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Research Article

Comparison of ResNet50 and ResNet101 Feature Extraction for Tea Leaf Disease Classification Using Support Vector Machine

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Abstract:
Introduction: Tea leaf diseases can substantially reduce crop quality and productivity, making early and accurate diagnosis important for effective disease management. This study compares ResNet50 and ResNet101 as pretrained deep feature extractors combined with Support Vector Machine (SVM) to determine whether a deeper residual architecture can improve discrimination among visually similar tea leaf disease classes. **Method**: Images were obtained from the Kaggle "Identifying Disease in Tea Leaves" dataset comprising eight classes. Data augmentation increased each class to 800 images, yielding 6,400 images that were divided into training and testing sets using an 80:20 ratio. ResNet50 and ResNet101 pretrained on ImageNet were used as fixed feature extractors, and the resulting feature vectors were standardized and classified using an RBF-kernel SVM. **Results and Discussion**: ResNet101–SVM achieved the best performance with 97.97% accuracy and precision, recall, and F1-score of 98%, substantially outperforming ResNet50–SVM, which achieved 89.15% accuracy, 90% precision, 89% recall, and 89% F1-score. The deeper ResNet101 architecture provided more discriminative representations for visually similar disease patterns, although a small number of misclassifications remained. **Conclusion**: ResNet101 combined with SVM provides a more accurate and reliable framework than ResNet50–SVM for multi-class tea leaf disease classification and offers a promising foundation for automated disease diagnosis systems.

Keywords: Tea Leaf Disease; ResNet50; ResNet101; SVM; Deep Learning.

1. Introduction

Tea ranks among the most widely cultivated and consumed agricultural commodities worldwide. Beyond its role as a beverage of cultural, economic, and health significance, tea underpins the economies of numerous countries across Asia, Africa, and parts of South America, with major producers such as China, India, and Sri Lanka supplying much of the global export market. Yet sustaining this demand is increasingly difficult: the tea industry must contend with climate change, deteriorating soil conditions, and a persistent burden of plant diseases. Tea leaf diseases in particular erode both yield and quality, making effective, sustainable disease management strategies essential [1],[2].

Growing public awareness of sustainability has simultaneously drawn greater attention to agricultural development. Public sentiment around agricultural programs and innovation increasingly favors efficiency, sustainability, and environmentally friendly technology adoption [3]. Within tea cultivation specifically, farmers and industry stakeholders remain acutely concerned about disease management, since outbreaks translate directly into income loss [4]. This concern reinforces the case for smart, image-based and AI-driven disease identification systems that can bolster production resilience and support farmer welfare amid today's agricultural pressures [5],[6].

This study proposes a hybrid approach for identifying diseases in tea leaves by integrating deep learning and machine learning methods to improve classification accuracy. The ResNet101 model, one of the deepest convolutional architectures in the Residual Network family, is utilized to extract features from tea leaf images automatically and efficiently. This feature extraction aims to capture complex and relevant visual characteristics of the leaf surface. The extracted features are then classified using the Support Vector Machine (SVM) algorithm, which has proven effective for handling multi-class classification problems with high generalization capabilities. The system is designed to recognize eight categories of tea leaf conditions: Anthracnose, algal leaf, bird eye spot, brown blight, gray light, healthy, red leaf spot, and white spot.

