

Fruits and Vegetable Diseases Recognition Using Convolutional Neural Networks

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Abstract: As they have nutritional, therapeutic, so values, plants were regarded as important and they're the main source of humankind's energy supply. Plant pathogens will affect its leaves at a certain time during crop cultivation, leading to substantial harm to crop productivity & economic selling price. In the agriculture industry, the identification of fungal diseases plays a vital role. However, it requires immense labor, greater planning time, and extensive knowledge of plant pathogens. Computerized approaches are developed and tested by different researchers to classify plant disease identification, and that in many cases they have also had important results several times. Therefore, the proposed study presents a new framework for the recognition of fruits and vegetable diseases. This work comprises of the two phases wherein the phase-I improved localization model is presented that comprises of the two different types of the deep learning models such as You Only Look Once (YOLO)v2 and Open Exchange Neural (ONNX) model. The localization model is constructed by the combination of the deep features that are extracted from the ONNX model and features learning has been done through the convolutional-05 layer and transferred as input to the YOLOv2 model. The localized images passed as input to classify the different types of plant diseases. The classification model is constructed by ensembling the deep features learning, where features are extracted dimension of 1×1000 from pre-trained Efficientnetb0 model and supplied to next 07 layers of the convolutional neural network such as 01 features input, 01 ReLU, 01 Batch-normalization, 02 fully-connected. The proposed model classifies the plant input images into associated labels with approximately 95% prediction scores that are far better as compared to current published work in this domain.

Keywords: Efficientnetb0; open exchange neural network; features learning; softmax; YOLOv2



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1 Introduction

The emergence of plant pathogens has a detrimental impact on crop development, then if plant pathogens are not identified timely, there would be a rise in food poverty. In general, major commodities like rice, maize, and so on., are important for guaranteeing the supply of food and agricultural development [1]. The early indicator and prediction seem to be the source of efficient prevention and treatment for crop ailments [2]. They play key responsibility for management and decision support systems for agricultural development [3]. For now, nevertheless, the observations made by seasoned farmers are indeed the predominant method for plant ailments identification in rural regions of advanced nations; this involves constant supervision of specialists, and that could be extremely costly in agricultural activities. Besides that, in some remote regions, farmers might have to go hundreds of miles to reach experts, which makes consultation too costly [4]. Nevertheless, that technique could be achieved in small regions and might not be well generalized. Plant pathogens detection through a computerized algorithm is a significant task, as it can prove beneficial in tracking vast areas of the crops, and thereby automatically diagnose the pathogen as promptly as possible on leaf tissue [5]. Therefore, searching for a quick, automated, less costly, and reliable framework to perform the detection of plant ailments is of great practical value [6]. Usually, plant leaves are the first indicator for detection of the plant's pathogens, as well as the signs of most ailments that might start to occur on leaves [7]. As in previous years, the primary classification methods which were widely used during disease diagnosis in crops involve Random Forest (RF) [8–12], and many more. And since we all realize that perhaps ailments identification rates of classical techniques depend heavily upon on segmentation of lesion and hand-designed features through different frameworks, like moments of invariant, Gabor transformation and dimensionality reduction, etc. [13]. Nevertheless, the artificial developed features involve costly works and professional expertise, that have a certain subjective nature [14]. Primarily, that is not easy to determine that features are suitable and stable for disease detection from some of the derived features [15]. Other than, complicated environmental conditions, many approaches failed to accurately leaf segmentation, which can proceed to inaccurate recognition of the disease outcomes [16]. Therefore, that automated identification of disease is also a tough challenge owing to the difficulty of infected plant leaves [17]. More lately, deep convolutional models, are rapidly utilized to address certain challenges [18]. While very good findings have been documented in literature, inquiries so far have utilized datasets with the minimal diversity [19]. Far more visual materials contain photos exclusively in innovative (laboratory) environments, not really in the actual wild environments. Throughout, photographs taken in cultivation area environments provide a wide diversity of history and an extremely unique of disease manifestations. Consequently, there seem to be a variety of features required to be learned for Convolutional Neural Network (CNN) and its derivatives, although training certain Neural networks often needs several labelled data and significant computing resources by scratch to determine the efficiency. Collecting the large number of the labelled database is certainly a difficult job [20]. Despite drawbacks, the latest studies have effectively shown the capacity of intelligent systems. Especially, the transfer learning models, that also mitigates the issues caused by traditional neural networks, i.e., these same remedies composed of utilizing a pre-trained model where parameters of last layers need to be extrapolated from the scratch that is normally utilized in the real time application [21]. The core contributing steps of the proposed study is manifested as follows:

- An improved localization model is constructed by a combination of the YOLOv2 model and ONNX model, where deep features are analyzed from the convolutional-05 layer and

transferred to the 09 tiny YOLOv2 models for more precisely localized the different types of plant diseases.

