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CNN TRANSFER LEARNING TECHNIQUES TO DETECT PLANT DISEASES

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Abstract
Every country's economy depends heavily on agriculture, and keeping the agricultural industry robust and productive depends on early identification of plant diseases. In addition to causing large crop losses, plant diseases can cause resource waste and financial hardship for farmers. The necessity for automated solutions is highlighted by the inefficiency and error-proneness of traditional disease identification techniques. This work investigates the application of sophisticated deep learning models for automated image classification-based plant disease identification. The accuracy of VGG16 was 95.1%, DenseNet-201 was 94.4%, MobileNet was 97.5%, Inception ResNetV2 was 97%, Inception V3 was 97.2%, and Xception was superior to all of them with a remarkable accuracy of 99%. This remarkable accuracy shows how deep learning has the ability to completely transform the diagnosis of plant diseases. Building on these findings, we suggest creating an intelligent web tool that uses the Xception model to anticipate crop diseases in real time. By examining photos of plant leaves, the program seeks to help farmers detect diseases, allowing for early intervention and a decrease in financial losses. The importance of deep learning in promoting sustainable agricultural methods and improving precision agriculture is highlighted by this work.
Keywords: disease prediction, transfer learning, early disease detection, Xception, VGG16, DenseNet201, Inception ResNet V2, Inception V3, MobileNet, deep learning, and plant disease detection.

1. Introduction

Plant diseases affect agricultural productivity and food security, making them a serious danger to global agriculture. Depending on the crop and disease, the Food and Agriculture Organization of the United Nations (FAO) estimates that plant diseases cause 20–40% of yearly losses in global crop production. Implementing prompt therapies and reducing these catastrophic losses depend on early and precise disease detection. Conventional disease diagnosis techniques frequently depend on expert visual inspection, which can be laborious, subjective, and occasionally unavailable, particularly in rural locations. This calls for the creation of effective and automated illness detection technologies. Even though they are still in use, traditional procedures frequently include serological assays, laboratory testing (such as growing pathogens or microscopy), and visual inspection. These techniques may not be scalable for wide areas or a variety of crops, and they can be labor-intensive and specialized equipment-dependent.
Convolutional Neural Networks (CNNs) are a potent tool for detecting plant diseases because of their impressive performance in picture classification tasks in recent years. CNNs can recognize illness patterns with accuracy because they can automatically learn complicated properties from photos. However, it frequently takes a lot of computer power and big datasets to train CNNs from scratch.
Transfer learning has become a viable strategy to deal with this issue. With smaller datasets, transfer learning applies previously learned models from large datasets (such as ImageNet) to new, related

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tasks. This method greatly cuts down on training time and enhances model performance, particularly when working with sparse data, as is frequently the case with datasets on plant diseases. By enabling more accurate disease diagnosis, transfer learning with CNNs has demonstrated encouraging results in improving crop yield forecast accuracy, which in turn aids in improved crop management and resource allocation. Studies have demonstrated that transfer learning can help increase disease classification accuracy by 5–15% or more when compared to training models from scratch, which indirectly translates to better yield prediction, though the precise percentage improvement varies depending on the particular dataset and model.

Using a number of well-known CNN architectures, including VGG16, DenseNet201, Inception ResNet V2, Inception V3, and Xception, this study investigates the use of transfer learning for plant disease identification. These models were picked because of their varied architectural styles and track records of success in a range of image recognition applications.

Our goal is to assess how well these pre-trained models perform in correctly categorizing different plant diseases by refining them on a particular plant disease dataset. In addition to identifying the best model for effective and trustworthy plant disease detection, this comparison analysis will shed light on the advantages and disadvantages of each design for this specific application. In the end, this research helps create reliable and easily usable tools that farmers and agricultural specialists may use to successfully fight plant diseases, increasing crop yields and ensuring food security. We can reduce losses and possibly help create a more productive and sustainable agricultural system by making early and accurate disease identification possible.

2. Literature Survey

Amara et al. [4] proposed Plant diseases are significant because they drastically lower agricultural output both in quality and quantity. This emphasizes the need of early diagnosis and screening for such disorders. The suggested method uses deep learning to automatically categorize banana-leaf-related disorders. In specifically, this employs a convolutional neural network using the LeNet architecture for the purpose of picture classification. The first findings show that the suggested method works well even when presented with difficult situations including inconsistent lighting, a busy backdrop, and pictures of varying quality, size, position, and orientation from the actual world. In agriculture and forestry, plant diseases result in significant output and economic losses.

