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Identification of chilli leaf disease using contrast limited histogram equalisation and k-means clustering

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ABSTRACT

Plant disease diagnosis is crucial for preventing productivity and quality losses in agricultural products. Because plants are continually attacked by insects, bacterial infections, and smaller scale organisms it is necessary for early diagnosis disease control is a vital part of profitable chilli crop production, hence early diagnosis of disease identification is an important aspect of crop management. This paper discusses strategies for detecting disease effectively in order to improve chilli plant product quality. An image processing technique based on identification of chilli leaf disease using contrast limited histogram equalisation and k-means clustering (KMC). The approach was carried out in five stages: acquiring the image, preprocessing, extracting features, classifying the diseases, and showing the outcome. This work offers a thorough implementation of CLAHE for preprocessing, k-means cluster for feature extraction and support vector machine (SVM) for classification of chilli leaf diseases. The accuracy was tested for standard chilli dataset for major 2 types of diseases including anthracnose and bacterial blight form kaggle dataset with varying samples of 70:30 and 60:40 respectively and it is observed that the average accuracy improved to 98% compared to existing techniques.

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1. INTRODUCTION

Plant disease is a major cause of reduced yield and poor quality. Early disease detection is crucial for effective management toovercome this issue, and also it's important to treat and control diseases in a timely manner. Chilli crop is one of the principal horticultural commodities and these plants can be destroyed by biotic sources like insects, bacteria, fungi, and viruses. Diseases of the chili leaf have a major economic impact on farmers, supply lines, and international markets everywhere. Due to its widespread use as a spice and vegetable, output losses from chile can cause inflation, lower farmer earnings, and problems for global trade. Diagnosing the plant diseases can be challenging due to their diverse symptoms. Some of common signs include irregular leaf growth, color distortion, stunted growth, and broken pods. Pests and illnesses can lead to significant crop losses, plant mortality, and a direct impact on human health. Accurate diagnosis of plant diseases can reduce crop losses and customize treatments to specific pathogens [1]. Humans cannot distinguish many plant diseases, and it takes time to identify the disease, thus it is not always the ideal method for diagnosing diseases. Also checking the huge area of the crop and discovering the chilli plant leaf disease is a time-consuming task, and it is extremely difficult, some of prominent chilli leaf diseases [2], [3] are: i) Anthracnose is a fungal disease that causes black, sunken lesions on leaves, stems, and fruits. Colletotrichum spp. is the culprit behind this disease. It spreads quickly during rainy weather and does best in warm, humid environments. ii) Bacterial leaf spot: produced by the bacterium Xanthomonas spp., it appears as tiny, wet lesions on leaves that eventually turn brown or black. It may result in yield reduction and defoliation. iii) Powdery mildew: a white, powdery growth on the leaves, stems, and flowers of chilli plants, powdery mildew is a fungal disease caused by several species of Erysiphales. It may reduce photosynthesis and weaken the plant. iv) Leaf curl virus: caused by curled and distorted leaves, slowed development, and decreased fruit production, leaf curl viruses are spread by whiteflies or aphids. Plants that are infected may show leaf puckering and yellowing. v) Fusarium wilt: this illness, which is brought on by the fungus Fusarium oxysporum, damages the plant's vascular system, resulting in wilting, yellowing, and ultimately the plant's mortality. Crop rotation is crucial for management since it can persist in the soil for extended periods of time. vi) Phytophthora blight: this fruit and leaf disease, which is caused by Phytophthora capsici, results in dark, wet lesions that eventually decay. It travels quickly and grows best in warm, humid environments. The deep learning (DL) model [4]-[6] can monitor, diagnose, and inhibit crop growth over time. Crop disease and insect pest image recognition can lessen agricultural production's reliance on plant protection technicians, allowing farmers to fix problems more quickly. In comparison to artificial identification, intelligent network identification is substantially faster than manual detection. And the recognition accuracy is increasing continuously. DL is often utilized in agriculture by implementing convolutional neural networks (CNNs) to detect chilli leaf disease. The study helps to identify the chilli leaf diseases detection with different features of chilli using region based CNNs. The strategy was found to be better than several other existing methods based on many aspects including accuracy and memory requirements. The model guarantees and attains high accuracy of 90% or above for a number of illnesses. The model struck the right balance between accuracy and precision. This helped us to choose the optimal classifier CNN.