- After localization, comprehensive features analysis is performed through a pre-trained EfficientNetB0 model and 07 layers CNN model with softmax layer for classification of different types of plant diseases.

The overall manuscript is organized as follows: where related work is discussed in Section 2, the proposed framework is explained in Section 3 and experimental outcomes are defined in Section 4, and finally obtained outcomes are written in Section 5.

2 Related Work

As of now, Deep Learning (DL) is a slicing technique for classification problems of land spread, which may also demonstrate support for certain distinct tasks. In the hyperspectral analysis, various kinds of Deep Neural Networks (DNNs) have produced remarkable outcomes [22]. In crop pattern tasks [23], and pathogens discovery [24]. In such investigations, the GoogLeNet [25] networks showed the best-classified outcomes. It was also suggested that if models are pre-trained, stronger findings were obtained. The researchers in [26] offer a detailed overview and easy-to-use empirical categorization of Machine Learning (ML) approaches to enable the plant network to implement the required ML techniques and best-practice guidelines for various attributes of biotic and abiotic stress correctly & effectively. Reference [27] reflects different forms of Parkinson's Disease (PD), diverse sophisticated ML methods for PD recognition, this summary also presents major inspection gaps that will aid in further research to recognize pathology. Reference [28] uses visualization and ML techniques to coordinate backwoods landscape on terrain database generated from the tool of Advanced Spaceborne Thermal Emission and Reflection Radiometer (ASTER) images to use Box Plot and Heat Map to explain the accumulated knowledge. Reference [29] to tweak & test slicing CNN Model for characterization of PD based on photos. Reference [30] reviewed the steps of a general structure for PD exploration & close investigation on methods of ML characterization for PD position. Reference [30] suggested a system using the K-nearest Neighbor (KNN) classifier for Leaf Pathogens Detection (PLDD) & classification. Reference [31] developed the programmed PLDD and order based on artificial intelligence for the snappy and easy place of the ailment and later characterized it and conducted anticipated solutions to cure the disease. The Global Pooling of Dilated CNN (GPDCNN) for PD recognition is suggested in [32]. References [33–36] based on the most recent progress on explorations related to ML for rational data analytics and diverse approaches related to existing computing requirements for various group applications. References [37–40] introduced new technique for leaf categorization using DL on the limited datasets. Reference [41] offers a range of approaches to discuss, optimization and allow multidisciplinary ML studies in the healthcare informatics. References [42–45] explored that practicality and probability of the pre-symptomatic tobacco disease identification utilizing hyperspectral analysis, together with technique for variable preference and ML. References [46–54] presented a novel model of identification of leaf disease based on DCNN process.

3 Proposed Framework

The proposed architecture contains two core steps as shown in Fig. 1, i.e., localization and classification. The localization model is built by a combination of two convolutional neural models, where deep features learning is performed using an open neural network such as ONNX and extracts features from the convolutional-05 layers and transferred as input to the tinyYOLOv2

model contains 09 layers. After localization, classification of different types of plant disease is implemented using dual-mode of the convolutional neural models i.e., firstly, deep features are extracted from pre-trained Efficientnetb0 model. The extracted features dimension of $1 * 1000$ is transferred to the next 07-layer convolutional neural model for deep features analysis. Later softmax layer is utilized to classified the plant diseases into corresponding classes.

