RESEARCH ARTICLE

Multi-Class Classification of Plant Leaf Diseases Using Feature Fusion of Deep Convolutional Neural Network and Local Binary Pattern

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ABSTRACT Plant diseases are one of the primary causes of decreased agricultural production quality and quantity. With ongoing changes in plant structure and cultivation techniques, new diseases are constantly arising on plant leaves. Thus, accurate classification and detection of plant leaf diseases in their early stages will limit the spread of the infection and support the healthy development of plant production. This work proposes a novel lightweight deep convolutional neural network (CNN) model for obtaining high-level hidden feature representations. The deep features are then fused with traditional handcrafted local binary pattern (LBP) features to capture local texture information in plant leaf images. The proposed model is trained and tested on three publicly available datasets (Apple Leaf, Tomato Leaf, and Grape Leaf). On the three datasets, the proposed approach achieves 99%, 96.6%, and 98.5% validation accuracies, respectively, and 98.8%, 96.5%, and 98.3% test accuracies, respectively. The results of the experiments show that the proposed approach can provide a better control solution for plant diseases.

INDEX TERMS Convolutional neural network (CNN), feature fusion, local binary pattern (LBP), multi-class classification, plant leaf diseases, precision agriculture, computer vision.

I. INTRODUCTION

One of the most critical areas of precision agriculture research is detecting diseases in plant leaves via image analysis. The traditional method of recording the severity of plant diseases is based on the visual examination of plant tissues by trained experts [1]. Expert systems in cultivation and management have become widely used due to the widespread adoption of digital cameras and the advancement of information technology in agriculture, considerably increasing plant production capacity [2]. However, pest and disease extraction and description characteristics in expert systems mainly depend on experts' expertise, resulting in high costs and low efficiency.

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Various artificial intelligence techniques for detecting and classifying plant diseases have been introduced. The most common techniques are the K-nearest neighbors (K-NN), logistic regression, decision tree, support vector machine (SVM) [3], and CNN. These techniques are used with different image pre-processing techniques to promote the extraction of features. The K-NN is a supervised learning algorithm. It is based on similarity measures for classifying the data. For K-NN, unlabeled objects are classified using neighboring labeled objects [4]. The Decision tree is a flow-chart learning algorithm. Each node denotes the decision attribute, the branches represent the possible outcomes from the nodes, and leaves signify the classes. However, decision trees possess certain limitations such as overlapping nodes and overfitting of data [5].

SVM is a common supervised learning model, which can be associated with learning algorithms for classification and

regression analysis based on statistical learning concepts. In the latest decade, SVMs have been widely used in image and text classification [6]. The previous machine detection approaches typically use traditional image processing techniques, such as noise removal, morphological operations, and image enhancement, for pre-processing diseased plant leaf images. Afterward, handcrafted feature extraction approaches capture low-level information about the leaves, such as color, shape, and texture. Sharif et al. [7] suggested a texture-feature-based method to identify diseases of citrus fruit plants. They used a hybrid feature selection method based on principal components and feature statistics analysis. Patil et al. [8] presented a content-based image retrieval system that uses leaf color, shape, and texture features to identify diseased soybean leaves. Sandika et al. [9] proposed a method for identifying grape leaf disease with a complex background. They evaluated the identification performance using various features, such as the Local Binary Pattern (LBP) feature, some statistical features in RGB planes, and different machine learning algorithms, such as Support Vector Machine (SVM) and Random Forest.

Recently, deep learning architectures have been used effectively for object identification, classification, and object segmentation tasks. CNN approaches have been the most common for deep learning tasks [10]. Selvaraj et al. [11] developed a banana plant sample dataset from various hotspots in Africa and Southern India, each with 17 diseased and one healthy class. They achieved an accuracy rate of 90% by using different CNN architectures like ResNet50, InceptionV2, and MobileNetV1.

To conduct their research, Zhang et al. [12] used the PlantVillage dataset images to get healthy and infected samples of peach plant leaves. After experimenting with the AlexNet architecture, they were enabled to get an accuracy rate of 99%. Other studies using the Plantvillage dataset images achieved accuracy rates varying between 97% to 99% in identifying maize [13], grape [14], and soybean [15] plant leaves disease classes using images with three diseased and one healthy class labels. With VGG CNN architecture, Fuentes et al. [16] achieved an accuracy rate of 90% using a dataset with nine classes of tomato diseases.

Additionally, Lu et al. [17] used a dataset having six diseased and one healthy class belonging to wheat plants and achieved an accuracy rate of 97% after conducting their experiments. Hu et al. [18] presented a system based on a modified deep convolutional neural network to detect tea leaf diseases. After completing the experiments, they achieved an average accuracy of 92%. Barbedo [19] used sample images covering 79 diseases in 14 different types of plants. After experimenting with the GoogLeNet architecture, various degrees of accuracy scores were obtained, all of which exceeded 75%. Too et al. [20] focused on multiple plant types and attained an accuracy rate of 81% using VGG architecture, and rates of 99% were obtained using other architectures. Additionally, Geetharamani et al. [3] focused on multiple plant types and used a dataset having 38 classes

of 14 different types of plants. They achieved an accuracy rate of 96%.

Ferentinos [21] achieved an accuracy rate of 98% using VGG architecture and a dataset of 25 different plants. When the recent studies based on apple leaf diseases were included in our work, it was observed that Liu et al. [22] achieved an accuracy rate of 97.62% using image pre-processing techniques with their CNN model. In contrast, other studies used traditional machine learning methods, which have garnered considerable expertise in identifying plant diseases. Still, they are constrained to the following procedures of image segmentation [23], feature extraction [24], and pattern recognition [25].

Although the basic CNN architectures, such as AlexNet [26], VGGNet [27], GoogLeNet [28], DenseNet [29], and ResNet [30], have been widely used in plant diseases classification, these architectures are limited by many drawbacks, including the need for many parameters and a slow calculation speed.

Although deep learning methods have been proven to be quite competent in displaying high-level and low-level features, they are less consistent in describing local spatial characteristics [31]. Consequently, we propose fusing the handcrafted and deep features better to capture the characteristics of the plant leaf images.

