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Plant Disease Detection using CAE and CNN

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Abstract: Plant illness recognition is a gigantic issue and frequently need proficient support to distinguish the sickness. Plants are susceptive to different illnesses in their developing stages. Early discovery of sicknesses in plants is one of the most difficult issues in farming. On the off chance that the sicknesses are not distinguished in the beginning phases, then they may unfavorably influence the all out yield, bringing about a diminishing in the ranchers' benefits. To conquer this issue, numerous scientists have introduced different cutting edge frameworks in light of Deep Learning and Machine Learning draws near. Nonetheless, the greater part of these frameworks either use a large number of preparing boundaries or have low characterization correctnesses. The proposed cross breed model requires lesser number of preparing boundaries when contrasted with different methodologies existing, we are attempting to. Our venture is pointed on making Application that distinguishes the sort of infection that impacted the plant from the pictures of the leaves of the plants. We are utilizing novel cross breed model in view of Convolution Autoencoder (CAE) organization and Convolutional Neural Network (CNN) for programmed plant sickness recognition. In this work, the proposed half and half model is applied to distinguish Bacterial Spot illness present in plants utilizing their leaf pictures; notwithstanding, it very well may be utilized for any plant sickness discovery involving any Image as info.

Keywords: Plant Disease Detection, Convolutional Autoencoder, Convolutional Neural Network, Deep learning in agriculture

I. INTRODUCTION

A plant can be effectively seen through actual appearance that it is contaminated or have some illness, but in this universe of modernization distinguishing the sort of sickness in plant and solution is minimal hard. India is an agrarian nation, and a significant piece of its economy relies upon the rural area. Around 75% populace of India relies upon the agrarian area either straightforwardly or in a roundabout way. Thusly, sickness free great quality yield creation is fundamental for the development of the nation's economy.

Like people, plants are additionally defenseless to different sorts of illnesses in their various phenoplasts. As of now, the customary procedure of visual review in people by visual examination makes it difficult to describe plant sicknesses. Progresses in PC vision models offer quick, standardized, and exact solutions to these issues. Classifiers can likewise be sent as connections during readiness. All you want is a web affiliation and a camera-prepared cell.

To resolve this issue, numerous analysts across the globe introduced various frameworks for programmed plant illness discovery with the assistance of different Machine Learning and Deep Learning strategies. These utilization an extremely big number of preparing boundaries. Subsequently, the preparation time and the forecast season of these frameworks are extremely high, or they require a machine with high calculation abilities.

Profound Learning strategies are propelled by the design of neurons present in the human cerebrum. These methods utilize Artificial Neural Networks (ANNs), and its different variations, like Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs) to distinguish the secret designs in information. There are two conspicuous benefits of Deep Learning procedures over the Machine Learning methods. In the first place, they consequently extricate different highlights from crude information, and thus there is no requirement for an additional a component extraction module.



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Second, Deep Learning procedures diminish how much time expected to handle enormous datasets of high aspects. Thusly, the Deep Learning methods are utilized to assemble the proposed crossover model.

These cutting edge frameworks utilize an extremely large number of preparing boundaries. Thusly, the preparation time and the forecast season of these frameworks are exceptionally high, or they require a machine with high calculation abilities. This exploration work attempts to diminish the quantity of highlights utilized for expectation utilizing the CAE network without a huge decline in the order exactness of plant sickness location. This, thus, diminishes the quantity of preparing boundaries by a huge component bringing about the reduction of preparing and forecast time.

Convolutional Neural Networks (CNNs) and Convolutional Autoencoders (CAEs) are two Deep Learning methods utilized in numerous PC vision applications because of their viability on picture information. Both these procedures use convolution activity to extricate different spatial and worldly elements from picture information. CNNs are utilized to characterize input pictures to their separate classes, though CAEs are utilized to proficiently decrease the dimensionality of a picture.

Dimensionality decrease involving CAE in the proposed model outcomes in decrease of number of preparing boundaries of the model. The remainder of the paper is partitioned into four segments. Area 2 examine a few best in class frameworks for programmed plant illness recognition present in the writing. In Section 3, the material and techniques used to plan proposed cross breed model is portrayed. The outcomes acquired by the model are introduced in Section 4 of the paper. Eventually, Section 5 finishes up the paper.

