Classification of Diseases in Rice Crops using Deep Convolutional Neural Networks for Agricultural Applications

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Abstract:
Agricultural crops are the important sources of energy, and are the primary way to resolve the crisis of global warming. There are various diseases that affect the agricultural crop health with the potential to source disturbing social, economical, and ecological losses. Over number of agricultural crops, rice acts as the major grain all over the world, and hence it is important to identify the type of the disease that attack the rice crop at early as possible in such a way to choose the proper pesticide to be used. This paper proposes a deep convolutional neural network (Deep CNN) based disease classification strategy for rice crop with the aid of the significant features of the input image. The proposed strategy possesses enhanced convergence characteristics and capable to deal with dataset of larger size. The effectiveness of the proposed model is deliberated by comparing the performance with the existing methods, in terms of the performance metrics, such as accuracy, precision, and recall. The accuracy, precision, and recall of the proposed method are attained to be 95.9181%, 94.2515%, and 97.125%, respectively, which shows the superiority of the proposed method in classification of diseases in rice plant.

Keywords: Agriculture, rice crop disease classification, crop health, pesticide, deep Convolutional neural network.
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1. Introduction

Rice, maize and wheat are the three commonly used crops of food sources throughout the world [7]. Among the three, rice exhibit the most sown filed, the largest total production and the maximum yield per unit, and acts as one of the major grains all over the world [8]. It has been predicted that by 2050, the population of the world will become more than nine billion [9]. Yet, the diseases in rice crop have been acutely deteriorating the production of rice. As a result, it is an immense task for the agricultural society to make sure the food security of such a huge population. During the growing stage of rice, various diseases are often escorted, such as sheath blight, rice blast, rice curl disease, leaf smut, bacterial leaf blight disease, and brown spot and so on. These diseases crop up in throughout the rice crop. Among the number of diseases, leaf smut, brown spot, and bacterial leaf blight are the three common diseases with the largest probability of occurrence and exhibit huge influence [4]. The crop diseases not only affect the production of crop, but also lead to ecological pollution. According to a recent survey, a loss of about 10–15% of rice crop production is originated by diseases [10]. In some cases, it may reach up to 40–50% or even no profits, leading to huge losses in economy to the cultivators who have worked hard for a year.

This is due to the reason, farmers usually do not be familiar enough about the diseases of rice crops, so they cannot completely know the event of each disease and its specific features, and thus cannot judge the disease and use the pesticides in time. Hence, high, low, or even wrong pesticides may be used, affecting the cure of disease and harm the environment and the soil. Thus, it is necessary to identify the disease and the type of disease as quick as possible to use the correct pesticide. Generally, the detection of diseases in rice plant depend either on visual estimation of the indications or the investigational outcomes by culturing pathogens in

lab. The visual estimation is a biased strategy and lead to error, and culturing the pathogens is a long time process and may not present the result in time [11]. In addition, both the traditional strategies need experts to recognize the diseases and it is hard for the farmers to access the experts with their interior agriculture field. These limitations have encouraged the researches to analyze different algorithms and design automatic methods to identify and categorize diseases in the rice plant, and simultaneously stimulate the farmers to select the right pesticides for the rice cops in such a way to increase the production [4].

This paper introduces a deep learning model to classify the diseases that affect the crops at different stages of growth. The deep CNN classifier executes the classification process in an effective way with its superiority in terms of accuracy when trained with large rate of data. The significance of the proposed model depends on the use of the imperative features that assists in enhancing the effectiveness of proposed classification model. This research provides a detailed elucidation of proposed model, and with the results, the efficiency of the proposed classification model can be validated. In addition, comprehensive evaluation is provided on the basis of the performance of the conventional classification strategies to analyze the superiority of the proposed method of disease classification in rice plants.

The contribution and the key topics discussed in the study are,

- The proposed model designs an automated deep strategy model to classify the diseases in rice plants using the images taken from the crop field.
- The significant features of the crop extracted from the input image plays a vital role in the enhancement of the performance of the proposed classification model.
- The proposed model is analyzed with the conventional methods in terms of performance measures to validate the effectiveness of the proposed strategy.

The rest of the paper is organized as: section 2 presents the survey of the recent strategies of crop disease classification with the challenges associated with them. Section 3 describes the proposed Deep CNN model in the classification of diseases in rice plants. Section 4 deliberates the outcomes of the proposed model, and section 5 concludes the paper.

2. Literature survey

This section deliberates the existing methods of classification of diseases in plants and the challenges associated with the existing model that acts as the motivation for the development of the proposed model.