A growing body of work has applied deep learning and machine learning together for tea leaf disease classification, often drawing on techniques originally developed in adjacent domains. For instance, one investigation extracted ResNet-50 features from brain tumor MRI scans and then compared several classical classifiers—Naive Bayes, Decision Tree, SVM, K-Nearest Neighbors, and Random Forest—finding that SVM and KNN performed best, reaching 0.95 and 0.96 accuracy respectively [7]. Elsewhere, SVM and Gradient Boosting models tuned through Particle Swarm Optimization were evaluated on five disease categories plus healthy leaves, with the optimized SVM reaching 91.68% accuracy [4]. A separate effort trained a VGG-16 CNN to distinguish three conditions—healthy, brown blight, and algal spot—attaining 97.7% test accuracy, while another comparison pitted MobileNet against NasNet Mobile across six disease categories, with MobileNet's 95% accuracy surpassing NasNet Mobile's 88% [3]. Collectively, these findings illustrate how different deep learning architectures and optimization schemes each contribute to improved classification outcomes. Beyond tea leaf disease specifically, hybrid ResNet–SVM pipelines have also gained traction: pairing a ResNet50 extractor with PCA and SVM yielded over 98% cross-validated accuracy on the 38-class PlantVillage dataset [16], and a modified ResNet50 variant was used for wheat leaf disease classification [17]. The pairing generalizes well outside agriculture too—ResNet101 features combined with a Bayesian-optimized SVM reached up to 100% accuracy on steel surface defect data [18]—while ensemble strategies combining ResNet50 with lightweight networks such as MobileNetV2 have supported tomato leaf disease classification [19], and ResNet101 features evaluated against multiple feature-selection and classifier combinations, SVM included, have been applied to leukemia detection from blood-smear images [20]. Despite this evidence that ResNet-based features work well across domains, few studies have directly compared ResNet50 against ResNet101 as feature extractors feeding a single classifier such as SVM for multi-class tea leaf disease classification specifically.

Within the narrower scope of tea leaf disease detection itself, several recent contributions have pushed toward more specialized network designs. Kalita and colleagues benchmarked feature-level against output-level ensembling across four pretrained backbones—ResNet-18, VGG-16, InceptionV3, and MobileNetV2—for an eight-class tea leaf disease task, obtaining 95.6% accuracy when PCA-reduced features were fed to a Random Forest and 98.3% when the models' output probabilities were pooled instead [21]. Closer in spirit to the present work, Bhagat and Kumar paired deep-learning-derived features with a kernelized SVM for tea leaf disease prediction [22], following essentially the same feature-extraction-then-SVM philosophy adopted here. Bhuyan and co-authors devised Res4net-CBAM, embedding a convolutional block attention module within a residual network, and reported 98.27% average recognition accuracy on their own tea leaf disease image collection [23]. Heng and colleagues instead proposed a hybrid pooling scheme to sharpen automatic tea leaf disease identification within a deep neural network [24], and Soeb and co-authors turned to the YOLOv7 detector for real-time detection and identification of tea leaf diseases [25]. Taken together, this body of tea-specific work points to the value of pairing deep feature representations with lightweight or attention-driven refinements tailored to this disease domain.

This research focuses on evaluating the performance of a tea leaf disease image classification model that combines deep learning-based feature extraction using the ResNet101 architecture with the Support Vector Machine (SVM) algorithm. Experiments are conducted on a dataset consisting of eight tea leaf disease classes: Anthracnose, algal leaf, bird eye spot, brown blight, gray light, healthy, red leaf spot, and white spot, with the aim of analyzing the effectiveness of this combined approach in enhancing model accuracy and generalization capability. The proposed method is expected to generate richer and more discriminative image feature representations while leveraging the precision classification strength of SVM. Thus, this study aims to contribute significantly to the development of accurate and automated digital image-based diagnostic systems for tea leaf disease detection.

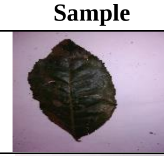
Specifically, this study addresses two research questions: (1) whether a deeper residual feature extractor, such as ResNet101, improves class separability for visually similar tea leaf diseases when paired with an SVM classifier; and (2) how sensitive the resulting classification performance is to the choices made during dataset balancing and augmentation.

2. Method

The dataset used in this study was obtained from the Kaggle platform "Identifying Disease in Tea Leaves" (https://www.kaggle.com/datasets/shashwatwork/identifying-disease-in-tea-leafs), consisting of eight classes as presented in Table 1. Each class was augmented to 800 images prior to splitting, yielding 6,400 images in total, which were then partitioned into training and testing subsets using an 80:20 split (test_ratio = 0.2) performed independently within each class folder—equivalent in effect to a stratified split—resulting in 5,131 training images and 1,281 test images. No fixed random seed was set for this split, so exact reproduction of the same train/test partition would require re-running the split with a fixed seed. Because augmentation was performed before the train-test split, augmented variants of the same source image could in principle appear in both subsets; this is acknowledged as a limitation in the Discussion section, and future revisions of the pipeline should split the data first and augment only the training portion to eliminate this risk.

