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*Research Article*

# A Lightweight Maize Leaf Disease Recognition Using PCA-Compressed MobileNetV2 Features and RBF-SVM

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**Abstract:** The integration of Artificial Intelligence (AI) into precision agriculture has significantly improved plant disease recognition; however, many existing deep learning models remain computationally expensive and feature-redundant, limiting their deployment on low-power and edge devices. To address these limitations, this study proposes a lightweight framework for maize leaf disease recognition based on serial deep feature extraction, dimensionality reduction, and machine-learning–based classification. A pre-trained MobileNetV2 network is employed as a fixed feature extractor to obtain discriminative visual representations, while Principal Component Analysis (PCA) is applied to reduce feature dimensionality by approximately 76%, retaining 95% of the original variance and improving computational efficiency. The compressed features are subsequently classified using a Radial Basis Function Support Vector Machine (RBF-SVM), optimized via grid search and cross-validation. Experiments conducted on a four-class maize leaf disease dataset (Northern Leaf Blight, Common Rust, Gray Leaf Spot, and Healthy), with class imbalance handled during training, demonstrate that the proposed MobileNetV2–PCA–SVM pipeline achieves 97.58% accuracy, 96.60% precision, 96.59% recall, and 96.59% F1-score, outperforming the DenseNet201 + Bayesian-optimized SVM baseline (94.60%, 94.40%, 94.40%, and 94.40%, respectively). This improvement corresponds to a 2.98% accuracy gain, a 55% reduction in error rate, an 86% reduction in model parameters (20.31M to 2.75M), and an 85% reduction in model size (81 MB to 12 MB). These results indicate that the proposed framework provides a compact and efficient solution with strong potential for deployment in resource-constrained agricultural environments.

**Keywords:** Deep feature extraction; Edge computing; Lightweight model; Maize leaf disease recognition; MobileNetV2; Plant disease classification; Precision agriculture; Smart agriculture.

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## 1. Introduction

Crop diseases remain a major constraint on agricultural productivity, particularly in staple crops that support global food systems. In maize (Zea mays), foliar diseases such as Gray Leaf Spot, Northern Leaf Blight, and Rust can severely reduce yield and crop quality, with losses exceeding 50% under severe infestation conditions [1], [2]. Effective disease management therefore, depends on early and accurate diagnosis, which is often challenging to achieve at scale using manual field inspection alone. Visual symptoms on leaves provide critical diagnostic cues, making image-based analysis a promising foundation for automated disease monitoring systems [3]. Recent advances in artificial intelligence (AI) and computer vision have further enabled the development of practical, data-driven tools that support timely intervention and sustainable crop management in precision agriculture [4]–[6].

Deep learning approaches, particularly Convolutional Neural Networks (CNNs), have demonstrated strong performance in automatic plant disease recognition by learning hierarchical and discriminative features from leaf images [3], [7], [8]. Well-known architectures such as VGGNet, ResNet, and DenseNet have achieved high classification accuracy in controlled experimental settings. Nevertheless, their deployment in real-world agricultural environments remains challenging. Most CNN-based models require large and well-balanced datasets to

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generalize effectively, whereas agricultural image data are often affected by environmental variability, inconsistent illumination, background clutter, and limited sample availability [9], [10]. These factors frequently introduce domain shift and overfitting, reducing robustness and limiting applicability in smallholder or resource-constrained farming contexts [11].

In addition to data-related challenges, high-capacity CNN architectures are computationally expensive, requiring substantial memory and processing resources for both training and inference [7]. Such complexity limits deployment on low-power or embedded devices commonly used in field monitoring systems. Consequently, lightweight CNN architectures have gained increasing attention due to their ability to provide efficient yet discriminative feature representations suitable for mobile and edge-based agricultural applications. Among these, MobileNetV2 [12] is particularly notable for its inverted residual structure and depth-wise separable convolutions, which enable a favorable balance between computational efficiency and representational capability.

Although lightweight CNNs reduce computational cost, the direct use of high-dimensional deep feature vectors may still introduce redundancy and irrelevant information. Dimensionality reduction techniques, such as Principal Component Analysis (PCA), offer an effective mechanism to retain the most informative components while discarding correlated and noisy features [13], [14]. When applied after deep feature extraction, PCA further improves computational efficiency and can enhance discriminative capability by emphasizing essential visual patterns relevant to disease classification.

In parallel, classical machine learning classifiers—particularly Support Vector Machines (SVMs) continue to demonstrate strong generalization performance on small or moderately imbalanced datasets. When combined with nonlinear Radial Basis Function (RBF) kernels, SVMs can model complex decision boundaries and improve separability between visually similar disease classes [14]. Integrating CNN-based deep feature extraction with optimized kernel-based classifiers, therefore, represents a promising hybrid approach that combines the representational strength of deep learning with the robustness of statistical learning [15], [16].

Despite these advances, several gaps remain in existing maize disease recognition studies. First, many works emphasize overall accuracy while underreporting recall performance for diseased classes, even though false negatives are particularly costly in agricultural decision-making. Second, the individual contributions of deep feature extraction, dimensionality reduction, and classifier choice are often insufficiently analyzed, limiting methodological transparency. Third, although lightweight deployment is frequently claimed, efficiency gains are rarely supported by explicit architectural justification or feature compression analysis. Finally, systematic evaluation of model components through ablation and controlled experiments remains limited in prior studies.

