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Leaf Disease Prediction Using Fast Enhanced Learning Method

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Abstract *- More than 75% of world poverty can be reduced by the process of Agriculture. Based on the previous studies, due to the increase in plant disease, 40% of production in agriculture is in the loss. To prevent and control plant diseases, the key link is to detect the disease in the leaf parts. This paper takes tomato leaves with 10 classes, and apple leaves with 4 classes, grapes leave with 4 classes, Corn or maize leaf with 4 classes, and potato leaves with 3 classes as experimental data [18]. The Plant Village dataset available online has been collected for the purpose of training and testing the algorithms. For the process of training, the dataset has been classified into two major classes as healthy and unhealthy. And it was further classified into subclasses based on the category of disease. For the texture-based feature GLCM, haralick texture has been used, and the color histogram is used for color feature extraction, and for shape-based feature Hu moments, Zernike moments have been used. Then the proposed algorithm has been trained to predict the disease and the exact type of the disease the plant got affected with more accuracy. The corn disease has been tested with various existing algorithms like logistic regression, linear discriminant analysis, KNN, Classification and regression tree, Random Forest, Naïve Bayes with an accuracy of 78.0625,77.1875, 75. 5625, 77.75 ,85.3125, 55.375 and 78.125 respectively. Further, the images have been tested using the proposed algorithm as well, which gives an accuracy of 99.76%. Similarly tested for apple, grapes, potato, and corn or maize. When compared with the mentioned existing algorithms, the proposed extreme learning algorithm predicts the disease with more accuracy.*

Keywords - *Image Classification, Leaf Disease, CNN, K-Means clustering, NN Classifier, SVM*

I. INTRODUCTION

In recent years the global food production has become an international issue. During the late 2008's, a sudden increase in the prices of food have brought a universal crisis in some developing countries which caused economic and political instability. In the next 40 years, due to the increase in the population, the demand for food would surely increase. It is estimated that an additional 70% of the food product may be required to meet these needs by 2050[6]. Presently over 1 billion of the world's population suffer from various stages of malnutrition due to insufficiency of food supply, and just about twice that inhabitants don't have ingress to adequate vitamins or nutrients in order to meet daily nutrition needs. The reactionary in production of agriculture can be ascribed to a variety of reasons; the destruction occurred by pathogens and pests play a vital role in yield losses entire the world [1].The dropping in the crop yield because of pathogenic infections ranging from 20% to 40%. Around 12% of soybean, rice, maize, and barley are because of pathogens, potatoes and groundnuts appraise around 24%, and cotton and wheat are assessed to be around 50% and 80%. The remaining 30% to 40% loss is due to diseases[17]. Altogether the commercial deprivation cause of infections is guessed around 40 billion dollars yearly in the USA alone. So as to decrease the persuasive damage in farms while growing, harvesting, and post-harvesting process. To increase productivity and to make certain the agricultural longevity and preventing the yield are extremely important[4].

This chapter depicts how an image processing technique is used in the identification of symptoms in tomato plant disease by analyzing the colored images and recognizing the color and shape of the leaf. A software named LABVIEW for capturing the RGB color model image of the tomato leaf. Python coding was used for enabling the recognition process for determining the disease caused to tomato leaf. Before extracting the leaf image from the background, the given image is enhanced to store information on the affected pixels. To differentiate between the color of a tomato and a non-tomato leaf efficiently, the color model is used [7].

This part introduces an inventive approach to instinctively grade and detect the diseases on plants such as Bacterial Blight and some different plant disease spots. Profiling of the plant volatile natural components and molecular techniques were used in detecting diseases from their vital functions such as transpiration, pollination, fertilization, photosynthesis, germination [3].

A. MOTIVATION AND JUSTIFICATION

Direct and Indirect methods are used in the identification and detection of diseased crops. Indirect detection of the serological and molecular methods is used when a huge number of samples need to be examined using high-throughput analysis. During this process, pathogens that cause disease to plants such as fungi, bacteria, viruses are detected. Besides different plant parameters like transpiration, photosynthesis, temperature changes, morphological changes for detecting plant disease comes under indirect methods.

B. RESEARCH OBJECTIVES

The crucial objective of this section is to identify the disease caused to the leaf in order to minimize the yield loss.

1) Implementing existing methods like image classification, segmentation, and feature extraction
2) Discussing the advantages and disadvantages of direct and indirect methods.
3) Developing a new technique for feature extraction, classification of leaf disease, and segmentation for detection.