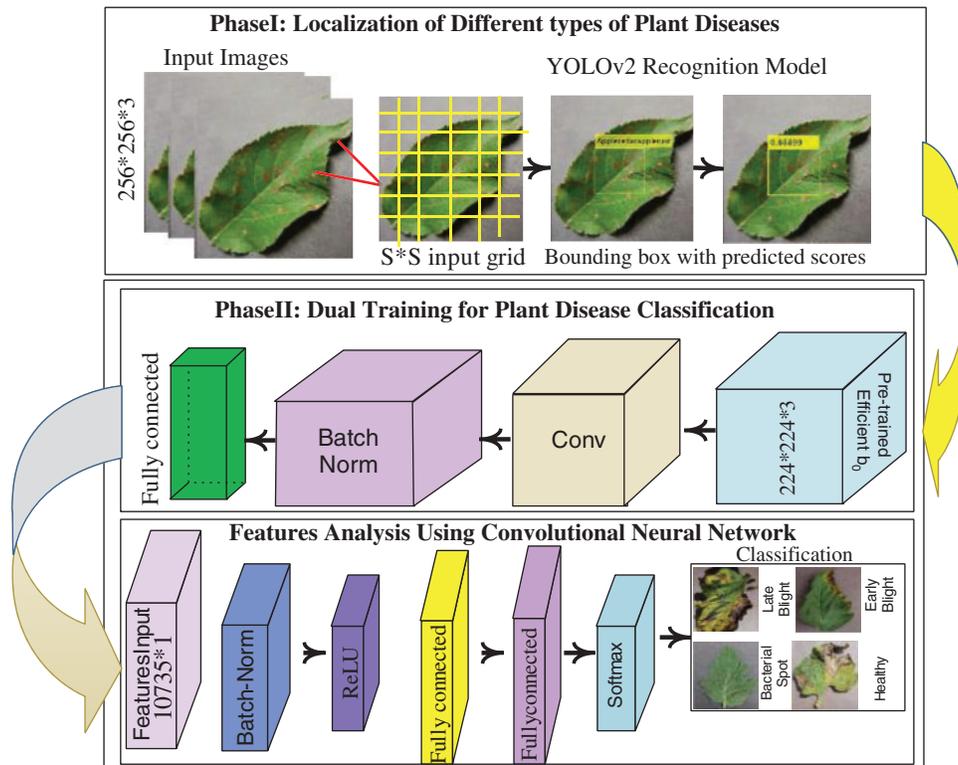


Figure 1: Core steps of the proposed architecture

3.1 Localization of Different Types of Plant Disease Using YOLOv2-ONNX Model

YOLOv2 model is utilized for the localization. For localization, a new framework is proposed by the combination of ONNX and the tinyYOLOv2 model. The ONNX model comprises the 35 layers such as 01 input, 02 element-wise affine, 08 batch-norm, 09 convolutional, 01 regression, 08 LeakyReLU, 06 max-pooling.

The proposed localization model is constructed by using 24 layers of the ONNX model i.e., 01 input, 02 elementwise affine, 06 convolutional, 05 batch-normalization, 05 LeakyReLU, 05 max-pooling that are transferred as an input to the 09 layers of tiny YOLOv2 model, and trained on tuned parameters that are manifested as [Tab. 1](#). The flow diagram of the proposed localization model is drawn in [Fig. 2](#).

[Tab. 1](#), shown the learning parameters that are selected after the experimentation for more precise localization. The activation units of localization model are given in [Tab. 2](#).

