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Transfer learning-based texture-enhanced convolutional neural networks over plant disease identification

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ABSTRACT

The global agricultural productivity and food security take serious threats due to the presence of plant diseases; thus, early and accurate diagnosis becomes the key to successful management of the disease. The traditional diagnosis techniques that rely on visual observation are time-based, subjective, and cannot be implemented on a large scale. Recent development in machine learning and computer vision provides possible solutions to automated plant disease detection. This paper suggests a plant disease identification with transfer learning (PDD-TL) model with the preprocessing, segmentation, feature extraction, and disease prediction phases. In the initial stages, median filtering is used to simplify the image quality, after which cells affected by the disease are segmented with the help of the integration of adaptive pixels in joint segmentation (IAPJS) algorithm. Multi-texton and pyramid histogram of oriented gradients (PHOG) are the discriminative features extracted. The classification of the disease is done with a new triple convolutional activation CNN with transfer learning (CNN-TCA-TL). In contrast to the current methods that use either a pure deep learning method or handcrafted features, the framework proposed explicitly employs both the use of texture descriptors and transferable deep representations, which retain fine-grained structural details. The experimental findings prove that CNN-TCA-TL has an accuracy of 0.92 which will prove that it is effective.

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1. INTRODUCTION

The diseases that affect plants are a great problem to agricultural output and economy worldwide as well as food security. Preservation of yield loss, early interventions, and elimination of overuse of pesticides are critical to be achieved through early and proper detection [1]. Conventional diagnosis through the use of expert visual inspection is time consuming, subjective and impractical in large scale farming and the world has been losing up to 20-40% of major crops yearly to plant diseases. This highlights the importance of high-speed, high level of reliability and automation in detection.

Convolutional neural networks (CNNs) and deep learning have become one of the useful methods to diagnose plant diseases via leaf imaging, which classifies healthy and diseased leaf samples based on automatic feature learning [2]. Nevertheless, the performance of CNN is reliant on huge, tagged datasets, which are often limited in farming. This is overcome by transfer learning that modifies the existing models [3]. Also, the inclusion of texture characteristics, which describe spatial patterns of pixels, may augment CNN discrimination by transforming the structure of diseased leaves [4]. Building on these insights, this study proposes a novel plant disease detection with transfer learning (PDD-TL) method that integrates CNNs with texture feature extraction for improved accuracy [5]. This work makes the following contributions:

Contributing contrast limited adaptive histogram equalization (CLAHE) filtering technique that filters the input image and preprocess the image for the further analysis. Proposing integration of adaptive pixels in joint segmentation (IAPJS) approach in the segmentation step that avoids excessive noise or over-segmentation within the preprocessed image.

- Along with this feature, pyramid histogram of oriented gradients (PHOG) and multi-texton-based features are extracted.
- Contributing CNN-TCA-TL model that involves additional convolutional layers to detect the plant disease effectively. Also, this model can possibly be reducing the information loss and provides better detected output.

2. LITERATURE SURVEY

Plant diseases are very harmful to food security and agricultural output. In order to control and treat plant diseases, the diseases need to be diagnosed in time and with accuracy. The traditional methods of illness detection involve manual search which is labour intensive and subject to errors.

Recent research explores a range of deep learning methods for agricultural image analysis, highlighting advancements in precision, efficiency, and adaptability. Table 1 shows approaches like Deep-GAN, Lite-MDC, DSGAN2, and hybrid CNN models have shown improvements in accuracy, speed, and resource optimization, with pre-trained layers reducing training time. The selection of optimizer, including the stochastic gradient descent (SGD), has also been proven to affect the performance of the model. Nevertheless, there are still limitations because of requirements on large-scale computing, small or non-diverse data, and the distance between laboratory outcomes and practice. The literature review refers to a variety of deep-learning methods, it can be reinforced through a direct comparison of the approaches and their results. Most of the current literature on texture-enriched CNNs uses small, single-crop datasets, which is not scalable, but demonstrates that application of handcrafted texture descriptors (including Gabor, LBP, and PHOG) can often improve feature discrimination. Transfer-learning methods are less expensive to train, and more accurate, but often overlook texture information and achieve heterogeneous behavior in different crop environments. This gap emphasizes the novelty of the combination of multi-texton and PHOG features with a transfer-learned CNN since our structure is based on the fact that the use of both texture sensitivity and pre-trained representations can lead to superior generalization and robustness of the novel methodology compared to the previous ones.