II. RELATED WORKS

The overview of the block diagram is shown in Fig.1. The training procedure is explained to the left side. The database consists of the trained images of the plant leaves with similar diseased mark images. These images indicate the accurate type and shape of diseases on leaf images [2]. Later the features are extracted from those images. Lastly, the model which is classified is trained by using the extracted features.

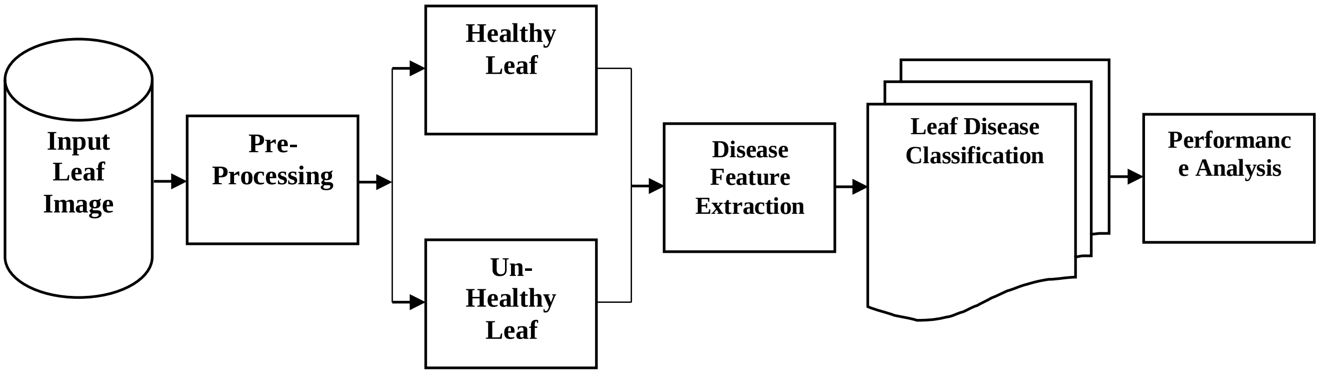

Fig 1 outline the proposed work

In this procedure, firstly, the input image undergoes pre-processing. Next comes segmentation, where the input image is segmented into 2 different categories, namely diseased and non-diseased. The non-diseased plants are excluded from leaving the diseased regions. Multiple features are extracted in the feature extraction step for describing each diseased region. After the features are generated, the before-trained classifier model is used to classify the regions. At the end, the detection results undergo validation and analysis using the performance metrics [5]. The proposed system is classified into 4 steps as

- Pre-processing,
- segmentation,
- feature Extraction and
- Classification.

A. PRE-PROCESSING

This is the foremost step in the detection of the diseased input leaf image. The input image was downloaded from the Plant Village dataset. The *training* directory containing 10000 images with 10 classes and *val* directory containing 1000 images with 10 classes were used before feeding images into the ML classifier. The images were resized to 500 X 500.

This conversion is applied for pre-processing. CIELAB is a device-independent system defined for classifying color according to human vision. In this conversion process, the RGB image is converted into CIELAB[8]

B. FEATURE EXTRACTION

After segmentation, the next task is to calculate the features from the diseased part of the leaf. The features are extracted based on texture, color, and shape. Haralick, Gray Level Co-Occurrence Matrix(GLCM), and Local Binary Pattern (LBP) methods are used for texture features. Shape-based features extraction performed by Hu Moment and Zernike moment, the meaningful shapes in the plant pixels are identified by the inherit values[13].

a) GLCM

The explicit texture of an image is recognized by the GLCM. Textural characteristics such as contrast, correlation, energy, entropy, and homogeneity may be computed from the produced GLCMs, for example. Image characteristics linked to second-order statistics[12] are estimated using this method. This technique is based on the belief that the information about texture is conveyed through a limited number of associational connections. To determine the degree of similarity between GLCM[10]. Some of them use 22 features, where we have taken only 6 features [“contrast”, “homogeneity”, “energy”, “correlation”, “Angular Second Moment (ASM)”, “dissimilarity”]. Then calculated the greycomatrix & greycoprops for an angle of 00, 450, 900, 1350. Then the final result is stored in a .csv file.