This paper proposes a deep convolutional neural network model (DCNN). The traditional convolution layers are replaced by deeper separable convolutions, which reduce the number of model parameters and iteration time. Then, the deep features are combined with the local binary pattern (LBP) features, where LBP efficiently captures the local information to supplement deep features.

We could summarize the main contributions of this paper in the following points:

1) The proposed DCNN model significantly reduces the training parameters and iteration times compared to the common transfer learning models such as AlexNet, GoogleNet, and VGG16.
2) An integrated model was developed by concatenating deep features and traditional handcrafted features (LBP). This model effectively captures the local spatial texture information found in images of plant leaves.
3) The proposed model was trained and achieved a high accuracy rate using different plant leaf disease datasets.

This work is arranged as follows: The proposed model is described in Section II. The experiments, the results, and the discussion are presented in section III. Finally, Section IV concludes this paper.

II. MATERIALS AND METHODS
A. DATASET
Three public datasets from PlantVillage [32] were utilized from a well-known repository to assess the efficacy of the proposed architecture. The first is the apple leaf dataset consisting of 3171 images before data augmentation. The
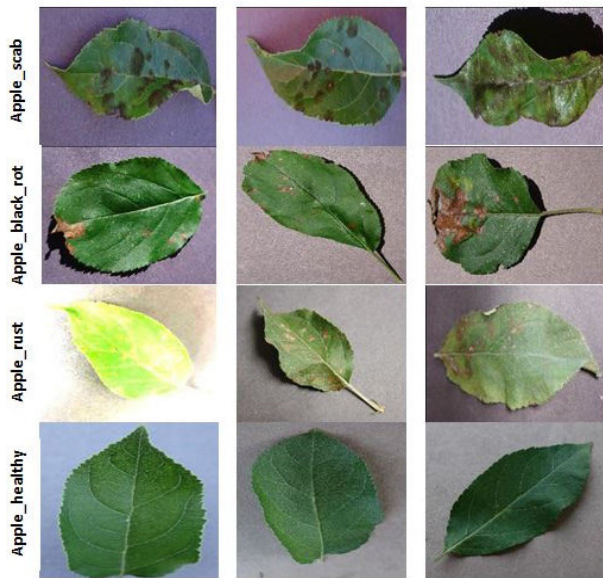
FIGURE 1. Image samples for each class in the apple leaf dataset [32].

TABLE 1. Number of images for each class in the apple leaf dataset [32].

Class	Samples	
	Before Augmentation	After Augmentation
Apple scab	630	1000
Apple Black rot	621	1000
Apple Cedar rust	275	1000
Apple healthy	1645	1645
Total	**3171**	**4645**

samples of these images are shown in Figure 1. The dataset is divided into four classes, as shown in Table 1. Scab includes 630 images, Black Rot 621, Cedar Rust 275, and Healthy 1645. We use data augmentation techniques on the apple leaf dataset to increase its size and handle the imbalanced cases reaching to 4645 images without affecting its biological properties. Only the most popular geometric transformation techniques are used, such as rotation, translation, flipping, scaling, and vertical translation. The data is split into training and testing datasets. The training dataset is further divided into training (80%) and validation data (20%) to avoid over-fitting [33].

Also, the tomato Leaf dataset was used, which contains 18160 images without using data augmentation. It was divided into ten classes. Figure 2 depicts one sample from each class. Each class has several images, as indicated in Table 2. The data was split similarly to the apple leaf dataset (training, Validation and testing). In addition, we used the grape leaf dataset consisting of 4062 images before using data augmentation. The data is divided into four classes, as indicated in Table 3. The samples of these images are shown in Figure 3. Also, we used data augmentation techniques on the grape leaf dataset to increase its size to 4639 images. The data was split similarly to the apple and tomato leaf dataset (training, validation, and testing).

TABLE 2. Number of images for each class the tomato leaf dataset [32].

Class	Samples
	Without Augmentation
Tomato Bacterial spot	2127
Tomato Early blight	1000
Tomato healthy	1591
Tomato Late blight	1909
Tomato Leaf Mold	952
Tomato Septoria leaf spot	1771
Tomato Spider Two-spotted mite	1676
Tomato Target Spot	1404
Tomato mosaic virus	373
Tomato Yellow Curl Virus	5357
Total	**18160**

TABLE 3. Number of images for each class in the grape leaf dataset [32].

Class	Samples	
	Before Augmentation	After Augmentation
Grape Black rot	1180	1180
Grape Black Measles	1383	1383
Grape blight Spot	1076	1076
Grape healthy	423	1000
Total	**4062**	**4639**

B. THE PROPOSED ARCHITECTURE

The proposed architecture fuses deep features with local binary pattern (LBP) features for plant disease classification, which includes two main phases: feature extraction, fusion, and classification. As shown in Figure 4, the proposed architecture first extracts the deep features of a plant leaf. It combines the local binary features with the deep features to generate the final distinctive features of a leaf image for plant disease classification. A deep CNN model captures the deep features while LBP effectively extracts the local texture information. We combine these two sets of features to obtain the final feature vector of plant disease samples.

In this research, we directly concatenate the extracted LBP features with deep features via the flattened layer in the proposed DCNN model. The combined features are then fed to the first fully connected layer, and softmax is applied for classification.

1) THE DEEP CNN ARCHITECTURE

The main advantage of using deep CNN for classifying images is that it eliminates a feature engineering process [27]. Figure 4 shows the deep CNN architecture for plant leaf disease classification. For the captured images, image pre-processing techniques such as image filtering, image sharpening, and resizing are implemented, where 64×64 sized images are fed into the proposed model, which consists of 3 convolutional layers (with kernel size 3×3), three max-pooling layers (with kernel size 2×2), and four dense (fully connected) layers.