2.1 Related works

The literature reviews of the existing methods are stated as, WeihuiZeng, and Miao Li [1] introduced a Self-Attention convolutional neural network that perform with enhanced effectiveness with its anti-interference capability and increased robustness. However, the ability of the developed method to deal with noise is noticeably weaker than the other methods. Hammad Masood *et al.* [3] introduced a method using the strategy named Mask RCNN that can be conveniently used in the field by the farmers without the need for technological knowledge. Feng Jiang *et al.* [4] developed a method using Deep learning and support vector machine (SVM) technology that can successfully find the diseased in rice leaf and offer technical support for the future crop fields. Lakshay Goyal *et al.* [5] designed a deep convolutional architecture for the classification of diseases that can learn from datasets of larger size in the presence of fewer amounts of resources. However, the data needed to train the model is high, which is one of the challenges of the above detailed deep learning based models. Dhruvil Shah *et al.* [6] developed the ResTS (Residual Teacher/Student) architecture that assisted in saving the gradients and reduced the problem of vanishing gradients. However, the reason for the improved performance and the way of enhancing the performance of the system was not deliberated. Dwi Ratna Sulistyaningrum *et al.* [19] used a multilayer SVM approach to classify rice plant diseases in leaf images. The accuracy value is calculated by employing a linear kernel in the SVM training process and scaling in the pre-image processing step. The technique, however, is unsuitable for huge datasets. Adiyarta et al. [20] planned to use image feature extraction and the k-NN classification approach to create a system for automated identification of rice leaf disease using digital image processing. However, the strategy does not scale well to huge datasets since computing distances between each data item would be prohibitively expensive. Maohua Xiao et al. [21] suggested a rice blast recognition approach based on principal component analysis and NN to address the problems of poor accuracy, inefficiencies, and objectivity in artificial rice blast identification. However, there are certain limitations in identifying lesions with similar form and colour.

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2.2 Problem statement

- The challenges associated with the existing methods of plant disease classification are deliberated as,
- Conventional strategies of crop disease detection may undergo the problem of tedious pre-processing step and are highly time consuming [1].
- The inadequate extraction of handcrafted features leads to the problem of image semantic gap [1].
- Overfitting is one of the major drawbacks, in which the deep learning models possess a wide gap in testing and training accuracy [5] [2].
- Machine Learning models are successful in handling different tasks, but they have a limitation of operating as a black box as they do not offer any data about how they prepare a particular decision [6].

3. Proposed method of deep learning based disease classification in rice plant

An optimization tuned deep learning model is proposed in this research to classify the different types of plant diseases at various stages of growth. The schematic representation of proposed model is depicted in figure 1.

In the initial step, the images of rice crop are subjected to pre-processing for the removal artefacts present in the raw image data. In order to isolate the required object from the input image data, segmentation of image is performed. The object is then analyzed using the proposed Deep CNN model with the provision of the features of the image as the training images. The features, such as color histogram features, Hu moment shape feature, and the Haralick texture are extracted from the image, with which the feature vector is developed based on feature concatenation. The trained Deep CNN model using the feature vector developed with the image features is tested with the test data, in such a way to classify the diseases of the plant, particularly the rice crop.

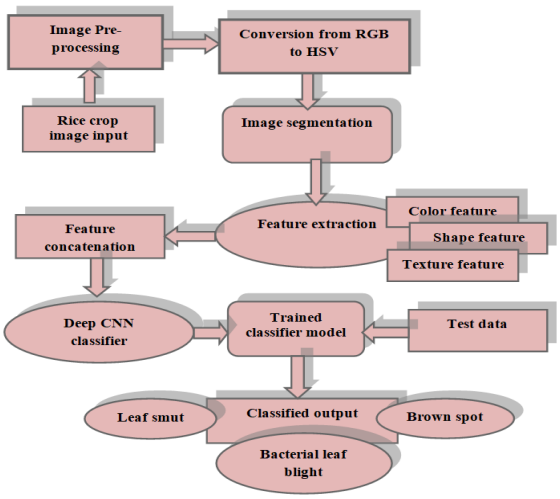

Figure 1. Schematic diagram of proposed plant disease classification model

3.1 Pre-processing of image

The pre-processing step is the initial steps of the proposed disease detection module, with the objective of getting rid of the artifacts that are present in the images taken from the crop fields comprising of nonlinear and non-stationary components. The pre-processing step is necessary in such a way to enhance the prediction accuracy of the proposed Deep CNN classifier. The raw rice crop image is normalized using the pre-processing step in such a way to subject it for the successive steps of the classification process [12].