Motivated by these limitations, this work presents a compact and efficient maize leaf disease recognition pipeline based on three sequential stages: (1) deep feature extraction using MobileNetV2, (2) feature refinement through PCA-based dimensionality reduction, and (3) classification using an optimized RBF-SVM. The proposed framework is designed to reduce computational complexity and feature redundancy while maintaining strong recognition performance under constrained data and resource settings. The main contributions of this study can be summarized as follows:

- Utilization of MobileNetV2 as a lightweight backbone for extracting discriminative maize leaf features with low computational overhead.
- Application of dimensionality reduction to minimize redundancy while preserving informative variance, leading to improved efficiency.
- Robust SVM-Based Classification: Replacement of the CNN softmax head with a grid-search-optimized RBF-SVM to enhance class separability under limited data conditions.
- Development of a serial and resource-efficient recognition framework suitable for deployment in mobile and edge-based agricultural systems.

The remainder of this paper is organized as follows. Section 2 reviews related work on deep learning and CNN–SVM-based plant disease recognition. Section 3 describes the proposed MobileNetV2–PCA–SVM methodology in detail. Section 4 presents the experimental setup, results, and performance analysis. Finally, Section 5 concludes the paper and outlines directions for future research toward scalable and deployable maize disease recognition systems.

## 2. Related Work

A substantial body of research has explored computational methods for plant disease recognition, ranging from early handcrafted feature–based approaches to modern deep learning–driven image analysis. These studies have investigated a wide variety of crops, imaging conditions, and classification strategies, with maize receiving particular attention due to its economic importance [3]. Existing work can be broadly categorized into methods based on handcrafted descriptors, deep convolutional neural networks, lightweight architectures for efficient deployment, and CNN-based pipelines that employ feature compression and classical machine learning classifiers such as Support Vector Machines (SVMs) [9].

Early studies relied on handcrafted descriptors, including color, texture, and shape features, for leaf disease detection. Although computationally lightweight, these approaches were highly sensitive to variations in illumination, background, and imaging conditions, resulting in limited robustness and inconsistent predictions [10], [13]. The introduction of Convolutional Neural Networks (CNNs) marked a major shift in agricultural image analysis by enabling automatic feature learning and hierarchical pattern extraction directly from raw images [17], [18]. Architectures such as AlexNet, VGGNet, and ResNet achieved notable improvements in classification accuracy across multiple crop species [19]–[21]. However, their large model size and high computational demands restrict deployment on low-power or embedded agricultural devices, particularly in real-time field applications [7], [22].

To overcome these limitations, lightweight CNN architectures such as MobileNet, ShuffleNet, and EfficientNet have been proposed to reduce computational cost while preserving representational capability [23], [24]. MobileNetV2, in particular, employs inverted residual blocks and depthwise separable convolutions, achieving an effective balance between efficiency and accuracy [25]. These architectural properties make MobileNetV2 well-suited for deployment in resource-constrained environments, and several studies have demonstrated its effectiveness for plant leaf disease recognition, including maize, tomato, and rice, with significantly reduced parameter footprints [15], [26].

Beyond architectural efficiency, feature redundancy remains a critical challenge in deep learning–based plant disease recognition. High-dimensional feature vectors often contain correlated or noisy components that can degrade discriminative performance. PCA has therefore been widely adopted as a dimensionality reduction technique to compress deep features while preserving the most informative variance components [14], [16]. By reducing redundancy, PCA improves computational efficiency and mitigates overfitting, thereby enhancing generalization across variable field conditions [11]. Several studies have shown that combining CNN-based feature extraction with PCA yields compact and discriminative representations without increasing model complexity [27]–[29].

For the classification stage, classical machine learning algorithms—particularly SVMs, continue to demonstrate strong generalization performance on small or moderately imbalanced agricultural datasets [30], [31]. When equipped with a nonlinear RBF kernel, SVMs can model complex decision boundaries and improve class separability for visually similar diseases [25]. Recent research indicates that replacing the softmax layer of CNNs with kernel-based SVM classifiers can enhance robustness and stability under limited data conditions, especially when deep features are used as input representations [4], [18].

Several studies have explored such CNN–SVM pipelines for plant disease recognition. For example, Dash et al. [3] employed DenseNet201 as a deep feature extractor followed by a Bayesian-optimized SVM classifier for maize disease classification, achieving high accuracy at the cost of increased computational complexity. Similarly, Pradeepa et al. [16] applied a CNN–SVM-based framework to rice leaf disease detection, demonstrating the benefits of kernel-based classifiers in improving class separability and reducing overfitting. These approaches highlight the effectiveness of combining deep feature extraction with statistical learning, particularly in data-limited scenarios.

In parallel, attention mechanisms have been introduced to improve feature discrimination and interpretability in plant disease recognition models. Modules such as Coordinate Attention (CA) and Efficient Channel Attention (ECA) enhance spatial and channel-wise feature emphasis, guiding networks toward the most informative lesion regions with minimal computational overhead [32]–[35]. These mechanisms have been successfully integrated into lightweight architectures such as MobileNetV2 and ShuffleNetV2, further improving accuracy and efficiency in agricultural image analysis [36].

Plant disease recognition research has evolved from handcrafted visual descriptors to deep CNN-based representations and, more recently, to serial pipelines that integrate deep feature extraction, dimensionality reduction, and kernel-based classification [3], [14], [37], [38]. These approaches have demonstrated that combining efficient architectures with feature refinement can significantly improve classification performance while reducing computational overhead. Despite these advances, challenges remain in balancing computational efficiency, accuracy, and generalization across varying field conditions. These open issues motivate the development of compact and efficient pipelines that are not only accurate but also practical for deployment in real-world agricultural environments.

