

Plant disease detection and classification: based on machine learning and Eig(Hess)-co-occurrence histograms of oriented gradients

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ABSTRACT

Agricultural districts provide high-quality food and contribute substantially to economic growth and population support. However, plant diseases can directly reduce food production and threaten species diversity. The use of precise, automated detection techniques for early disease identification can improve food quality and mitigate economic losses. Over the past decade, numerous methods have been proposed for plant disease classification, and in recent years the focus has shifted toward deep learning approaches because of their outstanding performance. In this study, we employ the Eig(Hess)-co-occurrence histograms of oriented gradients (CoHOG) descriptor alongside pre-trained machine-learning models to accurately identify various plant diseases. We apply principal component analysis (PCA) for dimensionality reduction, thereby enhancing computational efficiency and overall model performance. Our experiments were conducted on the popular PlantVillage database, which contains 54,305 images across 38 disease classes. We evaluate model performance using classification accuracy, sensitivity, specificity, and F1-score, and we perform a comparative analysis against state-of-the-art methods. The findings indicate that the approach we proposed achieves up to 99.83% accuracy, outperforming existing models. Additionally, we test the robustness of our method under various conditions to highlight its potential for real-world agricultural applications.

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1. INTRODUCTION

Agriculture has been indispensable to the smooth functioning of the global economy, providing basic food, employment, and income. It represents about 12% of Morocco's national income and employs approximately 31% of the population, as is the case in various low and middle-income countries that depend on agriculture [1]. In addition to its economic importance, agriculture is essential for ensuring food stability, supporting rural communities, and promoting socio-economic progress. Its influence extends to allied industries such as agro-processing and supply chains, amplifying their overall impact on national growth. Over the past five years, the agricultural sector's contribution to gross value added (GVA) to the Moroccan

the economy has grown from 11.16% [1], underscoring its pivotal role in driving economic growth and ensuring food security. However, plant diseases and pest infestations continue to pose major challenges, threatening both the quality and quantity of global food production and destabilizing economies reliant on agricultural outputs. Prophylactic treatments alone are inadequate, as they do not fully prevent agricultural epidemics and endemics. Combined systems for early identification, accurate diagnosis, and real-time management of crop diseases especially when combined with sustainable and modern crop protection practices have the potential to ensure not only stable production and prices, but also long-term agricultural resilience and profitability.

Classification is a critical component of automated plant disease detection, and accurate, timely recognition of illness is essential for informed decision-making in agricultural production. Infected plants often display symptoms such as sooty marks on stems, fruit, foliage, or flowers [2]. These distinctive markings can assist in identifying abnormalities. However, diagnosing plant diseases accurately requires specialized knowledge and considerable human resources, and manual analysis can be subjective and time-consuming. Misdiagnoses by farmers or specialists can lead to inappropriate treatments, which may damage crop quality and yield and even contaminate the environment if incorrect chemicals are applied [3]. Recent advances in machine learning and deep learning have revolutionized diagnostic technique for plant diseases.

Automated digestion and feature extraction have become more accessible, enabling more accurate image-based representations of disease symptoms. The recent accessibility of large image databases, powerful GPUs, and advanced computing software that are computationally less demanding has prompted a transition from classic methods to modern deep learning-based frameworks. While current models show encouraging results on specific datasets [4], they are typically trained on images with simpler backgrounds limiting their application in real agricultural settings where the diversity of images and complexity of backgrounds is high. Diversification and realism of a model's training datasets is necessary to improve generalization and confidence in predictions [5]–[7]. The novel contribution of this manuscript is the creation of a novel hybrid model for detection and classification of plant diseases. Unlike conventional approaches that rely solely on convolutional neural networks (CNNs), our method combines deep features extracted via an improved AlexNet architecture with handcrafted descriptors obtained from the Eig(Hess)-co-occurrence histogram of oriented gradients (CoHOG) algorithm, which captures fine geometric and textural characteristics. To better computational efficacy, we carry out principal component analysis (PCA) for dimensionality reduction, retaining essential information while minimizing redundancy. This fusion of deep and handcrafted features into a compact vector enhances the model's robustness and generalization capability, particularly on images captured under real-world conditions. Furthermore, we validate our model on two contrasting datasets PlantVillage and PlantDisease demonstrating performance superior to the state of the art, with accuracy reaching 99.83%, while maintaining stability across varying acquisition conditions. The rest of this paper is structured as follows: section 2 previous studies work in the range of content-based image retrieval (CBIR). Section 3 outlines the proposed method. Section 4 shows the findings from the experiment, which are compared to existing approaches in section 5. At last, section 6 concludes the paper and discusses prospective studies.

2. RELATED WORK

Traditional methods to diagnose plant diseases based on visual evaluation are subjective, expensive, time consuming and require considerable manual labour. These limitations have driven researchers to seek more effective solutions. Many studies now rely on machine learning methods to achieve high accuracy, reduced costs, and greater objectivity. In this section, we review key works in this area and highlight recent developments. Early efforts applied shallow CNNs with four to six layers to various crops, exploiting their flexibility and robustness. For example, Mohanty *et al.* [8] proposed an algorithm for both classification and preprocessing of rice plant images, and Ferentinos [9] identified diseases in rice fields. Chen *et al.* [10] improved upon these methods by combining CNNs with transfer learning strategies using architectures such as MobileNet and InceptionV3 for enhanced classification, recognition, and segmentation of plant diseases.