Tiwari et al. [6] used a pre-trained model VGG19 to extract the features and used multiple classifiers KNN, SVM and neural network for classification. The model also trained on the PlantVillage dataset to detect the early blight and late blight disease of potato leaves. They did not test their model on unseen data.

Durmus et al [10] project proposed to identify plant diseases in tomato fields and greenhouses. To this end, we used deep learning to identify a variety of tomato leaf diseases. The project attempted to have the robot execute the deep learning algorithm in real time. The robot will be able to identify plant illnesses while it freely roams the field or greenhouse under human control or on its own. Similarly, sensors installed in artificial greenhouses may utilize close-up photos of plants to identify illnesses. Symptoms of the diseases under investigation here include outwardly visible alterations to the leaves of the tomato plant. RGB cameras can detect these color shifts in the leaves. Previous research has relied on the use of conventional feature extraction techniques applied to photos of plant leaves in order to identify illnesses. Disease detection was the focus of this research, which employed deep learning techniques. To train the model, we utilized photos of tomato leaves from the Plant Village dataset. Choosing the right deep learning architecture proved to be the biggest challenge

Ismail, Aras M. and Abdulkadir Engur et al. [12] created three deep CNN models: deep feature extraction, and end-to-end training. 180 COVID-19 pictures and 200 chest X-rays were subjected to the authors' CNN model. The operating system's SVM classifier yielded 94.7% accuracy, and deep features from the ResNet50 model were acquired.

Alzubiet et al. [19] proposed a deep-learning by combining CNN and LSTM models. There are two steps in this paradigm. In the first stage, the LSTM model is employed, and in the second, the Inception model. These two models were fused together using a dense layer. This model encodes the input image by employing the LSTM and Inception model to citation the salient features from the given caption.

Additionally, the authors contrasted the suggested caption design with alternative techniques like GRU and 2D LSTM models.
Muhammad Loy [20] developed a model named "Generative Adversarial Network for Coronavirus Detection with Deep Transfer Learning (GAN)". The github repository contains the writing of Dr. Joseph Cohen. COVID-19, medical research, pneumonia, and standard photos gathered from Kaggle. Used Restnet18, Alexnet, Googlenet, and the other three deep transformation models for training after using GAN to achieve success. Restnet (normal, COVID-19, pneumonia, disease) obtained 80.6% accuracy in the first state. The accuracy index of Googlenet (usual and COVID-19) was up to 100% in the third case, whereas the Alexnet model (usual, COVID-19, disease) obtained an accuracy of 85.2% in the second case. The most accurate model, Googlenet, has overfitting problems.
B. Nigam et al [22] create COVID-19 diagnosis systems, deep learning models are utilized. Xception, EfficientNet, DenseNet121, VGG16, and NASNet are the architectures used, and multiclass classification is applied). In addition, regular patients, other patients, and positive COVID-19 individuals are taken into account. Pneumonia, the flu, and other illnesses related to the chest that fall under a different category are shown on chest X-ray images. VGG16 attains an accuracy of 79.01%, EfficientNet reaches 93.48, Xception reaches 88.03, NASNet reaches 85.03, and DenseNet121 reaches 89.96%.