The dataset, obtained from the Kaggle platform, originally contained unevenly distributed images per class before augmentation to 800 images per class (6,400 images total) prior to splitting into training and testing subsets.

Table 1. Distribution of the tea leaf disease dataset across eight classes

Class Label	Tea Class	Number of Samples	Sample
0	Anthracnose	97	
1	White spot	137	
2	Algal Leaf	109	
3	Red Leaf Spot	140	
4	Healthy	68	
5	Bird Eye Spot	98	

Class Label	Tea Class	Number of Samples	Sample
6	Brown Blight	113	
7	Gray Light	100	
Total Image			862

The **Figure 1** illustrates the research workflow for classifying tea leaf diseases using a combination of feature extraction with ResNet50 and ResNet101 architectures and Support Vector Machine (SVM) for classification. The process consists of the following stages: Tea leaf dataset, Preprocessing, Data Split, Feature Extraction ResNet50 and ResNet101, Classification, and Evaluation.

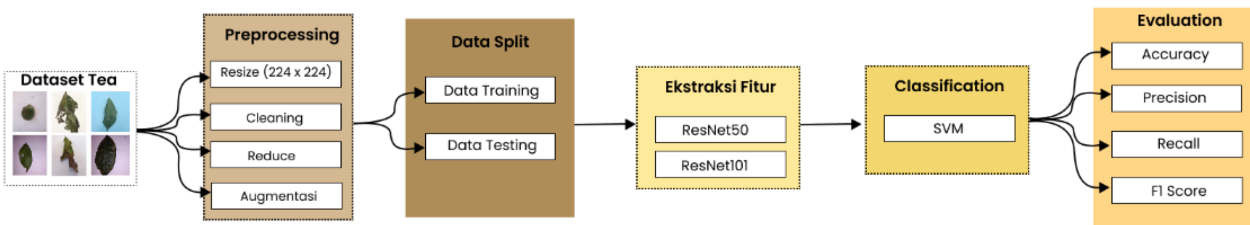


Figure 1. Research Workflow

Preprocessing

a. Resize
In this study, image preprocessing is performed to ensure consistent input data for each model. All images are resized to 128×128 pixels for the ResNet50 feature-extraction pipeline and to 224×224 pixels for the ResNet101 pipeline, matching the input resolution used for each backbone during feature extraction. This size standardization ensures that each image has a uniform resolution within a given pipeline, aligning with the input format required by the corresponding model architecture. Using two different input resolutions across the two backbones is noted as a limitation, since it introduces a confound when directly comparing ResNet50 and ResNet101 performance; a uniform input size across both pipelines is recommended for a stricter comparison in future work. Pixel values were normalized using each backbone's corresponding Keras preprocess_input function (BGR channel reordering with ImageNet mean subtraction, following the standard preprocessing used during pre-training), applied consistently to both the training and test images.

b. Cleaning
In the data cleaning stage, duplicate entries in the dataset are removed. This step aims to eliminate redundant information that could affect model accuracy and introduce bias during training. By removing duplicate entries, the quality of the dataset is improved, allowing the model to learn from cleaner, more relevant, and non-repetitive representations.

c. Reduce
An additional class-balancing step was explored during pipeline development, in which the minority classes were undersampled to match the smallest class (68 images), producing a reduced 6-class subset of 408 images. However, the feature extraction and classification experiments reported in this study were run on the full 8-class

dataset after augmentation (described below) rather than on this reduced subset; the undersampling step is reported here for completeness but does not correspond to the data used to produce the results in Table 2.

d. Augmentation

In the augmentation stage, the number of images in each of the eight classes—Anthracnose, algal leaf, bird eye spot, brown blight, gray light, healthy, red leaf spot, and white spot—was increased to 800 using image transformation techniques such as rotation, width/height shifting, shear, zoom, and horizontal flipping. This step enhances feature diversity and expands the dataset prior to the train-test split, ensuring that each class has a sufficient and balanced number of samples to support model training. As augmentation was applied before splitting the data (see Method: Dataset), this ordering is noted as a limitation in the Discussion section.