Based on selected grapevine and tomato diseases from the PlantVillage database [11], Karthik *et al.* [12] employed a multi-class classification approach using VGG16 with transfer learning. Barbedo [13] surveyed machine learning methods for crop disease classification, examining supervised approaches including naïve Bayes (NB), discriminant analysis (DA), k-nearest neighbors (k-NN), support vector machines (SVMs), decision trees (DTs), and random forests (RFs). Vardhini *et al.* [14] compared these with unsupervised techniques K-means clustering, fuzzy clustering, and Gaussian mixture models as well as pre-trained CNNs like AlexNet and GoogleNet for soybean disease classification. The emergence of generative networks has further accelerated data acquisition by overcoming traditional cost and time constraints. Mondal *et al.* [15] presented a framework combining model-agnostic meta-learning (MAML) with DeepLabV3 for leaf disease analysis and estimation, improving generalization on limited datasets. A conditional generative adversarial network (cGAN) was proposed by Abbas *et al.* [16] to enhance multi-leaf classification based on reference data. In another study,

a pre-trained MobileNet CNN achieved 96.58% classification accuracy for tomato leaf diseases. Hughes and Salathé [17] demonstrated that incorporating a weighted average fusion of gamma correction and multi-scale retinex with color restoration (MSRCR) preprocessing improved InceptionV3's recognition rate by 29.71%. Rehman *et al.* [18] introduced fusion techniques adapting DenseNet-121 [19] to accept both raw and segmented leaf images. Pal and Kumar [20] developed AgriDet, a deep learning-based detection framework for quantifying disease severity on plant leaves. Sunil *et al.* [21] proposed a multi-level feature fusion network based on ResNet-50 with an adaptive attention mechanism, enabling deeper insights at channel, spatial, and pixel levels. Finally, Anh and Duc [22] reviewed 160 studies across 50 plant leaf datasets, analyzing modern deep learning models (AlexNet [23], GoogleNet [24], ResNet [25], MobileNet [26], SqueezeNet [27], and YOLO [28]), whose contributions have been significant in providing reliable and scalable plant disease diagnostics.

3. MATERIALS AND METHODS

3.1. Approaches and resources

This research proposes an efficient conceptual framework within an experimental learning paradigm to enable reliable, adaptable deployment of plant disease-identification models in real-world settings. Our work leverages data from diverse sources ranging from curated, high-quality images to raw, field-captured samples to assess and enhance model generalization. We apply a suite of preprocessing techniques (normalization, resizing, and augmentation via flipping, rotation, and brightness adjustment) to standardize the input data, reduce domain inconsistencies, and increase the model's robustness across varying conditions.

To promote accurate feature extraction and classification, we optimize our deep learning architecture an enhanced AlexNet CNN with reduced complexity and faster computation and complement it with a new handcrafted descriptor, Eig(Hess)-CoHOG, which captures rich geometric and textural information from grayscale images. We then apply PCA to compress the high-dimensional Eig(Hess)-CoHOG vector into a 1×59 representation, preserving its discriminative power while reducing redundancy. This PCA-reduced vector is concatenated with the 1×64 deep feature vector, producing a compact 1×128 feature representation that integrates low-level handcrafted features with high-level learned features. This hybrid approach overcomes CNNs' typical inability to capture fine structural patterns without sacrificing the efficiency of deep architectures. We evaluate the model using comprehensive metrics accuracy, precision, recall, F1-score, and AUC-ROC across both controlled (PlantVillage) and real world (PlantDisease) datasets. Experimental results demonstrate high accuracy and stability under diverse conditions, confirming the framework's economic viability and practical applicability in agriculture. Conceptually, this hybrid architecture provides a novel, lean, and interpretable direction for future research in smart agriculture and image-based plant disease diagnosis.

3.2. Description of dataset

We evaluated our methods on two datasets, PlantVillage and PlantDisease. The most important difference between the two datasets is in the texture and complexity of the images. The PlantVillage dataset contains images taken under laboratory conditions with uniform smooth grey backgrounds and very minimal noise, thus it is quite a "perfect" dataset for evaluating models, whereas PlantDisease contains images collected in the wild, where lighting conditions and natural backgrounds are variable, thus it represents a more complex dataset. This allows us to evaluate the proposed model's reliability and ability to generalize in both ideal conditions and realistic field-like conditions.

3.2.1. PlantVillage dataset

The PlantVillage dataset is a primary open-source dataset for plant disease identification. The data contains 61,486 pictures across 39 species, including various plant leaf diseases and background images. In total, there are 54,306 images across 38 classes for individual diseases after excluding the background images. Each of these images contains an individual plant leaf on a uniform grey background, designed to mimic ideal input for automated analytical systems. This uniform background imitates the pre-processing step, in which individual leaves are masked from a larger canopy image by a smart monitoring system and extracted. The organization of the dataset and the many classes have made it a critical benchmark for developing and validating machine learning models for agricultural disease identification.