3. Methodology

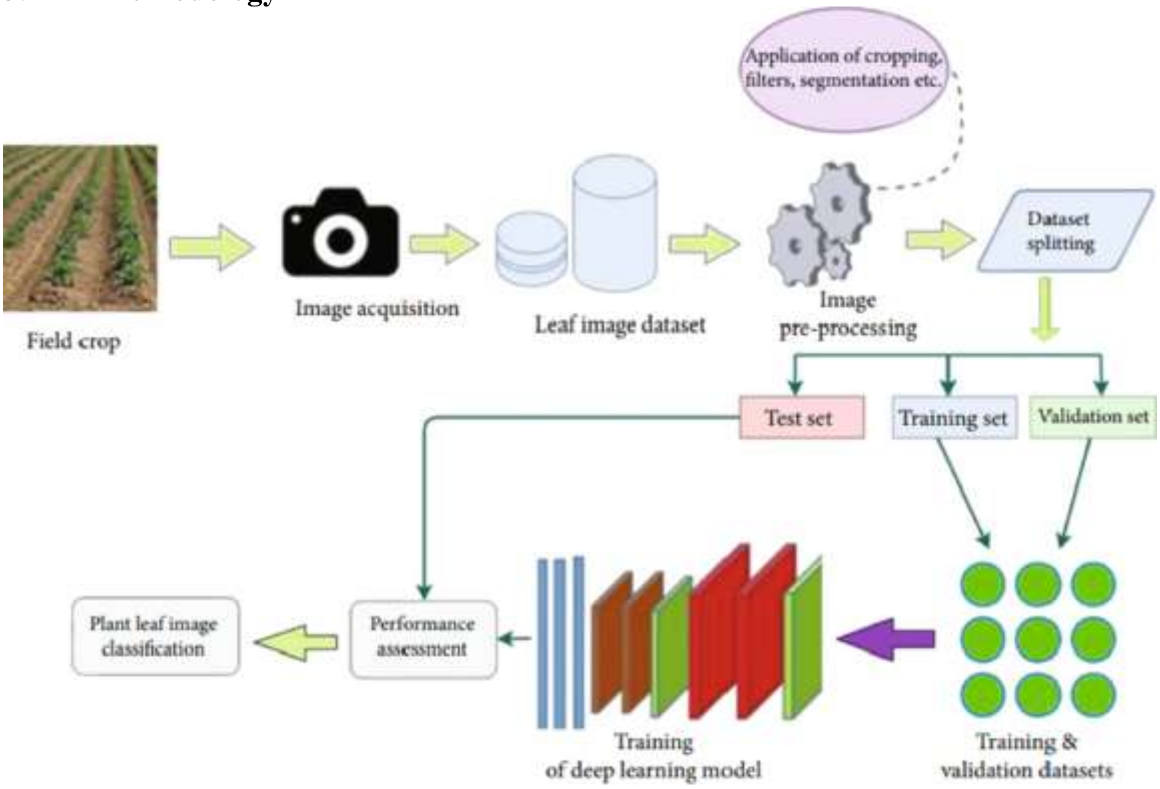

Figure: Architecture of proposed Methodology

Dataset Description:

For the project, we use dataset from the Plant Village for training, validation, and testing. The dataset has standardized images and includes healthy and diseased plant leaves images which were obtained from 10 different types of plants such as tomato, potato, pepper, grape, and apple. Every plant type is further subdivided into several disease classes, offering a comprehensive and varied dataset for testing, validation, and training.

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S. No	Plant Name	Class Names
1		Healthy
2	Apple	Leaf Scab
3		Black Rot
4		Leaf Rust
5	Bell Pepper	Healthy
6		Bacterial Spot
7	Cherry	Healthy
8		Powdery Mildew
9		Healthy
10		Black Spot
11	Citrus	Canker
12		Greening
14		Melanose
15		Healthy
16	Corn	Common Rust
17		Leaf Spot
18		Northern Leaf Blight
19		Healthy
20	Grape	Black Measles
21		Black Rot
22		Leaf Spot
23	Peach	Healthy
24		Bacterial Spot
25		Healthy
26	Potato	Early Blight
27		Late Blight
28	Strawberry	Healthy
29		Leaf Scorch
30		Healthy
31		Bacterial Spot
32		Early Blight
33		Late Blight
34		Leaf Mold
35	Tomato	Leaf Spot
36		Spider Mite
37		Target Spot
38		Mosaic Virus
39		Yellow Leaf Curl Virus

Table: The distribution of the dataset

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Disease Identification

Apple Black rot

Bellpepper Bacterial spot

Citrus canker

Corn Common rust

Grape Black rot

Peach Bacterial spot

PotatoEarly blight

Tomato YellowLeaf Curl

Corn Northern Leaf Blight

TomatoLeaf Mold

These photos of plant leaves reduce the need for manual inspection by aiding in the rapid identification of illnesses. This enables quicker treatment and improved crop health by making it simpler to identify plant diseases across vast agricultural fields.