Table 1: Building parameters of the proposed model

Optimizer	Adam
Epochs	500
Mini-batch-size	64
Rate of learning	0.0001

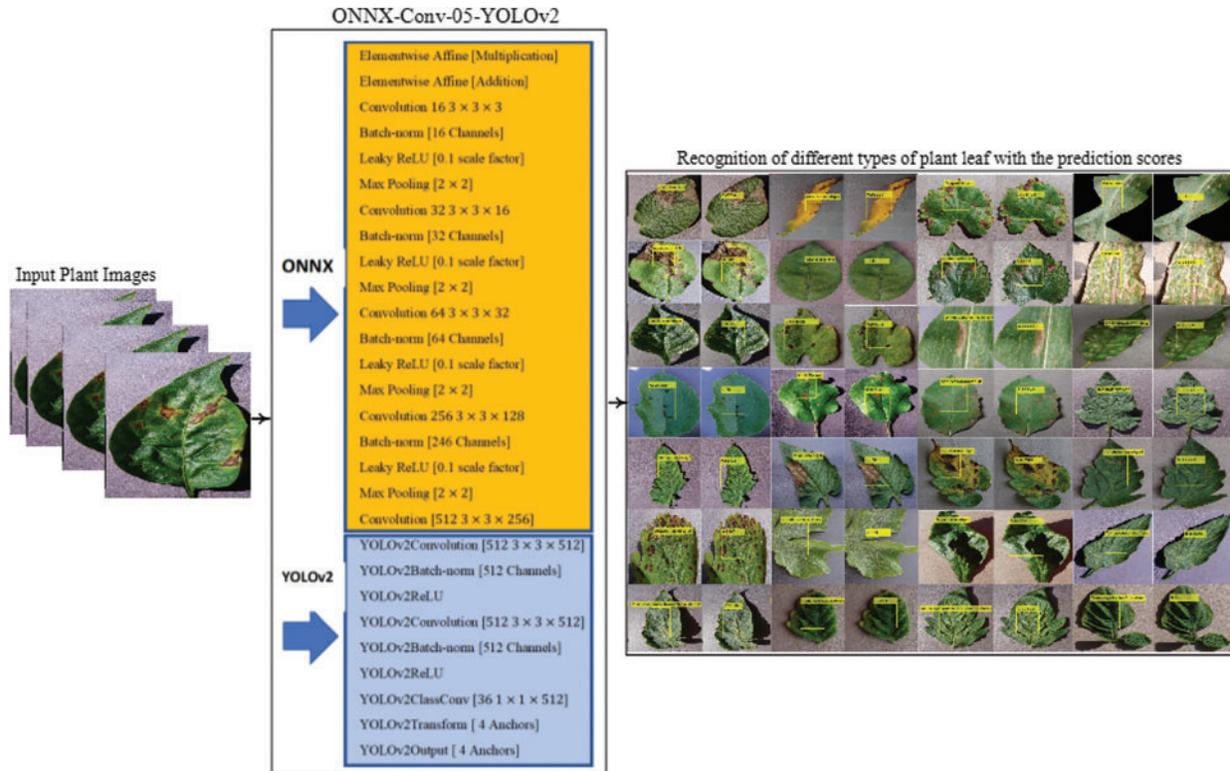


Figure 2: Proposed localization model

3.2 Features Extraction Using Efficientnetb0 Model

Efficientnetb0 [55] network consists of 290 layers, in which 65 convolutional, 49 batch-normalization, 65 sigmoid, 65 element-wise multiplication, 15 group convolution, 16 global average pooling, 09 addition, fully connected, softmax & classification. The input image size of $256 \times 256 \times 3$ is passed to the Efficientnetb0 model for features learning in a pipeline. The final feature vector length of $17984 * 1000$ is supplied to the convolutional neural network for further informative features analysis. The proposed model is trained on the tuned hyperparameters as given in Tab. 3.

The feature-length of $17984 * 1000$ that is obtained from the pre-trained Efficientnetb0 model that is supplied to the CNN model contains 07 layers were 01 features input layer, 01 batch-normalization, 02 fully connected layers, ReLU, softmax and classification. In this model again features are learned on 10-fold cross-validation with a variety of optimizer solvers such as adam, sgdm, and RMSProp. The best optimizer selection is still a difficult task, to overcome this

problem, thus in this study suitable optimizer is selected after the extensive experiment as shown in [Tab. 4](#).

Table 2: Activation units of the proposed localization model

Convolution	Affine elementwise	Batch-norm	Leaky-ReLU	Pooling	YOLOv2-transform
$128 \times 128 \times 16$	$128 \times 128 \times 3$	$128 \times 128 \times 16$	$128 \times 128 \times 16$	$64 \times 64 \times 16$	$4 \times 4 \times 120$
Convolution	Affine elementwise	Batch-norm	Leaky-ReLU	Pooling	YOLOv2-output
$64 \times 64 \times 32$	$128 \times 128 \times 3$	$64 \times 64 \times 32$	$64 \times 64 \times 32$	$32 \times 32 \times 32$	–
Convolution	–	Batch-norm	Leaky-ReLU	Pooling	–
$32 \times 32 \times 64$	–	$16 \times 16 \times 128$	$32 \times 32 \times 64$	$16 \times 16 \times 64$	–
Convolution	–	Batch-norm	Leaky-ReLU	Pooling	–
$16 \times 16 \times 128$	–	$8 \times 8 \times 256$	$16 \times 16 \times 128$	$8 \times 8 \times 128$	–
Convolution	–	Batch-norm	Leaky-ReLU	Pooling	–
$8 \times 8 \times 256$	–	$4 \times 4 \times 512$	$8 \times 8 \times 256$	$4 \times 4 \times 256$	–
Convolution	–	Batch-norm	ReLU-YOLOv2	–	–
$4 \times 4 \times 512$	–	$4 \times 4 \times 512$	$4 \times 4 \times 512$	–	–
Convolution	–	–	ReLU-YOLOv2	–	–
$4 \times 4 \times 512$	–	–	$4 \times 4 \times 512$	–	–
Convolution	–	–	–	–	–
$4 \times 4 \times 512$	–	–	–	–	–
Convolution	–	–	–	–	–
$4 \times 4 \times 120$	–	–	–	–	–

Table 3: Learning parameters of Efficientnetb0 model

Batch-size	08
Optimizer	Adam
Epochs	30

Table 4: Computation results of the proposed localization model

Optimizers	Batch-size	Training results (%)
RMSProp	8	92
Adam	16	97
Sgdm	64	95

[Tab. 4](#), shows the training outcomes that are computed after applying the number of optimizers and different batch-size, in which we observed that adam provides higher accuracy as compared to other optimizers. The parameters of the CNN model are manifested in [Tab. 5](#).

The features learning process of Efficientnetb0 model and 7 layers convolutional neural network as shown in [Fig. 3](#).

The classification results are computed on single fully-connected layer of model and also analyzed after supplied to the proposed selected 7 layers of CNN model as stated in [Tab. 6](#).

Table 5: Number of parameters of next convolutional neural network

Feature's input	999
Fully-connected	17984
Batch-norm	17984
ReLU	17984
SoftMax	4, 38

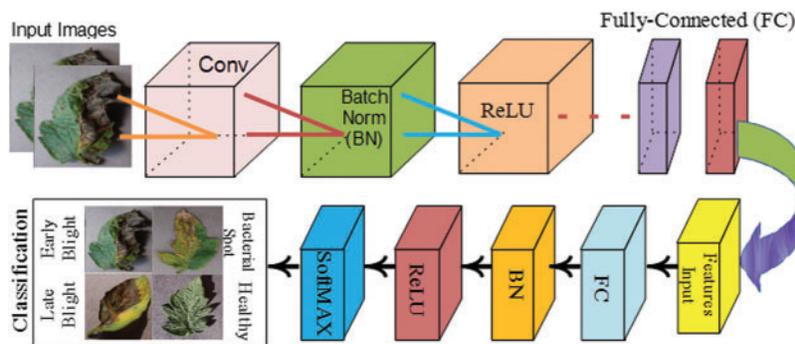


Figure 3: Classification of different types of plant diseases using convolutional neural network