## 3. Proposed Method

This section describes the dataset preparation, preprocessing pipeline, model architecture, and experimental configuration adopted for the proposed maize leaf disease recognition framework. The developed system follows a serial processing pipeline comprising three main stages: deep feature extraction with a pre-trained MobileNetV2 network, dimensionality reduction via PCA, and nonlinear classification with an optimized Radial Basis Function Support Vector Machine (RBF-SVM). The overall workflow of the proposed method is illustrated in Figure 1.

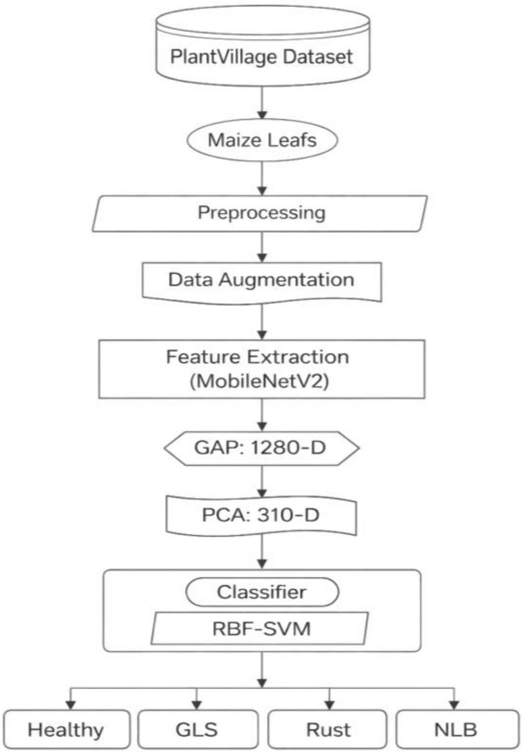

**Figure 1.** Workflow of the proposed maize leaf disease recognition framework based on MobileNetV2 feature extraction, PCA-based dimensionality reduction, and RBF-SVM classification.

### 3.1. Overview of the Framework

The proposed methodology begins with image preprocessing and class balancing to ensure representative learning across disease categories. Preprocessed maize leaf images are then passed through a pre-trained MobileNetV2 network to extract discriminative deep feature vectors from the global average pooling layer. These high-dimensional features are subsequently compressed using PCA to remove redundancy and reduce computational cost while preserving essential variance.

The PCA-reduced feature vectors are used to train an RBF-SVM classifier, with hyperparameters optimized via grid search cross-validation. During inference, the trained classifier predicts the disease class label for each input maize leaf image. This serial pipeline is designed to achieve a favorable balance between recognition accuracy, computational efficiency, and generalization capability under resource-constrained conditions.

### 3.2. Experimental Environment

All experiments were conducted using both a Google Colab GPU runtime and a local workstation to ensure reproducibility across different computing environments. The local workstation was equipped with an Intel Core i7 processor (2.60 GHz, x64-based), 16 GB of RAM, a 512 GB SSD, and an NVIDIA A100 GPU with 40 GB of VRAM. The operating systems used were Ubuntu 22.04 LTS and Windows 11 Pro.

The implementation was carried out in Python 3.10, using PyTorch 2.2.0 for deep feature extraction and Scikit-learn 1.4.2 for PCA computation, grid-search hyperparameter optimization, and SVM training. Additional libraries included OpenCV and Pillow for image preprocessing, NumPy and Pandas for numerical operations, and Matplotlib for visualization.

### 3.3. Dataset and Preprocessing

The maize leaf image dataset used in this study was obtained from the PlantVillage dataset, which was accessed via the Kaggle repository for ease of availability at https://www.kaggle.com/datasets/abdallahalidev/plantvillage-dataset. It is important to clarify that Kaggle served solely as a data hosting platform, and no additional or external datasets were incorporated in this work. All experiments were therefore conducted using a single, consistent dataset source, ensuring experimental transparency and fairness.

From the PlantVillage collection, maize-specific images were manually curated by selecting four visually distinct classes: Northern Leaf Blight (NLB), Common Rust, Gray Leaf Spot (GLS), and Healthy leaves. Representative samples from each class are shown in Figure 2. Prior to analysis, corrupted, duplicate, and blank images were removed to ensure dataset integrity and consistency. To enable reliable learning and fair comparison across classes, all images were resized to a uniform resolution of 224 × 224 × 3 pixels in accordance with the input requirements of the MobileNetV2 architecture. Pixel intensities were normalized to the range [0, 1] using Min–Max scaling. This normalization was applied uniformly across all data splits to stabilize training and improve numerical convergence.


(a) (b) (c) (d)

**Figure 2.** Sample maize leaf image used (**a**) GLS; (**b**) Rust; (**c**) NLB; (**d**) Health.

Given the moderate class imbalance observed in the dataset, random oversampling was applied to the training subset to reduce class skew and ensure more uniform class representation during learning. In addition, controlled data augmentation was applied exclusively to the training data to increase intra-class diversity and improve model generalization, rather than to balance the dataset artificially. Importantly, both oversampling and augmentation were applied only to the training subset to prevent information leakage into the validation and test sets. The dataset was partitioned into training (80%), validation (10%), and testing (10%) subsets using stratified sampling, thereby preserving the original class distribution in the evaluation data.