Data Augmentation

The model can handle noise and changes in real-world circumstances by augmenting the data with various transformations, which increases its resilience and conditional adaptability. In machine learning, especially in computer vision problems, a technique called "data augmentation" is commonly used to improve the variety of the training dataset by performing various transformations to the current data. Applying data augmentation to picture data means adding variability and making little alterations to the images while preserving the most crucial details. In order to help the model acquire robust features and avoid overfitting, data augmentation exposes it to a wider range of image alterations, such as rotation, flipping, or scaling.

- Rotation: To replicate various points of view, rotate the image by a specific angle (such as 90 or 180).
- Shear: To distort an image by moving one part of it in relation to another, apply a shearing transformation.
- Zoom: Using a zooming technique alteration to the picture that will enable you to see clearly by zooming in and out of it.

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Original Image Original Image Original Image

Rotate (20) Shear (30,10) Zoom (1.5)

Figure: Data Augmentation

Deep Learning Methods:

An artificial neural network's subfield of deep learning uses algorithms that are modelled after the way the brain works. With multiple convolutional filters, feature extraction in deep learning is accomplished independently. Different features are learned by each layer in the deep learning architecture. It can produce more feature maps by altering the filter's size. The problem is solved using this tensor of feature maps. By altering the several of convolutional layers, pooling techniques, activation functions, different deep learning architectures can be created. Several pretrained deep learning model are available, including ResNet50, Dense201, VGG16, Xception.

In our proposed model for plant disease identification, after preprocessing the input images, the dataset is split into training and testing sets (80%–20%). We employ a Xception architecture in the plant disease detection process to accurately classify plant diseases. Additionally, we utilize three pre-trained deep learning models Inception ResNet V2, Inception V3, DenseNet201, and Vgg16 for classification. The models achieve an accuracy of 97%,97.2%,88.89%, 94.4%, and 95.1%, respectively, demonstrating their effectiveness in plant disease identification.

	Diseased	**Healthy**	**Total**
Train	22307	15787	38094
Test	280	108	388
Total	22587	15895	32482

Table: Dataset used with proposed work

VGG16:

VGG16 is a deep convolutional neural network architecture consisting of 16 layers, featuring a series of convolutional and max-pooling layers followed by fully connected layers for classification. VGG16 is used in the project as a classification model for tasks involving the identification of plant diseases. It is simple to comprehend and apply due to its consistent filter sizes and uncomplicated construction. VGG16 performs well in picture classification tasks, such as correctly identifying plant diseases from input photographs, despite its simplicity. The study achieves accurate and efficient disease diagnosis by utilizing VGG16's shown efficacy, which enhances agricultural output and food security.

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The VGG16 model is appropriate for processing RGB images since it starts with an input layer that can handle images of size (224, 224, 3). In order to extract important features like edges and textures from the input images, it makes use of convolutional layers with tiny 3x3 filters. Max-pooling layers are added to the feature maps to further refine them; these layers decrease the spatial dimensions while preserving crucial information. After that, the model moves on to fully linked layers, which include two 4096-node layers that allow for the learning of intricate patterns for precise classification. Because it uses a SoftMax activation function, the final output layer is appropriate for problems involving multi-class categorization. With approximately 138 million parameters, VGG16 is computationally intensive but highly effective. Additionally, it is often used with pretrained ImageNet weights, allowing for transfer learning, which significantly enhances performance in tasks such as plant disease identification or other specialized image classification problems. VGG16 with 20 epochs and a batch size of 32 produced an accuracy of 95.1% in plant disease identification. The total parameters trained in VGG16 are shown in below.

Figure: Model summary and total parameters trained in VGG16

DenseNet201:

DenseNet is one of the deep learning Neural Network model useful for image segmentation. DenseNet consists of different dense Layers in dense block where every layer is connected to every other layers i.e., the feature map is added in every layer. DenseNet consists of Dense-block and Transition layer alternatively. Dense block has the 1x1 and 3x3 convolution layers of six iterations. In Dense block features are concatenated and every convolution layer connected to every other layer by that there will not have Vanishing gradient problem as in dense no down sampling i.e., feature size is same as input image size. Transition layer consists of 1x1 convolution and average pooling 2x2, with size two strides.

DenseNet-201 have a layer for each convolution and pooling, Dense block-1 have 1x1, 3x3 convolution layer of six iterations of two times, one layer for Transition layer-1, Dense block-2 have 1x1, 3x3 convolution layer of twelve iterations of two times, one layer for Transition layer-2, Dense block-3 have 1x1, 3x3 convolution layer of forty eight iterations of two times, one layer for Transition layer-3, Dense block-4 have 1x1, 3x3 convolution layer of thirty two iterations of two times. Total it has 201 layers so it is called as DenseNet-201.