Table 6: Selection of layers

Layers	Accuracy (%)
Fully connected layer of efficiengtnet-b0 model	94.6
<i>Fully connected layer of efficiengtnet-b0 model and 01 batch-normalization 02 fully connected 01 ReLU</i>	<i>96.46</i>
Fully connected layer of efficiengtnet-b0 model and 02 batch-normalization 03 fully connected 02 ReLU	95.40
Fully connected layer of efficiengtnet-b0 model and 04 batch-normalization 03 fully connected 02 ReLU	95.78

The empirical analysis from [Tab. 6](#), shows that, experiment is implemented on combination of different kinds of layers of CNN model, where we observed that bold italic layers provide improved results as compared to other selected layers. Therefore, the selected number of the layers are utilized for further experimentation.

4 Experimental Discussion

The presented study is evaluated on a publically available benchmark dataset such as plant village [56]. The datasets contain 38 classes. The dataset description is mentioned in Tab. 7.

Table 7: Description of the plant village dataset

Category	Classes	Training images	Testing images
Apple	Scab	2016	504
	Black rot	1987	497
	Cedar apple rust	1760	440
	Apple (healthy)	2008	502
	Blueberry (healthy)	1816	454
	Cherry (sour)	1683	456
	Cherry (healthy)	1826	421
Corn	Cercospora maize	1642	410
	Spot of gray leaf	1642	477
	Common rust	1907	465
	Healthy of maize	1859	477
	Northern leaf blight	1908	412
Grape	Black rot	1888	472
	Black measles	1920	480
	Healthy of corn	1692	423
	Grape leaf blight	1722	430
Orange	Orange citrus	2010	503
Peach	Spot of bacterial	1838	459
	Peach healthy	1728	432
Pepper	Bell healthy	1913	478
	Pepper	1988	497
Potato	Early blight	1939	485
	Healthy of pepper	1824	456
	Late blight	1939	485
Raspberry	Leaf mold	1781	445
Soybean	Septoria leaf spot	2022	505
Squash	Mite of two spider	1736	434
Strawberry	Target spot	1824	456
	Mosaic virus	1774	444
Tomato	Yellow leaf curl virus	1702	425
	Scab	1920	480
	Black rot	1926	481
	Rust cedar apple	1851	463
	Healthy (apple)	1882	470
	Healthy (blueberry)	1745	436
	Cherry (sour)	1741	435
	Cherry (healthy)	1827	457
	Cercospora maize spot	1790	448
	Spot leaf gray	1961	490

Tab. 7, shows the 12 different categories of fruits and vegetable plants such as apple, orange, grape, corn, pepper, potato, tomato, raspberry, soybean, and squash. These categories having 38 different classes. The classification results are computed on individual categories and a combination of different categories with class labels. The experiment is implemented on MATLAB2020Rb with an NVIDIA toolbox. The proposed model is classified on 10-fold cross-validation.

4.1 Experiment #1 Localization of Different Types of Plant Diseases

The original plant images of the fruits and vegetables are recognized with the actual class labels by utilizing a proposed YOLOv2 [57] framework. The proposed model is constructed by a mixture of the two-deep learning models such as ONNX and tinyYOLOv2 model, where a proposed model is trained on the selected learning parameters. The three different types of losses are utilized to reduce the error rate amongst predicted & actual class labels. The YOLOv2 losses are defined as follows:

The localization loss is utilized for the computation of the loss among the ground annotated masks and the predicted bounding box. The computation parameters of the localization loss are ground masks, bounding predicted box and position. The confidence loss computes the error among the detected objects and the actual masks in the i grid cell. The classification loss computes the mean square error between detected and predicted box in the i grid cell. The mathematical notations of the YOLOv2 losses is explained as:

$$\begin{aligned}
 & weight1 \sum_{i=0}^{gridcell^2} \sum_{j=0}^{boundingbox} 1_{ij}^{obj} \left[(x_i - \hat{x}_i) + (y_i - \hat{y}_i)^2 \right] \\
 & + weight1 \sum_{i=0}^{gridcell^2} \sum_{j=0}^{boundingbox} 1_{ij}^{obj} \left[\left(width_i - \sqrt{\widehat{width}_i} \right)^2 + \left(height_i - \sqrt{\widehat{height}_i} \right)^2 \right] \\
 & + weight2 \sum_{i=0}^{gridcell^2} \sum_{j=0}^{boundingbox} 1_{ij}^{obj} \left[(c_i - \hat{c}_i)^2 \right] \\
 & + weight3 \sum_{i=0}^{gridcell^2} \sum_{j=0}^{boundingbox} 1_{ij}^{noobj} \left[\left(width_i - \widehat{width}_i \right) + (c_i - \hat{c}_i)^2 \right] \\
 & + weight4 \sum_{i=0}^{gridcell^2} 1_i^{noobj} \sum_{c \in classes} \left[(p_i(c) - \widehat{p}_i(c))^2 \right]
 \end{aligned}$$

where s represents the number of grid cells, b denotes bounding boxes, x_i, y_i denote the center point of the jth bounding box and \hat{x}_i, \hat{y}_i signify the center point of the truth bounding masks. c identifies the confidence scores and p demonstrates the probability. The testing outcomes are given in Tab. 8.