II. RELATED WORK

This segment examines some cutting edge frameworks present in the writing utilized for programmed plant sickness location. Sanga et al. (Sanga et al., 2020) fostered a sickness identification device for banana plants with five distinct CNN models. These structures were VGG-16, ResNet-152, ResNet-50, ResNet-18, and InceptionV3. They tracked down that ResNet-152 beat others with a precision of 99.2%. They likewise fostered a versatile application so ranchers could undoubtedly distinguish illnesses in banana plants by transferring leaf pictures of their banana plants with their cell phones. This portable application utilized the InceptionV3 model for infection expectation with almost 100% certainty. The quantity of preparing boundaries utilized by their best performing model, i.e., ResNet-152, was 60 million, as referenced in the ResNet paper (He et al., 2016). One more comparative work was done in the paper created by Chohan et al. (Chohan et al., 2020). They utilized VGG-19 and InceptionV3 CNN designs for programmed plant illness identification utilizing the PlantVillage dataset. In their examination work, they likewise utilized information expansion to amplify the dataset falsely. The VGG-19 model outflanked the InceptionV3 model with 98% preparation precision and 95% testing exactness, as guaranteed by them in their paper. The quantity of preparing boundaries utilized by their best performing model, i.e., VGG-19, was 143 million, as guaranteed by (Simonyan and Zisserman, 2015) in their examination work. Ferentinos (Ferentinos, 2018) utilized five different current CNN models named AlexNet, AlexNetOWTBn, GoogLeNet, Overfeat, and VGG for plant sickness location utilizing the PlantVillage dataset. In his paper, he found that VGG beat other CNN structures with an exactness of 99.5% utilizing 138 million teachable boundaries, as referenced in the VGGNet paper (Simonyan and Zisserman, 2015). Mohanty et al. (Mohanty et al., 2016) dissected AlexNet and GoogLeNet CNN models' exhibition for plant sickness recognition utilizing the PlantVillage dataset. They performed 60 unique trials with the assistance of 60 distinct arrangements. They found that GoogLeNet with move learning performed best with a precision of 99.3%. The quantity of preparing boundaries utilized by GoogLeNet was around 7 million, as guaranteed in their paper (Szegedy et al., 2015).

Mohameth et al. (Mohameth et al., 2020) involved different current CNN structures and various classifiers for programmed plant infection identification on the PlantVillage dataset. They utilized VGG-16, ResNet50, and GoogLeNet CNN structures for include extraction, and for arrangement, they utilized k-Nearest Neighbor and Support Vector Machine (SVM) classifiers. They saw that SVM with ResNet-50 beat others with an exactness of 98%. As referenced in the ResNet paper, the quantity of preparing boundaries utilized by ResNet-50 was roughly 25 million (He et al., 2016). Comparable work was likewise finished by Tiwari et al. (Tiwari et al., 2020). They proposed a programmed infection discovery framework for potato plants. This framework utilized different CNN designs like VGG-19, VGG-16, and InceptionV3 for include extraction and various classifiers, for example, Logistic Regression, k-Nearest Neighbor classifier, Support Vector Machine (SVM), and Neural Network for sickness discovery. They reasoned that VGG-19 with Copyright to IJARSCT DOI: 10.48175/IJARSCT-4516 404