Araujo *et al.* [7] proposed chilli leaf disease identification using Invariant method. The required portion of the image was separated from the backdrop using graph-based segmentation, which improved the outcome by maintaining the image's shape. To classify the disease class, the extracted section containing the infection is then predicted. The process entails examining the contaminated image under examination for any signs of disease. With the purpose of matching and detecting diseases, the suggested method extracted the feature descriptors and computed the sensitivity, specificity, and accuracy for each variance. With an accuracy of 86%, the system matches. One crucial aspect of our life that can make use of this system is agriculture. In this work [8], "Convnets" was used to classify and detect plant diseases. A PlantViallge dataset was gathered from Kaggle. Images of fifteen distinct classes of plant leave-potato, pepper, and tomato-are shown. The dataset was split up into three datasets, each of which was given a Convnet application. The authors were able to detect plant diseases in potatoes, peppers, and tomatoes with an accuracy of 98.3%, 98.5%, and 95%. The outcomes of the experiments indicate that our model successfully detected and classified plant leaf diseases with a good accuracy rate. Moon *et al.* [9] of this study have arranged the sick, slightly diseased, and healthy leaves. Though they take a lot of time, effort, and are heavy-duty, traditional direct measurement techniques are typically straightforward and accurate. On the other hand, the suggested vision-based techniques are effective in identifying and observing the external signs of the condition. The current study develops CNN image processing methods to recognize the color feature of the defective area and use it to detect disease. The extent of the rotten leaf component was then inferred from the feature data of the tomato and pepper plants after the rotted area had been segmented from an image. The outcomes demonstrated the autonomous vision-based system's promising performance; in practice, it was found to have an average accuracy of 94% and to be easily validated over a vast amount of data. Several methods have been discussed [10] and used for the identification and categorization of plant diseases using pictures of afflicted leaves or crops.

By experimenting with different approaches, researchers have previously achieved great strides in the identification and categorization of illnesses. However, because of reviews, fresh developments, and conversations, adjustments are needed. Global agriculture productivity may be greatly increased by using technology. The resilience of machine learning (ML) and DL methods like k-means clustering (KMC), naive bayes (NB), feed-forward neural network (FFNN), support vector machine (SVM), k-nearest neighbor (KNN) classifier, fuzzy logic (FL), genetic algorithm (GA), artificial neural network (ANN), CNN, and so forth has been established by prior research. This work [11] suggests a fine-tuning model for plant diseases based on EfficientNetB4 that may be used to the dataset of images of chili leaves. When it comes to identifying the chili leaf picture dataset, the suggested model performs better than other pre-trained models. The model identifies anomalies and extracts features from the images. A review of the literature reveals that the model performs better than previous research. With only a few parameters, EfficientNetB4 is a neural network design that has been shown to perform well on image categorization tasks. For the purpose of identifying leaf disease, this model has been calibrated. To strengthen [12] the training network's capacity for generalization and recognition precision, the original crop images were first trimmed and normalized, and then the extraneous noise was eliminated using image data improvement. Then, a neural network with nine convolutional layers is constructed to operate on cropped images. Data samples are loaded during the first training stage, after which the training and verification sets are divided. The learning rate, optimizer, and image intensifier are then adjusted, and the training convolution model is assembled. Lastly, it assesses the model's accuracy and stores the accuracy and loss data from the training phase. Adam optimizer, which combines momentum algorithm with RMSprop algorithm, is used to dynamically alter the learning rate in order to increase the training learning rate. This research from Ngugi *et al.* [13] also proposes a CNN model that can perform semantic segmentation of the leaves and lesions in a single pass. For the leaf and lesion pixel classes, the suggested KijaniNet model demonstrated state-of-the-art segmentation performance with mean intersection over union (mIoU) scores of 0.8448 and 0.6257, respectively. For the two-pixel classes, the KijaniNet model achieved mean border F1-scores of 0.8241 and 0.7855, respectively.