Data augmentation was applied to the training subset to improve model generalization and mitigate class imbalance. Augmentation was performed in a class-wise manner, with more intensive augmentation applied to underrepresented classes (particularly GLS) to reduce distribution skew. The applied transformations included random rotation (±30°), horizontal and vertical flipping, and random zooming within the range of 10–20%. As a result, the effective number of training samples increased non-uniformly across classes, as reported in Table 1, while the validation and test subsets remained unchanged and free from augmented data. This strategy enhanced intra-class diversity and ensured a more balanced training distribution without altering the original dataset composition or introducing information leakage.

**Table 1.** Dataset composition before and after augmentation.

| Class | Original | After Augmentation |
|---|---|---|
| NLB | 985 | 1,695 |
| Rust | 1,192 | 1,717 |
| GLS | 513 | 1,637 |
| Healthy | 1,162 | 1,591 |

### 3.4. Deep Feature Extraction and Dimensionality Reduction

Deep feature extraction was performed using the MobileNetV2 architecture pre-trained on the ImageNet dataset. In this study, MobileNetV2 was employed exclusively as a fixed feature extractor without fine-tuning its convolutional layers to reduce training complexity and improve computational efficiency. The final classification head was removed, and the global average pooling (GAP) layer output was used as the deep feature representation. Consequently, each input maize leaf image was encoded into a 1280-dimensional feature vector capturing high-level spatial and textural characteristics relevant to disease discrimination.

To reduce feature redundancy and improve efficiency, PCA was applied to the extracted deep features as a dimensionality reduction step. PCA was fitted only on the training feature set, and the learned transformation was subsequently applied to the validation and test sets to prevent data leakage. The transformation retained approximately 95% of the original variance, reducing the feature dimensionality from 1280 to 310 components and yielding a compact yet discriminative feature representation suitable for efficient classification. The overall feature transformation process is illustrated in Figure 3.

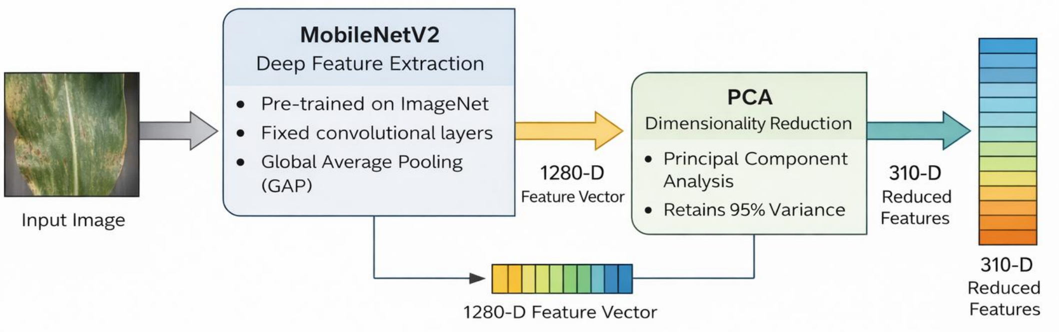

**Figure 3.** Serial feature transformation from MobileNetV2 deep features (1280-D) to PCA-reduced representations (310-D).

Formally, given a deep feature vector $x \in \mathbb{R}^{1280}$ extracted by MobileNetV2, PCA projects the feature into a lower-dimensional space as follows:

$$z = W^{\top}(x - \mu), \qquad z \in \mathbb{R}^{310} \tag{1}$$

where $\mu$ denotes the mean feature vector computed from the training set, and $W$ contains the eigenvectors corresponding to the top principal components that retain 95% of the total variance.

The PCA-reduced feature vectors were subsequently used as input to the RBF-SVM classifier for training and evaluation. All transformed features were stored as structured numerical arrays to ensure reproducibility and consistent experimental analysis.

### 3.5. RBF-SVM Training and Hyperparameter Optimization

The RBF-SVM was employed as the final classifier due to its strong ability to model nonlinear feature distributions and its robustness to overlapping class boundaries. The classifier was trained on PCA-reduced feature vectors, with the dataset partitioned into 80% training, 10% validation, and 10% test subsets.

An initial baseline model was trained using default parameters: regularization parameter $C = 1$, kernel type = RBF, kernel coefficient $\gamma = \text{scale}$, tolerance $\text{tol} = 1 \times 10^{-3}$, and no limit on the number of iterations until convergence. This baseline served as a reference for evaluating the impact of hyperparameter optimization.

To further improve classification performance, a grid search combined with 5-fold cross-validation was applied to the training set. The parameter search space included $C \in \{0.1, 1, 10, 100\}$, and $\gamma \in \{10^{-4}, 10^{-5}, 10^{-6}\}$. The combination yielding the highest mean validation accuracy was selected as the optimal configuration. The final optimized classifier was retrained using the combined training and validation subsets and serialized in binary .pkl format to ensure reproducibility and consistent deployment. Table 2 summarizes the hyperparameter ranges explored during the optimization process.

**Table 2.** Hyperparameter search space for RBF-SVM optimization.

| **Hyperparameter** | **Range** |
|---|---|
| Regularization ($C$) | 0.1, 1, 10, 100 |
| Kernel coefficient ($\gamma$) | $1\times10^{-4}$, $1\times10^{-5}$, $1\times10^{-6}$ |
| Kernel type | RBF |
| Tolerance | $1\times10^{-3}$ |

### 3.6. Evaluation Metrics and Visualization

Model performance was evaluated using four standard classification metrics: Accuracy, Precision, Recall, and F1-score. These metrics provide a balanced assessment of overall correctness, class-wise reliability, and robustness across disease categories. Let $TP$, $TN$, $FP$, $FN$ denote the numbers of true positives, false positives, true negatives, and false negatives, respectively. The evaluation metrics are defined as follows:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

$$\text{Precision} = \frac{TP}{TP + FP} \tag{2}$$

$$\text{Recall} = \frac{TP}{TP + FN} \tag{3}$$

$$\text{F1} - score = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \tag{4}$$

In addition to global performance, class-wise Precision, Recall, and F1 Scores were analyzed to assess the model's ability to correctly identify individual disease categories, particularly under moderate class imbalance. Visual performance analyses were conducted using confusion matrices and Receiver Operating Characteristic (ROC) curves to examine discriminative capability across classes. Training and validation accuracy plots were also included to provide insight into convergence behavior and model stability during optimization.