In DenseNet forward propagation, features are adding/concating to the next layers. DenseNet is advantage than ResNet because it has only skip connections but dense is having the fully forward propagation where one layer to each other layer in forward direction. DenseNet mainly have advantage of improve the vanishing gradient problem, reinforce feature propagation i.e., strong gradient flow, reassure feature reuse and substantially, decrease the no. of constraints. Dense201 trained for 20 epoch with batch size 32 produced and accuracy of 94.4%. Total Parameters trained in DenseNet201 shown in below.

Figure: Model summary and total parameters trained in DenseNet201

Xception:

Xception (Extreme Inception) is a deep learning neural network architecture that improves upon the Inception model by completely replacing standard convolution layers with depth wise separable convolutions. This architecture enhances computational efficiency while maintaining high accuracy in image classification and object detection tasks. In contrast to conventional convolutional networks, Xception can capture fine details with fewer parameters, making it especially helpful in image segmentation and plant disease detection.

The Xception architecture is more effective and able to recognize intricate patterns because it does not have the intermediary fully connected layers that Inception does. It is composed of two modules: one for feature extraction and the other for classification. Xception's primary characteristic is its dependence on depth-wise separable convolutions, in which depth-wise and spatial processing take place independently. This maintains the network's capacity to learn robust features while enabling a large reduction in the amount of computations.

Xception is that it has a good generalization capacity, making it a perfect choice for plant disease identification. The model improves feature extraction by utilizing depth-wise separable convolutions, which enables it to accurately diagnose diseases. Furthermore, Xception needs less calculations than ResNet and Inception, which makes it appropriate for deployment on resource-constrained devices like edge computing platforms and mobile devices. Xception achieved 99% accuracy after 20 epochs of training with a batch size of 32. The total parameters that were trained in Xception are displayed here.

block14_sepconv2 (SeparableConv2D)	(None, 10, 10, 2048)	3,159,552	block14_sepconv1_act[0][0]
block14_sepconv2_bn (BatchNormalization)	(None, 10, 10, 2048)	8,192	block14_sepconv2[0][0]
block14_sepconv2_act (Activation)	(None, 10, 10, 2048)	0	block14_sepconv2_bn[0][0]
avg_pool (GlobalAveragePooling2D)	(None, 2048)	0	block14_sepconv2_act[0][0]
predictions (Dense)	(None, 1000)	2,049,000	avg_pool[0][0]

Total params: [illegible] (87.40 MB)
Trainable params: [illegible] (87.19 MB)
Non-trainable params: [illegible] (213.00 KB)

Figure: Model summary and total parameters trained in Xception

Inception ResNetV2:

A convolutional neural network design called Inception ResNetV2 combines the advantages of the ResNet and Inception modules. It has residual connections and numerous parallel convolutional pathways for improved feature extraction and representation. For plant disease identification tasks in the project, Inception ResNetV2 is a potent classification model. Its complex architecture makes it possible to extract rich hierarchical information from input photos, which improves classification accuracy. The research offers strong and reliable plant disease diagnosis by utilizing Inception ResNetV2's sophisticated design. This allows for timely interventions to reduce crop losses and support agricultural sustainability.

The Stem is the first component of the Inception ResNetV2 architecture and is in charge of extracting the first features from input images. In order to reduce spatial dimensions while maintaining key characteristics, it uses multiple convolutional layers (3×3 filters) and max-pooling layers, creating a feature map that is used as input for deeper layers. The network then makes use of Inception-ResNet Blocks, which enable deeper networks to train well by fusing ResNet-style skip connections with Inception-style parallel convolutions. Three parallel convolution paths (1×1, 3×3, and 5×5 convolutions, bottlenecked by 1×1 convolutions) make up the Inception-ResNet-A block. A 1×1 convolution is then used to reduce dimensionality. To stabilize training, a skip connection is included. Using strided 3×3 convolutions, the Reduction Block 1 down samples feature maps, lowering spatial dimensions while preserving important data for more thorough feature extraction. The Inception-Reset-B block then enhances gradient flow and mid-level hierarchical feature extraction with its deeper 3×3 convolutions and skip connections. With an emphasis on high-level feature representations, the Reduction Block 2 further down samples the feature maps using strided convolutions. Last but not least, the Inception-ResNet-C block uses broader 1×1 and 3×3 convolutions to extract more abstract features while preventing vanishing gradients with skip connections. A Global Average Pooling (GAP)