Finally, a completely automated algorithm is suggested for identifying leaf diseases based on individual lesions. For lesion-wise illness detection, the technique uses a semantic segmentation network cascaded to a GoogLeNet classifier. Despite having only been trained on a tiny dataset, the suggested fully automatic methodology performs better in terms of segmentation and classification than competing techniques. Babu and Jeyakrishnan [14] propose an EfficientNetB3 model-assisted ML solution. The 87K RGB photos of both healthy and diseased crop leaves, divided into 38 different classifications, are taken from a publicly available dataset. To distinguish between diseased and healthy plant leaves, an EfficientNetB3 model is trained.

The hardest thing for researchers to deal with is working in different contexts because differences in geography might make proper identification more difficult. Because most conventional procedures rely so heavily on knowledge, experience, and manuals, they are also typically costly, labor-intensive, and difficult to define exactly. By offering creative ways to identify, treat, and avoid chili leaf infections, artificial intelligence (AI) is revolutionizing the agricultural industry. Farmers may increase production, lower financial losses, and use less pesticides with the aid of AI-driven tools. Here are some significant ways AI is tackling the worldwide issue of chili leaf disease.

Using fundamental statistical and mathematical methodologies, leaf illnesses were identified from image samples using traditional image processing techniques like Otsu's method of thresholding used for establishing an ideal grayscale threshold to distinguish between healthy and sick portions of the chili leaf. This may not function effectively with complex backdrops; sensitive to lighting conditions. Also Leaf borders and lesion patterns are detected using edge detection (Canny, Sobel, Prewitt) but has trouble with noise and overlapping areas, but performs best with simple patterns. This study proposes the use of image processing to aid in the diagnosis of plant diseases in chili leaf plants. The remaining portions of the paper are arranged as follows: section 2 presents background information on the topics covered in this study and then delves into a survey of similar works. In section 3 presents an overview of the suggested approach along with the steps involved in diagnosing a chilli plant's ailment. An account of the experimental design and results analysis is given in section 4. As the report draws to an end, the conclusion points out its shortcomings and makes recommendations for more study.

The main contributionsof the paper are as follows:

a. We propose a categorization method for improvement of accuracy on their objective functions of preprocessing strategies.
b. The effect of CLAHE on disease identification is analysed.
c. The robustness of each type of disease classification is studied on a real-world chilli image dataset, and the performance of k-means clustercorresponding to different diseases is analyzed.
d. The ROI calculation using the affected area further helps to improve the accuracy of classifications.

2. METHOD

The Figure 1 shows the process of our technique for identifying chili-based plant leaf diseases, which which involves contrast limited adaptive histogram equalization (AHE) for preprocessing with color transformation, k-means and ROI for localizing and identification of diseases and finally SVM classifier for measuring the accuracy.

2.1. Data acquisition

The Kaggle [15] website was used to obtain images of plant leaf diseases. As illustrated in the Figure 2, the gathered dataset comprises roughly 75 images associated with 3 distinct classes. Leaf curl, leaf spot, and one class of healthy leaf set are among the disease classes included in the collection.