## 4. Results and Discussion

This section presents the experimental results of the proposed maize leaf disease recognition framework, which uses MobileNetV2 deep feature extraction, PCA-based dimensionality reduction, and an optimized RBF-SVM classifier. The evaluation focuses on three key aspects: (1) the effectiveness of deep feature compression using PCA, (2) the performance of the optimized RBF-SVM classifier, and (3) comparative benchmarking against the baseline method proposed by Dash et al. (2023). All experiments were conducted following the protocol described in Section 3.

Model performance is analyzed using Accuracy, Precision, Recall, and F1-score, supported by visual interpretations including PCA variance curves, feature-space visualizations, confusion matrices, and comparative bar charts. Given the practical nature of plant disease diagnosis and the moderate class imbalance in the dataset, particular emphasis is placed on recall performance for diseased classes, as false-negative predictions (infected leaves classified as healthy) have more severe agronomic consequences than false positives.

### 4.1. Feature Extraction and PCA-Based Dimensionality Reduction

Deep feature extraction was performed using the pre-trained MobileNetV2 architecture, which produced a 1280-dimensional feature vector for each maize leaf image. These deep features encode high-level color, texture, and structural information relevant to distinguishing visually similar maize diseases. To reduce feature redundancy and improve computational efficiency, PCA was applied to compress the 1280-D feature vectors while preserving the most informative variance. The cumulative explained variance of the principal components is shown in Figure 4.

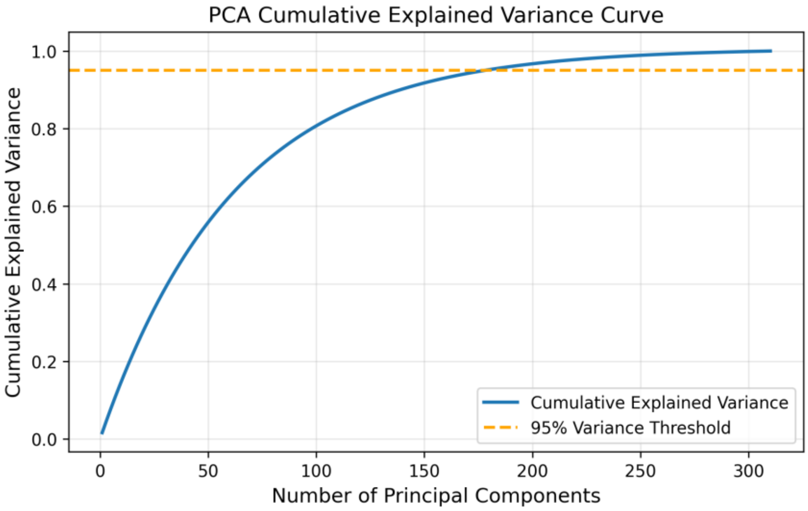

**Figure 4.** PCA cumulative explained variance curve for MobileNetV2 features

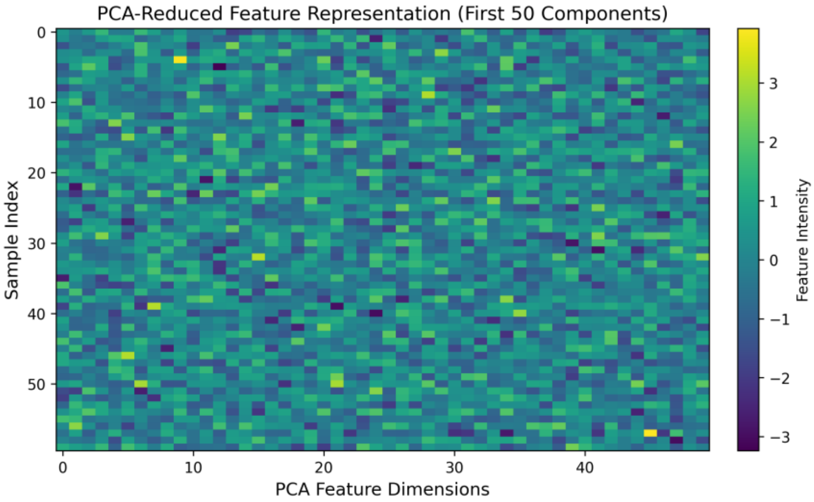

**Figure 5.** PCA-reduced feature representation heatmap.

Figure 4. demonstrates that approximately the first 300 principal components capture over 95% of the total variance, indicating that the dominant visual characteristics of all four classes—Healthy, Gray Leaf Spot (GLS), Northern Leaf Blight (NLB), and Rust—are well preserved after dimensionality reduction. Based on this analysis, 310 components were retained, achieving 95.01% variance preservation while reducing feature dimensionality by approximately 76%. This compression directly reduces memory usage and speeds up inference in the subsequent classification stage.

