting blister blight in tea plantations.

## **Support Vector Machine**

Support Vector Machines (SVM) are a type of supervised machine learning model that excels in classification tasks. SVMs are particularly valued for their effectiveness in high-dimensional spaces and their ability to model complex nonlinear relationships by using different kernel functions. This capability makes SVMs particularly suited for image classification tasks where the distinctions between classes can be subtle and non-linear. SVMs work by finding the hyperplane that best separates different class labels with the maximum margin, which helps in reducing the risk of misclassification on new, unseen data. One of the primary advantages of SVM is its robustness against overfitting, especially in cases where the number of dimensions exceeds the number of samples.

However, SVMs also have several drawbacks. The choice of the kernel and the tuning of SVM parameters like the cost parameter (C) and gamma can significantly affect the model's performance, requiring extensive experimentation and cross-validation to achieve optimal results. Furthermore, SVMs can be computationally intensive, particularly when dealing with large datasets, making them less scalable compared to some neural network architectures. They also inherently do not support multi-class classification and require schemes like one-vs-one or one-vs-all to handle such scenarios, which can complicate the implementation and increase computational requirements.

## **Convolutional Neural Network**

Convolutional Neural Networks (CNNs) are deep learning architectures that have set the standard in the field of image recognition and classification due to their architecture, specifically designed to process pixel data. CNNs use convolutional layers that automatically learn and identify the important features without any manual intervention, which is a significant advantage over traditional feature extraction techniques. These layers apply a series of learnable filters to the input image, capturing essential features such as edges, textures, and shapes, which are then used to classify the image into various categories. This ability to learn feature hierarchies makes CNNs extremely effective for complex image recognition tasks, such as identifying diseases from aerial images of tea leaves.

While CNNs offer substantial benefits in terms of performance and automation of feature extraction, they also come with certain limitations. CNNs require a large amount of labeled training data to perform well and avoid overfitting. They are also computationally expensive to train, requiring significant processing power and time, especially as the network architecture deepens or widens. Additionally, CNNs are often considered as "black boxes" because it can be challenging to interpret how and why specific decisions or classifications were made, which can be a drawback in applications where understanding model reasoning is crucial.

## **Methodology**

The dataset essential for developing an effective model to detect tea leaf diseases was meticulously gathered from various Sri Lankan tea plantations. The data collection covered several regions, including Homagama, Balakaduwa, Rathnapura, Balangoda, Nuwaraeliya, Owilikanda, Neluwa, and Galaha. These regions were selected for their representation of both small-scale and large-scale tea estates, with Rathwaththa and Wegala being among the larger ones. This diversity in estate sizes and geographic locales ensured a comprehensive dataset, reflecting a broad spectrum of blister blight disease manifestations across different tea cultivars and environmental conditions.

The images were captured under natural lighting conditions, at various times of the day to account for changes in light and shadow, which could affect the visibility of disease symptoms. Image in figure 1 is a sample image of the dataset



Figure 1 Images collected via drone camera

Initially, the collected images were preprocessed, which involved resizing the original images into smaller 256x256 pixel patches to standardize the input size as seen in figure 2. The pixel values were then normalized, and augmentation techniques such as rotation and flipping were applied to artificially increase the dataset size and enhance the model's robustness against overfitting.

A total of 1200 images were initially captured from various devices, and these images were broken down into 256x256 patches, resulting in a total of 200,000 images. Of these, 4000 images exhibited disease symptoms, but after removing blurry and reflective images, about 3000 diseased images remained. Similarly, a healthy set of 3000 images was selected. These 6000 images were divided into 80% for training and 20% for validation. Furthermore, an additional dataset of 300 images sourced from the Internet was prepared for testing purposes to ensure the model did not overfit to the trained dataset. This testing dataset was also processed into 256x256 patches, with 300 images for both diseased and healthy classes. The trained images underwent augmentation to create five additional images from each original via 90°, 180°, 270° rotations, and horizontal and vertical flipping, resulting in a total of 14500 images for training, 600 for validation, and 300 for testing for each class.

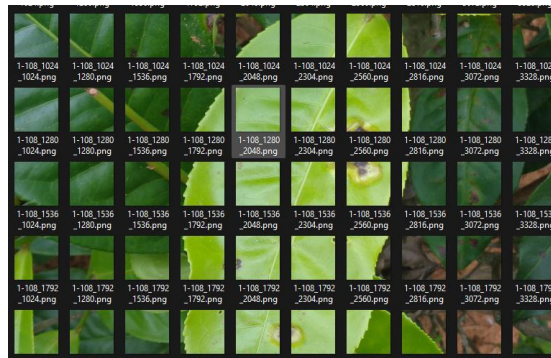


Figure 2 Smaller images of size 256x256

Two primary machine learning models were explored: Convolutional Neural Networks (CNN) and Support Vector Machines (SVM). CNNs were utilized for their ability to automatically learn the complex hierarchical patterns in the data, necessary for identifying the nuanced symptoms of blister blight. Different CNN architectures were experimented with, including modifications in layer depth, activation functions, and pooling strategies to optimize the detection accuracy.