The convolution layers operate as feature extractors from the images. As a result, the first convolutional layer in the proposed model has 32 filters, increasing to 128 filters in
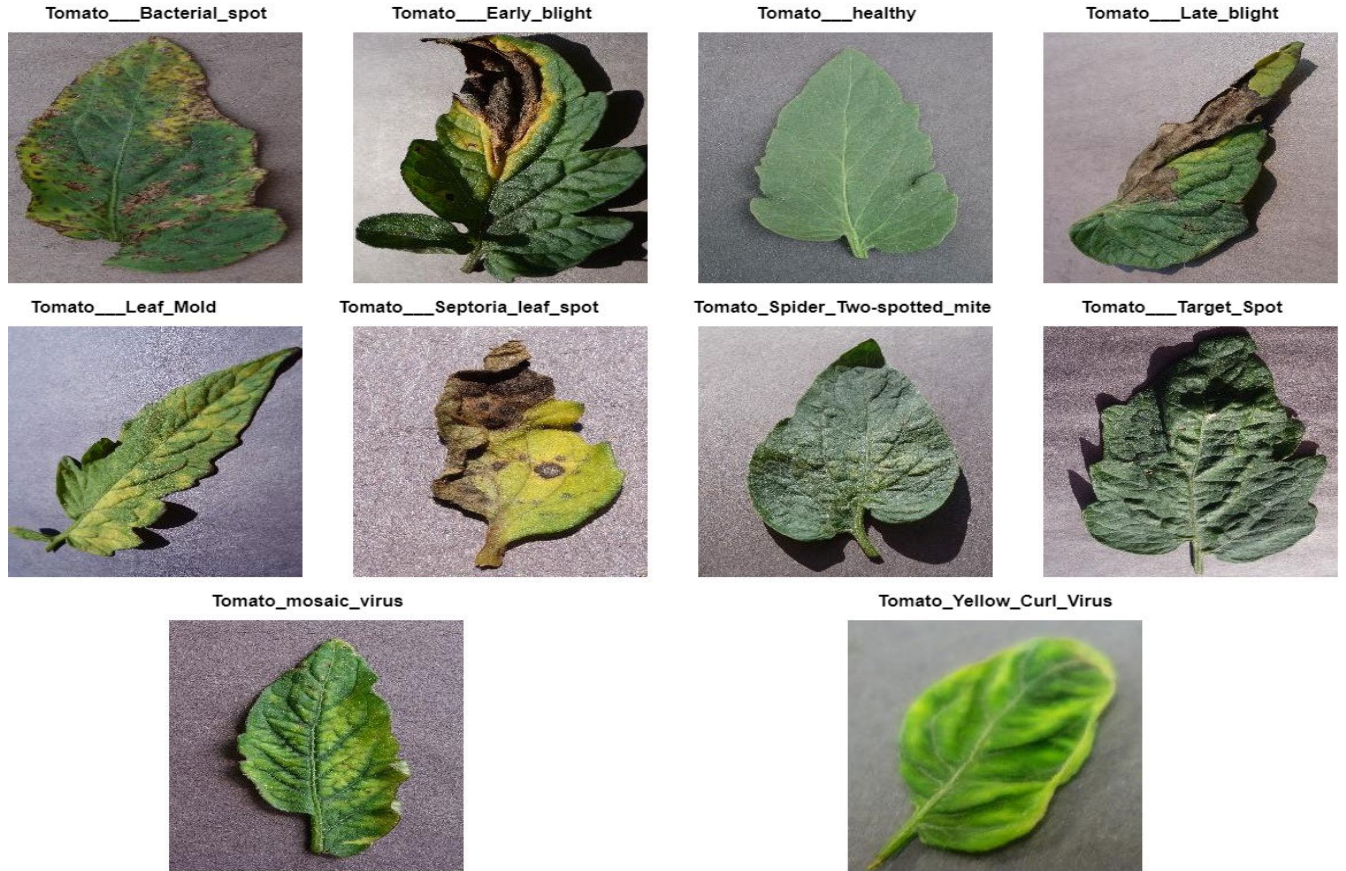
FIGURE 2. Image samples for each class in the tomato leaf dataset [32].

the last convolutional one. The studies show that gradually raising the filter sizes affects the model's performance [34].

Max-pooling layer was implemented after each convolutional layer to minimize the dimensionality of the convolutional layer image outputs. The output feature on the (n-th) local receptive field can be estimated in the (m-th) pooling layer, as shown in equation (1) [35]:

$$x_n^m = down(x_n^{m-1}, p) \tag{1}$$

where *down*( ) is the downsampling function, (x_n^{m-1}) is the feature vector from the previous layer, and (p) is the pooling size.

Before the fully connected layers process, the flattened process converts the last pooling image outputs to one-dimensional images. Finally, the classification process is performed by the softmax layer, which is mathematically written by [35] as:

$$softmax(z)_j = e^{z_j} / \sum_{k=1}^{K} e^{z_k} \quad \text{(for } j = 1, \ldots, K) \tag{2}$$

where (K) denotes the dimension of the (z) vector.

Dropout is a regularization technique for reducing overfitting, which removes certain artificial neurons from the network. In the proposed model, the chosen dropout values are 0.2 and 0.4. The proposed model's convolutional and fully connected layers used a Relu activation function that can adaptively learn a rectifier's parameters.

The proposed model is trained based on the loss function, which is the sum of the cross-entropy between real and predicted values [36]:

$$loss = -\sum_{x=0}^{n} \sum_{y=0}^{m} r_{xy} log p_{xy} \tag{3}$$

where, (r_{xy}) denotes the real value of the (x-th) instance belonging to class (y). Moreover, (p_{xy}) represents the corresponding predicted probability associated with the (x-th) instance of the class (y).

This study includes 4 class labels for apple and grape leaf diseases and ten classes for tomato leaf diseases. The softmax function is a preferred multiclass classification solution [34]. Therefore, deeper convolutional layers and the right choice for the proposed deep CNN model parameters achieved high accuracy and significantly reduced the number of training parameters and iteration time.