To further illustrate the structure of the PCA-transformed feature space, Figure 5. presents a heatmap visualization of the first 50 principal components across 60 representative maize samples. Each row corresponds to a sample, and each column represents a principal component dimension. The heatmap shows smooth intensity variations across components and samples, indicating that PCA effectively decorrelates redundant feature dimensions while preserving meaningful variance patterns. This compact representation facilitates more stable learning in the RBF-SVM classifier, leading to improved convergence behavior and enhanced generalization performance in downstream classification.

### 4.2. Training and Optimization of the RBF-SVM Classifier

The PCA-reduced feature vectors were used to train the RBF-SVM classifier using a five-fold cross-validation strategy combined with grid-search hyperparameter optimization. The trend of training and validation accuracy across folds is illustrated in Figure 6, providing insight into model stability and generalization behavior during optimization.

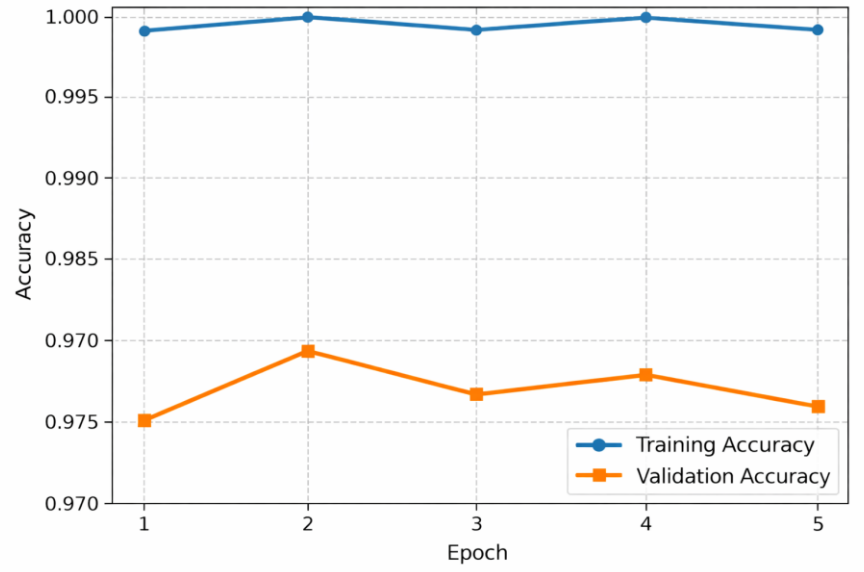

**Figure 6.** Training and validation accuracy across five epochs.

As shown in Figure 6, training accuracy remained consistently above 99.9% across all folds, while validation accuracy ranged between 97.0% and 97.8%. The small gap between training and validation performance indicates minimal overfitting and confirms that the PCA-compressed feature space supports stable kernel learning.

Based on grid-search results, the optimal hyperparameters were identified as C=10 and $\gamma = 1 \times 10^{-5}$. Using this configuration, the final model achieved 100% validation accuracy and 97.58% test accuracy. The combination of feature compression and kernel optimization also contributed to faster convergence and reduced computational complexity, supporting the suitability of the proposed framework for lightweight deployment.

### 4.3. Test Set Performance and Confusion Matrix Analysis

The classification performance of the optimized RBF-SVM model was evaluated on the held-out test set to assess its generalization capability. Figure 7. shows strong diagonal dominance, corresponding to an overall test accuracy of 97.58%. Only minor confusion was observed between Gray Leaf Spot (GLS) and Northern Leaf Blight (NLB), which share similar visual characteristics in early stages of disease. From an agricultural perspective, recall for diseased classes is of primary importance, as false-negative predictions (infected leaves classified as healthy) can delay treatment and result in greater yield loss. The proposed model achieved consistently high recall across all disease categories, particularly for Rust and NLB, indicating strong sensitivity to disease symptoms and a low false-negative rate.

The detailed per-class performance metrics are summarized in Table 3, which shows balanced precision and recall across all categories. Notably, the Healthy class achieved perfect recall, ensuring that diseased leaves were not misclassified as healthy, while the Rust and NLB classes achieved near-perfect F1 Scores, confirming strong discriminative capability and robust generalization.

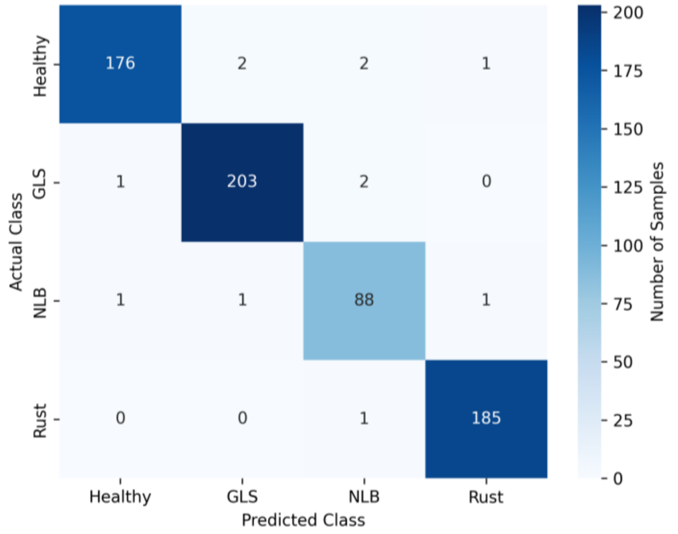

**Figure 7.** Confusion matrix test results of the RBF-SVM classifier

**Table 3.** Per-class classification performance of the proposed MobileNetV2–PCA–RBF-SVM model on the test set.

| Class | Accuracy (%) | Precision (%) | Recall (%) | F1-score (%) |
|---|---|---|---|---|
| Healthy | 100.00 | 100.00 | 100.00 | 100.00 |
| GLS | 93.46 | 94.70 | 93.46 | 94.08 |
| NLB | 95.54 | 93.16 | 95.54 | 94.37 |
| Rust | 98.94 | 100.00 | 98.93 | 99.46 |
| Macro Avg. | – | 96.97 | 96.98 | 96.97 |
| Weighted Avg. | 97.09 | 97.11 | 97.09 | 97.09 |

