Prediction of Rice leaf Diseases

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Abstract:

Rice diseases has adverse consequences on crop yield, and the right finding of rice illnesses is the way to stay away from these impacts. In any case, the current sickness analysis techniques for rice are neither precise nor effective, and exceptional hardware is frequently required. In this review, a programmed finding strategy was created and executed in a cell phone application. The strategy was created utilizing profound learning in view of a huge dataset that contained 33,026 pictures of six sorts of rice infections: leaf impact, bogus filth, neck impact, sheath curse, bacterial stripe illness, and earthy colored spot. The center of the strategy was the Ensemble Model in which submodels were coordinated. At long last, the Ensemble Model was approved utilizing a different arrangement of pictures. Results showed that the three best submodels were DenseNet-121, SE-ResNet-50, and ResNeSt-50, as far as a few credits, for example, learning rate, accuracy, review, and illness acknowledgment exactness. In this way, these three submodels were chosen and incorporated in the Ensemble Model. The Ensemble Model limited disarray among the various sorts of infection, diminishing misdiagnosis of the illness. Utilizing the Ensemble Model to analyze six kinds of rice illnesses, a general exactness of 91% was accomplished, which is viewed as sensibly great, thinking about the appearance likenesses in certain sorts of rice infection. The cell phone application permitted the client to utilize the Ensemble Model on the web server through an organization, which was helpful and proficient for the field determination of rice leaf impact, bogus muck, neck impact, sheath scourge, bacterial stripe illness, and earthy colored spot.

1. Introduction

In the Indian financial area, horticulture assumes a significant part and contributes a second spot in rice creation. Roughly every one of the states in India rehearsing rice development which are Tamil Nadu, West Bengal, Punjab, Uttar Pradesh, Assam, Bihar, and so forth Agribusiness area is giving its portion around 19.9% to the absolute GDP[1]. Rice is one of the dominatingly utilizing food grains in India. The development and nature of rice plants get influencing by infections which further suggests the benefit of the cultivating. The various assortments of illnesses might happen in individual rice crop which is challenging to distinguish to the ranchers with their restricted information acquired through the experience. For this accuracy and early distinguishing proof of plant infections finding programmed information handling master framework is urgently imperative. Along these lines the sound and fruitful development is suitable[2,3].

The strong calculation of profound learning has been entered in the field of horticulture for settling the various kinds of issues, for example, weed and seed discovery, plant sicknesses order, organic product counting, root division, and so forth Profound learning is a progression of AI procedure which effectively prepares an enormous measure of information and naturally learns the elements of the info and gives the result in light of the choice guidelines. CNN is powerful in handling the visual symbolism. It is a feed forward counterfeit neural organization which has three different layers input layer, stowed away layer, and result layer. The secret layer is made out of convolutional layer, pooling layer standardization layer, and completely associated layer and it contains set of programmed learnable boundaries (loads) through which it can become familiar with the spatial relationship of the info information and play out a characterization task[3-6].

Move learning is a strategy by which a pre-prepared convolutional neural organization can be reused for another issue. Along these lines the preparation season of the model can be diminish when contrasted with the model created without any preparation and gives an upgraded exhibition to the proposed model[7-9]. Move learning can be used to make a model that can be utilized as a proper component extractor by wipe out the last completely associated layers or by adjusting the last couple of layers that will work more explicit to the concerned dataset[10-15].

2. Related Work:

Over the past decades, researchers have used computer vision technology in agriculture for estimating crop yields (Gong et al., 2013; Deng et al., 2020), detecting crop nutritional deficiencies (Xu et al., 2011; Baresel et al., 2017; Tao et al., 2020), estimating geometric sizes of crop (Liu et al., 2019), and recognizing weeds (Jiang et al., 2020). Several different approaches of computer vision have also been used for the diagnosis of crop diseases, such as image processing, pattern recognition, support vector machine, and hyperspectral detection (Ngugi et al., 2020). Multi-spectral remote sensing images of tomato fields were used for cluster analysis to differentiate healthy tomatoes from diseased ones (Zhang et al., 2005). The shape and texture features of rice bacterial leaf blight, sheath blight, and blast were extracted using a support vector machine. A genetic algorithm and a support vector machine were used to detect the diseased leaves of different crops (Singh and Misra, 2017). Islam et al. (2018) detected the RGB value of an affected portion, and then used Naive Bayes to classify rice brown spot, bacterial blight, and blast. Infrared thermal imaging technology that provides temperature information of crop has also been used to detect tomato mosaic disease and wheat leaf rust (Zhu et al., 2018). Although some of these existing methods could achieve reasonably high accuracies for crop disease diagnosis, most of them rely on manual extraction of disease features. As a result, the expression ability is limited, and it is difficult to generalize when results are applied. Also, some methods