The achieved outcomes show, proposed localization method provides 1.00 localization scores that are far better as compared to recently published work. This approach might be utilized as a real-time application for the localization of the different types of plant diseases. The proposed method localization outcomes are shown in Fig. 4.

Table 8: Results of localization method

Classes	Average precision (Ap)	Log miss rate
Scab	1.0	0.0
Black rot	1.0	0.0
Apple of cedar rust	1.0	0.0
(Healthy) apple	1.0	0.0
Blueberry (healthy)	1.0	0.0
Cherry (sour)	1.0	0.0
Cherry (healthy)	1.0	0.0
Leaf maize cercospora spot	1.0	0.0
Spot gray leaf	1.0	0.0
Common rust	1.0	0.0
Healthy of maize	1.0	0.0
Northern leaf blight	1.0	0.0
Black rot	1.0	0.0
Black measles	1.0	0.0
Healthy of corn	1.0	0.0
Grape leaf blight	1.0	0.0
Orange	1.0	0.0
Bacterial spot	1.0	0.0
Peach healthy	1.0	0.0
Bell healthy	1.0	0.0
Pepper	1.0	0.0
Early blight	1.0	0.0
Healthy of pepper	1.0	0.0
Late blight	1.0	0.0
Leaf mold	1.0	0.0
Spot of septoria leaf	1.0	0.0
Two-spotted spider mite	1.0	0.0
Target spot	1.0	0.0
Mosaic virus	1.0	0.0
Yellow leaf curl virus	1.0	0.0

4.2 Experiment #2 Classification of Different Types of Plant Diseases

In this experiment, input images are classified into related class labels. The classification outcomes are computed on training and testing plant images as given in [Tab. 9](#).

The results in [Tab. 9](#) display, proposed method attained kappa scores of 0.964 and an accuracy of 96.46%. Whereas 100% accuracy achieved on Leaf Mold, Two-spotted spider mite, Bacterial spot, Orange Haunglongbing (Citrus greening) classes of plant leaves. The proposed method achieved outcomes above 99% are Cherry (healthy), Cedar apple rust, Common rust, Northern Leaf Blight, Healthy of corn, Grape Leaf blight, Target Spot, and Cherry (healthy) classes of plant leaves. The classification results on the individual classes of the different types of fruits and vegetables as shown in [Tab. 10](#).