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layer turns feature maps into a single vector, a Fully Connected (Dense) layer processes the extracted features, and a SoftMax layer generates class probabilities for multi-class classification (e.g., identifying various plant diseases). These layers make up the final classification head. There are various benefits to using the Inception ResNetV2 model for plant disease diagnosis. It enhances gradient flow and avoids vanishing gradients by fusing effective training (ResNet) with multi-scale feature extraction (Inception). By capturing both fine-grained and abstract information, it improves classification accuracy. Its computational efficiency also makes it appropriate for large-scale agricultural applications, guaranteeing precise and timely plant disease diagnosis. Beginning ResNetV2 achieved 97% accuracy after 20 epochs of training with a batch size of 32. The following displays the total parameters trained in Inception ResNetV2.

Figure: Model summary and total parameters trained in Inception ResNetV2

InceptionV3:

A convolutional neural network architecture known for its deep and complex architecture, InceptionV3 captures rich spatial information by utilizing many parallel convolutional paths with different filter sizes. For tasks involving the identification of plant diseases, InceptionV3 is used as a classification model in the project. Its advanced architecture makes it possible to extract features from input photos efficiently, which results in precise disease classification. Utilizing InceptionV3's strong architecture and potent feature representation capabilities, the project identifies plant illnesses with high accuracy, enabling preventative measures to protect crop health and improve agricultural sustainability.

The InceptionV3 architecture uses deep feature extraction to identify plant diseases effectively and accurately. It starts with the Stem, which reduces spatial dimensions while maintaining important information by extracting initial features using 3×3 convolutions and max-pooling. After that, the model moves on to the Inception Blocks, where parallel convolutional layers with varying kernel sizes record both large-scale and fine-grained spatial patterns to provide a thorough feature representation.

There are several Inception Modules in the network: Reduction Block 1 is used for down sampling after Module A uses 1×1, 3×3, and 5×5 convolutions to extract a variety of features. Wider convolution filters (1x1, 3x3, and 7x7) are added in Module B to improve feature extraction, while Reduction Block 2 further refines high-level representations. High-dimensional feature learning is the main focus of Module C, which also maintains skip connections for effective training and steady gradient flow. InceptionV3 achieved 97.2% accuracy after 20 epochs of training with a batch size of 32. The total parameters that were trained in InceptionV3 are displayed here.

Figure: Model summary and total parameters trained in InceptionV3

MobileNet:

A lightweight convolutional neural network architecture called MobileNet was created with effective inference on mobile and embedded devices in mind. It uses depth-wise separable convolutions to keep accuracy high while lowering computational cost. Based on input photos, MobileNet is used in the research as a classification model to identify plant illnesses. It is perfect for real-time disease detection

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applications because of its small size, which enables quick deployment and operation on platforms with limited resources. The project uses MobileNet's effective design to quickly and accurately classify plant illnesses, allowing for prompt treatments to reduce crop losses and improve agricultural productivity.

The first convolution layer in the MobileNet architecture is in charge of extracting the most fundamental features. Using a conventional 3x3 convolution with 32 filters, this layer preserves spatial resolution while capturing important edge and texture features from input images. The model then makes use of depthwise separable convolutions, a crucial MobileNet advancement that drastically lowers computing cost. The two steps of each separable convolution are pointwise convolution (1×1 Conv), which projects the output into a higher-dimensional space, and depthwise convolution, which applies a single filter per input channel. MobileNet is able to maintain robust feature extraction capabilities while achieving great efficiency because to this combination. To provide robust and efficient learning, the network consists of 13 depthwise separable convolution layers, each of which is followed by batch normalization and ReLU activation.