3.2 Conversion of RGB image to HSV image

The image in the form of RGB is initially made in the arrangement of BGR form, which is nothing but the reverse order of RGB with no influence on accuracy or color vitality [13]. Then the BGR image is converted into HSV form in such a way to describe the color of the image with more recognizable comparisons, like color, brightness, and vitality [12].

3.3 Image segmentation

Image segmentation is an important constituent of image analysis system, and acts as one of the most tedious tasks in image processing, and responsible for the quality of final outcome of the model. In the proposed plant disease classification model, image segmentation is a process of partitioning the HSV image into different regions in order to remove the white spaces in the image [14].

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3.4 Feature extraction

The next important step in the proposed plant disease classification module is the extraction of the significant features from the input rice crop image. The feature extraction strategy is used for the need to develop the feature vector from a normal vector. It involves in selecting the features that are most important to carry out the classification process [14]. The features that are desirable to be extracted in the proposed plant disease classification system are the color, shape and texture features.

3.4.1 Color histogram feature

The visual features are the most uncomplicated visual features of an image due to the fact that human eye is highly responsive to colors. Color feature acts as the basic characteristic of the content of images, and with the assistance of color features, human can identify the images and the objects included in the image [15]. The color histogram is the method for representing the color feature in the proposed disease classification module in rice crops. The feature size of the color histogram is$[40 \times 1]$, and the feature is represented as C_f.

3.4.2 Hu moment shape feature

Most of the image classification strategies make in use of only the color features, and neglect the important shape feature. The proposed classification model considers the extraction of Hu moment shape features, which possess rotation, translation and scale invariance of the input image to be processed [15]. The size of the Hu moment shape feature is$[40 \times 7]$, and is represented as S_f.

3.4.3 Haralick's texture feature

The Haralick's texture feature based on the gray level co-occurrence matrix (GLCM) is utilized to capture the textural patterns of the rice crop images. Haralick features are the statistical features generally evaluated over the whole image. These values are used to deliberate the entire texture of the image with the values, including sum of variance and entropy. The extraction of Haralick's feature comprise of two steps for the extraction of feature. Initially, the GLCM is evaluated in the first step, and in the second step, the texture features based on GLCM are evaluated [15]. The size of the Haralick's texture feature is $[40 \times 13]$, and is represented as H_f.

3.4.4 Feature concatenation

The feature vector is obtained by concatenating the features extracted from the image of rice crop that contains the important data about the plant disease to be analyzed for categorization. The extracted features are combined together to develop the feature vector that acts as the input to the Deep CNN classifier [16], and the feature vector thus developed is expressed as,

$$F = \{C_f, S_f, H_f\} \quad (1)$$

The feature vector represents the characteristics of the significant features of rice crop image data, and the dimension of the feature vector is $[120 \times 21]$. The feature vector is then given as the input to the Deep CNN classifier, which classifies the disease of the rice crop as leaf smut disease, Brow spot disease, or bacterial leaf blight disease.

3.5 Classification of diseases in rice crop using Deep CNN model

In this section, the process of disease classification using the images taken from the crop fields is performed, where the Deep CNN classifier involves in the classification process. The significance of using deep CNN [16] is that the classifier performs the process of classification without the need for any human intervention. In addition, Deep CNN is capable of executing the classification process with the data size of larger size.

3.5.1 Structure of Deep-CNN classifier:

The configuration of the deep CNN classifier consists of number of layers, where each layer performs a particular task, where the convolutional layers develop the feature maps, and the classification layers is responsible for generating the final output. Figure 2 depicts the structure of deep CNN classifier.

Input layer: Initially, the input image from the crop field is pre-processed to remove the artifacts in the image, and the features extracted from the image data is fed to the input layer of the deep CNN classifier.

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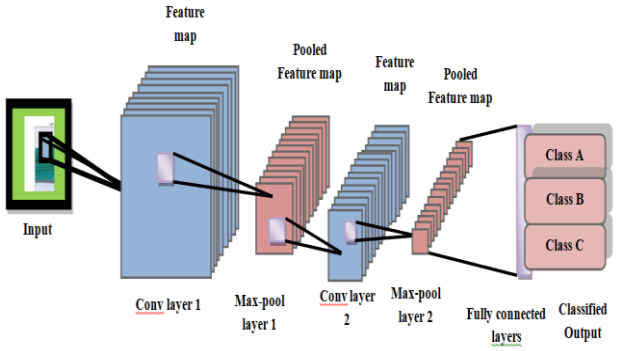