2) LOCAL BINARY PATTERN
Local binary patterns (LBP) are regarded as one of the most powerful texture descriptors. It was first introduced by Ojala et al. [37] and is used to represent the local features of an image, which are the important points of an image. The
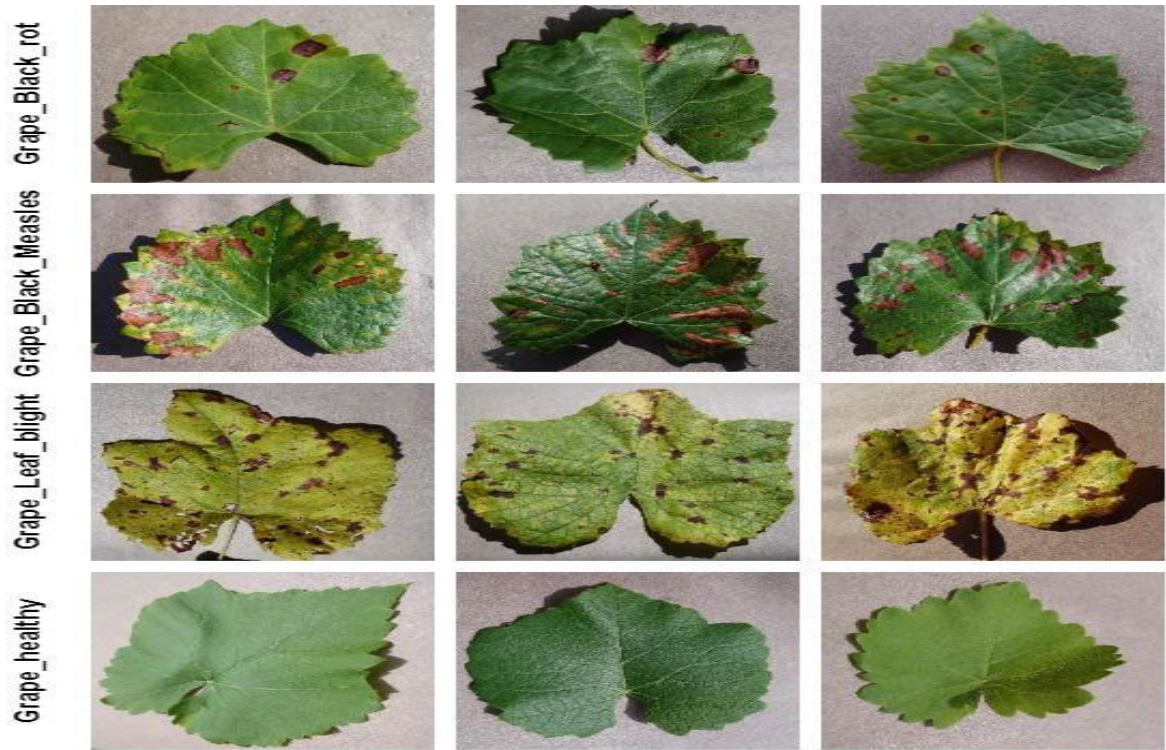
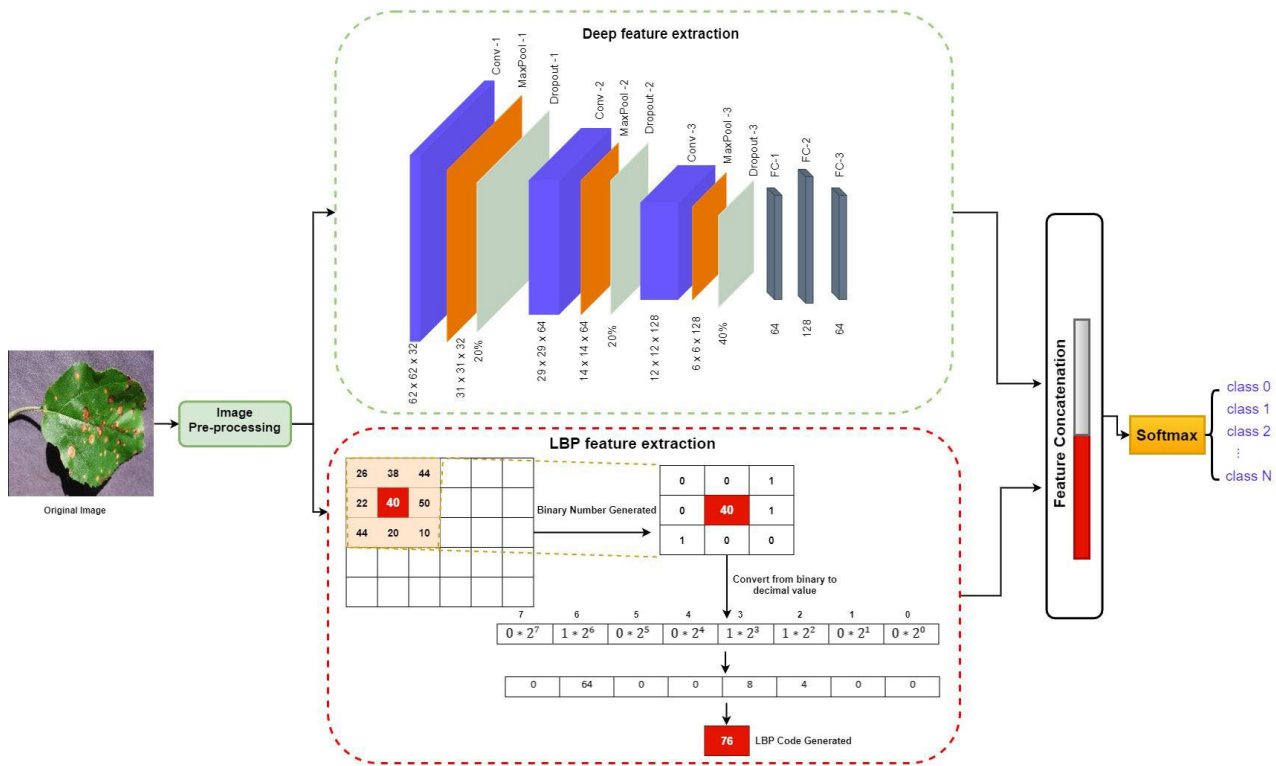**FIGURE 3.** Image samples for each class in the grape leaf dataset [32].