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Logistic Regression beat others with an exactness of 97.8%. The quantity of preparing boundaries utilized by VGG-19 was roughly 143 million, as guaranteed in the VGGNet paper (Simonyan and Zisserman, 2015). Khamparia et al. (Khamparia et al., 2020) proposed a Deep Convolutional Encoder Network framework for occasional yields illness distinguishing proof. They considered 900 leaf pictures of three yields: potato, tomato, and maize, disseminated in six classes (i.e., five unhealthy and one solid). They accomplished 100 percent preparing precision while the testing exactness of their model was 86.78%. Since the preparation exactness was a lot higher when contrasted with the testing precision, so quite possibly the prepared model overfitted on the preparation information. In their paper, they have additionally referenced that their framework utilized around 3.3 million preparation boundaries, which is a lot higher than the quantity of preparing boundaries 9,914 utilized in the proposed work. They have involved Autoencoder and CNN for occasional harvest illness ID. Then again, the proposed novel mixture model depends on CAE and CNN. In addition, the proposed model likewise accomplishes higher testing exactness than the testing precision of the model proposed by Khamparia et al. (Khamparia et al., 2020). Pardede et al. (Pardede et al., 2018) planned a framework for programmed sickness discovery for corn and potato plants with CAE and SVM classifiers' assistance. They removed leaf pictures of potato and corn plants from the PlantVillage dataset. They accomplished 87.01% and 80.42% exactness in identifying sicknesses in potato and corn plants, separately. According as far as anyone is concerned, best in class frameworks that anyone could hope to find in the writing for plant illness recognition utilize an exceptionally big number of preparing boundaries going from 3.3 million to 143 million (He et al., 2016; Khamparia et al., 2020; Simonyan and Zisserman, 2015; Szegedy et al., 2015). A synopsis of these exploration works has been introduced in Table 1. All of the above-examined research works have a significant weakness that all examination works utilized an exceptionally big number of preparing boundaries. Besides, preparing a model with an exceptionally big number of preparing boundaries requires either a great deal of preparing time or a machine with high calculation power. This propelled us to pursue lessening the quantity of preparing boundaries utilized for plant illness identification absent a lot of decline in the grouping exactness. Thus in this paper, a clever crossover model is suggested that lessens the dimensionality of information leaf picture utilizing CAE prior to grouping it involving CNN for plant illness location. The dimensionality decrease of plant leaf pictures before order lessens the quantity of preparing boundaries by a huge variable, which is the significant finding of this exploration work.

III. MATERIAL AND METHODS

This segment examines the material and techniques which are utilized to plan the model. Segment 3.1 gives an essential comprehension of CNN and CAE, which is useful to figure out the proposed work. In Section 3.2, the proposed half breed model is depicted exhaustively. The trial design to execute the proposed model is introduced in Section 3.3.

3.1 Background concepts

vThis segment portrays the essential ideas of Convolutional Neural Network (CNN) and Convolutional Autoencoder (CAE) which are utilized to plan the proposed crossover model.

3.1.1. Convolutional neural network (CNN)

Convolutional Neural Network is a Deep Learning method that utilizes convolution activity rather than straightforward lattice increase. When contrasted with other Deep Learning methods, CNN manages pictures most productively. It extricates different spatial and worldly highlights from input pictures, which assume a huge part in picture characterization and other PC vision errands. The design of a run of the mill CNN contains one Input layer, one Output layer, a bunch of Convolutional layers (each with an enactment work), Pooling layers, and Fully Connected layers (each with an initiation work). The Convolutional layer present in the CNN plays out the convolution activity. The underlying Convolutional layers of a CNN extricate the straightforward lower-level highlights of a picture, and the Convolutional layers present toward the finish of the organization separate the complex more elevated level highlights of a picture.

It tends to be presumed that after every convolution activity, the size of result include map is diminished. All in all, the size of the information picture lessens after every convolution activity and becomes zero after certain convolutions. Thus, it restricts CNN's profundity by putting an upper bound on the quantity of Convolutional layers present in a CNN. Further, the components present on the edges and corners are utilized not exactly the components present in that frame of mind of the info lattice. To handle these two issues, cushioning is utilized in the Convolutional layers present in the CNN.



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Cushioning is utilized to grow the information grid by attaching the layers of zeroes to the information lattice's line. Accordingly, the information lattice region is expanded on which the convolution activity must be performed, which guarantees that the size of the information grid doesn't diminish after convolution activity. It additionally guarantees that the components present on the edges and corners are likewise used by adding different cushioning layers. There are two kinds of cushioning: Valid Padding and Same Padding.

To extricate the non-straight highlights from pictures, different non-direct enactment capacities like Sigmoid, Hyperbolic Tangent, Rectified Linear Unit (ReLu), and so forth, are utilized in CNNs after the convolution activity. Subsequent to applying non-straight enactment capacities, it is performed to pool activity. Pooling activity is utilized to decrease the quantity of preparing boundaries and subsequently lessen the dimensionality of the component map it gets from its first layer. It figures a solitary result esteem in view of certain measurements from its area. A portion of these measurements are Max Pooling, Average Pooling, and so forth. Max Pooling picks the most extreme worth from its area, and Average Pooling processes the typical worth in its area.