Figure 2. Design of Deep CNN classifier

Convolutional layers: The feature maps are the confine features gathered from the input and these maps are generated from the individual conv layers for leading the classification process effective. In addition, the neurons between the layers are interconnected with each other using weight measures. The output of the conv layers is formulated as,

$$\left(Y_j^i\right)_{q,h} = \left\{\left(D_j^i\right)_{q,h} + \sum_{l=1}^{J_1^{w-1}} \sum_{n=-J_1^q}^{J_1^q} \sum_{r=-J_{21}^q}^{J_2^q} \left(Z_{j,l}^q\right) * Ylq-1q+n,h+y \right.$$

(2)

where, $*$ indicates the convolutional operator, $\left(Y_j^i\right)_{q,h}$ represents the fixed feature map from Y^{th} convolutional layer centered atq, h. Let us consider that the weights of the convolutional layers be represented as, $\left(Z_{j,l}^q\right)$and $\left(D_j^i\right)$ be the bias. The parameters l, n and r indicates the feature maps producing the output from each convolutional filter.

Batch Normalization Layer: This layer is placed among the conv layers and the ReLU layer to improve the training feature of the Deep CNN classification model. This layer helps in normalizing the activations and gradients of the network, assisting in effective training.

ReLU Layer: The maps from the consecutive convolutional layers are conversed using the non-parametric layer known as ReLU layer, which does not inhibit any bias or weight.

Max Pooling Layer: In this layer, the feature maps generated using the conv layers are down-sampled to lower the spatial size and data. The dimension of the max pooling layer is $[1 \times 1]$.

Fully connected layers: The feature maps of convolutional layer are sent to the fully connected layer, where the final processing is executed to generate the final output as,

$$Qa_i^j = k\left(V_j^i\right) \text{ with}$$

$$\left(Y_j^i\right) = \left\{\left(D_j^i\right)_{q,h} + \sum_{l=1}^{J_1^{w-1}} \sum_{n=-J_1^q}^{J_1^q} \sum_{r=-J_{21}^q}^{J_2^q} \left(Z_{j,l}^q\right) * Ylq-1q+n,h+y \right.$$

(3)

Softmax Layer: The output from fully connected layer is normalized with the softmax activation function so as to enable the effective processing in the classification layer.

Classification Layer: The final layer of Deep CNN is the layer for classification that make in use of the possibilities produced from the softmax activation function to all the inputs to assign the class for all the input rice crop image data. Hence, the diseases are finally classified as leaf smut disease, Brow spot disease, or bacterial leaf blight disease in the classification layer using the rice crop image.

4. Results and discussions:

The outcomes of the proposed disease classification module and the comparative study for proving the performance of the proposed Deep CNN classifier in disease classification in rice crop is discussed in this section.

4.1 Experimental setup

The experimentation of proposed Deep CNN classifier is executed in PYTHON tool installed in Windows 10 OS and 64-bit OS with 16GB RAM.

4.2 Dataset description

The dataset used in the proposed classification strategy is the rice leaf diseases database [17] comprising of three directories, such as bacterial leaf blight disease, brown spot disease, and leaf smut disease each containing 40 rice crop images per directory.

4.3 Evaluation metrics:

The effectiveness of proposed classification strategy is tested using the metrics described as below,

4.3.1 Accuracy

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The accuracy of the system is characterized as the degree of closeness to the obtained quantity to the real quantity. It is expressed mathematically as,

$$Accuracy = \frac{True\ Positive + True\ Negative}{Real\ positive + Real\ negative} \quad (4)$$

4.3.2 Precision:

The evaluation of the proportion of total number true Positive values to the sum of true positives and false positives is termed as precision, and is expressed as,

$$Precision = \frac{True\ Positive}{True\ Positive + False\ Positive} \quad (5)$$

4.3.3 Recall:

The term recall is defined as the ratio of True Positive values to the number of real positive cases as,

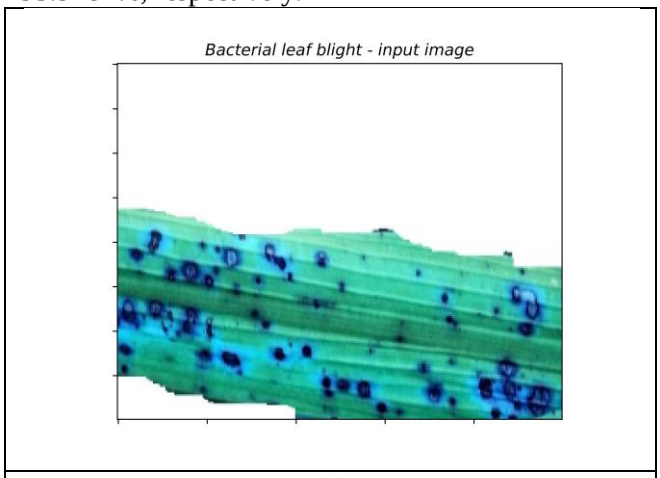
$$Recall = \frac{True\ Positive}{No\ of\ real\ positive\ cases} \quad (6)$$