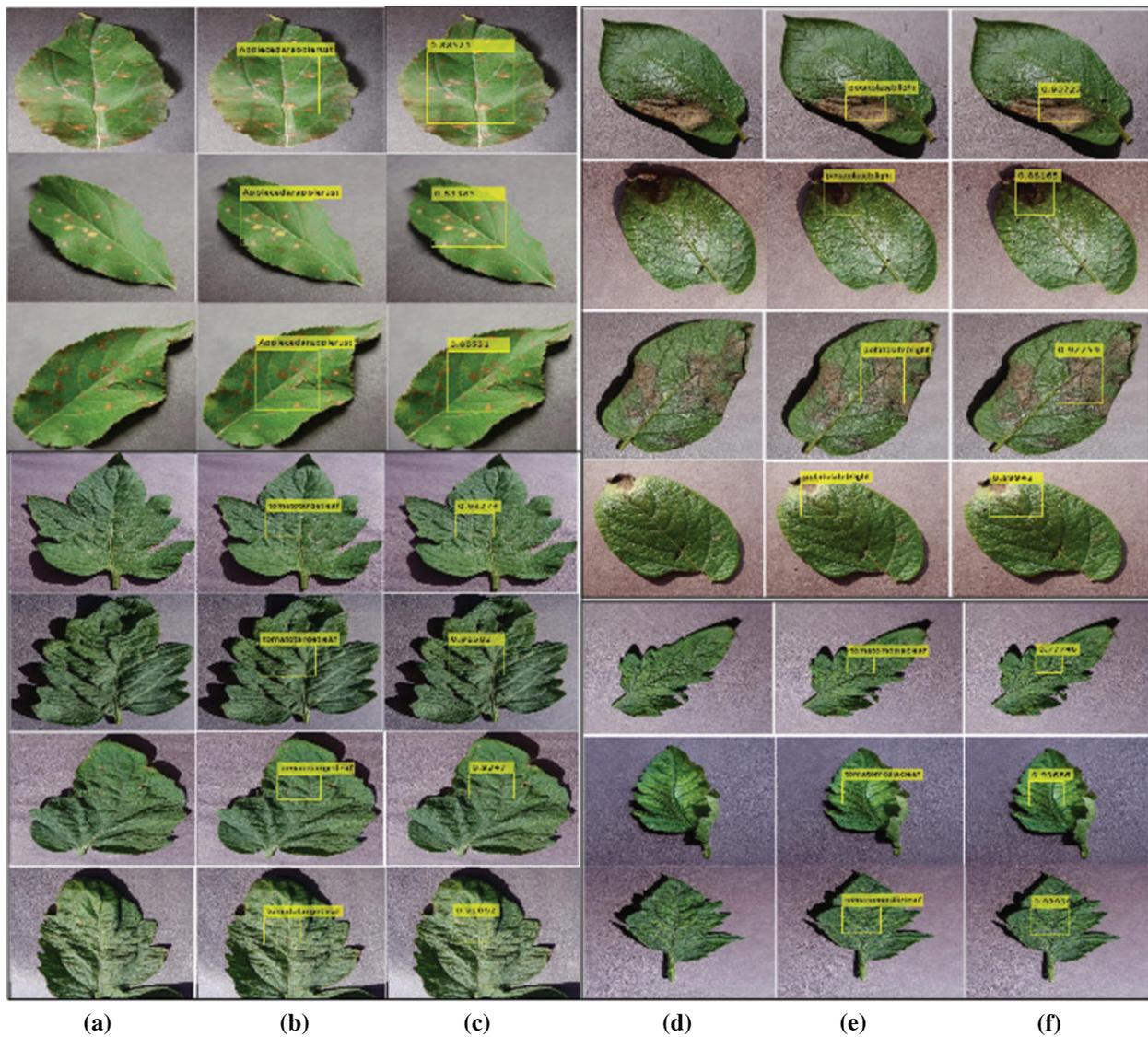


Figure 4: Shows plants diseases (a, d) input images (b, e) plant localization (c, f) localized with predicted

Tab. 10, shows the classification results on different types of apples. The 1.0 precision score was achieved on the apple plant, whereas 99.5% and 98.82% precision scores on healthy classes of apple and blueberry respectively. The proposed method achieved 1.0 precision scores on benchmark classes of the apple plant leaves. The classification outcomes of variants corn types as shown in Tab. 11.

The classification accuracy on testing images of the corn leaves is 99.95%, 98.06%, 98.14%, 99.92%. The classification outcomes on grape plant diseases as given in Tab. 12.

Table 9: Classification outcomes on input images

Classes	Training results		Testing results	
	Accuracy = 96.46%		Accuracy = 96.403%	
	Kappa = 0.964		Kappa = 0.963	
	Precision (%)	Recall (%)	Precision (%)	Recall (%)
Black rot	50	17.808	98.859	91.422
Cedar apple rust	99.39	99.79	100	92.807
Apple (healthy)	98.53	99.48	98.024	99.143
Blueberry (healthy)	99.34	97.97	96.569	96.806
Cherry (sour)	98.96	98.58	92.195	100
Cherry (healthy)	99.04	99.75	90.947	100
Maize cercospora leaf spot	99.56	99.61	92.371	100
Gray leaf spot	89.16	97.47	100	92.99
Common rust	99.47	99.84	99.318	100
Healthy of maize	97.79	90.98	96.174	100
Northern leaf blight	99.83	99.89	98.439	100
Black rot	97.82	96.80	97.54	100
Black measles	96.61	98.09	99.842	100
Healthy of corn	99.12	99.88	96.017	100
Blight of grape	98.99	99.94	93.776	100
Orange haunglongbing (citrus greening)	98.90	100	99.101	99.799
Bacterial spot	95.97	100	99.946	76.894
Peach healthy	98.90	98.16	98.088	99.706
Bell healthy	96.39	98.29	98.024	99.62
Pepper	98.39	95.41	97.35	99.791
Early blight	98.96	97.55	98.878	99.773
Healthy of pepper	94.21	97.02	99.947	97.172
Late blight	97.09	98.11	98.18	99.888
Leaf mold	98.25	100	98.178	100
Septoria leaf spot	98.61	98.90	99.152	99.499
Two-spotted spider mite	99.94	100	98.171	100
Target spot	99.71	99.49	98.124	100
Mosaic virus	99.50	98.16	97.456	100
Yellow leaf curl virus	94.06	91.80	95.412	100
Scab	85.93	88.80	99.683	80.564
Black rot	89.08	92.53	97.891	90.636
Cedar apple rust	92.08	96.76	96.201	95.74
Apple (healthy)	91.86	85.17	89.309	90.625
Blueberry (healthy)	90.17	91.33	92.068	96.053
Cherry (sour)	91.40	77.03	88.907	83.229
Cherry (healthy)	93.37	99.72	95.508	99.947
Maize cercospora leaf spot	97.59	97.70	98.994	98.39
Gray leaf spot	95.11	96.93	77.091	99.933