Table 1: GLCM texture compared using tomato plant, disease classes.

	dissimilarity_0	correlation_0	homogeneity_0	contrast_0	ASM_0	energy_0	label
0	19.54118404	0.1848	0.05036	624.123	0.00054	0.02328	Potatohealthy-112-
1	24.89253539	0.1162	0.03909	987.014	0.00048	0.02185	Potatohealthy-116-
2	21.13899614	0.2368	0.04796	713.484	0.00052	0.02272	Potatohealthy-95-
3	32.33783784	0.25017	0.0315	1769.82	0.00042	0.02043	Potatohealthy-142-
4	29.63127413	0.03206	0.03908	1455.63	0.00046	0.02148	Potatohealthy-120-
5	22.38931789	0.34864	0.04723	865.513	0.00048	0.02202	Potatohealthy-115-

Table 1 calculates greycomatrix and greycoprops of potato plant disease classes using 6 metrics, namely “contrast”, “homogeneity”, “energy”, “correlation”, “Angular Second Moment (ASM)”, “dissimilarity” for an angle of 0^0, 45^0, 90^0, 135^0. It shows few results of class label Potatohealthy for an angle 0^0.

b) HU MOMENTS

It extracts the features from the image by using the OpenCV function cv2.HuMoments() flattened. It means the moment of the image converted into the vector using flatten (). Hu Moments are a set of seven numbers that are image transformation invariant and can be calculated using central moments. In the first six, you'll find translation, size, and rotation. The sign changes at the last moment for picture reflection. The most popular are Hu Moments, which can be found in a number of locations [11].

c) ZERNIKE MOMENT

These are used as shape descriptors and undergo orthogonality property. For achieving scale variance and translation, an extra normalization process is required. Image centroid is used to achieve translation normalization.

$$A_{mn} = \frac{m+1}{\pi}\int_x\int_y f(x,y)[V_{mn}(x,y)]^*\, dx\, dy \qquad (1)$$
$$\text{where } x^2 + y^2 \leq 1$$

Where x2 represents the normalized image's intensity value and Vmn* represents the complex conjugate of a Zernike polynomial of degree n with angular dependence.

d) COLOR HISTOGRAM

OpenCV's cv2.calcHist() function used to extract Color Histogram features from the image. The picture, channels, mask, histSize (bins), and ranges for each channel are the arguments it expects (typically 0-256). The histogram is then normalized using the OpenCV normalize () function, and a flattened version of the normalized matrix is returned using the flatten () function ().

C. CLASSIFICATION

The proposed work undergoes 4 th step as classification. Just feature extraction is not sufficient for finding the image from a pre-processed image. this chapter deals with Naive Bayes, KNN, RF, Logistic Regression, Decision Tree, Linear Discriminant Analysis, support vector machine, and Enhanced learning approaches

The data set is divided into a pre-defined K non-overlapping subgroup or cluster, with each data point belonging to only one group. It is an iterative algorithm. It aims to make the inter-cluster data points so close that the clusters are kept as distinct as possible. Data points are assigned to a cluster such that a minimum amount of the squared distance between the data points and the center of the cluster. The less heterogeneity between clusters, the greater the uniformity of the data points in the same cluster. Feature extraction is a critical factor of pattern recognition and machine learning activities, which is the first step towards identifying the leaf disease.

As a magic instrument for distinguishing cells, the morphologic features may thus be employed:

- Mean - Mean is the average pixel size of the image’s brightness within the zone of interest.
- Area – The area in which the blast cell surface occupies space.

Standard Deviation - Evaluate and analyze the average, extra-large, or extra small by using the Standard Deviation.

a) DECISION TREE

The Data Science and Machine Learning practitioners can find Decision Tree training useful. A Random Forest classifier, which is the outcome of a number of several decision trees working together, is frequently created. Decision trees are employed by interrogating a specific record in the dataset. If a decision has been made, a follow-up question is asked about each time. A decision tree, which is a network made up of nodes and guided connections, can be used to address questions. They have three varieties of anatomy:

node with no incoming or outgoing edges Internally linked structures has precisely one inbound and two outbound edges. Each leaf or terminal node has exactly one inbound edge.

A decision tree is a learning algorithm that utilizes a decision model to make a prediction. It generates a result using a non-parametric predictive method. Various algorithms, including ID3, CART, and others, are employed to find the most diverse set of data. We found the best results for the CART algorithm here. First, you consider the tree's characteristics, then the root node. The judgment model is proven by comparison. This method is repeated before the correct classification or forecast is achieved.

Gini Score = 1- (pk * (1 — pk)) for classification. Where pk denotes the proportion of same-class inputs found in a given disease category.

b) NAIVE BAYES

Naive Bayes classifiers are a very simple and fast classification method. This is equivalent to every other classifier having n features (e.g., inputs) and p instances (x) that are a subset of such features, just like other classifiers. The steps to study are to understand a conditional probability model.

$$p(Cy|x1,x2,...,xy) \qquad (2)$$

For each of the dataset's y groups, have a probability distribution: We can see how you can use these conditional probabilities later to make a decision. If the feature set of features grows, the volume of data used grows. To simplify the analysis, we can conclude that features are independent of class. Even if this isn't valid in the modern universe, it yields a single succinct classifier.