FIGURE 4. The proposed architecture for plant leaf disease classification (CNN + LBP).

classic LBP operator is defined as a 3×3 pixel window. The center pixel of this window is used as a threshold; if the value of the neighboring pixel is less than the threshold value, the pixel value is labeled 0. Otherwise, it is labeled 1. This
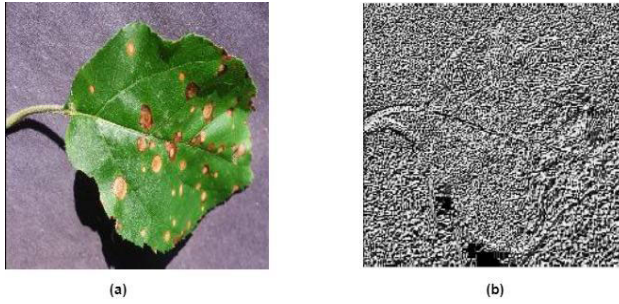
FIGURE 5. Illustration of LBP features' extraction: (a) original image; (b) extracted LBP image.

approach will generate an 8-bit binary number that will be converted to a decimal value, as shown below:

$$LBP_{I,J}(g_c) = \sum_{j=0}^{J-1} G(g_j - g_c)2^j \qquad (4)$$

where:

$$G(m) = \begin{cases} 0, & m < 0 \\ 1, & otherwise. \end{cases} \qquad (5)$$

In equation (4), $g_c = g(m, n)$ is the center pixel at (m, n) position, and $g_j = g(m_j, n_j)$ is a neighboring pixel of the central pixel g_c. The LBP features extraction of an image sample is indicated in Figure 5.

III. EXPERIMENTAL RESULTS AND DISCUSSION

Tensorflow and Keras frameworks implemented the proposed method and different transfer learning CNN models. A free cloud service from Google, Collaboratory (or Colab) performs the training and testing processes.

The hyper-training parameters are standardized for the proposed and reviewed transfer learning models. The data were divided into training, validation, and testing. For all experimental configurations, the batch size, learning rate, and epoch were set to 32, 0.01, and 50, respectively. Also, we used an early stopping mechanism to prevent over-fitting during the training process.

Accuracy, Precision, Recall, F1 score, (AUC-ROC) curve, and Confusion Matrix [38] are performance measures that have been computed to evaluate the reliability of the proposed method, defined as follows:

$$Accuracy = \frac{t_p + t_n}{t_p + f_p + f_n + t_n} \qquad (6)$$

$$Precision = \frac{t_p}{t_p + f_p} \qquad (7)$$

$$Recall = \frac{t_p}{t_p + f_n} \qquad (8)$$

$$F1\ score = \frac{2t_p}{2t_p + f_p + f_n} \qquad (9)$$

where t_p, t_n, f_p, and f_n represent true positive, true negative, false positive, and false negative, respectively.

Initially, we compared the proposed deep CNN model's effectiveness to common transfer learning models such as

TABLE 4. Comparison of the proposed deep CNN model and the transfer learning-based models for apple leaf disease classification.

Model	Precision	Recall	F1-Score	Accuracy
Proposed CNN model	**97.0%**	**97.0%**	**97.0%**	**97.8%**
VGG16	96.7%	96.5%	96.4%	96.0%
GoogleNet	95.0%	95.0%	95.0%	95.0%
AlexNet	91.0%	91.0%	91.0%	92.0%

TABLE 5. Comparison of the proposed deep CNN model and the transfer learning-based models for tomato leaf disease classification.

Model	Precision	Recall	F1-Score	Accuracy
Proposed CNN model	**96.0%**	**96.0%**	**96.0%**	**96.0%**
VGG16	95.0%	95.0%	95.0%	95.0%
GoogleNet	94.0%	94.0%	94.0%	94.8%
AlexNet	91.0%	91.0%	91.0%	91.0%

TABLE 6. Comparison of the proposed deep CNN model and the transfer learning-based models for grape leaf disease classification.

Model	Precision	Recall	F1-Score	Accuracy
Proposed CNN model	**97.0%**	**97.0%**	**97.0%**	**97.0%**
VGG16	96.0%	96.0%	96.0%	95.8%
GoogleNet	96.0%	96.0%	96.0%	95.6%
AlexNet	96.0%	96.0%	96.0%	95.5%

TABLE 7. Number of trainable parameters of different CNN models for apple leaf dataset.

Model	Number of Parameters
Proposed CNN model	**405,060**
VGG16	134,276,932
GoogleNet	6,237,492
AlexNet	23,976,004

AlexNet, GoogleNet, and VGG16. The results for apple, tomato, and grape leaf disease classification are indicated in Table 4, Table 5, and Table 6, respectively, using different performance metrics. These tables show that the highest metric scores are achieved by the proposed CNN model, showing that the proposed CNN model effectively extracts useful information in plant leaf disease images. Table 7 shows the trainable parameters of the proposed CNN model and the three reviewed CNN models. The proposed Deep CNN model has fewer parameters and higher calculation speed than others.