3.2.2. Plant disease dataset

The plant disease dataset is an important component of assessing the robustness and generalization of the models we presented. It provides a benchmark for assessing performance when no preprocessing techniques are used, including object masking or noise reduction; this dataset was augmented offline based on the original dataset which we provided as a link in this GitHub. Although our dataset does not have any

noise reduction it contains almost 87,000 RGB images of sound and diseased crop leaves across 38 different categories. The complete dataset was divided within training and validation sets in an 80/20 ratio, while preserving the original directory structure.

3.3. Experimental design and configuration

The experimental models were tested on a dataset specifically chosen to evaluate stability and generalization at fairly compromised data conditions, without stepped or other pre-processes, noise removal or mask segmentation. We used average precision and average recall to measure performance. The code was written in Python in Anaconda environment using Windows 10, running on hardware that had 2.2 GHz Intel Core i5 CPU, 12 GB of 1600 MHz DDR RAM, Intel HD Graphics 5000 GPU to 1536 MB of ROM. The software included libraries such as Keras, OpenCV, NumPy, CuDNN, Theano, utilizing Anaconda3 which included NVIDIA's CuDNN as well as CuMeM with the backend of Theano, for optimized memory and performance when running deep learning, as well as excellent image-processing across multiple platforms (Linux, Windows, Mac, iOS, Android, and Java). These elements together ensure the algorithm achieves a high-level of precision and scalability for real-world applications. Figure 1 shows the proposed approach.

Input Images were initially resized via bicubic interpolation in MATLAB, to $227 \times 227 \times 3$, and then run through the algorithm in two main steps: i) an improved AlexNet using CNN and ii) the Eig(Hess)-CoHOG algorithm. The enhanced AlexNet extracts deep features, yielding a 1×64 feature vector, while Eig(Hess)-CoHOG produces complementary handcrafted features. To reduce dimensionality, we apply PCA to the Eig(Hess)-CoHOG vector, compressing it to 1×59 without significant information loss. These PCA-reduced features are concatenated with the AlexNet features to form a composite 1×128 feature vector, combining the strengths of both methods. The following sections offer comprehensive explanations of the AlexNet CNN, the Eig(Hess)-CoHOG algorithm, and PCA.