4.4 Experimental results:

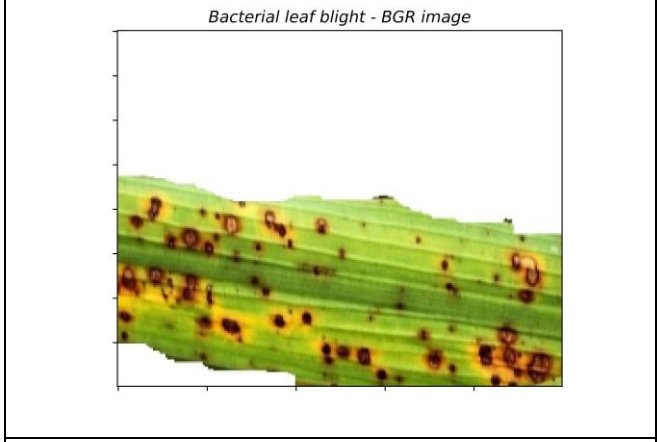
The experimental results of the proposed plant disease classification model are deliberated in this section. Figure 3 shows the experimental results of the proposed model. Figure 3 (a) is the input bacterial leaf blight image, figure 3 (b) is the BGR image of bacterial leaf blight image, figure 3 (c) shows the HSV image of bacterial leaf blight image, and figure 3 (d) shows the segmented image of bacterial leaf blight image. Figure 4 (a) is the input leaf smut disease image, figure 4 (b) is the BGR image of leaf smut image, figure 4 (c) shows the HSV image of leaf smut image, and figure 4 (d) shows the segmented image of leaf smut image. Figure 5 (a) is the input brown spot image, figure 5 (b) is the BGR of brown spot image, figure 5 (c) shows the HSV of brown spot image, and figure 5 (d) shows the segmented image of brown spot image.

4.5 Comparative analysis of methods involved in classification of diseases in rice plants

The performance of Deep CNN model is evaluated against the existing methods, such as Support vector machine (SVM) [4], K-Nearest neighbor (K-NN) [18], and the Neural network (NN) classifier [18]. The performance analysis of the methods in terms of the performance indices, such as accuracy, precision, and recall is depicted in figure 6. The analysis in terms of accuracy is depicted in figure 6(a). The accuracy of the methods, such as SVM, KNN, NN, and the proposed Deep CNN for the training percentage of 40% are 85%, 88.7654%, 89.7654%, and 90.865%, respectively. The accuracy of the methods, such as SVM, KNN, NN, and the proposed Deep CNN for the training percentage of 80% are 90.0531%, 93.8185%, 94.8185%, and 95.9181%, respectively.



(a)



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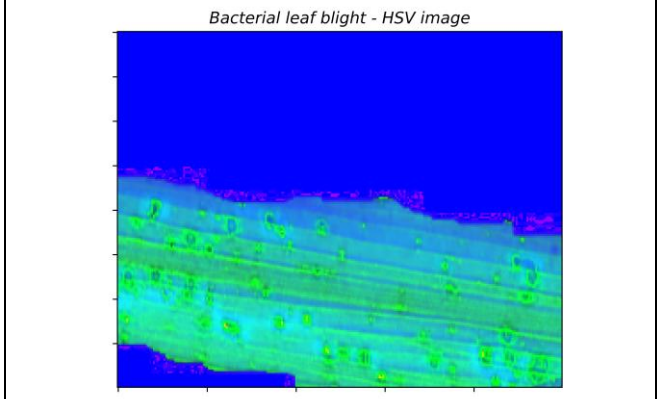

(c)