need special equipment that is not always readily available to users. All these drawbacks make it difficult to apply these methods for crop disease diagnosis.

Deep learning technology can be implemented in crop disease diagnosis methods to overcome the drawbacks. In recent years, deep learning has been widely used in image classification, object detection, and content recommendation. In fact, there have been researchers who used deep learning to detect diseases of various crops. Lu et al. (2017a) proposed an in-field automatic disease diagnosis system, which could achieve identification and localization for wheat diseases. Ozguven and Adem (2019) first applied a convolutional neural network (CNN), Faster R-CNN, to images of sugar beet leaves to detect spot disease. Karlekar and Seal (2020) proposed SoyNet that was applied to soybean leaf images for disease diagnosis. Deep learning also plays an important role in disease diagnosis of many other crops, such as tomato (Rangarajan et al., 2018; Agarwal et al., 2020), cassava (Sambasivam and Opiyo, 2020), tulip (Polder et al., 2019), and millet (Coulibaly et al., 2019). Deep learning has also been applied for detecting rice crop diseases. For example, Kamal et al. (2019) combined a depthwise separable convolution architecture with Reduced MobileNet. In terms of recognition accuracy, there have been various claims. Chen et al. (2020) used Enhanced VGGNet with Inception Module through migration learning, which had an accuracy of 92% in the classification of rice diseases. Rahman et al. (2020) proposed a two-stage small CNN architecture, which achieved 93.3% accuracy with smaller model sizes. Some efforts have been made to improve the accuracy. For instance, Picon et al. (2019) used a dataset of five crops, 17 diseases, and 121,955 images, then proposed three different CNN architectures that incorporate contextual non-image meta-data. ArnalBarbedo (2019) proposed a method of image classification based on individual lesions and spots, testing 14 plants and 79 diseases, which improved the accuracy compared with using original images.

Relying on a single predictive model may cause machine learning algorithm to overfit (Ali et al., 2014; Feng et al., 2020). To solve this problem, ensemble learning with a set of algorithms to combine all possible predictions was used (Dietterich, 2000). With the development of computer technology, ensemble learning was used for prediction in disease diagnosis (Albert, 2020), soybean yield (Yoosefzadeh-Najafabadi et al., 2021), protein binding hot spots (Hu et al., 2017), and wheat grain yield (Fei et al., 2021). Since the above studies have proven the feasibility of ensemble learning, ensemble technology would be used in this research to improve the accuracy of disease diagnosis.

In summary, deep learning is a promising technology for disease diagnosis of various crops with which high accuracy can be achieved. Existing research on the use of deep learning for rice diseases dealt with a limited number of rice diseases. Various types of rice diseases have been observed in rice fields, such as rice leaf blast, false smut, neck blast, sheath blight, bacterial stripe disease, and brown spot. The aim of this study was to increase the accuracy, efficiency, affordability, and convenience of rice disease diagnosis. The specific objectives of this study were to (1) develop a deep learning network model for diagnosing six different types of rice diseases, (2) evaluate the performance of the model, and (3) implement the diagnosis method in a cloud-based mobile app and test it in an application.