Table 1. Advantages and challenges of some recent plant disease detection techniques

Source	Technique	Advantages	Limitations
[6]	D-GAN	It achieved higher precision.	Using fewer samples to generate higher-resolution images will need more work.
[7]	Lite-MDC	Exhibits excellent precision and efficiency in real-time calculations and memory requirements.	Testing this approach directly on gadgets with less computing capability, such as cellphones or agricultural robots, may be the next step.
[8]	Improved vision transformer (IVT) and ResNet9	The SGD optimizer produced the best accuracy, whereas the Adam optimizer produced consistent results.	To tackle the difficulties of real-time data processing, the scientists want to develop a compact DNN in subsequent work.
[9]	Deep-learning models	Exhibits improved adaptability and durability in dealing with wide range of crops and illnesses.	Future studies should focus on improving the model's effectiveness and efficiency in practical situations.
[10]	DSGAN2	With processing time of 98 ms, suggested model outperformed most of the current models in simulated testing.	In order to improve the models further in future versions, researchers could add new datasets with a greater range of rice plant varieties and diseases to the training data.
[11]	CNN+CAE	Suggested hybrid model has low training and prediction times.	Because the CAE's encoder network's layers are pre-trained, there are less values required to be changed when training the whole hybrid model.
[12]	CNN	Using visual representations, it correctly determines the disease kind.	Future studies should concentrate on creating applications that expand the current approach to include all plant leaf species.
[13]	Deep learning	It was more accurate.	It was tested using a very small dataset.

In recent research, different methods have been proposed including GAN-based, lightweight CNNs, transformer-based models, and hybrid models [6] through [13].

3. METHOD

According to Figure 1, the PDD-TL architecture is divided into four distinct stages: preprocessing, segmentation, feature extraction, and disease prediction. Preprocessing first gets raw data ready for further analysis. Median filtering is used in this work to guarantee the consistency and quality of the data. Following that, a segmentation process is carried out to separate regions of interest within plant pictures using the IAPJS technique, with a particular focus on areas that may be impacted by diseases. In the joining phase, the IAPJS makes changes to the pixel values. Key properties derived from those segmented regions are identified and quantified using feature extraction after segmentation, which is essential for the subsequent categorization of diseases [14]. Because there are several features to extract, this study specifically extracts a few key aspects like multi-texton and PHOG. Lastly, a new CNN using transfer learning (CNN-TL) system called CNN-TCA-TL uses triple convolutional activation (TCA) to categorize the presence and impact of diseases based on features that have been retrieved. Figure 1 shows the entire recommended model.