After demonstrating the effectiveness of the proposed CNN model and its ability to extract useful information in plant leaf disease images, we demonstrated the efficacy of the proposed feature fusion framework. Also, the study is conducted on three datasets (Apple Leaf, Tomato Leaf, and grape leaf datasets). The results are shown in Figure 6, Figure 7, and Figure 8 for the apple leaf, tomato leaf, and grape leaf datasets, respectively.
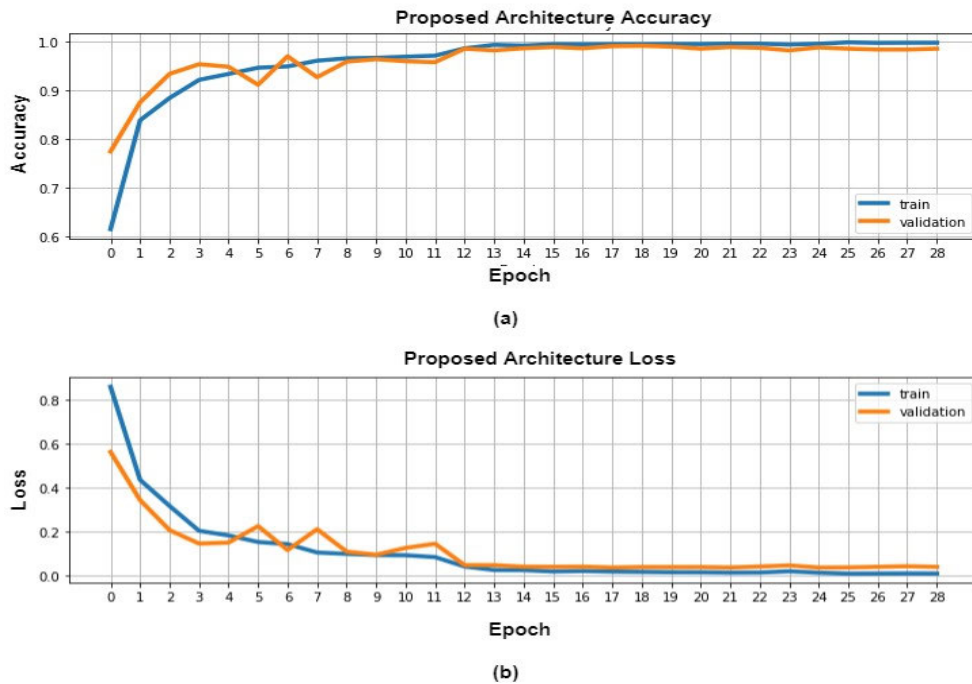
FIGURE 6. Classification accuracy of the proposed architecture (CNN + LBP) with apple leaf dataset: (a) Training and validation accuracy; (b) Training and validation loss.
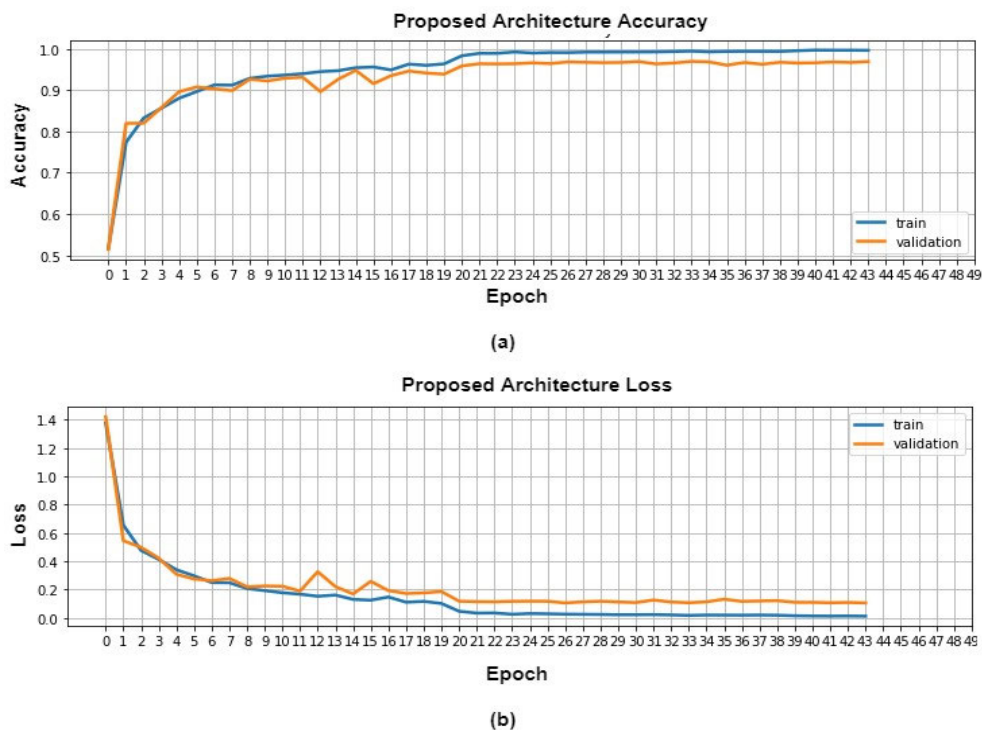

FIGURE 7. Classification accuracy of the proposed architecture (CNN + LBP) with tomato leaf dataset: (a) Training and validation accuracy; (b) Training and validation loss.