Feature Extraction

a. ResNet50 Feature Extraction

Once preprocessing is complete, each image is passed through a ResNet50 backbone pre-trained on ImageNet (input resolution 128×128) to obtain a fixed-size visual feature vector. Since no pooling layer follows the final convolutional block, the resulting 4×4×2048 feature map is flattened directly into a 32,768-dimensional vector per image. The backbone's weights remain frozen throughout, serving purely as a fixed feature extractor rather than being fine-tuned. Every image is processed individually through this ResNet50 pipeline (**Figure 2**), yielding features that capture the image's inherent visual characteristics [8],[9],[10]; each resulting vector is labeled by class and retained for subsequent analysis and model training.

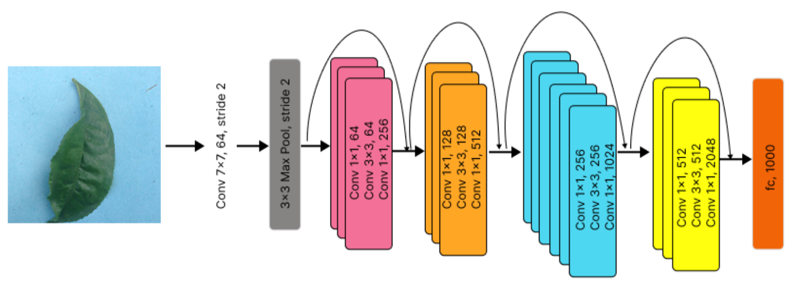


Figure 2. ResNet50 Architecture

b. ResNet101 Feature Extraction

For the deeper backbone, ResNet101—pre-trained on ImageNet and accepting a 224×224 input—serves as the feature extractor. Extending the ResNet family to 101 layers, it relies on identity shortcut connections to implement residual learning (Figure 3), and its stacked residual-block structure allows it to learn increasingly complex visual features without the accuracy degradation typically seen in very deep networks [11],[12]. As with ResNet50, no pooling layer is appended after the final convolutional block, so each preprocessed image yields a 7×7×2048 feature map that is flattened into a 100,352-dimensional vector [13]; backbone weights are likewise frozen and used only for feature extraction. These vectors encode key pattern, texture, and structural information and are labeled by class before storage, later serving as input to the classification stage (Figure 3).

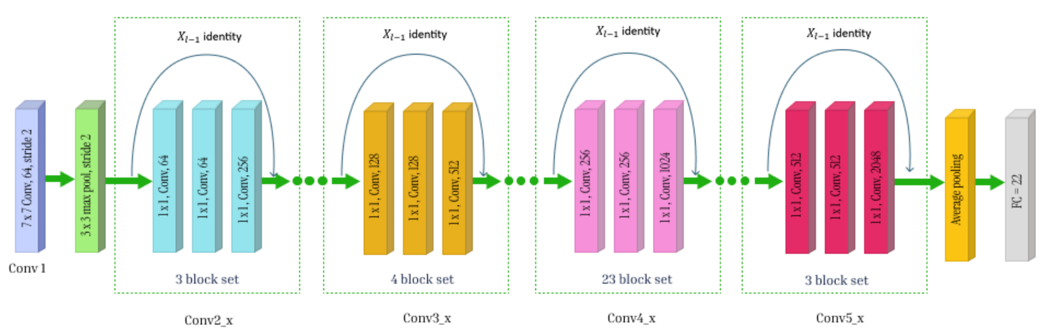


Figure 3. ResNet101 Architecture

Classification

a. Super Vector Machine (SVM)