c) LOGISTIC REGRESSION

If the dependent variable is a binary variable, logistic regression is your best option (binary). Regression research, as all others predict Using logistic regression to characterize data and explain nominal, ordinal, or interval-level, or ratio-level independent variables' E logistic regressions can be complicated at times; the ISTAT program simplifies the analysis and explains the outcomes The technique is a lot like linear regression

To estimate a value, parameters (the Greek capital letter Beta are used) (y). The value being modeled is binary rather than continuous, making the performance far-prediction linear regression inaccurate

$$y = (1 + e^{(b0 + b1*x)} / e^{(b0 + b1*x)} \qquad (3)$$

The single input value coefficient is b1, and the bias or intercept expression is b0. The predicted output is y, and the bias or intercept expression is b0 (x). In order to use your training data as input data, you must know the b coefficient (a constant real number) for each column of your input data. When you write a formula in a register or in memory, the coefficients in equation b's represent the precise expression of the formula that you will put there.

d) LINEAR DISCRIMINANT ANALYSIS

When it comes to supervised classification issues, Linear Discriminant Analysis (LDA) is a dimensionality reduction approach that is extensively utilized. In group distinctions, such as dividing two or more classes, it is used to express group differences. Higher-dimensional characteristics are projected onto a lower-dimensional environment and vice versa. We have two groups, for example, and we need to be able to distinguish between them efficiently. Classes can be distinguished by a variety of features. Using only one characteristic to differentiate them can result in some overlap, as seen in the picture below. Because of this, we will keep increasing the number of characteristics required for accurate categorization in the future.

The fundamental equation of generalized linear model is

$$g(E(y)) = \alpha + \beta x1 + \gamma x2 \qquad (4)$$

Where g is the link function, E(y) denotes the target variable, and $\alpha + \beta x1 + \gamma x2$ denotes the linear predictor $((\alpha, \beta, \gamma)$.

e) SVM (SUPPORT VECTOR MACHINES)

SVM stands for supervised machine learning model, and it is used to solve two-group classification issues by employing classification methods. There are several ways to identify the two kinds of data points. We want to have the largest range of the two classes of data points. Reinforcing the difference between capacities offers better data classification. Decision hyperplanes are good for classifying data. Many different classes are allocated to each point on the hyperplane. Also, the number of functions for the hyperplane is: If the hyperplane has two features, it's just linear. As the number of input variables grows, the hyperplane becomes two-dimensional. Features amount to clutter; it is difficult to imagine. Support vectors are points which impact the hyperplane in relation to the x- and y-coordinates. These are the classifier's support vectors. It will be changed if the support vectors are removed. These will help us to train our SVM.

If a dataset is linearly separable, we can use the Hard Approach or find two parallel planes that divide it and determine each class separately. However, since most datasets are not linearly separable, we must resort to a two-term approach. When the data is in a higher-dimensional space, the second solution is to use a Non-Linear Kernel (one that must satisfy the Mercer condition). The issue you'll have to deal with is:

$$minimize1 \;/\; 2\|w\|^2+C\sum i=1n\xi i \;, \; subjecttoyi[xi\cdot w+b]\geq 1-\xi i \qquad (5)$$

The hyperparameter is C, and the distance from the point to the boundary line is i. The margin size is 1/ ||w||, the hyperparameter is C, and the distance from the point to the boundary line is i. Finally, we must decide the best margin and penalty balance. The only parameter we can use is C since the optimization problem and calculus are committed to the calculators.

f) RANDOM FOREST

In general, the random forest works without hyper-parameter tuning. Because of its ease of use and applicability, it is also used (It may be applied to both classification and regression problems.). We'll go through the random forest method, its variation, and how to use it in this tutorial. Our tree learning algorithm is random.

Hyperparameters are used in random forest models to improve prediction or run more efficiently. Let's examine the random forest function's hyperparameters in sklearn.

Hyperparameters : n_estimators , max_features , min_sample_leaf (increases the predictive performance), n_jobs, random_state, oob_score (used for cross validation) (helps to increase the model speed)

g) K-FOLD CROSS-VALIDATION

The cross-validation model is the most likely to accurately predict the model's performance. A simple way of explaining it is to say it would be to say that split the dataset into k parts, here K = 10 chosen, splitting of the dataset is known a fold.

This technology was conceived out of necessity, and therefore a method that emerged from it was cross-validation. "Conducting a holdout (or split) experiment", "testing the model performance on the other" is a computational procedure that first partitioned the dataset into holdout samples, then trained the models on one of that data subset, and then assessed their overall performance on the remaining samples. In an effort to reduce complexity, we perform several different subsets of the same data sets of data for each round of cross-validation. To approximate the overall performance of the model's predictive capacity, we take the average of these many estimates. In the case of the cross-validation method, the models were estimated with greater accuracy. The result of performing cross-validation is k distinct performance scores, which may be summarized.