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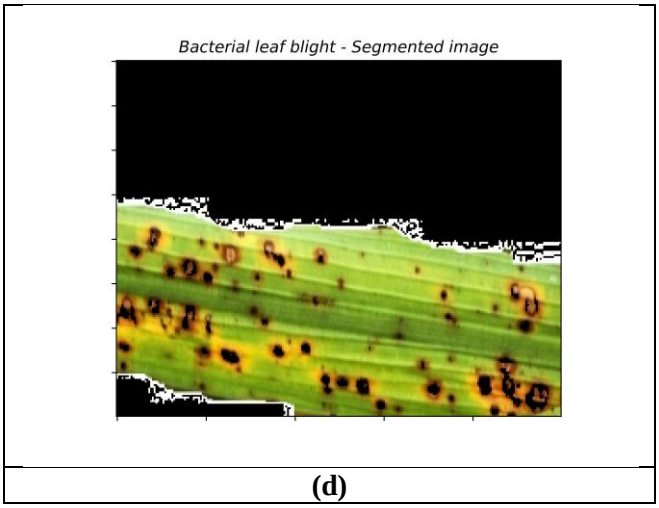
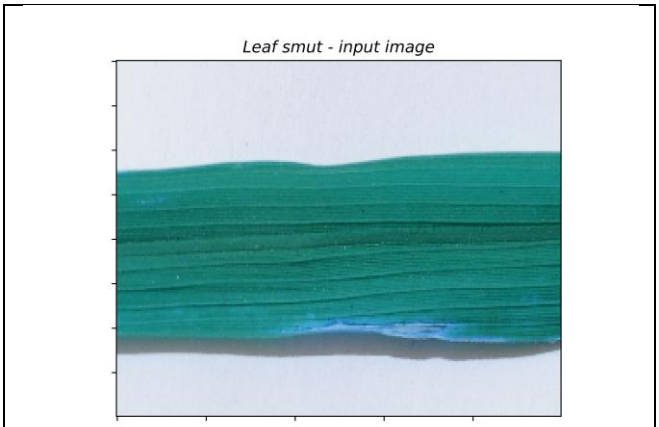
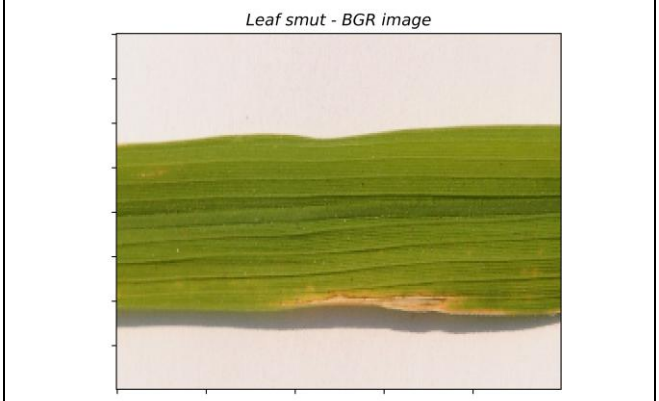


(d)

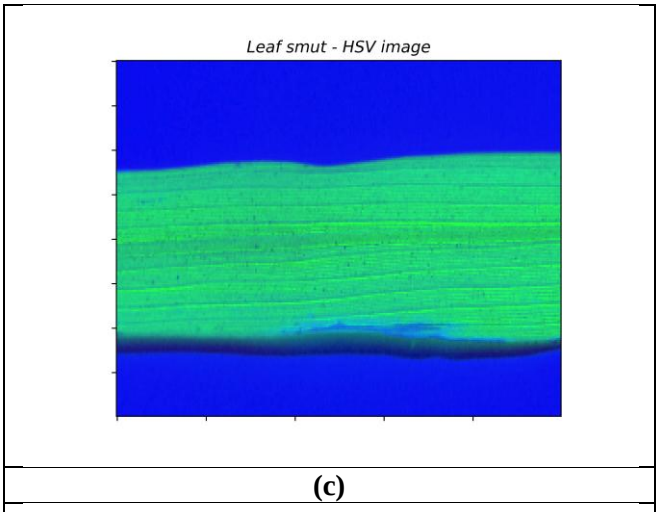
Figure 3. Experimental results, (a) input image 1, (b) BGR of input image 1, (c) HSV of input image 1, (d) segmented image 1



(a)



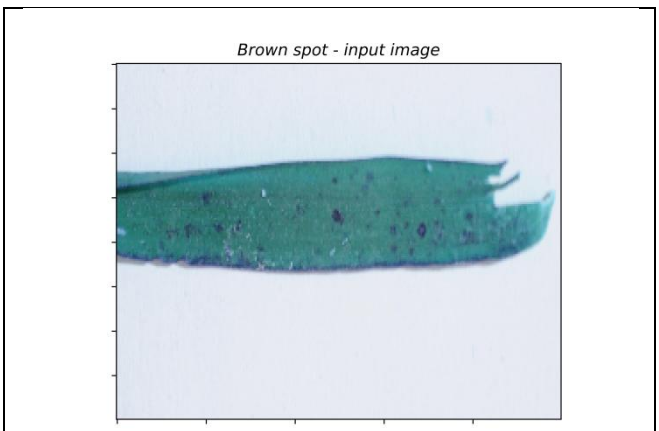
(b)



(c)