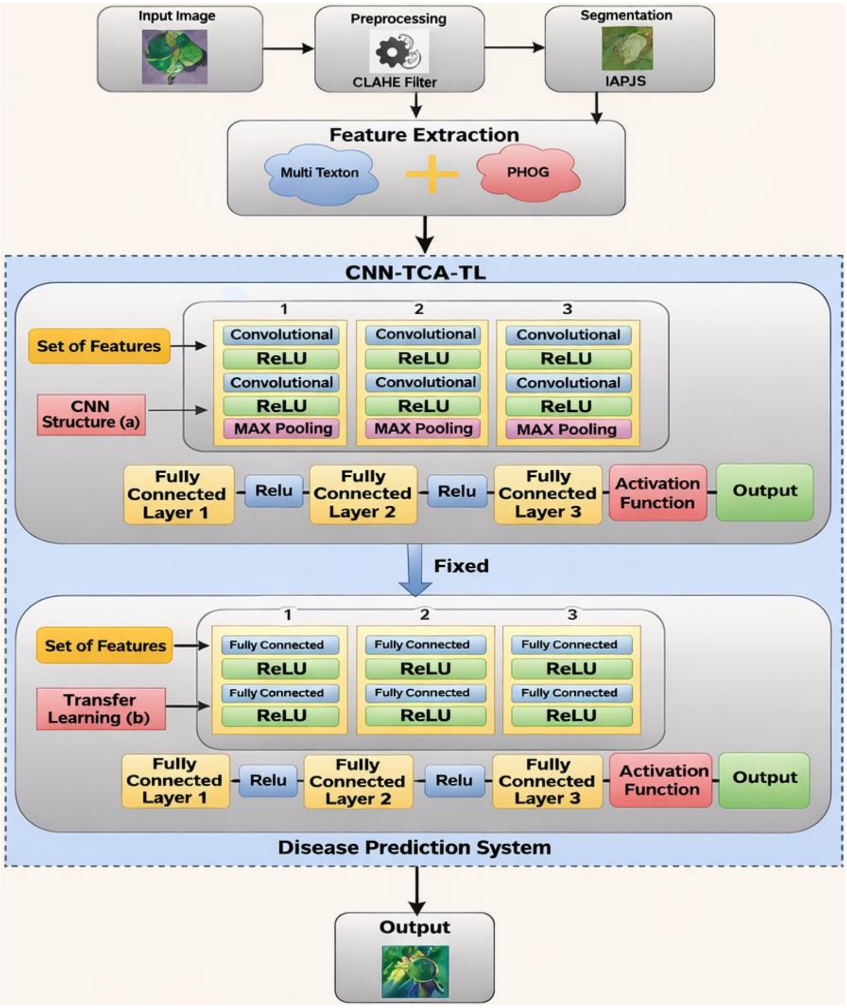

Figure 1. The overall design of the suggested method for classifying and detecting plant diseases

The framework consists of the hybrid property of fusing feature directly into the CNN pipeline of multi-texton and PHOG descriptors, TCA block, which preserves fine texture structures before pooling, and a transfer-learning mechanism, which incorporates the handcrafted features to fine-tune the pre-trained weights. Compared to previous texture-enhanced or standard transfer-learning models, this end-to-end design allows representing richer texture, achieving a faster convergence, and being more accurate.

3.1. Preprocessing using contrast limited adaptive histogram equalization filtering

To identify plant diseases, picture preprocessing is necessary because it enhances the extraction of features and quality of images to use in accurate classification. A well-known optical method is the CLAHE which is used to enhance the contrast of a picture without over-enhancing noise. Unlike the conventional histogram equalization, CLAHE utilizes contrast enhancement of each tile (small part of the picture) [15]. In so doing it eliminates over brightness variations and preserves local details. The CLAHE algorithm has the mathematical appearance as (1):

$$I_{CLAHE} = 255 * \frac{I(p,q)-I_{min}}{I_{max}-I_{min}} \quad (1)$$

Here in (1), I_{min} and Imax are the lowest and greatest pixel intensity values, respectively, and 255 is the highest level of an 8-bit greyscale image. I (p, q) is the intensity of a pixel at (p, q), or the local values. By applying a clip limit to disperse histogram values and prevent over-enhancement, contrasting weakness is addressed at CLAHE.

CLAHE on plant leaf images enhances the clarity of diseased areas in plant leaf images, which comprise spots, lesions, and discolorations and helps deep learning models to make correct classifications. CLAHE maintains the local texture information and contrast and thereby makes CNNs and other classification systems capable of differentiating between diseased and healthy areas of the plant, resulting in better disease detectability [16].

3.2. Integration of adaptive pixels in joint segmentation approach for image segmentation

At this step, the proposed IAPJS algorithm, which is a variant of the deep joint segmentation (DJS) algorithm, is used on the picture that was processed earlier [17]. This technique relies on similarity in areas and distance between segmentation points and deep areas in the image to determine the most optimal segments. DJS algorithm consists of three major stages that include segmentation point generation, region fusion, and joining.

To use pixels with a threshold and mean calculation, the original image is first cut into grids as in Figure 2. This step aims at establishing the first portions of the image. Then, through area fusion regions formed by merging regions according to their similarity and shared bi-constraints, we come up with new mean values. To further narrow down the segmentation, identified points by mapping in grids with minimum mean values are merged. Identification of the best segments is done during the segmentation point formation stage depending on the distance between the deep points and segmentation points. The reading of mean square error (MSE) is used to find this evaluation and ensure that the final segmentation captures the underlying architecture and the characteristics of the image appropriately.