3.1.2. Convolutional Autoencoder (CAE)

Autoencoder is a self-managed learning calculation that involves a Neural Network for portrayal learning. Portrayal learning is a method wherein a framework figures out how to encode input information. Autoencoders are utilized to plan input information to some lower-layered space or packed area portrayal. To do this, a bottleneck is presented in the organization, which upholds the framework to become familiar with the packed space portrayal of information. An Autoencoder involves four parts: Encoder Network, Bottleneck Layer, Decoder Network, and Reconstruction Loss. Encoder Network is a Neural Network that encodes input information to a compacted space. The Bottleneck layer is the last layer of the Encoder Network, and its result is known as encoded input information. Give there are N layers access an Encoder Network in which the last layer i.e., Nth layer is Bottleneck Layer.

Decoder Network is likewise a Neural Network that takes the result of the Bottleneck Layer as information and attempts to reproduce the first information. The quantity of layers in the Decoder Network is equivalent to the quantity of layers in the Encoder Network yet in the converse request. The last layer of the Decoder Network delivers the boisterous recreation of info information.

There are various sorts of autoencoders, like Undercomplete Autoencoder, Deep Autoencoder, Convolutional Autoencoder, and so forth. A CNN based autoencoder is known as Convolutional Autoencoder (CAE). It utilizes Convolutional and Down Sampling (Pooling) layers for encoding the information picture to its packed area portrayal. Essentially, Up Sampling and Convolutional layers are utilized to recreate the first picture utilizing its compacted space portrayal. Since this examination work manages plant leaf pictures, so CAE has been utilized to acquire the compacted space portrayal before arrangement, in the proposed cross breed model. The model lessens the size of leaf pictures to such an extent that the unmistakable highlights of leaf pictures are not lost and are additionally utilized in grouping. Because of packed area portrayals of leaf pictures, the quantity of highlights is decreased essentially, which ultimately diminishes the quantity of preparing boundaries and lessens the time taken for the preparation of mixture framework and time taken for order by the crossover framework

3.2 Proposed Work

In this examination work, a clever cross breed model is intended to consequently distinguish plant sicknesses. This model purposes two profound learning procedures: CAE and CNN. To start with, the CAE network has been prepared to decrease the dimensionality of the information leaf pictures. The dimensionality decrease of the leaf pictures has been done to such an extent that the significant highlights of the leaf pictures are not lost. This has been guaranteed by applying as far as possible on Reconstruction Loss of CAE. In the wake of decreasing the dimensionality of leaf pictures, the result of the Encoder Network of CAE, (i.e., compacted area portrayals of leaf pictures) is utilized as contribution to the CNN. With the assistance of CNN, the info leaf picture has been named either an unhealthy leaf or a sound leaf. The block chart of the proposed crossover model is displayed in Fig.

The most common way of planning the proposed crossover model includes two stages. The initial step is making a CAE network that decreases the dimensionality of the info leaf pictures from 256×256 to 32×32 .

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The CAE network likewise contains a Decoder Network that is utilized to remake the first information (for this situation, leaf pictures) from the encoded information. The preparation of CAE network is done to such an extent that the Reconstruction Loss is limited .This guarantees that the CAE network diminishes the dimensionality of the leaf pictures without losing its significant highlights.

Subsequent to diminishing the dimensionality of info leaf pictures, the CNN has been applied to characterize the information leaf pictures as either an infected leaf or a sound leaf. The result of the Bottleneck Layer of the CAE is taken as the contribution for the CNN. As currently examined, the proposed model has been made by connecting the layers of the encoder organization of CAE and the layers of the CNN.

Since the layers imported from the encoder organization of CAE are pre-prepared subsequently, preparing boundaries of these layers are excluded while registering the preparation boundaries of the half and half model. Consequently, the absolute teachable boundaries utilized in the proposed work can be determined as the amount of teachable boundaries of CAE and cross breed model. Since CAE utilizes 4,163 teachable boundaries, and the half and half model purposes 5,751 teachable boundaries so the complete teachable boundaries utilized in this exploration work is 9,914.

3.3 Dataset Description

The proposed cross breed model has been applied to recognize sicknesses from leaf pictures of plants present in the PlantVillage dataset. The dataset contains 54303 of sound and unfortunate leaf pictures separated into 38 classifications by species and illness.