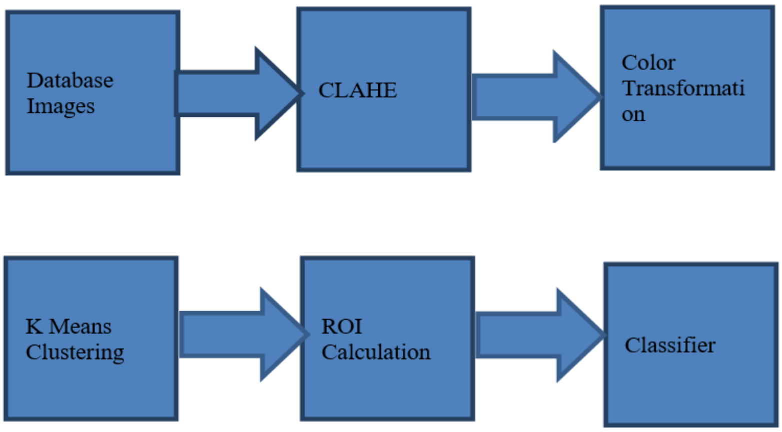

Figure 1. Proposed methodology

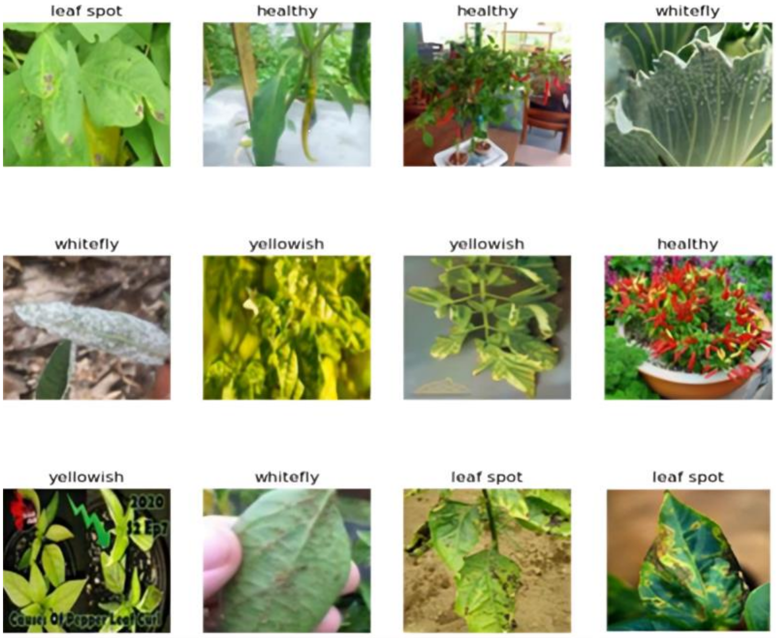

Figure 2. Kaggle dataset samples

2.2. Pre processing

In many computer vision applications, such as the diagnosis of chilli leaf disease, preprocessing is an essential first step. It entails prepping the input image for the model's analysis by implementing a number of strategies pre-processing is done to improve the image's quality so we can analyze it more successfully. Through preprocessing, we can get rid of undesired distortions and enhance certain properties that are crucial for disease classifications. Pre-processing seeks to enhance the input image's quality, remove noise or artifacts, and extract important traits that will aid in the detection of illnesses. Pre-processing methods that are frequently applied in computer vision applications include as follows:

a. Image resizing: each image is resized to a predefined size (IMAGE_SIZE, IMAGE_SIZE).
b. Resizing helps ensure that all images in the dataset have the same dimensions, which is necessary for training the SVM model.

2.2.1. CLAHE enhancement

The adaptive technique distributes the image's brightness values by computing multiple histograms, each of which represents a distinct part of the image, in contrast to normal histogram equalization [16]. It therefore does a good job of bringing out the local contrast and edges in each area of an image. To improve the input image's contrast and edges, AHE [17] is applied. Using the enhancement characteristic on each community pixel, this method calculates the transformation function. THE CLAHE involves the following steps i) histogram equalization: in order to create a more uniformly distributed image, traditional histogram equalization extends the dynamic range of pixel values. But it can also increase noise, producing unwanted artifacts, particularly in low contrast areas. ii) Adaptive approach: by segmenting the image into smaller areas known as tiles, CLAHE outperforms conventional histogram equalization. Next, each tile is subjected to separate histogram equalization instead of the image as a whole. iii) Contrast limiting: CLAHE uses a contrast limiting strategy to avoid overly amplifying noise in areas with low contrast. The cumulative histogram within each tile is limited to a predetermined value, sometimes referred to as the "clip limit." Pixels that go over this threshold are reassigned to adjacent bins, which lessens the noise amplification while maintaining the enhancement of local contrast. iv) Interpolation: the process of applying histogram equalization to individual tiles and then combining them to create the final enhanced image. The borders between tiles can be smoothed out using interpolation techniques to prevent artifacts.