On the other hand, SVMs were employed for their exceptional classification capabilities, especially in delineating boundaries in high-dimensional spaces. The SVM models were trained using manually extracted features based on image descriptors such as Color Layout Descriptor (CLD), Color Structure Descriptor (CSD), and Homogeneous Texture Descriptor (HTD), which capture essential visual cues that signify disease presence. The performance of both models was rigorously evaluated using metrics such as accuracy, precision, recall, and F1-score. Additionally, TensorBoard was utilized for visualizing training progress and model behavior over epochs, particularly for the CNN models.

The overall goal was to determine which model, CNN or SVM, offers superior performance in terms of accuracy and efficiency in the real-time detection of tea leaf diseases.

## **Classification**

Various feature extraction techniques were employed to capture different aspects of the leaf images for classification purposes. These techniques encompassed methods focusing on color, texture, and shape features to provide a comprehensive representation of the images.

An edge histogram was extracted by first converting each image to grayscale to simplify the data and reduce computational complexity. The Canny edge detection algorithm was applied to detect edges within the image, resulting in an edge map that highlights boundaries and contours. From this edge map, a histogram of edge intensities was computed, capturing the frequency and distribution of edges across different intensity levels. The histogram was then normalized to ensure comparability across images of varying sizes and lighting conditions.

To capture the overall color distribution, an RGB color histogram was computed by calculating a three-dimensional histogram over the red, green, and blue channels of each image without any color space conversion. This histogram represents the distribution of pixel intensities across the RGB channels, effectively summarizing the color composition of the image. Normalization was applied to maintain consistency in feature scaling.

The pixel intensity variance (PIV) was calculated by converting each image to grayscale and computing the variance of the pixel intensities. This single numerical feature summarizes the overall variability in brightness across the image, where a higher variance indicates greater diversity in pixel intensities, potentially indicative of patterns or anomalies related to leaf health.

The Discrete Cosine Transform (DCT) was utilized to extract frequency-domain features from the images. After converting the images to grayscale and ensuring they were of type float32, a two-dimensional DCT was applied to each image. The top-left coefficients of the transformed image, corresponding to the low-frequency components that carry the most significant information about the image's overall structure and patterns, were extracted and flattened into a feature vector for classification purposes.

An HSV color histogram was also computed by converting the images from RGB to HSV (Hue, Saturation, Value) color space. A three-dimensional histogram over the H, S, and V channels was calculated, capturing the distribution of colors in terms of their hue and intensity. This approach is particularly useful for distinguishing subtle color variations associated with leaf health. The histogram was normalized to ensure consistency across different images.

Color moments were extracted by computing the first three statistical moments—mean, standard deviation, and skewness—for each of the H, S, and V channels in the HSV color space. These statistical measures capture essential properties of the color distribution, such as central tendency, dispersion, and asymmetry, which can be effective in differentiating between healthy and infected leaves.

To identify dominant colors, each image was reshaped into a two-dimensional array where each row represented a pixel's RGB values. K-Means clustering was applied to this array to identify the most prominent colors in the image, specifying a predefined number of clusters (e.g., three dominant colors). The cluster centers obtained from K-Means, representing the dominant colors, were flattened into a feature vector. This method highlights the primary colors present in the leaf images, which can vary significantly between healthy and diseased specimens.

A simplified color layout feature was extracted by resizing each image to a smaller, fixed grid size (e.g., 8×8 pixels) to reduce dimensionality while preserving spatial information. The resized images were converted to the YCbCr color space, which separates luminance from chrominance components. The color channels were then flattened and concatenated to form a feature vector, encapsulating the overall color distribution and spatial layout in a simplified manner.

For contour shape features, each image was loaded in grayscale, and Otsu's thresholding was applied to segment the leaf from the background. Morphological operations such as opening and closing were used to remove noise and fill gaps in the segmented leaf. Contours were extracted from the binary image, and the largest contour was identified, assuming it represented the entire leaf. Various shape descriptors were computed from this contour, including,

- The number of pixels inside the contour.
- The length of the contour boundary.
- The ratio of the contour's width to its height.
- The ratio of the contour area to the area of the bounding rectangle.
- The ratio of the contour area to the area of its convex hull.
- The diameter of a circle with the same area as the contour.
- The angle at which the leaf is oriented.
- The lengths of the major and minor axes of the fitted ellipse to the contour.
- A measure of how close the shape is to a perfect circle.