### *4.3.1. ROC–AUC and Recall-Focused Evaluation*

To further evaluate the robustness of the proposed framework under moderate class imbalance, ROC and Precision–Recall (PR) curves were generated. Unlike overall accuracy, these metrics provide a more informative assessment of recall behavior and class separability, which are critical in agricultural disease diagnosis, where false-negative predictions have severe consequences.

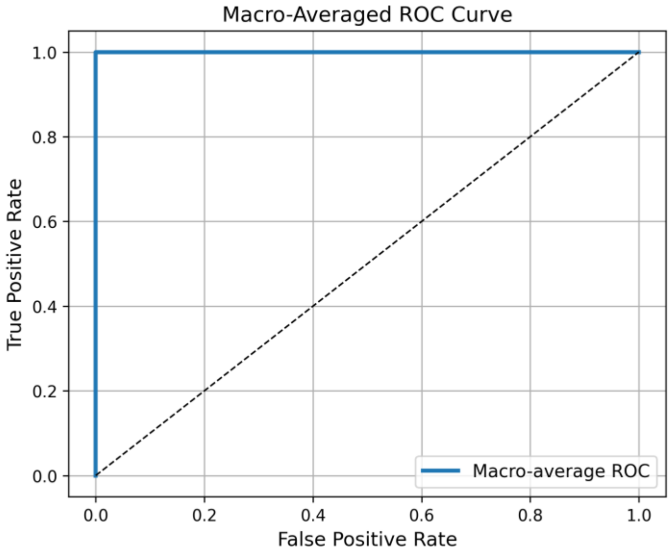

**Figure 8.** Macro-averaged ROC curve of test results.

The macro-averaged ROC curve is shown in Figure 8. The curve exhibits a high true positive rate across a wide range of false positive rates, indicating strong separability between healthy and diseased samples as well as among visually similar disease categories such as GLS and NLB. The high area under the curve (AUC) confirms the effectiveness of the deep feature representation and the optimized kernel-based decision boundary.

To complement the ROC analysis, the macro-averaged Precision–Recall (PR) curve is presented in Figure 9. The PR curve demonstrates that the proposed model maintains consistently high recall while preserving strong precision, reinforcing its suitability for real-world crop monitoring where missing infected leaves is more costly than false alarms.

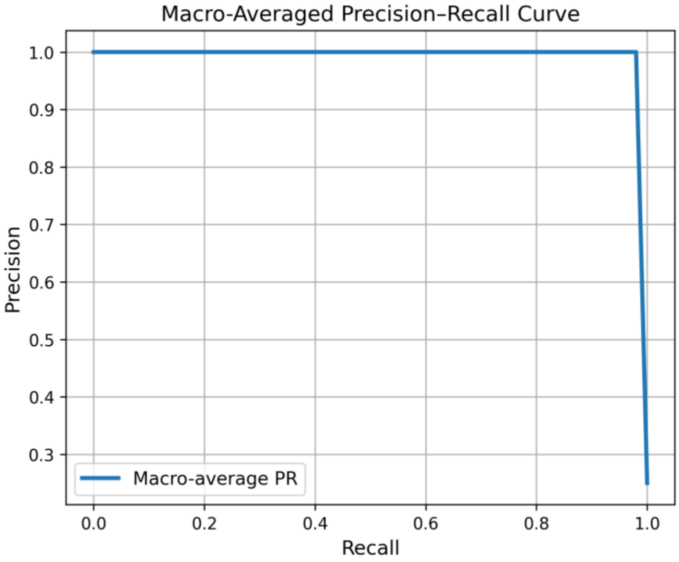

**Figure 9.** Precision–Recall curve of test results.

Together, the confusion matrix analysis (Figure 7), ROC–AUC evaluation (Figure 8), and Precision–Recall curve (Figure 9) provide consistent evidence that the proposed MobileNetV2–PCA–RBF-SVM framework achieves robust, recall-oriented performance and reliable class discrimination under practical agricultural conditions.

### 4.4. Ablation Study

An ablation study was conducted to evaluate the individual contributions of hyperparameter optimization, PCA-based dimensionality reduction, and data augmentation to the overall performance of the proposed framework. The results of the ablation experiments are summarized in Table 4.

**Table 4.** Ablation analysis of the proposed framework.

| Model | Configuration | Feature Dimension | Accuracy (%) | Description |
|---|---|---|---|---|
| A | Default RBF-SVM (Baseline) | 1280 | 96.63 | Default parameters, no optimization |
| B | Optimized RBF-SVM (No PCA) | 1280 | 97.09 | Grid-search tuned, no dimensionality reduction |
| C | MobileNetV2 + PCA + Optimized RBF-SVM (No Augmentation) | 310 | 97.22 | PCA applied, without data augmentation |
| D | Proposed MobileNetV2 + PCA + Optimized RBF-SVM | 310 | 97.58 | Full configuration with PCA and augmentation |

The ablation results in Table 4. demonstrate that the performance gains of the proposed framework are the cumulative effect of several complementary design choices rather than a single component. Hyperparameter optimization alone (Model B) already provides a measurable improvement over the baseline, confirming the importance of kernel tuning for capturing nonlinear class boundaries in deep feature space.