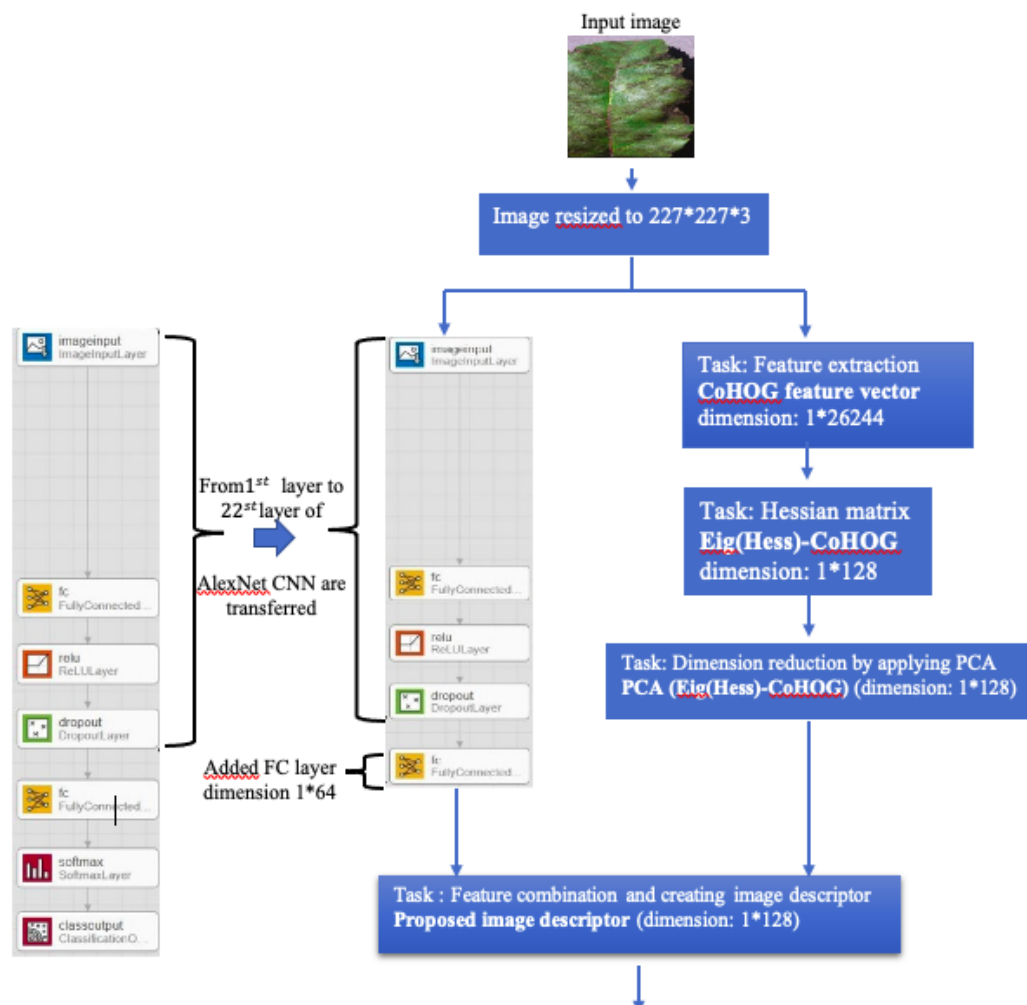


Figure 1. Our proposed descriptor

3.3.1. PCA

In this article, PCA [29] was utilized as a key dimensionality reduction technique to enhance the performance and efficiency of the proposed plant disease classification model. The handcrafted features extracted using the Eig(Hess)-CoHOG descriptor, although rich in geometric and textural information, initially produced a high-dimensional feature vector. Such high dimensionality often introduces redundancy, increases computational load, and may degrade model generalization due to overfitting. To mitigate these issues, PCA was applied to transform the correlated features into a new set of uncorrelated, orthogonal components ranked by the amount of variance they capture from the original data. By selecting the top components that preserved more than 95% of the total variance, the feature vector was reduced to a more manageable size of 1×59 without significant loss of discriminative power. This reduced vector retained the most meaningful structural and textural cues from the leaf images. Subsequently, the PCA-compressed feature vector was concatenated with a 1×64 deep feature vector extracted from the improved AlexNet CNN. The resulting composite feature vector of size 1×128 effectively combines low-level handcrafted descriptors with high-level semantic features, enabling a robust and computationally efficient classification pipeline. Overall, PCA played a crucial role in balancing model complexity and accuracy, improving training speed, reducing memory usage, and enhancing the model's ability to generalize across diverse datasets.

3.3.2. Improved AlexNet architecture

The AlexNet architecture is a strong neural network when it comes to feature extraction and is composed of 25 layers. We propose an improved AlexNet architecture in this research to optimize efficiency, and performance. The resulting task was to optimize the AlexNet architecture by removing the last three fully connected layers; they are also typically the costliest layers to develop. Instead, we replace them with one fully connected layer of size 1×64 . In theory, optimization reduces the total number of parameters significantly while reducing our cost, but we can maintain or improve performance in relation to the original design. In practice, our updated architecture maintained similar representations as prior to optimization with improved performance. The fully connected layers are typically used for identifying and classifying the most relevant, high-level features; and consequently, the need for manually developed features is no longer applicable. Essentially, the design is well balanced, allowing maximum performance while remaining quite simple. Because optimization needed to be simple enough to develop an effective, smart neural network to be able to extract features efficiently and appropriately.

3.3.3. The Eig(Hess)-CoHOG descriptor

The Eig(Hess)-CoHOG algorithm [30] can be classified as a shape-based image descriptor. The Eig(Hess)-CoHOG algorithm allows for the extraction of structural and textural information; this is accomplished by combining Hessian-based curvature with a CoHOG. In this case, the resulting feature representation is very discriminative, which is advantageous for use in agricultural applications, since plant diseases usually represent deviations in leaf outlines, leaf textures, and leaf vein patterns. The algorithm first computes the Hessian matrix $H_\sigma(x, y)$ for every pixel of a grayscale image $I(x, y)$ defined as:

$$H_\sigma(x, y) = \begin{bmatrix} \frac{\partial^2 I}{\partial x^2} & \frac{\partial^2 I}{\partial xy} \\ \frac{\partial^2 I}{\partial xy} & \frac{\partial^2 I}{\partial y^2} \end{bmatrix} \quad (1)$$

with $\frac{\partial^2 I}{\partial x^2}$ and $\frac{\partial^2 I}{\partial y^2}$ are the second partial derivatives with respect to x and y respectively;

$\frac{\partial^2 I}{\partial xy}$ is the cross partial derivative;

The local curvature of the matrix, by means of its eigenvalues, provides a method to detect geometrically significant areas like corners, ridges, or blobs. The features are stable to image rotation and reasonably robust to illumination changes. At the same time, CoHOG is used for encoding the orientation of gradients. Whereas HOG only captures local edge orientation information, CoHOG captures spatial distribution information pertaining to gradient orientation pairs and therefore provides a richer means of textural and structural context. Eig(Hess)-CoHOG descriptor is built as.

- Step 1: Calculate the eigenvalues of the Hessian matrix at every pixel as a way to identify curvature features.
- Step 2: For each important eigenvalue area, calculate CoHOG features by using local gradient co-occurrence at different distances and angles.
- Step 3: Combine both the curvature-based and co-occurrence features into one descriptor vector that shows both shape and texture.