The classification stage combines the extracted features with a Support Vector Machine (SVM). Before training, every feature vector is standardized to zero mean and unit variance using a scaler fitted only on the training data and then applied to the test set. SVM's appeal here lies in its strength at separating high-dimensional data by maximizing the margin between classes[14]. We configure the SVM with a Radial Basis Function (RBF) kernel (C = 1.0, gamma = 'scale', random_state = 42) to capture nonlinear boundaries between visually similar disease classes, relying on scikit-learn's default one-vs-one strategy and uniform class weights for the eight-class task—appropriate given the dataset's balance after augmentation. Because the RBF kernel is used, the margin-maximization formulation below operates implicitly within the higher-dimensional feature space $\varphi(x)$ induced by the kernel function $K(x, x') = \exp(-\gamma\|x - x'\|^2)$, rather than acting directly on the raw feature vector x. This general margin-maximization objective is expressed as

$$w^T x + b = 0 \tag{1}$$

Where w is the weight vector, x is the (kernel-transformed) feature vector, and b is the bias term. The optimization seeks to minimize the loss function:

$$\frac{1}{2} ||w||^2 \tag{2}$$

Subject to the constraint:

$$yi(w^T x + b) \geq \tag{3}$$

Here y_i denotes the class label (1 or −1). Because an RBF kernel is used, the SVM implicitly maps the data into a higher-dimensional space and identifies the hyperplane offering the widest margin between classes within that space [15], as illustrated in **Figure 4**.

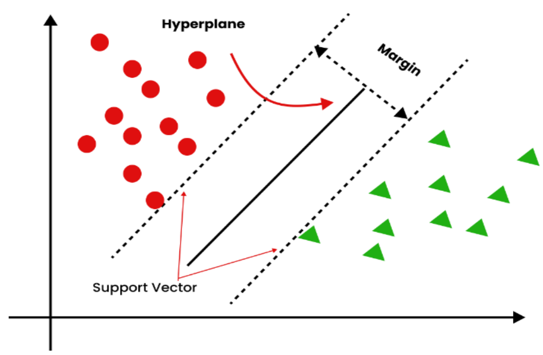


Figure 4. SVM Architecture

3. Results and Discussion

In the testing phase, two feature extraction approaches were employed, namely ResNet50 combined with SVM and ResNet101 combined with SVM, to classify eight categories of tea leaf diseases on a held-out test set of 1,281 images. The performance of both models was assessed using accuracy, precision, recall, and F1-score as evaluation metrics, macro-averaged across the eight classes (the test set is approximately class-balanced, since each class was augmented to an equal 800 images before the 80:20 split). The experimental results demonstrated that the ResNet101 + SVM configuration consistently outperformed the ResNet50 + SVM approach across all evaluation measures.

Table 2. Evaluation Results of SVM Models with Different Feature Extraction Approaches

Algorithm	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
ResNet50 + SVM	89.15	90	89	89
ResNet101 + SVM	97.97	98	98	98

As shown in Table 2, both models demonstrated strong classification performance; however, the ResNet101 + SVM combination consistently outperformed ResNet50 + SVM across all evaluation metrics. The ResNet101 + SVM achieved an accuracy of 97.97%, with precision, recall, and F1-score values each reaching 98%, highlighting its robustness and stability in distinguishing between disease categories. In comparison, the ResNet50 + SVM model yielded an accuracy of 89.15% and an F1-score of 89%, which still indicates a satisfactory level of classification performance. Figure 5 presents a more detailed comparison of precision, recall, and F1-score across different classes for the ResNet50 + SVM model. While this model achieved high performance in most classes—particularly for algal leaf, healthy, red leaf spot, and white spot—a slight reduction in recall was observed in the anthracnose and gray light categories. This suggests that certain samples from these disease classes were not correctly identified, leading to misclassifications. The superior performance of ResNet101 + SVM can be attributed to its deeper architecture, which allows the extraction of more discriminative and high-level features from the tea leaf images. This advantage provides a stronger basis for accurate disease classification, thereby offering a reliable framework for early detection and potentially improving disease management strategies in tea cultivation.