Eng-exploratory molecular imaging Cross-validation divides the dataset is randomly into k groups or folds, and each of these groups receives an extra sample of the test dataset. At this point, the model is only used as k-1 times while the initial fold is used for analysis. - time K iterations are performed, the technique is applied to a separate subset of the results to assess the impact of variations in each fold or population

III. ENHANCED LEARNING METHOD (ELM)

Algorithm

```
Begin
Input: Leaf data D_ImageNet = $\{x_i, y_i\}_{i=1}^{m}$
Output: model M, Accuracy A, Classifier H
$x_i = \{x_1, x_2, \dots \dots . x_n\}$
F = $\{f(x_1), f(x_2), \dots . f(x_n)\}$
F- Set of input features
$q_i$ – query features.
For feature f=1 to n, do
    Learn $F_n$ based on $D_{1..m}$
    Perform feature matching between database feature and query feature
    d(p,q)=$\sqrt{\sum_{i=1}^{N}(q_i - x_i)^2}$
    Append all the distance values
    results = max (d(p,q))
    If results< threshold
        Defected leaf
    Else
        Normal Leaf
End for
End
```

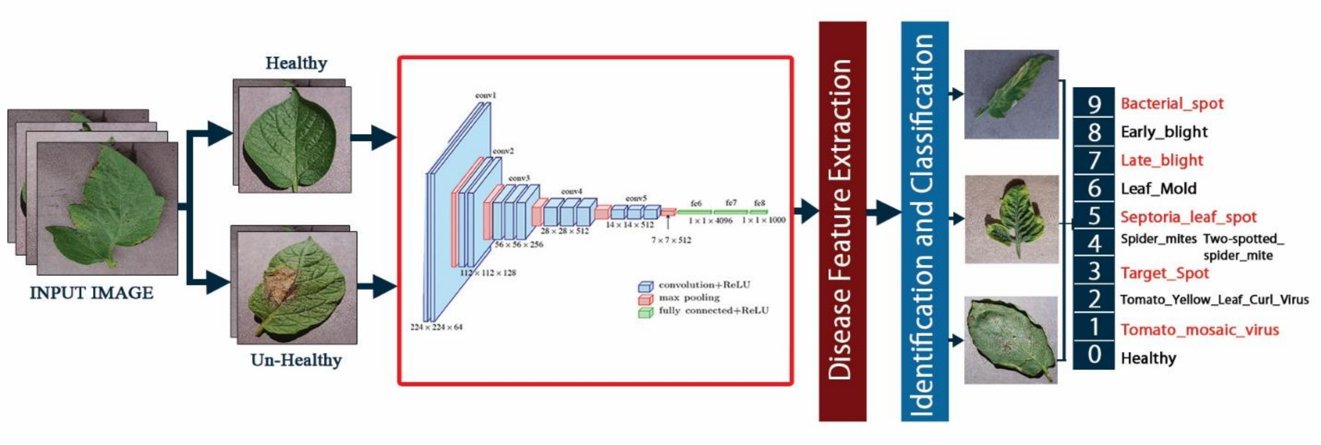

Fig 2: Enhanced learning Architecture

Fig.2 are split into train and test images, and training images are used to train and fit the model and test images to evaluate the model's performance on an unknown dataset. The image pixel data of train and test are stored as an array format of defined dimensions. Then the resultant image array is normalized to ensure the pixel has a similar data distribution. The Output column, which is to be predicted, is removed from input data and stored as a "categorical value" in the output column for the Model fitting. The Neural convolutional system is utilized for training and testing. Each information of the image will go through a progression of convolution layers with filters (Kernels), Pooling, completely associated layers (FC), and apply Softmax capacity to characterize the images. Provide the input images into the first convolution layer, which has 32 units and a kernel size of 3*3 and has a relu activation function to introduce non-linearity, and padding is the same as it applies padding to the input image so that the input image gets fully covered by the filter and specified stride. Figure 3 shows the machine learning-based classification model.