3.3.4. Categorical cross-entropy loss

For model performance optimization, the categorical cross-entropy loss function was implemented, which is typical for multi-class multi-label classification problems. This loss function measures how different the predicted probability distribution is to the true label distribution for a given sample. The loss on a single training example let be:

$$\mathcal{L} = -\sum_{i=1}^C y_i \cdot \log(\hat{y}_i) \quad (2)$$

where $\mathcal{L}$: Total loss computed for one training instance,

C: total number of class,

y_i : actual label for class i (1 correct class, 0 all others),

$\hat{y}_i$: the SoftMax layer's output representing the predicted probability for class i .

The loss was reduced with the Adam optimizer learning rate of 0.001. During training, the model fine-tuned weights iteratively with back-propagation and a stochastic gradient descent, to obtain optimal parameters that minimized the training loss. The model was trained for 30 epochs, and the loss values were tracked and plotted at each epoch for both training and validation sets

4. RESULTS AND DISCUSSION

These metrics together establish a comprehensive framework for evaluating the effectiveness and reliability of the proposed fashion. They illustrate how the model balances accuracy against different types of errors and guide researchers and practitioners in refining the approach for real-world applications. We tested the proposed method on two datasets PlantVillage and PlantDisease across multiple runs. The results, summarized in Tables 1 (in A, 2 and 3, demonstrate the method's efficiency under various training conditions. The model's results for each plant disease class on both the PlantVillage and PlantDisease datasets are detailed in Table 1. Precision (%), F-score (%), and accuracy (%) were reported for each class during training (10 and 30 iterations) and validation (after 10 and 30 iterations). On PlantVillage, the model achieved very high training and validation precisions, as well as F-scores for most classes. For example, in the "Apple - Apple Scab" class, the training precision increased from 94.6% (10 iterations) to 97.5% (30 iterations), and the F-score reached 93% after 30 iterations. Continuing with examples from our previous *Scripts & File Organization* chapter, the model, after 30 iterations, achieved validation precisions and F-scores close to 100% for some classes such as "Apple - Healthy," "Blueberry - Healthy," and "Corn (Maize) - Healthy." This suggests that the model performed quite well on the PlantVillage dataset. On the other hand, overall performance on the PlantDisease dataset was generally lower than on PlantVillage; however, it was still meaningful. For "Apple - Apple Scab" on the PlantDisease dataset, the training precision was 92.2% (10 iterations) and 95.8% (30 iterations), with an F-score of 86% at 30 iterations. The model also performed quite well on some classes like "Orange - Huanglongbing (Citrus Greening)" and "Grape - Esca (Black Measles)," with F-scores around 80%–82%. This suggests that these two classes may be particularly important to distinguish within the PlantDisease dataset. For most other classes, increasing the number of iterations from 10 to 30 led to improved precision and F-scores.

Table 2 provides an overall performance summary of the proposed fashion on the PlantVillage dataset, focusing on precision and loss for training and validation after 10 and 30 training iterations. We focused on each metric: training precision (%), validation precision (%), training loss, and validation loss. after 10 training iterations, the method attains a training precision of 94.96% and a validation precision of 92.3%, along with the training and validation losses of 0.1875 and 0.2016, respectively. After 30 training iterations, the training precision improved to 98.64%, and the validation precision increased to 93.5%. Moreover, the training loss significantly decreased to 0.0623, while the validation loss for 30 iterations was not shown in the table. As noted, the model's training performance improved significantly, and the results from training on the PlantVillage dataset indicate that additional training leads to better convergence and overall improved performance for the proposed model. Table 3 offered the accuracy and loss of the proposed fashion on the PlantDisease dataset after 10 and 30 iterations of training. Similar to Table 2, it includes training accuracy, validation accuracy, training loss, and validation loss. After 10 iterations on the PlantDisease dataset, the training accuracy was 82.25% and the validation accuracy was 83.11%, with training and validation losses of 0.3247 and 0.2803, respectively. After 30 iterations, the training accuracy improved to 85.43% and the validation accuracy to 87.26%, while the training loss decreased to 0.1543. However, the validation loss for 30 iterations is not reported. These results indicate consistent improvement with additional training on the PlantDisease dataset, although the precision scores for PlantDisease remain generally lower than those for the PlantVillage dataset.