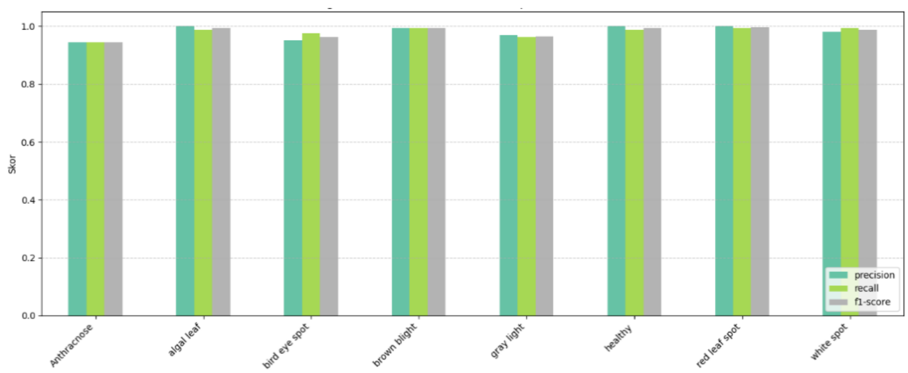


Figure 5. Class-wise classification results of the ResNet50 + SVM mode

Figure 5 showing the precision, recall, and F1-score obtained for each class. The model achieved strong performance in most categories, particularly for algal leaf, healthy, red leaf spot, and white spot, while a slight decrease in recall was observed in the anthracnose and gray light classes.

To further examine the misclassifications, Figure 6 presents the confusion matrix of the ResNet50 + SVM model. Most predictions are located along the diagonal, indicating that the model achieved satisfactory accuracy in classifying the images. However, several notable errors occurred in the anthracnose class, where a number of samples were misclassified as brown blight. In addition, mispredictions were also observed in the brown blight class, which were incorrectly classified as white spot. These errors can be attributed to the visual similarities between classes, such as spot patterns or severity levels that are difficult to distinguish visually, thereby affecting the model's prediction accuracy. Including one or two representative misclassified test images alongside this figure is recommended to illustrate these failure modes concretely

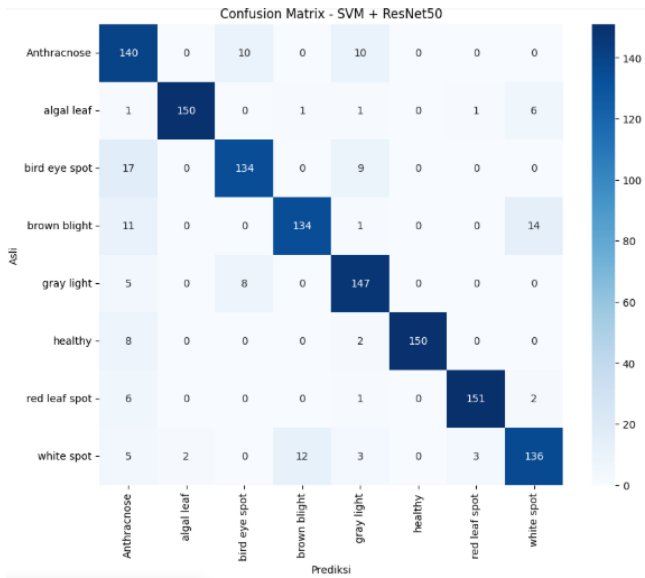


Figure 6. Confusion matrix of the ResNet50 + SVM model

Most predictions are correctly aligned along the diagonal, indicating reliable classification performance. However, misclassifications are observed in the anthracnose class, where several samples were predicted as brown blight, and in the brown blight class, which was occasionally misclassified as white spot. These errors are likely due to visual similarities among the classes, such as spot patterns and severity levels, which make accurate differentiation more challenging.