The model uses strided convolutions for down sampling at particular layers (2, 4, 6, and 12) to handle picture input efficiently. A stride of 2 halves the spatial dimensions, allowing for more abstract and in-depth feature extraction. A Global Average Pooling (GAP) layer reduces the number of parameters and mitigates overfitting by converting feature maps into a single vector following the convolutional feature extraction procedure. To create class probabilities for multi-class plant disease classification, the recovered feature vector is lastly run through a fully connected (Dense) layer and then a SoftMax activation function. MobileNet is the perfect option for real-time agricultural applications because of its streamlined architecture, which enables it to identify plant diseases effectively and accurately. MobileNet trained for 20 epoch with batch size 32 produced and accuracy of 97.5%. Total Parameters trained in MoblieNet shown in below.

```
model.summary()
```

conv_pw_13_bn (BatchNormalization)	(None, 7, 7, 1024)	4,096
conv_pw_13_relu (ReLU)	(None, 7, 7, 1024)	0
global_average_pooling2d (GlobalAveragePooling2D)	(None, 1, 1, 1024)	0
dropout (Dropout)	(None, 1, 1, 1024)	0
conv_preds (Conv2D)	(None, 1, 1, 1000)	1,025,000
reshape_2 (Reshape)	(None, 1000)	0
predictions (Activation)	(None, 1000)	0

Total params: 4,253,864 (16.23 MB)

Trainable params: 4,231,976 (16.14 MB)

Non-trainable params: 21,888 (85.50 KB)

Figure: Model summary and total parameters trained in MobileNet

4. Experimental Results

The results of the experimental evaluation showed how well the suggested method classified and detected plant diseases. Tests on the dataset revealed that the DenseNet and Xception models performed better on classification tasks. Xception outperformed the others with a remarkable 99% accuracy rate, as well as remarkable precision, recall, and F1 scores. These outcomes demonstrate that the model can effectively detect plant illnesses and manage challenging field circumstances.

Users were able to upload plant photos and get real-time results by integrating these models into a web application built with Flask. Throughout testing, the system operated flawlessly and produced precise disease classifications and detection results. Its potential to help farmers and researchers diagnose plant diseases effectively is validated by this real-world application, which will ultimately improve crop health management and yields.

i) Accuracy: The accuracy of a test is its ability to differentiate the patient and healthy cases correctly. To estimate the accuracy of a test, we should calculate the proportion of true positive and true negative in all evaluated cases. Mathematically, this can be stated as:

$$Accuracy = \frac{tp + tn}{tp + fp + fn + tn}$$

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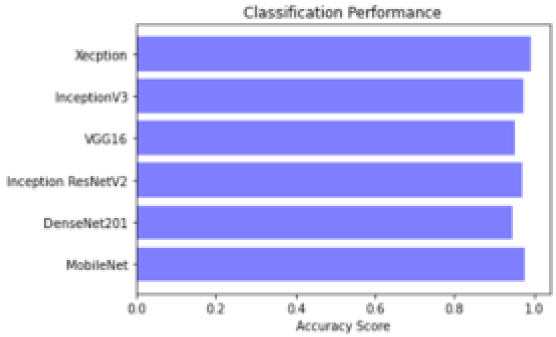

Figure: Accuracy Score

ii) Precision: Precision evaluates the fraction of correctly classified instances or samples among the ones classified as positives. Thus, the formula to calculate the precision is given by:

$$Precision = \frac{tp}{tp + fp}$$

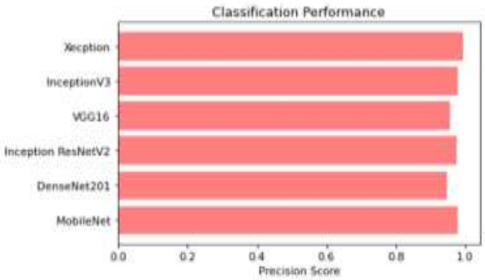

Figure : Precision Score

iii) Recall: Recall is a metric in machine learning that measures the ability of a model to identify all relevant instances of a particular class. It is the ratio of correctly predicted positive observations to the total actual positives, providing insights into a model's completeness in capturing instances of a given class.