More importantly, the introduction of PCA (Model C) not only reduces the feature dimensionality by 75.8% but also yields a further accuracy gain, indicating that dimensionality reduction acts as an effective feature refinement mechanism rather than a lossy compression step. This finding highlights that removing redundant components can improve class separability while simultaneously reducing computational cost.

Finally, the full configuration achieves the highest accuracy, showing that data augmentation contributes additional robustness by increasing intra-class variability, particularly for visually similar diseases such as GLS and NLB. Together, these results confirm that the proposed pipeline is both computationally efficient and performance-preserving, validating its suitability for lightweight and deployable maize disease recognition systems.

## 5. Comparative Benchmarking with Existing Work

To validate the effectiveness of the proposed framework, a comparative evaluation was conducted against the DenseNet201 + Bayesian-Optimized SVM model proposed by Dash et al. (2023), which represents a recent and competitive approach for maize leaf disease recognition. The comparison was performed using identical dataset splits and evaluation protocols to ensure fairness. The quantitative results are summarized in Table 5.

**Table 5.** Performance comparison with existing methods.

| Model | Accuracy (%) | Precision (%) | Recall (%) | F1-score (%) |
|---|---|---|---|---|
| Dash et al. [3] | 94.60 | 94.60 | 94.10 | 94.30 |
| Alpsalaz et al. [2] | 94.97 | 94.88 | 94.76 | 94.85 |
| Proposed Model | 97.58 | 96.60 | 96.59 | 96.59 |

The proposed model achieved a 2.98% improvement in accuracy and a 2.29% gain in F1-score over the baseline, demonstrating consistently superior classification reliability across all metrics. More importantly, the improvement in recall confirms that the proposed method reduces false-negative predictions, which is critical in agricultural disease diagnosis where undetected infections may lead to delayed treatment and yield loss. Unlike the baseline DenseNet-based approach, the proposed framework achieves these gains while using a significantly more compact representation, indicating that performance improvements arise from feature refinement and kernel optimization rather than model over-parameterization. This confirms that the proposed pipeline offers a more efficient and scalable alternative for practical deployment.

In addition to accuracy, model efficiency was evaluated in terms of parameter count and memory footprint, as summarized in Table 6.

**Table 6.** Model efficiency comparison.

| Model | Parameters (M) | Model Size (MB) | Accuracy (%) | F1-score (%) |
|---|---|---|---|---|
| Dash et al. [3] | 20.31 | 81 | 94.60 | 94.30 |
| Proposed Model | 2.75 | 12 | 97.58 | 96.59 |

The proposed framework achieves an 86.5% reduction in model parameters and an 85% reduction in storage size, while simultaneously improving classification accuracy by nearly 3%. This efficiency gain is primarily attributed to the lightweight design of MobileNetV2 and the application of PCA-based feature compression, which together reduce computational overhead without sacrificing discriminative power.

These results demonstrate that the proposed MobileNetV2–PCA–RBF-SVM framework offers a favorable trade-off between accuracy and efficiency, making it particularly suitable for real-time, edge-based agricultural monitoring systems with limited computational resources.

## 6. Conclusions

This study investigated whether a compact, efficient maize leaf disease recognition pipeline could achieve high diagnostic performance without relying on large or computationally intensive deep networks. The experimental results demonstrate that this goal can be achieved by combining lightweight deep feature extraction with systematic feature refinement and optimized kernel-based classification. By employing MobileNetV2 as a fixed feature extractor and applying PCA for dimensionality reduction, the proposed framework effectively reduces feature redundancy while preserving the most discriminative visual information. The optimized RBF-SVM classifier further exploits this compact feature space to produce robust decision boundaries, particularly for visually overlapping disease classes such as Gray Leaf Spot and Northern Leaf Blight. Together, these design choices confirm that efficiency-oriented architectures can maintain, and in some cases improve, classification reliability compared to heavier deep learning models.

Beyond accuracy, the proposed framework significantly reduces model complexity and memory footprint, making it well-suited for deployment on resource-constrained platforms. This confirms that lightweight, serial feature-processing pipelines remain a practical and effective alternative for real-world agricultural applications where computational resources and energy consumption are limited. Despite the encouraging results, several limitations should be acknowledged. First, the experiments were conducted using publicly available datasets captured under controlled imaging conditions, which may not fully reflect the variability encountered in real field environments, such as illumination changes, background clutter, and partial occlusion. Second, the evaluation focused on four common maize disease classes, and the generalization of the framework to rarer diseases or multi-infection scenarios remains to be investigated. Third, MobileNetV2 was employed as a fixed feature extractor to prioritize efficiency, leaving domain-specific fine-tuning as a potential direction for further performance enhancement. Finally, although computational efficiency was analyzed, direct deployment and benchmarking on embedded or edge devices were not included in this study.

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**Data Availability Statement:** The dataset used in this study consists of maize leaf disease images obtained from the PlantVillage dataset, which is publicly available via the Kaggle repository at: https://www.kaggle.com/datasets/abdallahalidev/plantvillage-dataset. Only the maize (corn) subset was used in this work, comprising four classes: Healthy, Gray Leaf Spot, Northern Leaf Blight, and Common Rust. Kaggle served solely as a data hosting platform, and no additional datasets were incorporated. The processed feature representations and experimental splits generated during this study are available from the corresponding author upon reasonable request. No new image data were created as part of this research.

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