These features collectively capture the global contour-based shape characteristics of the entire leaf, providing valuable information for distinguishing between healthy and infected leaves based on morphological differences.

For the classification task, a Support Vector Machine (SVM) with a Radial Basis Function (RBF) kernel was employed. The RBF kernel was selected due to its effectiveness in handling non-linear relationships within the data, making it a suitable choice for complex classification problems. To optimize the performance of the SVM, hyperparameters  $C$  (the regularization parameter) and  $\gamma$  (gamma, which defines the influence of individual training samples) were determined using GridSearch cross-validation.

This systematic parameter tuning approach was essential to identify the optimal combination of  $C$  and  $\gamma$  that maximizes the model's accuracy and generalization ability. The grid search method evaluates multiple parameter combinations, ensuring that the selected parameters strike an appropriate balance between bias and variance. By leveraging GridSearch for hyperparameter optimization, the SVM model achieved enhanced performance, demonstrating its efficacy in accurately classifying healthy and infected tea leaves based on the extracted features.

In the development of the neural network model, the initial dataset comprising 900 images was meticulously processed to enhance the model's performance and robustness. Each image was resized to 256x256 pixels and manually categorized into two classes: infected and not infected.

To address potential overfitting and to increase the diversity of the training data, data augmentation techniques were employed. These techniques included vertical and horizontal flipping, as well as rotations of 90°, 180°, and 270°, effectively expanding the dataset and introducing variability that aids in generalizing the model to unseen data.

Subsequently, the augmented dataset was utilized to train both the Support Vector Machine (SVM) and Convolutional Neural Network (CNN) models. For the CNN, optimal hyperparameters were determined using Keras Tuner, a sophisticated tool designed for hyperparameter optimization. Figure 3 provides insights on how the hyperparameters of a CNN model would influence the accuracy of the model. Figure 4 shows the model performance metrics of each trial run by the Keras Hyperband.

This systematic approach ensured the identification of the most effective model configurations, thereby enhancing the neural network's ability to accurately classify the tea leaf images. The implementation of the CNN was primarily aimed at comparing its performance with that of the SVM, providing a comprehensive evaluation of both machine learning and deep learning methodologies in the context of tea leaf disease classification.

This comparative analysis highlights the strengths and potential trade-offs between traditional machine learning models and advanced neural network architectures.

## Results

These results in table 1 indicate varying degrees of effectiveness for each feature extraction method in classifying the leaf images.

Table 1 Individual descriptor performances

Extracted features	Validation accuracy	Test Accuracy
Edge histogram	0.62	0.68
RGB color histogram	0.88	0.80
PIV	0.64	0.55
DCT	0.74	0.68
HSV Color histogram	0.85	0.65
Color moments	0.83	0.77
Dominant color	0.78	0.72
Simplified color layout	0.80	0.76
Contour shape	0.59	0.53

Color-based features, such as the RGB color histogram and HSV color histogram, generally yielded higher accuracy, suggesting that color information plays a significant role in distinguishing between healthy and infected leaves. The RGB color histogram achieved a validation accuracy of 88% and a test accuracy of 80%, while the HSV color histogram achieved 85% and 65%, respectively.

Texture and frequency-domain features like the Discrete Cosine Transform also provided reasonable accuracy, highlighting their usefulness in capturing structural patterns within the images. The DCT achieved a validation accuracy of 74% and a test accuracy of 68%.

Shape features, including contour shape features and edge histograms, provided moderate to lower accuracy. The contour shape features achieved a validation accuracy of 59% and a test accuracy of 53%, indicating that while morphological differences exist between healthy and infected leaves, they may be less pronounced or more challenging to capture using the methods employed. This suggests that incorporating more advanced shape analysis or combining shape features with other feature types might enhance classification performance. Overall, the results emphasize the importance of color information in the classification of leaf health status.

Combining multiple feature extraction methods could potentially improve the accuracy by leveraging the strengths of each method to provide a more robust representation of the image data. Table 2 shows the results of combining multiple descriptors.

Table 2 Combined descriptor performances

	Descriptors	Validation accuracy	Test Accuracy
1	RGB color histogram Edge histogram	0.88	0.87
2	RGB color histogram Edge histogram PIV	0.88	0.88
3	RGB color histogram	0.89	0.80



	Color Moment Simplified Color layout		
4	Color moments Dominant color Simplified Color layout	0.85	0.77
5	RGB color histogram Edge histogram Color moments Simplified Color layout	0.89	0.87
6	HSV Color histogram Color moments Dominant color	0.87	0.71