On the Apple dataset, the proposed approach achieves 99.9% and 99% training and validation accuracies, respectively, and reduces the training and validation loss rate to 0.0034 and 0.0398, respectively. On the Tomato dataset, the proposed approach achieves 99.4% and 96.6% training and validation accuracies, respectively, and reduces the training
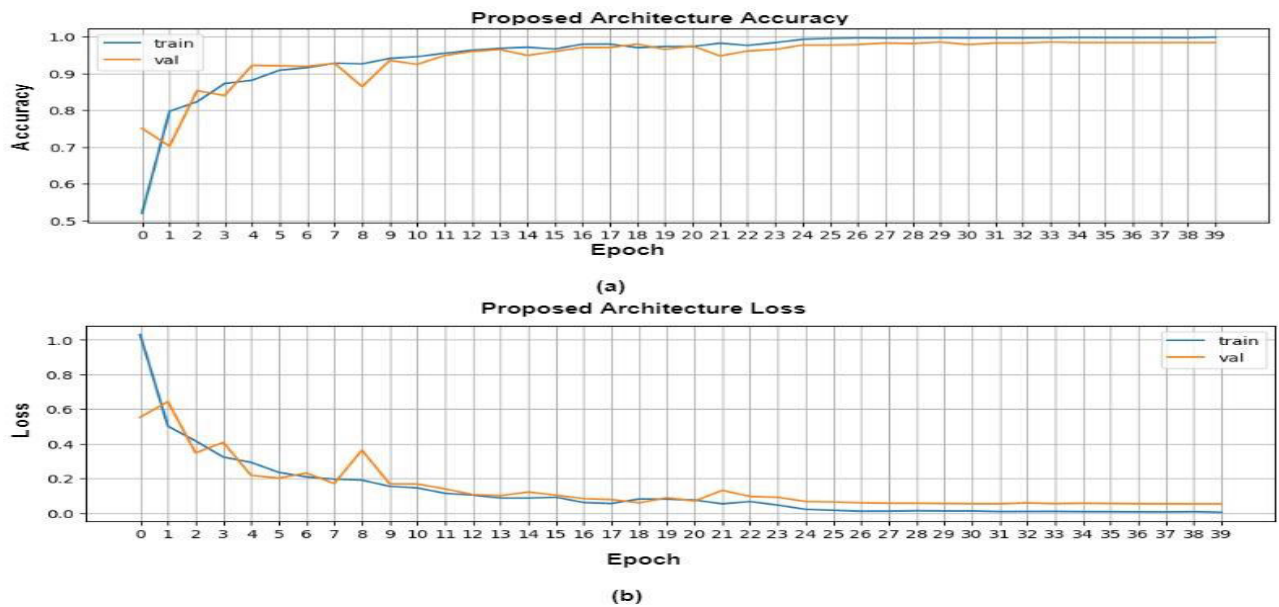
FIGURE 8. Classification accuracy of the proposed architecture (CNN + LBP) with grape leaf dataset: (a) Training and validation accuracy; (b) Training and validation loss.
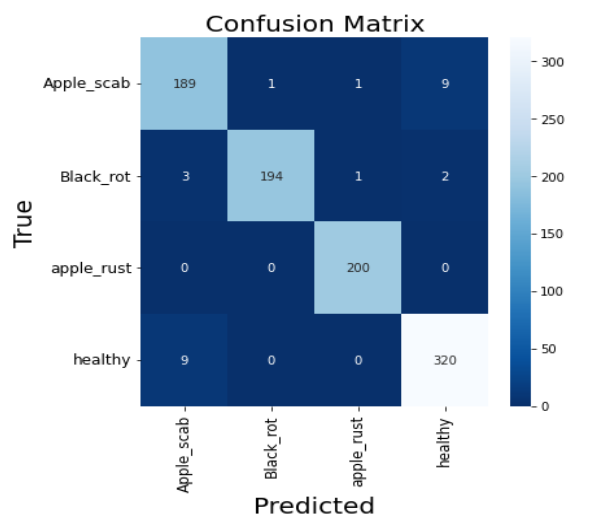

FIGURE 9. Confusion matrix obtained by the proposed architecture (CNN + LBP) with apple leaf dataset.
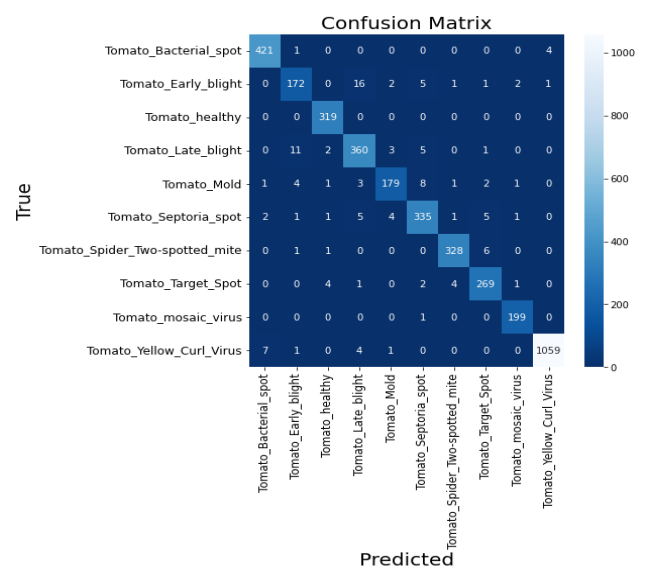

FIGURE 10. Confusion matrix obtained by the proposed architecture (CNN + LBP) with tomato leaf dataset.

and validation loss rate to 0.0184 and 0.1683, respectively. The proposed approach achieves 99.6% and 98.5% training and validation accuracies on the Grape dataset, respectively, and reduces the training and validation loss rate to 0.0129 and 0.0557, respectively. The proposed feature fusion method outperforms the individual features by fusing the deep and LBP features. For identifying plant leaf diseases, the proposed method is the most discriminative. The confusion matrix of the proposed feature fusion method on the three datasets is shown in Figure 9, Figure 10, and Figure 11. Also, the Area Under the Receiver Operating Characteristic (AUC –ROC) curve is one of the popular performance

measures for evaluating the learning algorithms' performance. Figure 12, Figure 13, and Figure 14 shows each class's AUC –ROC curves of the proposed method for the three datasets.

Table 8 shows the performance of the proposed methodology compared with that of other state-of-the-art methods.

After analyzing the results in Table 8, it is possible to conclude that the suggested model outperformed existing plant leaf disease classification methods. More precisely, in the case of the Apple data set, the proposed method achieves a 1.6% higher disease identification accuracy than
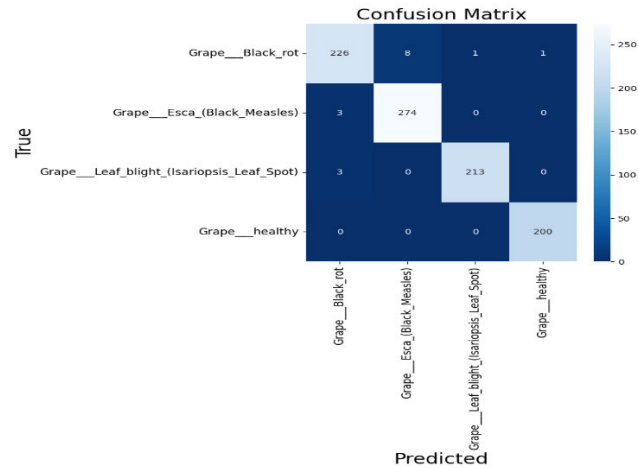
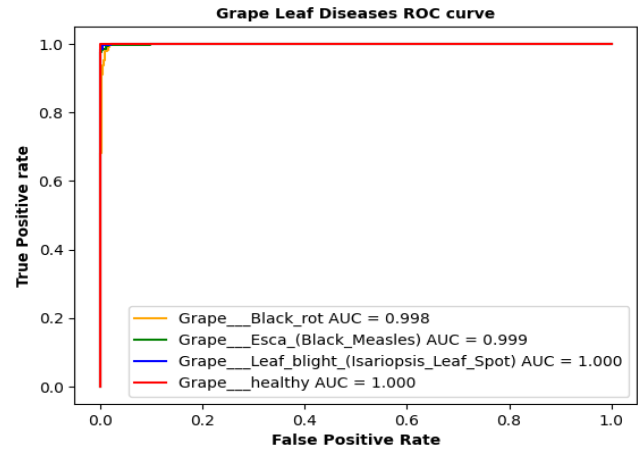**FIGURE 11.** Confusion matrix obtained by the proposed architecture (CNN + LBP) with grape leaf dataset.