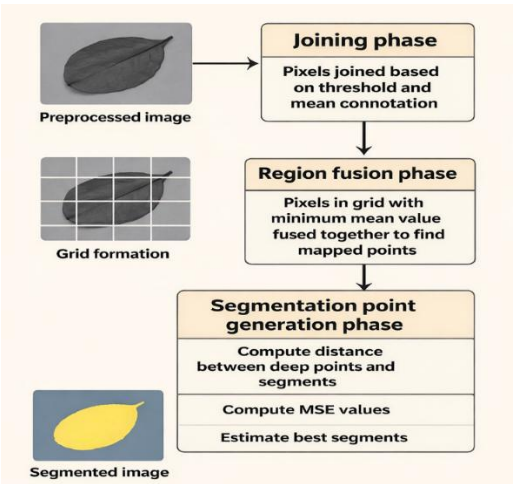

Figure 2. Procedure for suggested APIJS approach

3.3. Feature extraction: multi-texton and pyramid histogram of oriented gradients

Multi-texton features are extracted through a systematic procedure of extracting the complex textual patterns that are representational of different plant pathologies. First, a median filter is used to preprocess the images that have been acquired of leaves to successfully eliminate the noise without distorting the necessary details of the edges. Segmentation methods are then used to isolate regions of interest, i.e., diseased parts of the leaf.

After segmentation, the process of the multi-texton feature extraction commences whereby the texture patterns in the segmented regions are analyzed. This includes the process of recognition of basic micro-structures that are called textons and constitute the basic texture perception elements. These textons are then quantified to create a characterization of the texture [18]. This can be mathematically expressed as in (2):

$$T_f = \{t1, t2, t3, \dots, tn\} \tag{2}$$

where Tf represents the collection of features of extracted texton, and Ti represents the count of occurrence of an i-th texton in the region. To boost the discriminative power of the feature set, these multi-texton features are commonly used in combination with PHOG descriptors which encode shape and edge attributes on various scales. Multi-texton and PHOG features integrate to give a strongly represented character that summarises both the textual and structural properties of the sick regions [19].

The two are then combined as a feature vector as an input to machine learning classifiers to identify and classify plant diseases correctly. New deep learning-based methods have also enhanced accuracy and strength of the plant disease detection systems. This integrative strategy has shown a higher accuracy of plant disease detection because it has been shown to effectively represent the richness of the interactions of the texture and shape features related to different plant pathologies.

3.3.1. Texton detection

The process of identifying plant diseases begins with examining the color distributions and edge orientations in leaf photos. In order to identify edges, gradients are calculated using the Sobel Operator. In order to capture color variations that are symptomatic of diseases, RGB colors are split into 64 bins per component. Six pre-established patterns—two more for enhanced performance—are used for texton detection. These textons process edge orientation and color quantization maps in 2×2 pixel windows, acting as masks to draw attention to particular aspects. This creates six maps for every feature, per texton type.

These maps are then used to create histograms that summarize the frequency for texton detections. This thorough method makes it possible to analyze and categorize plant diseases using visual traits seen in photos of leaves.

3.3.2. Pyramid histogram of oriented gradients -based features

The PHOG features are derived through several systematic processes designed to obtain local and spatial data of leaf photos to identify plant diseases. In order to enhance the quality of the further analysis, the received leaf pictures are initially preprocessed with the help of a median filter that eliminates noise without losing edges [20]. To make sure that the extraction of features focuses on the relevant places, they can then be segmented using image segmentation methods to isolate the region of interest that in most cases is the diseased parts of the leaf [21]. After segmentation, each pixel in the gradient-magnitude of the image, M (x, y) and orientation 0 (x, y) is computed to begin a PHOG feature extraction.

$$\mathrm{S}(i,j) = \sqrt{\mathrm{H_x}(i,j)^2 + \mathrm{G_x}(i,j)^2} \tag{3}$$

$$\emptyset(i,j) = tan^{-1}\frac{\mathrm{H}_y(i,j)}{H_x(i,j)} \tag{4}$$

In (3) and (4), $H_x(i,j)$ and $H_y(i,j)$ are the horizontal and vertical gradient values of the image intensity that are generally determined with the help of Sobel operators. The image is subdivided, according to these gradients, into a grid of local cells, which is organized into a grid, and, inside a cell, a histogram of gradient orientations is built. These histograms are weighted with the respective magnitude of gradients so as to emphasize critical edge information.