Table 1. Class-wise performance on PlantDisease dataset and PlantVillage dataset

	PlantVillage dataset					PlantDisease dataset				
	Training precision %		Validation precision %		F1-score (%)	Training precision %		Validation precision %		F1-score (%)
	10	30	10	30		10	30	10	30	
	Iterations	Iterations	Iterations	Iterations		Iterations	Iterations	Iterations	Iterations	
Apple - Apple Scab	94.6	97.5	93	92.2	95.8	82.6	86	81.2	84.4	83.55
Apple - Black Rot	94.2	97	92	92	95.4	81.5	84.4	80.5	83.3	82.4
Apple - Cedar Apple Rust	96	97.8	93.5	92.8	97	83.5	87.7	83	85.3	84.8
Apple - Healthy	97.3	98.8	93	93.8	99	87.5	91.4	86	89.3	88
Blueberry - Healthy	97.1	100	92	95	98.7	86	90.9	85.5	87.8	87
Cherry (Sour) - Powdery Mildew	93.5	95.6	89	90	95	81	85	80.3	82.8	82.2
Cherry (Sour) - Healthy	97.2	97.5	91	92.6	99	86.3	91	85	88.1	87.6
Corn (Maize) - Cercospora Leaf Spot	94.1	95.4	92	90.3	95.4	82	85.8	81	83.8	83.15
Corn (Maize) - Common Rust	95.4	98.5	93	93.4	97	83.4	87.5	82.8	85.2	84.7
Corn (Maize) - Northern Leaf Blight	94.9	100	91	95	96.4	83	86.9	82.3	84.8	84.25
Corn (Maize) - Healthy	98.1	100	94	95	100	88	93.1	87	89.8	89.4
Grape - Black Rot	93.8	97.3	91.3	92.3	95.3	81	84.8	80	82.8	82.15
Grape - Esca (Black Measles)	92.2	96.1	90	91	94	79.6	83.7	78.7	81.4	80.85
Grape - Leaf Blight	93.4	97.8	91	92.6	95	81	85.3	80.4	82.8	82.5
Grape - Healthy	96.5	100	94.2	95	98.6	85.6	90	84.7	87.4	87
Orange - Huanglongbing (Citrus Greening)	90.5	96.8	88.2	91.5	91.7	80	82.7	77.9	81.8	80.6
Peach - Bacterial Spot	91.3	97.5	89	92.5	93.2	81	83.8	79.3	82.8	81.7
Peach - Healthy	97	100	94	95	98.6	86	89.9	84.7	87.8	87.1
Pepper (Bell) - Bacterial Spot	92.4	97.5	91	92.5	94.3	80.4	84.2	79.8	82.2	81.65
Pepper (Bell) - Healthy	97.8	100	94.7	95	99.5	87	91.7	86.5	88.8	88.5
Potato - Early Blight	95	100	93	95	96.3	82	85.5	81	83.8	83
Potato - Late Blight	95.6	100	92.5	95	97	83	87	82.4	84.8	84.3
Potato - Healthy	97.3	100	95	95	99	86.5	91.3	85.8	88.3	88
Raspberry - Healthy	96.7	100	94	95	98.3	85	89.8	84.6	86.8	86.55
Soybean - Healthy	97.4	100	95.3	95	99.1	87	91.6	86.2	88.8	88.4
Squash - Powdery Mildew	93.2	98	91.1	93	94	81	84.9	79.5	82.8	82.05
Strawberry - Leaf Scorch	92.4	97.5	90	92.5	93	80	83.7	78.7	81.8	81.05
Strawberry - Healthy	96.8	100	94.7	95	98.4	85.4	90.1	84.8	87.2	86.8
Tomato - Bacterial Spot	93.5	97	91	92	94	80.5	84.6	79	82.3	81.6
Tomato - Early Blight	94.8	98	91.7	93	96.1	82	86	81.2	83.8	83.25
Tomato - Late Blight	95	100	92	95	96.5	82.7	86.7	82.1	84.5	84
Tomato - Leaf Mold	93.2	98	91.5	93	95	81	85	80.4	82.8	82.3
Tomato - Septoria Leaf Spot	94.3	100	92.2	95	95.7	81.5	85.5	80.9	83.3	82.8
Tomato - Spider Mites	91.7	96.6	90.6	91.6	93	79.4	83.4	78.6	81.2	80.65
Tomato - Target Spot	92.8	97.7	91.7	92.7	94	80.3	84	79.7	82.1	81.5
Tomato - Yellow Leaf Curl Virus	97.4	100	95.5	95	99	85.6	90.3	85	87.4	87
Tomato - Mosaic Virus	96.7	100	94.1	95	98	84.4	89	83	86.2	85.65
Tomato - Healthy	97	100	95	95	99.2	87	91	86	88.8	88.2

Table 2. The proposed approach's precision and loss after 30 training epochs on the PlantVillage dataset

	Iterations	Training precision %	Validation precision %	Training loss	Loss of validation
Plantvillage	10 Iterations	94.96	92.3	0.1875	0.2016
Database	30 Iterations	98.64	93.5	0.0623	

Table 3. The proposed approach's precision and loss after 30 training epochs on the PlantDisease dataset

	Iterations	Training precision %	Validation precision %	Training loss	Loss of validation
PlantDisease	10 Iterations	82.25	83.11	0.3247	0.2803
Dataset	30 Iterations	85.43	87.26	0.1543	

5. COMPARATIVE ANALYSIS OF DEEP LEARNING AND HYBRID METHODS

To thoroughly test the efficacy of the proposed combined model, comparative experimental tests were conducted across five popular pre-trained CNN architectures: DenseNet-201, VGGNet-19, Inception V3, ResNet-50, and a hybrid model based on the architecture of Inception and VGGNet called INC-VGGN. These five models were selected because of their popularity and known effectiveness in various vision tasks.