FIGURE 14. AUC-ROC curve obtained by the proposed architecture (CNN + LBP) with grape leaf dataset.
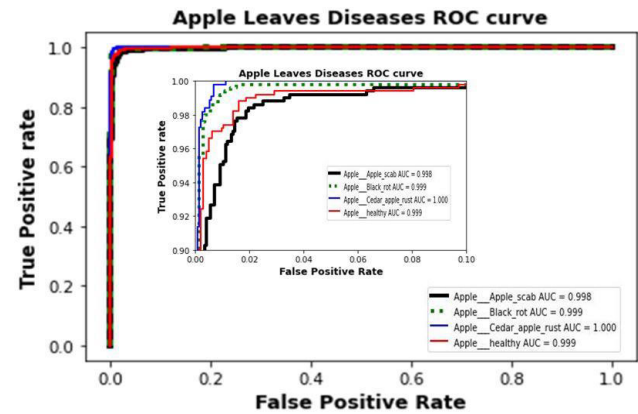

FIGURE 12. AUC-ROC curve obtained by the proposed architecture (CNN + LBP) with apple leaf dataset.

TABLE 8. Results comparison with existing methods for the three datasets (apple, tomato and grape leaf).

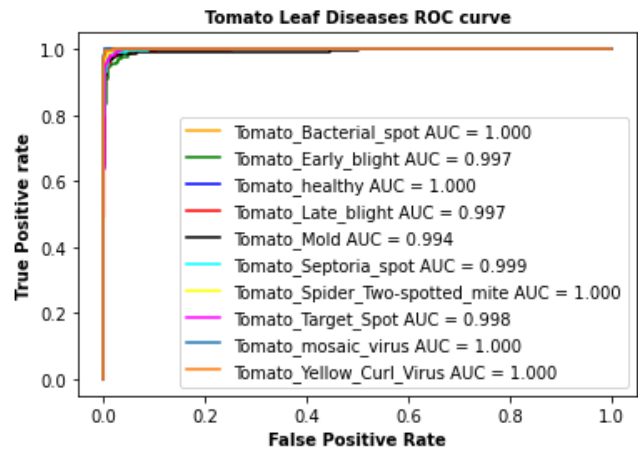| Dataset	Authors	Method	No. classes	Accuracy
Apple leaf	Wang et al. [39]	VGG16	4	90.40%
	Khan et al. [40]	LBP, M-SVM	4	97.20%
	Bracino et al. [41]	GPR, quadratic SVM	3	83.30%
	Hasan et al. [42]	DWT, color histogram	3	98.63%
	Proposed	**Deep feature + LBP**	**4**	**98.80%**
Tomato leaf	Agarwal et al. [43]	CNN Model	10	91.20%
	Durmus et al. [44]	AlexNet and SqueezeNet	10	95.65%
	Elhassouny et al. [45]	MobileNet	10	90.30%
	Proposed	**Deep feature + LBP**	**10**	**96.50%**
Grape leaf	Ahil et al. [46]	CNN Model	4	95.66%
	Tang et al. [47]	ShuffleNet V1	4	97.79%
	Akshai et al. [48]	DenseNet	4	98.27%
	Proposed	**Deep feature + LBP**	**4**	**98.30%**

FIGURE 13. AUC-ROC curve obtained by the proposed architecture (CNN + LBP) with tomato leaf dataset.

the best existing method for the same problem with four classes. Similarly, in the tomato leaf dataset, the proposed method outperforms all the deep learning models in the table,

demonstrating a superior accuracy improvement between 6.20%-0.85%. Finally, for the case of the Grape leaf dataset the proposed method shows a higher accuracy up to 2.64%. The proposed methodology achieves these impressive results using a lightweight model, significantly reducing computing time, which makes the proposed methodology an excellent option for detecting diseases in crops, especially in edge computing systems. Overall, the results highlight the superior performance of the proposed method over existing approaches in terms of absolute recognition accuracy values and computational efficiency.

IV. CONCLUSION

Accurate, with few parameters, and high calculation speed CNN model is developed. Furthermore, a feature-fusion-based method for classifying plant leaf diseases is proposed. The proposed method enables deep features to be fused with handcrafted features extracted by LBP. The proposed model used three public PlantVillage datasets (Apple Leaf, Tomato Leaf, and Grape Leaf datasets) for the training and testing. The performance of the proposed architecture outperformed the existing classification methods by achieving the highest accuracy reaches 99%, 96.6%, and 98.5% validation accuracies, respectively, and 98.8%, 96.5%, and 98.3% test accuracies, respectively, for the three datasets.

While the proposed method performs satisfactorily for the examined problems, there is potential for further research directions. Firstly, studying different LBP variants [49] in the same fusion scheme would be valuable in determining the most appropriate texture features for each case. Additionally, the proposed method should be tested in leaf diseases of other crops and evaluated for its performance in real-time applications. These future studies would enhance the proposed method and expand its potential applications in practical crop disease detection.

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