This process is repeated at several levels of a spatial pyramid to sample many multi-scale structural features, with the image being down sampled to obtain features at different resolution levels. The last PHOG feature is the sum of the orientation histograms of all the cells of each level of the pyramid which gives a complete description of the shape as well as the spatial layout.

In addition, the combination of PHOG characteristics and multi-texton histograms contributes to the overall level of discriminative capabilities since the use of complementary texture data is provided [22]. This joint representation has the ability to effectively encode complex visual patterns related to the symptoms of plant diseases, and, therefore, enhance the accuracy of classification. This combination of features extraction approach has been specifically useful in isolating the minor differences between the diseases in various plants, which results in more precise and certain recognition of diseases [23].

3.4. Disease prediction via CNN-TCA-TL

The extracted feature set is then fed into CNN-TCA-TL model after the feature extraction process. This is a variation of CNN-TL [24] model. According to CNN-TCA-TL model, CNN structure initially trains feature set, which uses convolutional and activation function on two occasions and subsequently the transfer learning to utilize the pre-trained models and improve the entire performance in the context of selected tasks such as detection of plant diseases.

3.4.1. CNN-TCA-TL model

The model is organized into the following main stages:

- Input layer: accepts the extracted features as input.
- TCA module: a sequence of three convolutional layers, each followed by rectified linear unit (ReLU) activation and batch normalization, allowing deeper and more abstract feature extraction.
- Pooling layers: max pooling is applied after each convolutional block to reduce spatial size and retain significant information.
- Fully connected layers: aggregate the extracted features to prepare them for classification.
- Output layer: uses Sigmoid activation for binary outputs or Softmax activation for multi-class scenarios [25].

3.4.2. Key hyper parameters

Several hyper parameters can determine the behavior of the proposed CNN-TCA-TL model, and the learning process, feature extraction, and their optimization. These parameters have been chosen with great care to make training effective, enhance convergence and strong performance classification. A list of the main hyper parameters used in this study is the following:

- 64 into 128 into 256 filters (progressively on the TCA layers)
- Kernel size: 3×3
- Pooling size: 2×2
- Activation: ReLU in the intermediate layers; Sigmoid/Softmax in the output
- Optimizer: SGD (learning rate=0.001, momentum=0.9)
- The loss function is categorical cross entropy
- Batch size: 32
- Training epochs: 50

3.4.3. Transfer learning

Transfer learning helps overcome the difficulty of efficient prediction in another field by using the knowledge acquired in one source domain in which a model is first trained using large data sets [26]. The approach saves a lot of time that is usually spent to train a model in the target domain, and this domain has no direct relation with the source domain. CNN transfer learning has been shown to be effective in image classification: in the first instance, a CNN is conditioned in the source domain. It is then frozen and re-used in parts of its hidden layers followed by retraining of fully connected layers of the deep layers on target domain datasets.

4. RESULTS AND DISSCUSSION

The experiments used the PlantVillage Apple Leaf subset, a publicly available benchmark dataset curated by the PlantVillage research initiative at Pennsylvania State University. It provides 3,172 expert-verified RGB images of apple leaves in four categories—Apple Scab, Black Rot, Cedar Rust, and Healthy. Each image, originally 256×256 px, carries manual class annotations identifying the disease type, with no pixel-wise masks required because each frame contains a single leaf. For training, images were resized to 224×224 px, normalized, and divided into a 70 : 15 : 15 train/validation/test ratio, with augmentation (flips, ±15° rotations, brightness variation, Gaussian noise) to enhance diversity. To assess cross-crop generalization, a supplementary multi-crop PlantVillage collection of about 6,000 labeled images (including tomato, potato, and grape leaves) following the same expert-labeling protocol was also employed. The dataset includes images of the leaves of apple plants. A comprehensive analysis for the CNN-TCA-TL models and its variations, including those with conventional segmentation, conventional feature extraction, conventional classifier, and no feature extraction is shown in Table 2.