It is called SAME because, for stride 1, the output will be the same as the input. And again same convolution layer with the same parameters is used, followed by pooling with 2*2 filter. Dropout Layer comes last. It refers to dropping out units (hidden and visible) in a neural network associated with probability. The dropout layer prevents the overfitting of data. This is repeated twice with modified units and finally followed by a fully connected Dense layer as the Output layer. It has softmax regression units as same as the number of classes to output 7 different classes. Adam optimizer is used instead of stochastic gradient descent to update network weights iterative based on training data, and it can handle sparse gradients on noisy problems. Learning rate annealer is set monitoring the accuracy value of the model if it stays the same after no of epochs with no improvement after which learning rate will be reduced. Learning rate annealing is you start learning at high LR and decrease it when you get closer to the local minimum. ImageDataGenerator() function from Keras is used for data pre-processing and augmentation. Finally, the model is run for 50 epochs (an epoch is single forward and backward propagation) with a batch size of 12 images. Then validation and testing are done, evaluating the performance of the model.

Resnet is commonly used for classification purposes in pattern recognition and image identification. The picture is resized with its shorter side arbitrarily tested in [256,480] for scale increase. A 224×224 yield is arbitrarily examined from a picture or its even flip, with the per-pixel mean subtracted. Residual Network: Based on the above plain system, an alternate route association is embedded (Fig. 2, right), which transforms the system into its partner lingering rendition. The personality alternate routes F(x{W}+x) can be legitimately utilized when the info and yield are of similar measurements. At the point when the measurements increment, it thinks about two alternatives: The easy route performs character planning, with additional zero passages cushioned for expanding measurements. This choice presents no extra boundary. The alternate projection route in F(x{W}+x) is utilized to coordinate measurements (done by 1×1convolutions).

A. INPUT LAYER

The first input layer considered all the resized augmented data on this layer

B. CONVOLUTIONAL LAYERS

Convolutional layers are used for the computation of all the tasks related to all the layers, and it is also called a primary layer in CNN. It performs the task related to input convolution, and it sends the output of these layers to the next convolutional layer. The process continues to learn all the low-level features up to the high-level features and also learn all the deep specific features.

C. MAX-POOLING LAYERS

The Max-pooling layers are presented in between the convolutional layers, which are responsible for pixel reduction and reduction of computational reduction. The pooling layer works almost every pixel to reduce the computational cost. It just works like filters that are applied to the image, which is responsible for noise reduction. It also applied to the feature map. The pooling layer size is smaller than the feature map. The size of the pooling layer has 2x2 strides of 2 pixels, which means the reduction of the pooling layer will be the size of a factor of 2 of the feature map. In our methodology, the Max-Pooling layer is added in between convolutional layers to find out the max value for the feature map.

D. SOFT MAX LAYER

In softmax layer converts the given input from the previous layer into probabilities. Numerous multi-layer neural systems end in a penultimate layer that yields genuine esteemed scores that are not helpfully scaled and which might be hard to work with. Here the softmax is extremely helpful on the grounds that it changes over the scores to standardized probabilities

E. FULLY CONNECTED LAYER

The size of the feature map was separated and diminished in light of the convolution and max pool layers in the information pictures. The last output depends on the classes got by the completely associated layer. The Resnet the cfirst layer does the separating in the given info pictures with the components of 236x236x3 alongside the 110 parts of measurements 12x12 in which 236x236 is width and tallness, and 3 speaks to depth, which RGB individually. The element map got from the convolutional layer is passed to the following layer, which further diminished the element guide and went to the following convolutional layer. Lastly, it arrives at the completely associated layer. The fourth and fifth layers having more kernels; in the fully connected layer, the number of neurons is more than 4000. It is interconnected with each layer in the network, and it also had an activation function in all the previous layers.

F. TRAINING AND TESTING

During this training and testing phase, the images were taught by the layers that represented them in the network. Disease classification is done exclusively in the new layer that is created in the network due to the activation function that is essential for data training and the proper classification of disease. Following training, parameters were included as epochs, learning rate, and batches to extract 70% of the learned model from the dataset. The model was trained with batches ranging from 1 to 10 and epochs ranging from 1 to 10.

IV. RESULTS AND DISCUSSION

This experiment evaluates the contribution of each type of classifier in the detection of disease-affected parts in leaves. It takes KNN, Naive Bayes, ANN, SVM, and ELM as the classifiers. Detection accuracy analysis for classification based on plant disease crops using all classifiers shown in Table 3.1

Table 2. Accuracy analysis of different classification methods

Tomato Leaf disease								
Metrics	LR	LDA	KNN	CART	RF	NB	SVM	**ELM**
Accuracy	0.75925	0.76375	0.79375	0.72475	**0.91025**	0.6145	0.75925	**0.9976**
Error Rate	0.24075	0.23625	0.20625	0.27525	0.08975	0.3855	0.24075	**0.0024**