The ResNet101 + SVM model demonstrated superior classification performance compared to the previous model, as visualized in Figure 7. The precision, recall, and F1-score values across all classes were consistently high and stable, with most approaching near-perfect levels. Classes such as white spot, healthy, algal leaf, and red leaf spot recorded exceptionally high and consistent scores across all three metrics, indicating the model's strong ability to accurately recognize and differentiate images from these categories, with red leaf spot in particular maintaining the same stable performance it already showed under ResNet50. Furthermore, the recall scores for the anthracnose, gray light, and bird eye spot classes showed significant improvements over the ResNet50 model, highlighting the enhanced capability of ResNet101 in detecting all relevant samples correctly. Overall, this figure illustrates that the deeper ResNet101 architecture was able to extract visual features of tea leaves more effectively, resulting in more accurate and balanced predictions.

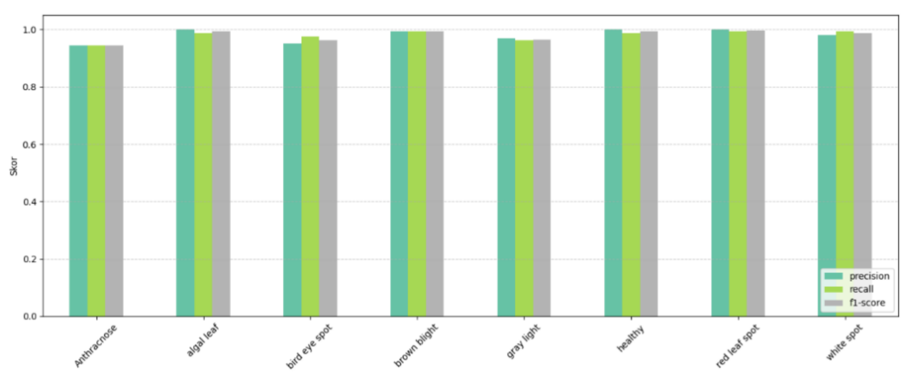


Figure 7. Class-wise classification results of the ResNet101 + SVM model

The precision, recall, and F1-score values are consistently high across all classes, with several categories such as white spot, healthy, algal leaf, and red leaf spot achieving near-perfect scores. Significant improvements are also observed in the anthracnose, gray light, and bird eye spot classes compared to the ResNet50 + SVM model, indicating the enhanced capability of ResNet101 in correctly detecting samples across all categories. These results highlight the effectiveness of the deeper ResNet101 architecture in extracting discriminative visual features of tea leaves, leading to more accurate and balanced classification outcomes.

To provide a clearer understanding of the prediction distribution, Figure 8 presents the confusion matrix of the ResNet101 + SVM model on the test data. The results show that most predictions are located along the main diagonal, indicating that the model consistently classified images correctly across all classes. The number of misclassifications was very small and scattered sporadically, with most classes experiencing only one or two mispredicted samples. For example, in the *anthracnose* class, five samples were classified as *bird eye spot*, while one *white spot* sample was incorrectly predicted as *algal leaf*. Nevertheless, no dominant pattern of misclassification was observed, suggesting that the model achieved excellent generalization across all categories. With such a low error rate, this confusion matrix further reinforces the superiority of the ResNet101 model in supporting an accurate and reliable tea leaf disease classification system.