3. Materials and Methods

Data Acquisition

Profound learning requires countless preparation pictures to accomplish great outcomes (Barbedo, 2018). Along these lines, a sum of 33,026 pictures of rice infections were gathered more than a 2-year time span for the improvement of an illness finding model. Among these pictures, 9,354 were for rice leaf impact, 4,876 were for rice bogus filth, 3,894 were for rice neck impact, 6,417 were for rice sheath scourge, 6,727 were for rice bacterial stripe, and 1,758 were for rice earthy colored spot infections. The qualities of rice leaf impact are huge axle molded sores with grayish focuses and earthy colored edges. For misleading filth illness, the microorganism is parasitic that taints rice blossoms and transforms them into rice bogus muck balls, which is the main noticeable element of rice bogus filth. For rice neck impact sickness, hub and neck injuries frequently happen simultaneously and have a comparable trademark, a blackish to a grayish earthy colored tone. For rice sheath curse sickness, injuries on the leaves are normally sporadic in shape, and after a time of disease, the middle is typically grayish white with earthy colored edges. For rice bacterial stripe infection, on youthful injuries, the microscopic organisms overflow dew and dry out the plant, leaving yellow dots that in the end foster orange-yellow stripes on the leaves. For rice earthy colored spot sickness, the spots are at first little round, dim brown to purplish brown, and completely created spots are round to elliptic with light brown to dim focuses and rosy earthy colored edges. Model pictures of every infection are in the Supplementary Material. The pictures were from four areas in China: (1) Baiyun Base of The Guangdong Academy of Agricultural Sciences, Guangzhou, Guangdong, (2) Laibin, Guangxi, (3) Binyang, Guangxi, and (4) the Chinese Academy of Sciences, Hefei, Anhui. These pictures were taken utilizing cell phones with high goal (more than 1 megapixel), so the attributes of rice infections could be plainly caught. To get ready for model turn of events, the pictures were parted into a preparation set, an approval set, and a test set with a proportion of 7:2:1. This proportion was arbitrarily applied to all the six infection classifications; hence, the relating picture quantities of these sets were 23,096; 6,684; and 3,246.

Picture Preprocessing

Picture preprocessing and information improvement are performed to decrease the overfitting of models, as shown in Figure 1. Before the model peruses the picture, the short side of the picture was scaled to 256 pixels, and the long side was scaled relatively to lessen the computational strain of the model. Then, at that point, irregular relative change was applied to the picture, which could arbitrarily interpret, turn, scale, distort, and cut the picture. Simultaneously, Gaussian haze and picture flipping were applied haphazardly. At last, the resized picture was haphazardly trimmed to a 224 × 224 pixels square region as the genuine preparation picture. These cycles leaned toward growing the informational index and decreasing the over-fitting of the model on the first dataset without adjusting the qualities of rice illnesses.

FIGURE 1

Figure 1.Steps of the image preprocessing for expanding dataset and reducing the overfitting of models.

Then, the mean and standard deviation of the ImageNet dataset were applied for standardization to make picture shading dispersion as comparable as could really be expected. As the quantity of pictures of various sorts of illnesses was not equivalent, an over-testing activity was taken on for few rice earthy colored spot pictures in the preprocessing, with a proportion of multiple times. This interaction was rehashed for each preparing age; consequently, the quantity of pictures that each model read was different in each preparing age, and the quantity of picture tests in the dataset was expanded thusly.

Convolutional Neural Network (CNN) Models

The construction of the convolutional neural organization impacts the exhibition of the last model. It was important to analyze the exhibition of various organizations in the conclusion of rice infections. Five organization structures were chosen and tried, and they were: ResNet, DenseNet, SENet, ResNeXt, and ResNeSt. These organizations are portrayed beneath.

ResNet (He et al., 2016) is a generally utilized organization model, which utilizes remaining squares to upgrade the profundity of the CNN. The construction of the leftover square is displayed in Figure 2A. By straightforwardly associating the information and the result, ResNet can decrease the issues of angle vanishing and inclination blast, along these lines extending the quantity of organization layers and accomplishing better impacts. DenseNet (Huang et al., 2017) utilizes a thick association, which interfaces each layer to each and every other layer (Figure 2B). Since DenseNet permits highlights to be reused, this can create many elements with few convolution parts. Accordingly, it can lessen slope misfortune and upgrade the spread of highlights, and the quantity of boundaries is enormously diminished. SE-ResNet (Hu et al., 2020) presents the "Crush and-Excitation" block, which can lay out the connection among channels and adaptively recalibrate the reactions of the channel-wise element. The SE square can be included various organizations. Figure 2C shows the SE block with ResNet. ResNeXt (Xie et al., 2017) is a superior variant of ResNet that was intended to have a multi-branch design and