$$Recall = \frac{tp}{tp + fn}$$

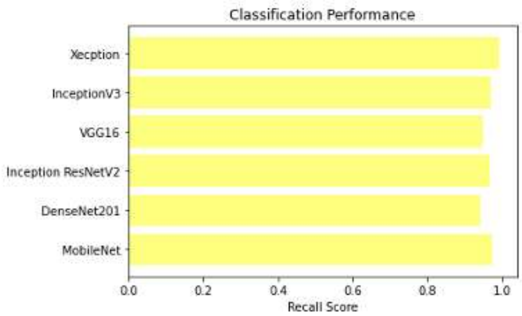

Fig.6.Recall Score

iv) F1-Score: A machine learning evaluation metric called the F1 score measures how accurate a model is. It integrates a model's precision and recall scores. The accuracy measure calculates the number of times a model correctly predicted the whole dataset.

$$F - measure = \frac{2 \times (recall \times precision)}{recall + precision}$$

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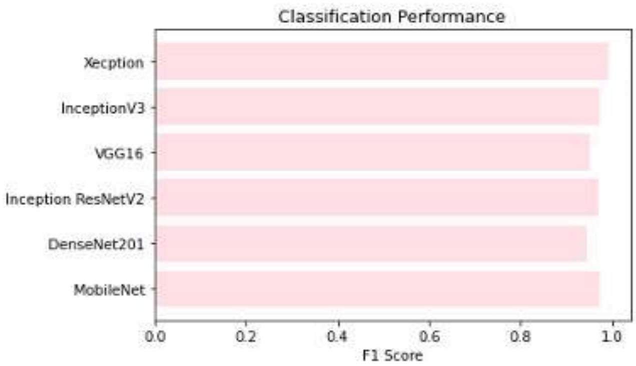

Figure: F1 Score

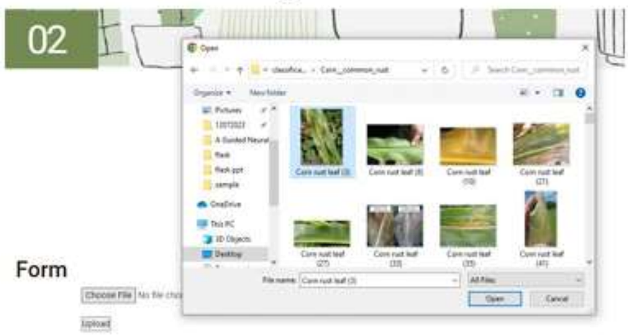

Figure: upload image

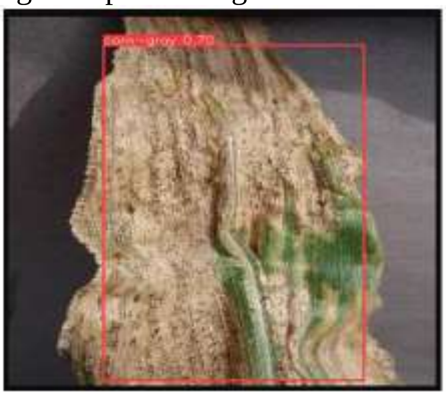

Figure: .result

DL Model	Accuracy	Precision	Recall	F1_score
DenseNet201	0.944	0.945	0.943	0.944
VGG16	0.951	0.955	0.949	0.952
Xception	0.991	0.993	0.991	0.992
Inception ResNet V2	0.970	0.974	0.967	0.970
MobileNet	0.975	0.978	0.973	0.975

Figure:.Accuracy graph

5. Conclusion and Future Scope

Enhancing agricultural productivity, reducing financial losses, and ensuring food security at the global level all rely on an early and correct detection of plant diseases. This research examines the effectiveness of Convolutional Neural Networks (CNNs) using deep learning for plant disease classification. DenseNet-201 recorded 97% accuracy, Xception recorded the highest accuracy of 99%, ResNet-50 recorded 88%, and VGG16 recorded 95% accuracy, showing the high performance of state-of-the-art architectures in disease detection. These findings illustrate that deep learning models, particularly Xception and DenseNet-201, are highly efficient at identifying plant diseases, making them perfect for real-world agricultural usage.

By minimizing the requirement for manual inspection and enabling quick response, the integration of automated AI-based plant disease detection systems can potentially revolutionize modern precision agriculture. Future advancements can focus on expanding datasets, improving models for edge and mobile platforms, such as real-time monitoring using the Internet of Things, and enhancing interpretability using explainable AI. Plant disease detection systems based on deep learning have the capability to significantly boost food production, encourage sustainable agriculture, and reduce pesticide misuse by embracing this technology, which leads to a stronger and better agricultural system.

6. References

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