Apple Leaf disease								
Metrics	LR	LDA	KNN	CART	RF	NB	SVM	**ELM**
Accuracy	0.946	0.949	0.935	0.933	0.98	0.639	0.951	0.9912
Error Rate	0.054	0.051	0.065	0.067	0.02	0.361	0.049	0.0155

Corn or Maize Leaf disease								
Metrics	LR	LDA	KNN	CART	RF	NB	SVM	**ELM**
Accuracy	0.78063	0.77188	0.75563	0.7775	0.85313	0.55375	0.78125	0.995
Error Rate	0.219375	0.228125	0.244375	0.2225	0.146875	0.44625	0.21875	0.005

Potato Leaf disease								
Metrics	LR	LDA	KNN	CART	RF	NB	SVM	**ELM**
Accuracy	0.968	0.9416	0.9591	0.97	0.9866	0.54667	0.9675	0.9989
Error Rate	0.032	0.0584	0.0409	0.03	0.0134	0.45333	0.0325	0.0575

Grape Leaf disease								
Metrics	LR	LDA	KNN	CART	RF	NB	SVM	**ELM**
Accuracy	0.9468	0.9493	0.9356	0.9331	0.98	0.6393	0.9512	0.9942
Error Rate	0.0532	0.0507	0.0644	0.0669	0.02	0.3607	0.0488	0.0142

In the existing approaches such as LR, LDA, KNN, CART, RF, NB, SVM. The Random Forest classifier Performs better than other existing ML approaches. But Comparatively less than the Proposed Method.

Tomato Leaf Disease ["Bacterial_spot", "Early_blight", "Late_blight", "Leaf_Mold", "Septoria_leaf_spot", "Spider_mites Two-spotted_spider_mite", "Target_Spot", "Tomato_Yellow_Leaf_Curl_Virus", "Tomato_mosaic_virus", "healthy"]				
Labels	precision	recall	f1-score	support
0	0.95	0.96	0.96	100
1	0.92	0.8	0.85	88
2	0.94	0.92	0.93	105
3	0.87	0.97	0.92	110
4	0.95	0.79	0.86	94
5	0.87	0.92	0.89	96
6	0.84	0.91	0.87	101
7	0.96	0.98	0.97	89
8	0.96	1	0.98	106
9	0.99	0.95	0.97	111
accuracy			0.92	1000
macro avg	0.92	0.92	0.92	1000
weighted avg	0.93	0.92	0.92	1000

Corn or maize leaf Disease ["Blight" - 0 , "Common_Rust" - 1, "Gray_Leaf_Spot" - 2 , "Healthy" - 3]				
	precision	recall	f1-score	support
0	0.72	0.75	0.73	106
1	0.94	0.9	0.92	87
2	0.74	0.75	0.75	100
3	0.98	0.98	0.98	107
accuracy			0.84	400
macro avg	0.85	0.84	0.85	400
weighted avg	0.84	0.84	0.84	400

Grape leaf Disease ["Grape Black Measles", "Grape Black rot", "Grape Healthy", "Grape Isariopsis Leaf Spot"]				
	precision	recall	f1-score	support
0	0.72	0.75	0.73	106
1	0.94	0.9	0.92	87
2	0.74	0.75	0.75	100
3	0.98	0.98	0.98	107
accuracy			0.84	400
macro avg	0.85	0.84	0.85	400
weighted avg	0.84	0.84	0.84	400

Potato leaf Disease ["Potato Late blight", "Potato Early blight", "Potato Healthy"]				
	precision	recall	f1-score	support
0	0.97	0.98	0.98	105
1	1	1	1	103
2	0.98	0.97	0.97	92
accuracy			0.98	300
macro avg	0.98	0.98	0.98	300
weighted avg	0.98	0.98	0.98	300

Apple Healthy leaf Disease ["Apple Healthy", "Apple Black rot", "Apple Scab", "Cedar apple rust"]				
	precision	recall	f1-score	support
0	1	1	1	87
1	1	0.97	0.99	106
2	0.96	1	0.98	100
3	1	0.99	1	107
accuracy			0.99	400
macro avg	0.99	0.99	0.99	400
weighted avg	0.99	0.99	0.99	400

Table 3 Classification report for Random Forest classifier compared different plant disease

A. PERFORMANCE ANALYSIS OF FEATURE EXTRACTION APPROACHES

In this experiment, this work will evaluate the contribution of each type of feature extraction approach in the plant disease detection techniques[9]. This experiment takes texture, shape, color features into consideration to extract the disease-affected part. For classifier, this experiment uses the ELM approach as the classifier, which gives the best result, as shown in Table 3.1. Five performance metrics are mentioned in section 1.10. From five performance metrics, this experiment takes only two parameters, such as detection accuracy and error rate analysis[16]. Table 3.8 shows that detection accuracy and error rate analysis of LBP, Zernike moment, and color moment methods give the best results for extracting the affected parts in leaves[14][15].