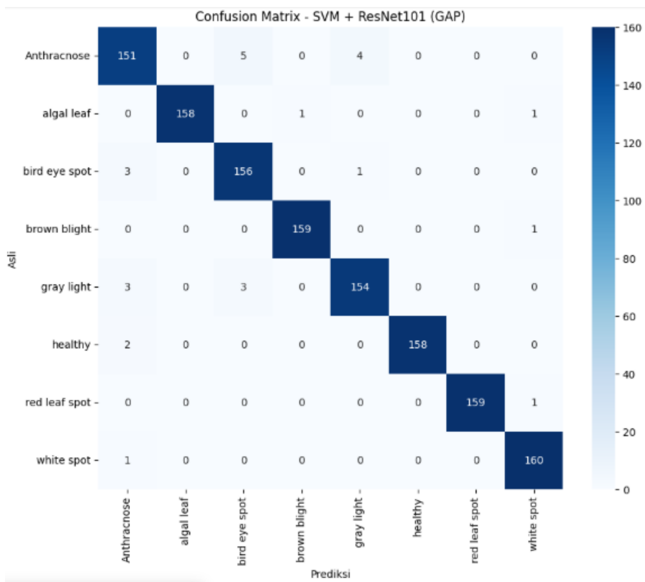


Figure 8. Confusion matrix of the ResNet101 + SVM model on the test dataset

Most predictions are correctly aligned along the main diagonal, indicating highly accurate and consistent classification across all classes. Misclassifications are minimal and sporadic, with only a few cases such as *anthracnose* samples predicted as *bird eye spot* and a single *white spot* sample misclassified as *algal leaf*. The absence of any dominant error pattern highlights the strong generalization capability of the model. These results further demonstrate the robustness and reliability of ResNet101 in supporting accurate tea leaf disease classification.

Based on the obtained results, it is evident that the approach of tea leaf disease classification using deep learning-based feature extraction provides a significant improvement in performance compared to direct classification without additional feature extraction. In this study, two model combinations were tested, namely ResNet50 + SVM and ResNet101 + SVM, with the findings showing that utilizing a deeper network architecture such as ResNet101 yields more optimal classification outcomes. The ResNet50 + SVM model demonstrated fairly good performance with an accuracy of 89.15%, while its precision, recall, and F1-score values ranged between 89–90%. However, certain limitations were identified, particularly in detecting the anthracnose and gray light classes, where the model tended to experience reduced recall. This decline can be attributed to visual similarities between classes, such as leaf spot patterns or coloration. In addition, external factors such as lighting conditions and image capture angles may also affect the model's accuracy in distinguishing between classes. As this evaluation is based on a single train-test split, future work should repeat the split multiple times or adopt k-fold cross-validation and report the mean and standard deviation of each metric to quantify the stability of these results. A fixed-feature-extractor-plus-SVM design was adopted throughout this study; future work should also compare this approach against an end-to-end fine-tuned CNN baseline to quantify the added value of the fixed-feature + SVM pipeline relative to full fine-tuning.

Meanwhile, the ResNet101 + SVM model achieved a substantial performance improvement, with an accuracy of 97.97% and precision, recall, and F1-score values consistently reaching 98% across nearly all classes. These results indicate that the ResNet101 architecture, with its deeper layers and more complex feature representation capabilities, was able to capture finer visual differences between tea leaf disease categories. Consequently, the combination of ResNet101 and SVM proved to be more effective in producing accurate and stable classification results. Nevertheless, challenges remain in differentiating visually similar classes and in handling variations in image quality collected from field conditions. Therefore, future development can be directed toward integrating more diverse image datasets as well as applying augmentation strategies or more adaptive fine-tuning methods to enhance the model's robustness against noise and real-world environmental conditions

4. Conclusion

This study demonstrated the effectiveness of deep learning-based feature extraction approaches for tea leaf disease classification by combining convolutional neural network architectures with Support Vector Machines (SVM). The experimental results confirmed that employing deeper architectures such as ResNet101, when paired with SVM, significantly improved classification performance compared to ResNet50 + SVM. The ResNet50 + SVM model achieved satisfactory results with an accuracy of 89.15% and balanced precision, recall, and F1-score values. However, its performance declined when dealing with classes that exhibit strong visual similarities, such as anthracnose and gray light, suggesting the limitations of shallower networks in capturing subtle distinctions between classes. In contrast, the ResNet101 + SVM model delivered superior outcomes, achieving 97.97% accuracy with consistently high precision, recall, and F1-scores of 98% across nearly all classes, thereby highlighting the advantages of deeper feature representations. Overall, the findings suggest that the ResNet101 + SVM framework is a more reliable and stable approach for tea leaf disease classification. Future research can be focused on enhancing model robustness by incorporating more diverse and larger-scale image datasets, implementing advanced augmentation techniques, and exploring adaptive fine-tuning strategies. Such improvements will enable the development of an even more accurate and generalizable system to support early detection and effective management of tea leaf diseases in real-world agricultural environments.

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