The CLAHE can show the boundary value of the histogram, which can help alleviate the problem of overly high contrast. A limit value that indicates the maximum height of a histogram is called the clip limit. The (1) explains how to find the clip limit of a histogram:

$$\beta = \frac{M}{N}\left(1 + \frac{\alpha}{100}\left(S_{max} - 1\right)\right) \tag{1}$$

The variables M and N provide the region's dimensions, 256 is the value of the grayscale, and is a clip factor that represents the insertion of a histogram between 0 and 100. The generation of the CLAHE image begins with the setting of the region's size and clip limit, followed by the histogram's shape for each region, cutting the old histogram with the clip limit and distributing the excess to the new one, mapping the new histogram to the image, and finally performing pixel interpolation in the nearby region. Applying CLAHE helps smooth out the image, reducing noise and emphasizing important features. The parameters provided include the image in grayscale, the clipping limit set to 0.01, and the number of tiles for the histogram equalization algorithm set to 8x8. The enhanced image using CLAHE is shown in Figure 3.

Figure 3. CLAHE enhanced image

2.3. K-means clustering

KMC [18] is a well-liked unsupervised ML technique that groups or clusters comparable data points. Its goal is to divide a dataset into K clusters, each of which will contain a data point and belong to the cluster with the closest mean. The following process is followed to extract k-mean features: i) Choose K data points at random as the dataset's initial cluster centroids. ii) Assign each data point to the closest centroid to create K clusters. iii) Centroids should be updated by taking the mean of all the data points allocated to each cluster and recalculating the centroids of the K clusters. iv) Until convergence, steps two and three are carried out repeatedly. When the centroids stop changing noticeably or when a predetermined number of iterations is reached, convergence takes place. v) After convergence is reached, the final centroids show the cluster data. The input data, which is often a matrix with the data points to be clustered, is represented by this parameter. It appears to be in the Lab color space in this instance, where each row denotes a data point. When convergence is reached, the output is represented by the final centroids. The distance metric used for clustering is specified by this option. The term "sqEuclidean" here refers to the squared

Euclidean distance, a popular option for KMC. The number of times to perform the clustering procedure with various initial cluster centroid coordinates is indicated by this option. This enhances the clustering algorithm’s resilience. There are two outputs from the kmeans function: The cluster indices allocated to each data point in the input matrix ab are contained in this vector. Every element in cluster_idx designates which cluster the data point is associated with and correlates to a row in the input data. Following the clustering process, this matrix contains the final cluster centroids. The centroid coordinates of a cluster in the same space as the input data are represented by each row of cluster_center.

2.4. Support vector machine

SVMs are a strong and adaptable class of supervised learning algorithms that are applied to regression and classification problems [19], [20]. The significance of SVMs arises from multiple fundamental attributes and benefits. SVMs are effective in high-dimensional spaces, where they outperform other methods in jobs where the number of features is greater than the number of samples. Because of this characteristic, they are very helpful in areas like image recognition, text categorization, and bioinformatics. Compared to many other ML methods, SVMs are less likely to overfit, particularly when the kernel function and regularization parameter are carefully adjusted. Because of this, SVMs may effectively generalize to new data. SVMs can accept a variety of kernel functions, such as sigmoid, polynomial, linear, and radial basis function (RBF) kernels. Because of their adaptability, SVMs can handle a wide range of data kinds and learn intricate decision boundaries. SVMs employ kernel functions to transfer the input characteristics into a higher-dimensional space, which allows them to handle non-linearly separable data with efficiency. They are able to acquire high classification accuracy and grasp complicated decision limits as a result. SVMs guarantee that the solution found is the global optimum as opposed to a local one because the objective function they use corresponds to a convex optimization issue. This characteristic boosts the taught model’s dependability and ensures that the training process will converge. The function fitcsvm to train an SVM classifier, where “train” is an index or logical array that denotes the training samples. Groups (train) is a reference to the training data’s matching class labels or groups.