Table 4 Accuracy and Error rate analysis of Feature Extractions

Classifier	**Performance Metrics**	**Feature Extractions**				
		Texture		**Shape**		**Color**
		GLCM	**Haralick Texture**	**Hu Moments**	Zernike moment	**Color Hstogram**
LR	**Accuracy**	0.5593	0.75925	0.75925	0.5593	0.75925
	Error Rate	0.4408	0.2408	0.2408	0.4408	0.2408
LDA	**Accuracy**	0.5636	0.76375	0.76375	0.5636	0.76375
	Error Rate	0.4365	0.2363	0.2363	0.4365	0.2363
KNN	**Accuracy**	0.318	0.79375	0.79375	0.318	0.79375
	Error Rate	0.682	0.2063	0.2063	0.682	0.2063
CART	**Accuracy**	0.5246	0.72475	0.72475	0.5246	0.72475
	Error Rate	0.4755	0.2753	0.2753	0.4755	0.2753
RF	**Accuracy**	0.6450	**0.9103**	**0.91025**	0.6450	**0.91025**
	Error Rate	0.3550	0.0898	0.0898	0.3550	0.0898
NB	**Accuracy**	0.415	0.6145	0.6145	0.415	0.6145
	Error Rate	0.586	0.386	0.386	0.586	0.386
SVM	**Accuracy**	0.5593	0.75925	0.75925	0.5593	0.75925
	Error Rate	0.4408	0.2408	0.2408	0.4408	0.2408

Table 5 Accuracy and Error rate analysis of Proposed method

Classifier	**Performance Metrics**	**Tomato Disease (10 classes)**	**Corn or Maize Disease (4 Classes)**	**Apple Disease (4 Classes)**	**Potato Disease (3 Classes)**	**Grapes Disease (4 Classes)**
		Label Binarizer (transformation)	**Label Binarizer (transformation)**	**Label Binarizer (transformation)**	**Label Binarizer (transformation)**	**Label Binarizer (transformation)**
ELM	**Accuracy (%)**	0.9976	0.995	0.9912	0.9989	0.9942
	Error Rate (%)	0.0024	0.005	0.0155	0.0575	0.0142

Table 3 illustrates the summaries of accuracy and error rate analysis for the feature extraction method with different algorithms. The plant leaves classify into three categories based on the type of texture, shape, and color. It is observed that Haralick belongs to the texture feature, and it performs the best accuracy and error rate among all the Five plant crops. The shape feature includes Hu Moments and Zernike moment. It can be seen that the Hu moment method obtains the best results in all categories other than the two existing approaches. For all accuracy and error rate, from beginning to end, crops were detected by both color histogram and color moments based on the color. Each color histogram shown in Table 5 represents crops, where all crops are highlighted in the analysis with the highest attention values. It is already proved that ELM has fast learning speed and good generalization performance than other classifiers. It is observed from Table 5. The experimental results also prove this. From the experimental results listed in In Feature extraction, the Local Binanzier technique is used for texture, as it can produce better results even in the image rotation process. Local Binanzier transformation is more suitable for recovering attacks operations. From the experimental results listed in the above tables.

In this chapter, various plant leaf disease detection techniques are taken for analysis and comparison purposes. The comparison is done as three steps of the work such as segmentation, feature extraction, and classification. This work utilizes the supervised machine learning methods classifiers, feature extraction techniques, and segmentation methods for the comparison process. As shown in Table 5, the ELM classifier obtains an average accuracy of 99.1%. Precision, f-score, and recall values also have shown better results. From these results, it is observed that ELM performs best other than the existing approaches. Similar experiments are also conducted for segmentation, and feature extraction approaches. The resultant accuracy indicates that the Haralick for texture, Hu moment for shape, and color Histogram for color features performs best in the feature extraction. So, the three approaches, namely such as segmentation using KNN, feature extraction using LBP, Hu moment, color Histogram, and ELM classifier, are used for the development of new automated leaf disease detection techniques.

V. CONCLUSION

In this paper, various plant leaf disease detection techniques are taken for analysis and comparison purposes. The plant leaves were classified into three categories based on the type of texture, shape, and color. It is observed that Haralick belongs to the texture feature, and it performs the best accuracy and error rate. Hu moment method obtains the best results in all categories other than the two existing approaches. ELM classifier obtains a higher accuracy of 99.76% for tomato disease. Precision, f-score, and recall values also have shown better results.

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