(d)

Figure 4. Experimental results, (a) input image 2, (b) BGR of input image 2, (c) HSV of input image 2, (d) segmented image 2



(a)

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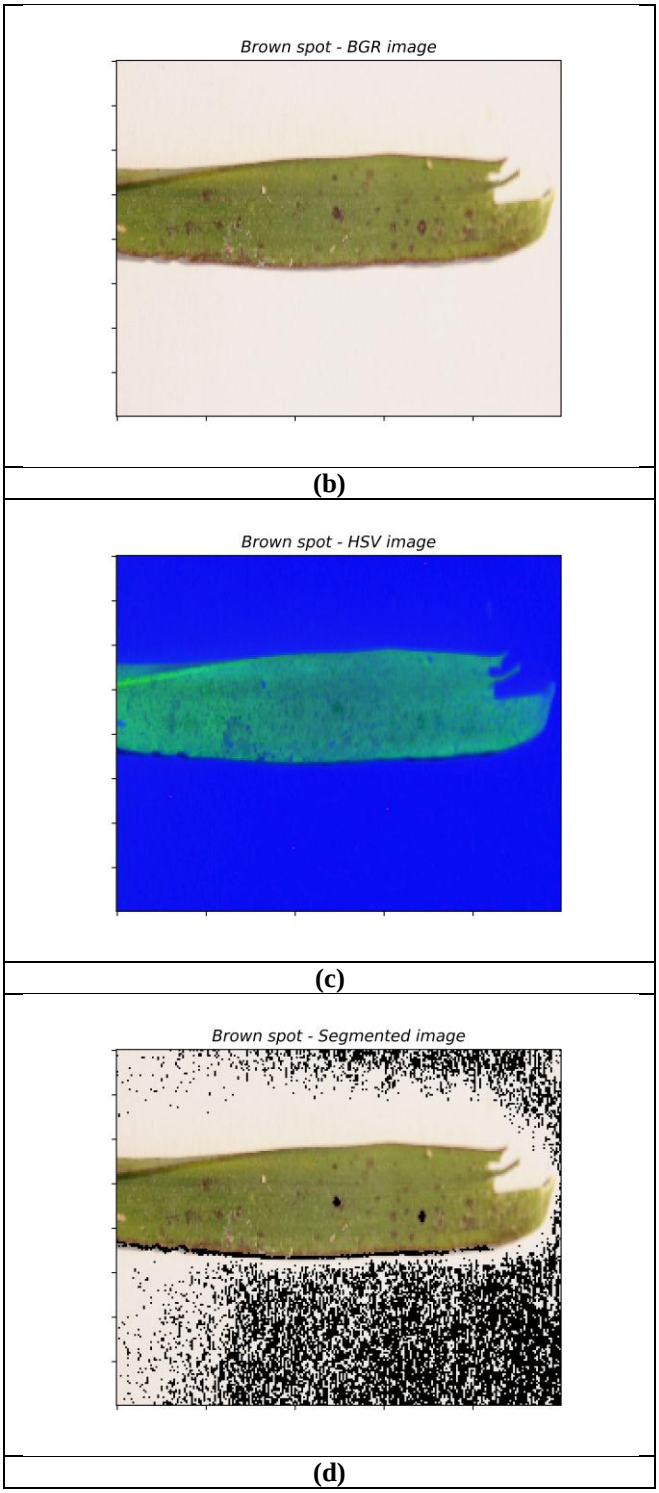
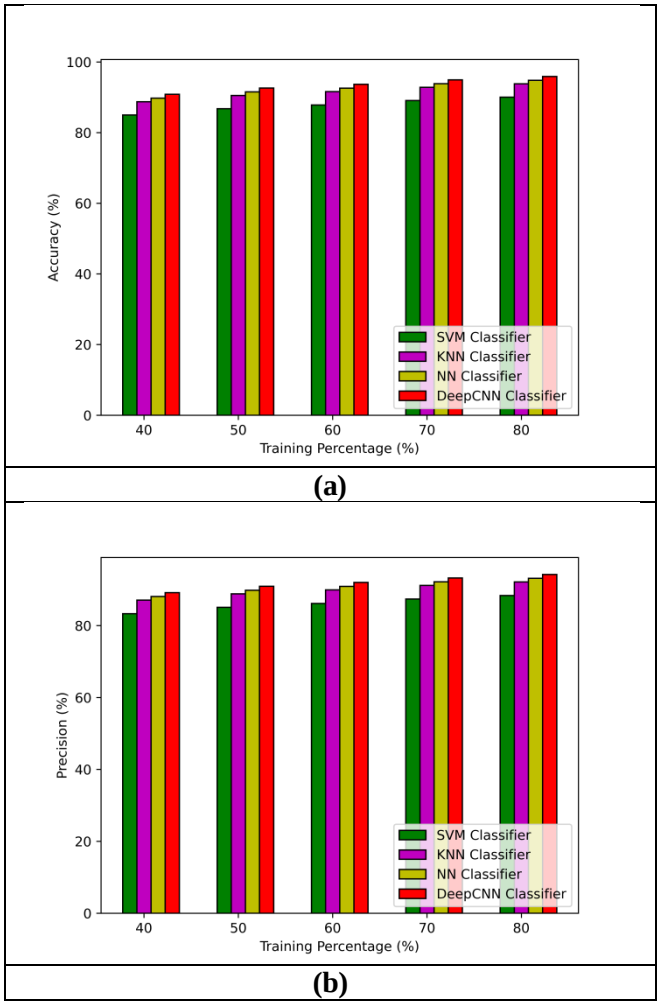