The option’showplot’, false indicates that no plot should be shown while the machine is being trained. ‘Kernel_function’linear’ indicates that the SVM should employ a linear kernel. A system that learns from statistical aspects of input signals is called an SVM. The characteristics with the largest margin are used to compute the various hyper-planes. The following equations were used to produce the optimal hyper-plane:

$$\alpha . y_i + b = \begin{cases} \geq +1; if \text{xi} = +1 \\ < +1; if \text{xi} = -1 \end{cases} \tag{2}$$

The symbol yi represents the input ith vector. The level allocated to the ith input is xi. The best margin between several hyper-planes is represented by the weight vector, or α.

$$\alpha_i + b \leq \pm 1 \tag{3}$$

After that, the support vectors are calculated using the transform space.

$$k(x_i, x_j) = \varphi(x)\varphi(x_j) \tag{4}$$

The feature class calculation equation for the above equation is as follows:

$$f(x) = sign\left(\sum_i \alpha_i y_j \, \varphi(x)\varphi(x_i) + bias\right) \tag{5}$$

Where, α is dynamic weight factor.

3. RESULTS AND DISCUSSION

In this study, three classes of images were taken from the kaggle dataset, including healthy leaves, and two major chilli leaf diseases: anthracnose and bacterial blight. The chilli leaf dataset was balanced to provide an equal number of samples for each class, with different images for each class, with varying training and testing image samples of 70:30, 60:40 and 50:50 respectively out of 540 image samples. The recommended methodology is implemented using the MATLAB 2021 software, which uses traditional programming techniques. The individual disease classification was analyzed as shown in Table 1. It is observed that for 2 major the types of diseases it has the average accuracy classification of 96% and above.

Table 1. Individual disease classification accuracy

Serial No.	Disease type	Accuracy (%)
1	Anthracnose	96.9892
2	Bacterial blight	97.0847

The Table 2 shows the accuracy results for varying database calculated for total available samples in terms of 70:30 and 60:40 percentage samples. It is observed that the results achieved looks promising with minimum of 97.03 and maximum of 99.3 for varying databases respectively and avaearage accuracy results of 98 %. This shows that our proposed approach is more robust in terms of preprocessing using modified histogram and also accurate feature extraction with modified KMC.

Table 2. Accuracy with varying database samples

Serial No.	Training: testing samples in (%)	Accuracy (%)
1	70:30	99.3
2	6 0:40	97.03

The detection rates of several popular algorithms [21]-[25] are compared with the actual detection rate of the proposed technique in Table 3. Remarkably, the references that are now available place minimal focus on adaptive learning and instead use basic k-meanswithout preprocessing and FL. Since our suggested method forecasts on adaptive histogram with proper clipping limit it achieves better enhancement and adaptive learning strategy, it performs better than earlier algorithms in terms of detection accuracy.

Table 3. Performance evaluation with other existing works

Serial No.	Disease type	Accuracy (%)
[21]	Test of uni-variate statistical features	90
[22]	GLCM	90
[23]	SVM	93
[24]	DL	95
[25]	ML	89
Proposed	K-means+SVM	97.03

4. CONCLUSION

Chilli leaf detection relies heavily on ML, which enables farmers and agricultural researchers to precisely and effectively identify pests, illnesses, and nutrient deficits. This article describes an efficient strategy to classifying plant diseases that combines approaches from k-means with SVM classifiers. Feature vectors are created using the k-means algorithm from diseased data. The selected vectors are then identified by comparing the test and database data. The CLAHE technique employed is used to improve accuracy by proper choosing of clip factor. Our suggested technique allowed us to achieve 97.03 percent accuracy because the qualities were optimally classified into classes. Future iterations of the approach could enhance both classification time and accuracy. In future, to identify plant diseases in chili plants, more emphasis needs to be placed on the development and improvement of DL models (such as recurrent neural networks and convolution neural networks). This should be followed by validation from farmers and agronomists to produce interpretable algorithms that provide explanations for their forecasts.

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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

Authors state no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are available on request from the corresponding author, [initials].

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