Model performance was evaluated across key metrics including training precision, validation precision, training loss, and validation loss, after 10 and 30 training iterations. As indicated in Table 4, the proposed model outperformed the other methods on all metrics across all iterations. After only 10 training iterations, the proposed model achieved a training precision of 94.96% and a validation precision of 92.3%, with a training loss value of 0.1875 already outperforming most competing models even after 30 iterations. Following 30 iterations, the proposed model further increased its training precision to 98.64% and validation precision to 93.5%, achieving a training loss of 0.0623 and a validation loss of 0.2016. These results indicate not only rapid convergence but also the strong generalization ability of the proposed model as designed.

Table 4. Accuracy and error rates of different technique after 30 training iterations

Methods	10 Iterations		Training loss	30 Iterations			
	Training precision %	Validation precision %		Training precision %	Validation precision %	Training loss	Loss of validation
DenseNet201	80.27	76.30	0.573	84.20	79.00	0.445	0.499
ResNet50	65.20	64.70	1.003	70.40	69.70	0.834	0.844
InceptionV3	85.60	82.30	0.409	92.10	85.00	0.258	0.372
VGGNet19	65.20	66.70	1.164	74.20	74.80	0.916	0.903
INC-VGGN	93.90	90.20	0.212	97.60	91.80	0.086	0.241
Proposed technique	94.96	92.30	0.187	98.64	93.50	0.062	0.202

In contrast, DenseNet-201, while capable of achieving relatively high precision, ultimately underperformed when compared with the proposed method. After 30 training iterations, it achieved a training precision of 84.2% and a validation precision of 79.0% but also reported a training loss of 0.4451 and a validation loss of 0.4987. Although these metrics suggest that DenseNet-201 learned some features effectively, it is clear there is a lack of performance in feature discrimination compared to the hybrid method. The overall performance of ResNet-50 was lower than that of the other examined architectures. After thirty iterations, its training precision was only 70.4% and validation precision 69.7%, while the training and validation losses remained high at 0.8338 and 0.8442, respectively. These results indicate poor overall convergence on the plant disease dataset. The relatively low performance of ResNet-50 may be due to its sensitivity to initialization and learning rate factors that are particularly problematic for heterogeneous and noisy domains like plant pathology images. Inception V3 performed better, achieving 92.1% training precision and 85.0% validation precision after 30 iterations, along with a training loss of 0.2576 and a validation loss of 0.3717. While these findings are respectable, they still lagged behind the proposed model, particularly in validation accuracy, where fine-grained disease classification remains a challenge. VGGNet-19 delivered decent results due to its depth and straightforward architecture. After 30 training iterations, it achieved a training precision of 74.2% and validation precision of 74.8%, with relatively high training and validation losses of 0.9162 and 0.9026, respectively. These results indicate that identifying an optimal feature representation for generalization is difficult with complex plant disease datasets.

The hybrid INC-VGGN model performed better than the standard CNN models, achieving 97.6% training precision and 91.8% validation precision after 30 iterations, with low training and validation losses of 0.0856 and 0.2409, respectively. However, despite these strong results, it still failed to outperform the proposed method in terms of training speed and overall performance. The marked improvement delivered by the proposed model is due to its hybrid nature, wherein features derived from AlexNet were combined with handcrafted descriptors from Hilbert space-based (Hess)-CoHOG. The hybrid model utilized both types of representation the abstract, high-level hierarchical learning provided by CNNs and the texture-sensitive, rotation-invariant qualities of handcrafted descriptors. To decrease the size of the representation to a computationally friendly 1×128 vector while retaining discriminative information, the features were compressed using PCA.

This balance between feature richness and reduced dimensionality contributed to superior performance across all metrics. Overall, the comparative results substantiate that the hybrid model is robust and outperforms state-of-the-art CNN architectures tested in this study, particularly after training for 30 epochs. It represents a viable and promising approach for large-scale, real-world plant disease recognition where accuracy and efficiency are essential. Table 5 provides a similar analysis of the major deep learning architectures (and the proposed hybrid model) to better explain the relative advantages and disadvantages of each method analyzed in this study. Each method was assessed based on its computational characteristics, learning ability, and applicability to plant disease detection. Conventional CNN-based methods like AlexNet, VGGNet-19, ResNet-50, Inception V3, and DenseNet-201 each offer specific advantages such as fast training, deep feature extraction, or strong gradient flow but also present drawbacks like sensitivity to initialization, high memory requirements, and long training times. The INC-VGGN hybrid model, which fuses intermediate and visual styles from different architectures, offers some training advantages but introduces greater complexity and higher training costs. In contrast, the proposed model effectively addresses

these disadvantages by integrating deep learning with handcrafted features and dimensionality reduction. Its two primary advantages are their robustness to noise and rotation, and its high degree of accuracy in a compact representation demonstrates its applicability. Therefore, the proposed hybrid architecture has enough theoretical backing for future consideration and potential application in real-world deployment on farms. This comparative investigation not only validates the research relevance of the proposed hybrid model but also provides direction to other investigators and practitioners looking to select or alter their deep learning models as per contextual limitations.