Table 10: Classification of different types of apple diseases on training benchmark datasets

Classes	Training results				Testing results			
	ACC (%)	PRE	RE	F1e	ACC (%)	PRE	RE	F1e
Scab	99.9	1.0	1.0	1.0	99.02	1.0	0.96	0.98
Rot	99.97	1.0	1.0	1.0	99.74	1.0	0.99	0.99
Cedar rust	99.97	1.0	1.0	1.0	99.73	1.0	0.99	0.99
Apple (healthy)	99.89	1.0	1.0	1.0	99.5	0.99	0.99	0.99
Blueberry (healthy)	99.97	1.0	1.0	1.0	98.82	0.94	1.0	0.97

Table 11: classification outcomes on different types of corn (maize) leaves

Classes	Training results				Testing results			
	ACC (%)	PRE	RE	F1e	ACC (%)	PRE	RE	F1e
Cercospora	99.95	1.0	1.0	1.0	99.95	1.0	1.0	1.0
Gray spot	98.06	0.98	0.95	0.96	98.06	0.98	0.95	0.96
Rust	98.14	0.94	0.98	0.96	98.14	0.94	0.98	0.96
Healthy	99.92	1.0	1.0	1.0	99.92	1.0	1.0	1.0

Table 12: Classification outcomes on different types of grape leaves on training/testing dataset

Classes	Training results				Testing results			
	ACC (%)	PRE	RE	F1e	ACC (%)	PRE	RE	F1e
Black rot	99.95	1.0	1.0	1.0	99.54	0.98	1.0	0.99
Measles	98.06	0.98	0.95	0.96	98.46	0.96	0.98	0.97
Healthy	98.14	0.94	0.98	0.96	97.87	0.98	0.93	0.95
Leaf blight	99.92	1.0	1.0	1.0	99.82	0.99	1.0	1.0

Tab. 12, shows the classification of different types of grape diseases, which attained an accuracy of 99.95% on black rot, 98.06% on black measles, 98.14% healthy, and 99.92% on grape leaf blight. The testing classification accuracy is 99.54% on black rot, 98.46% on black measles, 97.87% on healthy, and 99.82% on grape leaf blight. Tab. 13, shows the comparison with recent existing works, where the five latest methods results are compared to the proposed methodology.

Tab. 13, shows results comparison i.e., [26,57–60] where a pre-trained VGG model has been employed for diseases orange detection [26]. The convolutional neural model has been utilized for Tomato classification and achieved 99.32% and 99.0% accuracy [57,58] respectively. While pre-trained AlexNet and modified convolutional network have been utilized for the classification of maize plant disease with 70.5% and 97.89% accuracy respectively [59,60]. As compared to recent latest studies, the present study provides a new feature learning model for plants diseases classification. In the literature, no work has been done for the detection of plant disease using 38 different categories of the plant village dataset. As we observed that from the existing literature method detects the one or two different types of plant disease such as tomato, maize, and

orange, however, the proposed technique detects the different types of fruits and vegetables more accurately. The comparison outcomes show results are superior as compared to existing methods.

Table 13: Proposed results comparison

Approaches	Year	Fruits/vegetable	Results (accuracy) (%)
[26]	2021	Orange	89.5
[57]	2018	Tomato	99.32
[58]	2021		99.0
[59]	2020	Maize	70.5
[60]	2019		97.89
Proposed Method		Tomato, Maize, Apple, Potato, Strawberry, Pepper, Peach, Grape Combination of 38 types of the plant diseases	99.01, 99.60, 99.30, 98.70, 100.0, 99.74 99.82, 99.95 96.403

5 Conclusion

AI is the field where information communication technology (ICT) reaches multiple application fields in the center of the space. The algorithms that dominate AI allow for making decisions. The big performers mostly in the domain are ML & DL. DL deals with layers and optimizers identical to the neural system of the human brain, which helps to create a consistent model that shows greater precision. Therefore, the proposed study developed two optimized models. In the localization phase, the YOLOv2-Conv5 model is utilized for localization of the different types of the plants and 1.0 precision scores with 0.0 log miss rate this provides a great impact in the domain of agriculture for localization of the different types of the plant. In the second phase, extricated deep features from the plant input using pre-trained Efficientnetb0 model and transferred as an input to the next 7-layer CNN for the analysis of the complex features. The classification model achieved accuracy of 99.01% on tomato, 99.60% Maize, 99.30% Apple, 98.70% Potato, Strawberry 100.0%, Pepper 99.74%, 99.82% peach, and 99.95% on Grape. Furthermore, classification results are also computed on the combination of different types of plant diseases and achieved an accuracy of 96.403%. In the future, this work might be utilized as a front-line tool.

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