Table 2. Performance analysis of proposed CNN-TCA-TL with other methods

Metrics	Model with conventional segmentation	Model with conventional feature extraction	Model without feature extraction	Model with conventional classifier	CNN-TCA-TL
MCC	0.70	0.72	0.68	0.69	0.91
Accuracy	0.72	0.70	0.73	0.70	0.92
NPV	0.69	0.73	0.68	0.67	0.89
Sensitivity	0.75	0.64	0.66	0.72	0.94
Specificity	0.74	0.65	0.67	0.73	0.95
F-measure	0.74	0.67	0.70	0.71	0.94

The primary purpose of this assay is to predict plant diseases during the Apple class. This assessment will attempt to deconstruct and contrast the input of individual elements in the model structure to general prediction capabilities as shown in Figure 3. The performance of each of the variants is evaluated to establish how each feature extraction approach, segmentation strategy, and classifier selection influences accuracy of disease prediction in agricultural settings. The sensitivity values of different models in the study of Table 2 give vital information on how effective they were in the identification of diseased plants in the Apple Class.

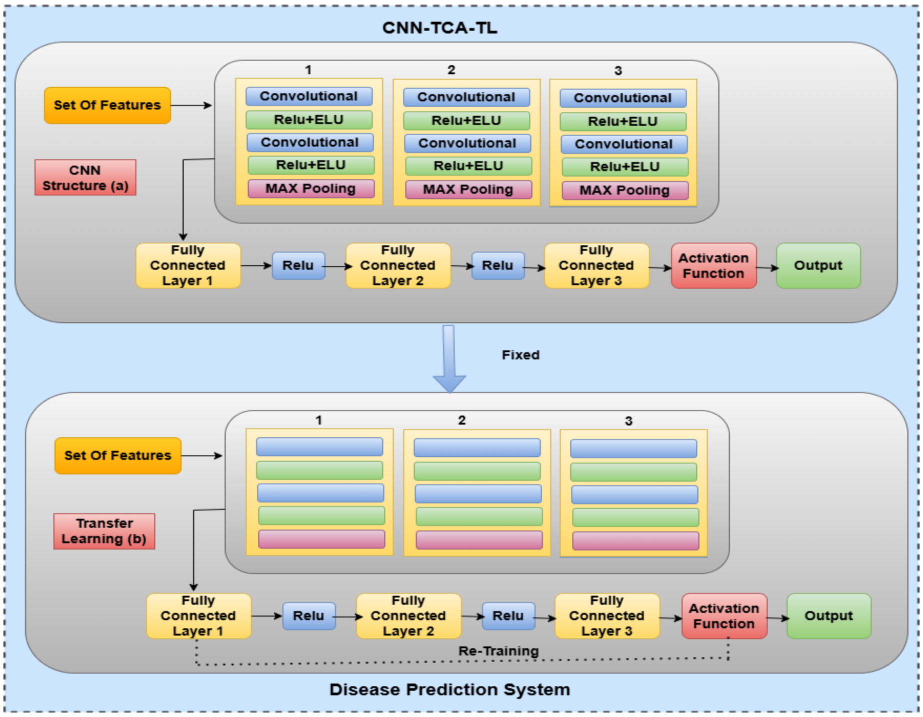

Figure 3. CNN-TCA-TL model

The graphical representation on Figure 4 indicates the variability with respect to other variants, including the ones with conventional segmentation (0.75), feature extraction (0.64), classifier (0.72), and more importantly, the model with no feature extraction (0.66) the CNN-TCA-TL approach records a sensitivity of 0.94, which indicates that the approach is highly effective in identifying instances of disease accurately. These results align with the recent research that has shown the effectiveness of deep learning-based plant disease detection platforms. This disparity points to the way in which feature extraction is essential to making the model more sensitive; without the process, models may not be able to collect the data necessary to detect an illness accurately. The high sensitivity of the CNN-TCA-TL model highlights that it has high degree of feature extraction, segmentation methods and classifier optimization that guarantees the ability to detect a disease.