Table 5. Key strengths and limitations of different deep learning techniques

Method	Positive aspects	Negative aspects
AlexNet	- Fast training - Simple architecture - Effective for basic image classification	- Shallow depth - Limited generalization on complex datasets
VGGNet-19	- Deep network with good feature extraction - Performs well with transfer learning	- High number of parameters - Requires more memory and computational resources
ResNet-50	- Residual connections enable deep training - Mitigates vanishing gradient problem	- Sensitive to learning rate and initialization - Longer training time
Inception V3	- Efficient multi-scale feature extraction - Good trade-off between depth and speed	- Complex architecture - Requires image input standardization
DenseNet-201	- Strong gradient flow - Feature reuse improves efficiency and accuracy	- Slower training due to dense connections - Memory-intensive - Increased architectural complexity - Higher training and inference time
INC-VGGN	- Hybrid architecture leverages VGG and Inception strengths - High classification accuracy	
Proposed model	- Combines deep and handcrafted features - Robust to noise and rotation - High accuracy with low dimension (1×128 vector)	- PCA may reduce subtle but useful features - Requires parameter tuning for fusion

5. CONCLUSION

For many years, plant diseases have been an important area of concern in agriculture and represent a considerable threat to food manufacturing security. In extreme cases these diseases can lead to total crop losses, with spillover effects that can include economic shocks, food scarcity and breaks in supply chains. Such challenges are particularly pronounced in developing geographies, where farmers lack access to modern agricultural technologies and the economic well-being of smallholder farmers are directly linked to crop yields. Plant diseases have social and environmental impacts in addition to their economic effects, fueling poverty, diminishing biodiversity, and leading to unsustainable farming practices. With increasing global population growth, and the coming threats of climate change, the drive for more innovative and efficient ways to combat plant diseases is critical. Among the information in agriculture, there is a great demand for the early identification of plant disease. Early detection of plant diseases is critically important in the field of agricultural information. Utilizing early detection through disease management enables timely intervention and the application of targeted treatments that may drastically reduce crop losses in the long run.

It also provides a means of decreasing reliance on chemical pesticides, which frequently cause soil degradation, water contamination, and detrimental effects on non-target organisms like pollinators. Early detection technologies have the potential to make a significant impact if they can show that they can help meet the principles of sustainable agriculture. Currently deep learning methods, especially CNNs, have shown outstanding performance on many problems involved in the field of disease diagnosis. Not only would these methods perform exceptionally on high-dimensional image data, but they also enable retraining on updated datasets, allowing them to be seamlessly adapted to changing agricultural conditions over time. This section presented an innovative method that combines CNN, specifically AlexNet, with the Hessian matrix to calculate the eigenvalues of the image surface. By incorporating the Hessian matrix, our approach enhances the model's ability to identify subtle textural features and variations in plant images that may otherwise go undetected. Furthermore, we used the PCA algorithm harnessed for minimizes size, enabling the extraction of essential information while decreasing computational overhead. This nesting addresses various practical purviews, such as processing time and scalability, which are critical for widespread adoption. The results of our experiments demonstrate the effectiveness of our proposed method achieving a notable screening accuracy of 91.83% on the PlantDisease dataset and an imposing 93.67% accuracy on the PlantVillage dataset. The results obtained show more than the reliability and robustness of our algorithm propose they also show also highlight its potential to has exceed existing algorithms in the field of plant disease classification.

The percentage of precision achieved could have transformative implications for agricultural practices, facilitating clarity of decisions for farmers and the use of technology in traditional farming systems. Furthermore, the results obtained show the ability of artificial intelligence to bridge the gap between cutting-edge research and practical applications in agriculture. In our future projects, we will propose deployment approaches on mobile devices using connected objects to facilitate the monitoring and automatic recognition of a broader spectrum of diseases at various locations in the plant at various stages of disease progression. The integration of this technology with mobile devices could democratize access to advanced diagnostic tools, particularly in rural and underserved areas. By empowering farmers with user-friendly and cost-effective solutions, such technologies have the potential to transform precision agriculture, reducing yield gaps and fostering resilience against environmental stressors.

In parallel, we goal to prolong the request of our algorithm to real-world situations, inclusive computer-aided diagnosis, thereby conducive to advancements in agricultural information systems. Beyond disease classification, our structure is allowed to be expanded to include predictive design, enabling stakeholders to anticipate disease outbreaks based on environmental and climatic data. This integration would not only improve crop management strategies but also inform regional and national policy decisions, contributing to a more sustainable and secure agricultural ecosystem. In addition, the approach could support the development of automated agricultural robots capable of performing tasks such as targeted spraying, harvesting, or pruning based on real-time disease detection. Moreover, the potential of this technology extends to interdisciplinary applications. For example, its integration into food supply chain systems could ensure quality control by identifying diseased crops during processing or storage, thereby minimizing food waste. We will collaborate with ecological monitoring systems to further exploit ecological monitoring technology to assess the health of natural plant populations, as well as for conservation efforts. We believe that through these interdisciplinary opportunities, our approach could serve as a critical tool to address global challenges, from food security to environmental sustainability.

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