Figure 5. Experimental results, (a) input image 3, (b) BGR of input image 3, (c) HSV of input image 3, (d) segmented image 3

The analysis in terms of precision is depicted in figure 6 (b). The precision of the methods, such as SVM, KNN, NN, and the proposed Deep CNN for the training percentage of 40% are 83.3333%, 87.0987%, 88.0987%, and 89.1983%, respectively. The precision of the methods, such as SVM, KNN, NN, and the proposed Deep CNN for the training percentage of 80% are 88.3865%, 92.1519%, 93.1519%, and 94.2515%, respectively. The analysis in terms of recall is depicted in figure 6 (c). The recall of the methods, such as SVM, KNN, NN, and the proposed Deep CNN for the training percentage of 40% are 86.2069%, 89.9723%, 90.9723%, and 92.0719%, respectively. The recall of the methods, such as SVM, KNN, NN, and the proposed Deep CNN for the training percentage of 80% are 91.26%, 95.0254%, 96.0254%, and 97.125%, respectively. The comparative discussion of the methods involved in the classification of diseases in rice crops is tabulated in table 1.



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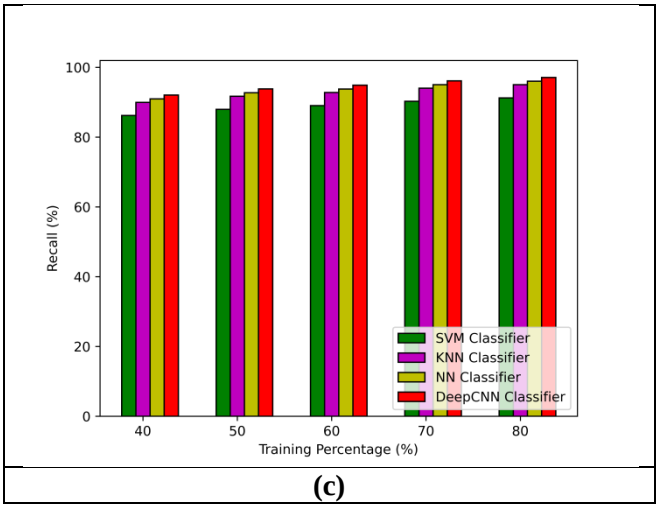

Figure 6. Comparative analysis, (a) accuracy, (b) precision, and (c) recall

Table 1. Comparative discussion

Metrics	Methods			
	SVM	KNN	NN	Proposed Deep CNN
Accuracy	90.0531	93.8185	94.8185	95.9181
Precision	88.3865	92.1519	93.1519	94.2515
Recall	91.2600	95.0254	96.0254	97.1250

Hence, from the discussion, it is evident that the proposed method is efficient in the classification of diseases in rice crops as compared with the existing methods.

5. Conclusion

This paper proposes a deep learning based classification model for the categorization of the diseases in rice plants. The input image from the crop field is initially subjected to pre-processing for the removal of artefacts. The pre-processed image is then fed to feature extraction process for the extraction of the significant features that assist in the performance enhancement of the proposed deep convolutional neural network (Deep CNN) classifier in classification of the diseases. The feature vector trains the Deep-CNN model and responsible for the accurate classification of crop diseases. The effectiveness of the proposed strategy is analyzed with the performance indices, namely accuracy, precision and recall. The measures of accuracy, precision and recall, are 95.9181%, 94.2515%, and 97.125%, respectively, which shows the effectiveness of the proposed method in effective disease classification. In future, the weights of the Deep CNN classifier will be optimally tuned to further increase the accuracy of the proposed model of crop disease classification.

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