To prepare the model, the leaf pictures of plants have been arbitrarily partitioned to such an extent that 70% of them structure the preparation dataset, and 30% of them structure the testing dataset.

3.4 Experimental Configuration

The tests acted in this examination work utilizes the Google ColabNotebook, which is a facilitated Jupyter journal administration that requires no arrangement to use, while giving access for nothing to processing assets. One can likewise utilize other programming dialects like Matlab, R, and so on, to carry out the proposed half breed model. Application Programming Interface (API) of Python has been utilized to frame the preparation and testing dataset. To make and prepare the model, the Keras API has been utilized. Also, Adam streamlining agent and Binary Cross-Entropy (BCE) misfortune have been utilized to prepare the proposed model with 5 ages. To try not to retrain of layers imported from the CAE organization, i.e., layer 1 to layer 8, False worth has been allocated to the teachable banner of these layers during the preparation period of the proposed mixture model. To forestall model overfitting, Early halting has been utilized with persistence esteem approaches 5 (i.e., in the event that the testing misfortune doesn't work on north of five sequential ages, then the preparation will stop)

IV. RESULTS AND DISCUSSION

This part examines the aftereffects of analyses acted in the flow research work. The aftereffects of the proposed model are shown. Some unique leaf pictures with their comparing reproduced leaf pictures are displayed in Fig. . The proposed model could accomplish an exactness of 98.74%. The brain organization could effectively recognize the plant leaf picture and grouped it to the right sickness with a precision of 97.89%. The model effectively distinguished 10861 testing pictures from 38 classes, 43444 preparation pictures from 38 classifications.

Subsequently, the proposed cross breed model requires exceptionally less preparation time and extremely less forecast time. The proposed model has two noticeable use cases. In the first place, it tends to be prepared and utilized for programmed plant sickness discovery on low computational power frameworks with less preparation time and expectation time. Second, the proposed model can likewise be prepared and utilized on cell phones. Running a Deep Learning model in versatile applications as opposed to sending the leaf pictures of plants to the cloud/server lessens the dormancy and gives information security to ranchers.

V. CONCLUSION

Illness identification in plants at the beginning phases is a hard and testing task. Numerous analysts have involveddifferent Machine Learning and Deep Learning strategies for programmed plant sickness recognition. Notwithstanding,Copyright to IJARSCTDOI: 10.48175/IJARSCT-4516www.ijarsct.co.in407

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the vast majority of these procedures either use a huge number of preparing boundaries or have a low characterization precision. In this paper, a model was proposed for programmed plant sickness discovery that depended on two Deep Learning strategies named Convolutional Autoencoder (CAE) organization and Convolutional Neural Network (CNN). The proposed model originally acquired packed space portrayals of leaf pictures utilizing the encoder organization of CAE and afterward involved the compacted area portrayals for arrangement utilizing CNN. Because of dimensionality decrease utilizing CAE, the quantity of highlights, and thus the quantity of preparing boundaries diminished essentially when contrasted with existing cutting edge frameworks. The proposed model could accomplish an exactness of 98.74%. The brain organization could effectively distinguish the plant leaf picture and grouped it to the right infection with an exactness of 97.89%. The model effectively identified 10861 testing pictures from 38 classifications, 43444 preparation pictures from 38 classes. Less preparation boundaries utilized in the proposed cross breed model altogether diminished the time expected to prepare the model for programmed plant sickness identification and the time expected to recognize the illness in plants utilizing the prepared model.

REFERENCES

- [1]. Many researchers across the world explored different Machine Learning (Es-saady et al., 2016; Islam et al., 2017; Krithika and Selvarani, 2017; Padol and Yadav, 2016)
- [2]. Deep Learning (Golhani et al., 2018; Ramesh and Vydeki, 2020; Sharma et al., 2019)
- [3]. Image Processing (Marwaha et al., 2012; Ngugi et al., 2020; Qin et al., 2016; Tewari et al., 2020)
- [4]. Soft Computing (Singh, 2019; Singh and Misra, 2017), and Semantic Web-based (Jearanaiwongkul et al., 2018; Marwaha et al., 2009) techniques to automate plant disease detection.