assembled convolutions to make channels more extensive (Figure 2D). ResNeXt can further develop exactness without expanding boundary intricacy while diminishing the quantity of super boundaries. ResNeSt (Zhang et al., 2020) proposes Split-Attention blocks in light of SENet, SKNet, and ResNeXt, which makes considerations gathered (Figure 2E). This design joins channel consideration and component map thoughtfulness regarding further develop execution without expanding the quantity of contentions.

FIGURE 2

Figure 2. Structures of different convolutional neural network (CNN) models tested. (A) Residual Block, (B) Dense Block, (C) SE Block with ResNet, (D) ResNeXt, (E) ResNeSt Block.

4. Results

Model Training and Testing Results

Performance Comparisons of the Five Network Submodels

After fine-tuning and training, the loss value was low for all the five submodels, and the minimum loss values of all the submodels were below 0.002 (Figure 3A). The learning rate was the same for all the submodels, and it was in the range of 0–0.001 (Figure 3B). The disease diagnosis accuracy on the training set of rice disease images was high for all the submodels, meaning all the submodels had fit the training set well, but that SE-ResNet-50, DenseNet-121, and ResNeSt-50 had better accuracies (over 99%) (Figure 3C). When the submodels were applied on the validation set and test set of images, the disease diagnosis accuracy was also high

for all the submodels, particularly for the SE-ResNet-50, DenseNet-121, and ResNeSt-50 submodels, which achieved accuracies of over 99% (Figure 3D).
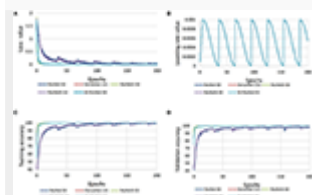
FIGURE 5

Figure 3.Comparisons in performance of the five different submodels. (A) Loss value, (B) learning rate, (C) validation accuracy, and (D) training accuracy.

Confusion matrix is a specific table that makes it easy to see if the model is mislabeling one class as another.

5. Discussion

Rice leaf blast, rice false smut, rice neck blast, rice sheath blight, rice bacterial stripe, and rice brown spot are common diseases during the growth of rice. The identification of these diseases is of practical importance and can provide ideas for the identification of other rice diseases in the future. In this study, the dataset was split into a training set, a validation set, and a test set using a ratio of 7:2:1. From the training results, the ratio made full use of the data obtained from the collection and enabled the model to learn the important features of each disease. Considering that the test set obtained from splitting this dataset has a large similarity with the training set, various disease images from different sources were collected to form an independent test set. The test results of the independent test set demonstrate that the network designed in this study is generalizable and can be applied in practice. Therefore, the division of the data set and the selection of the test set are appropriate for this study.

6. Conclusion

In this study, a dataset containing 33,026 images of six types of rice diseases was established. Based on these images, five submodels, ResNet-50, ResNeXt-50, DenseNet-121, ResNeSt-50, and SE-ResNet-50 were trained and tested, achieving over 98% accuracy and over 0.95 F1 score. Among them, DenseNet-121, SE-ResNet-50, and ResNeSt-50 performed well. Visual analysis confirmed the good learning status of the submodels on the characteristics of rice diseases. Subsequently, the Ensemble Model, an integration of these three submodels, produced accurate judgment of confusable diseases, according to the confusion matrixes analysis. As a result, the F1 scores reached more than 0.99 for each of the six types of disease. Being tested by independently sourced images, the Ensemble Model achieved 91% accuracy, indicating that it has enough generalization ability to be implemented in a rice disease diagnosis app for field applications. With a software system that included both servers and clients, the smartphone app provided high accuracy, easy operation, simplicity, and low-cost means for the recognition of rice diseases. The limitation was that the Ensemble Model has many parameters, which may

affect the speed of identification. Future studies will be carried out on network pruning to reduce the number of parameters.

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