To further justify performance, an error analysis indicated that model which did not deeply extract features tended to misclassify healthy leaf that had minor discoloration. It shows that to deal with minute variations in visuals, feature representation needs to be strong. CNN-TCA-TL model is stronger theoretically because it has the combined advantages: CNN is able to grasp the spatial patterns, TCA it owns the alignment of domain features and transfer learning enhances generalization. Combined, these make it more accurate in different data conditions.

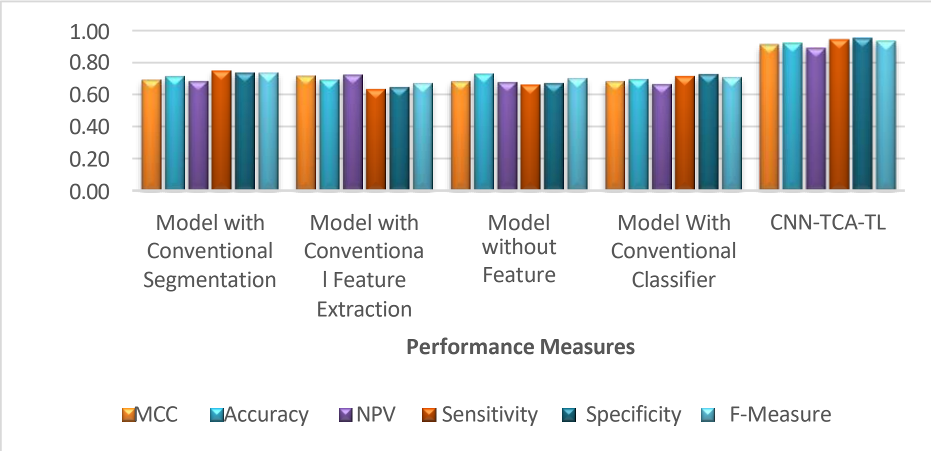

Figure 4. Graphical analysis of performance measures of all methods

4.1. Ablation study

The ablation analysis indicates that CNN and texture features complement each other in the proposed framework as Table 3 indicates. Performance was also much lower when no texture features were used whereas results were also lower when using only texture features. The best results were always obtained with the full hybrid model which proves that the combination of both types of features improves classification. The results of these studies highlight that structural and deep features should be used together to ensure high accuracy in detection of plant diseases.

Table 3. Ablation study

Model variant	Accuracy	Sensitivity	Specificity	F-measure
CNN-TCA-TL (full model: CNN+texture)	0.92	0.94	0.95	0.94
Without texture features (CNN only)	0.85	0.78	0.83	0.81
Texture features only (PHOG+Texton)	0.83	0.81	0.82	0.80
Without feature extraction	0.73	0.66	0.67	0.70

5. CONCLUSION

This paper suggested a hybrid vegetable disease recognition model combining both a texture-based extraction of plant features and a transfer learning-driven convolutional neural network. CNN-TCA-TL is a description that blends multi-texton and PHOG with deep learning that is effective in recording both the fined-grained texture patterns and high-level semantic features of plant leaves.

The experimental results show that the proposed model is good in terms of classification and has the accuracy of 0.92, sensitivity of 0.94, specificity of 0.95 and F-measure equal to 0.94. These findings suggest that the model has high success in terms of both separating successfully between normal and diseased plant samples and especially in visually similar classes of disease.

This enhancement in performance could be explained by the fact that handcrafted texture descriptors have been combined with deep feature representations, and this method is more effective to discriminate features and be resistant to classifications.

The research is also constrained by the application of regulated benchmark datasets that might not be a true-to-life scenario of agricultural variability including lighting conditions, complexity of the background and image noise. The next step in work is the validation of the model on various real-world data and the further optimization of the model to deploy it into real-time and onto edge devices and extension of the framework to handle several crops and other types of plant diseases.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

The authors declare that there is no conflict of interest regarding the publication of this paper.

DATA AVAILABILITY

The dataset used in this study is publicly available from the PlantVillage dataset. The data supporting the findings of this study are available from publicly accessible sources, and additional processed data and implementation details are available from the corresponding author upon reasonable request.

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