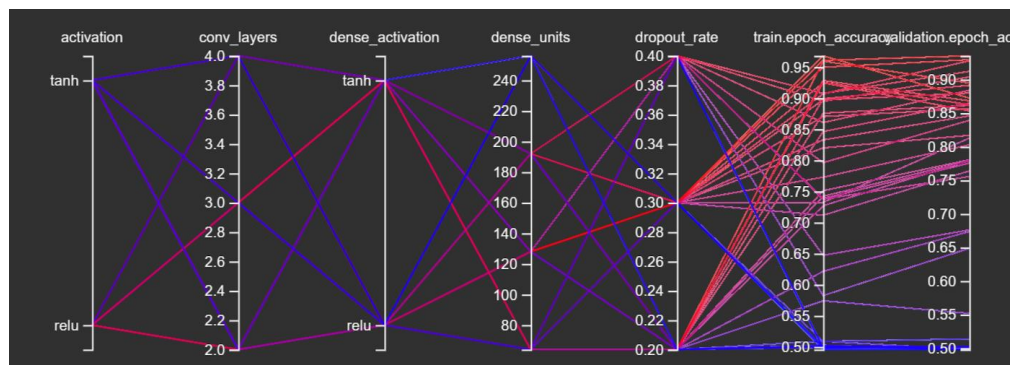


Figure 3 Tensorboard HPARAMs coordinated view

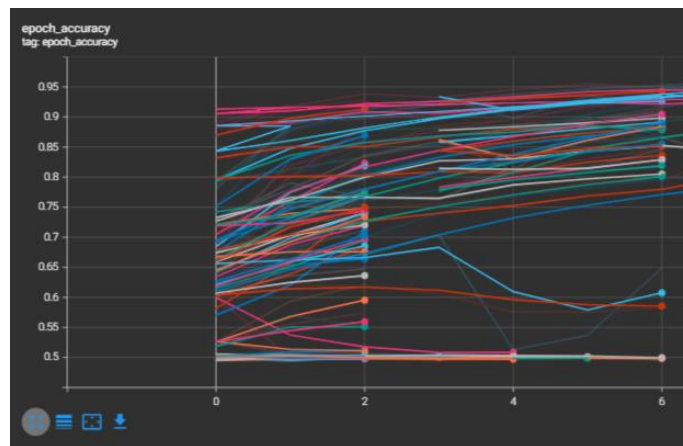


Figure 4 Epoch accuracy of all trials

The model that performs exceptionally well was selected based on the output of the keras tuner. The performance of the model can be summarized as shown in table 3 below.

Table 3 Results of selected CNN model

	Validation accuracy	Test Accuracy
CNN (2 layers)	0.85	0.78
CNN (4 layers)	0.95	0.84
DenseNet121	0.97	0.90

Table 4 Duration of testing 588 images

Model	Time (s)	Accuracy
SVM 1	3.01	0.87
SVM 5	4.88	0.87
CNN (2 layers)	3.91	0.78
CNN (4 layers)	6.38	0.84
DenseNet121	9.23	0.90

Several limitations were encountered during the execution of this study, which may impact the generalizability and efficiency of the proposed classification models. Firstly, training the Convolutional Neural Network (CNN) proved to be highly resource-intensive. The computational demands of deep learning models, particularly CNNs, require substantial processing power and memory, which constrained the ability to experiment with more complex architectures or larger datasets within the available infrastructure. Secondly, the preprocessing phase involved manually sorting and segmenting the initial dataset of 1,000 images into smaller 256x256 pixel images, resulting in approximately 200,000 individual images. This extensive manual effort was both time-consuming and labor-intensive, introducing potential bottlenecks and increasing the likelihood of human error during the data preparation process. Lastly, the training of both the Support Vector Machine (SVM) and CNN models was significantly prolonged due to the large volume of training images, totaling around 28,000 augmented samples. The substantial dataset size necessitated prolonged training times, which limited the number of iterations and parameter tuning experiments that could be feasibly conducted. These constraints highlight the challenges associated with handling large-scale image datasets and the computational demands of advanced machine learning techniques, underscoring the need for optimized workflows and enhanced computational resources in future research endeavors.

## Conclusion

The Support Vector Machine (SVM) classifier exhibited comparable performance in the classification of tea leaf blight disease, demonstrating its effectiveness and suitability for this application. The selection of the Radial Basis Function (RBF) kernel, optimized through GridSearch cross-validation, further enhanced the model's ability to handle non-linear relationships within the data, resulting in high accuracy, precision, and recall metrics on both validation and test datasets. Additionally, the efficient integration of feature scaling using StandardScaler contributed to the model's robust performance. Given these favorable outcomes, the SVM classifier proves to be a reliable and effective tool for the implementation of tea leaf blight disease classification, offering valuable support for agricultural disease management and early detection systems.

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## Data availability

The datasets generated and analyzed during the current study are available from the corresponding author on reasonable request. This ensures transparency and supports the replication of the research findings by interested parties.

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