

Ensemble Efficient Net and ResNet model for Crop Disease Identification

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Abstract: Crop diseases have the potential to cause devastating epidemics that threaten the global food supply, and their dispersal patterns vary greatly. Therefore, it is essential to predict crop diseases to improve production efficiency hence, many existing techniques diagnose the disease through optical and automatic examination of infected leaves but they require additional feature extraction modules to predict only a single disease which results in time-consuming erroneous prediction. Hence an Ensemble ResNet-Efficient Net Model has been proposed that provides effective classification results on crop diseases with balancing network depth, width, and resolution thereby having limited computational resources, and precise and timely prediction of multiple diseases in crop images. Also, the features are extracted more significantly with the swish activation function in ensemble models without the need for a separate module which neglects erroneous prediction due to gradient vanishing and multi-co linearity. The experiment is conducted on 1950 real-time crop images collected from Crop fields using ResNet, Efficient Net B4, and Efficient Net B7 models. The result obtained shows that the proposed ensemble ResNet-Efficient Net model has high accuracy and low loss when implemented in Python and is compared to other existing methodologies.

Keywords: Artificial intelligence, Crop diseases, Image Processing, ResNet, Efficient Net B4, Efficient Net B7, Modified U-Net, Fuzzy filtering

1.Introduction

The agricultural industry is a crucial and innovative framework for computer vision researchers nowadays. Agriculture's principal purpose is to create a diverse array of important and significant crops and plants [1-3]. Plants provide a significant portion of the world's food supply but diseases in plants cause output losses, which can be mitigated through continual monitoring. Agricultural researchers have recently concentrated their efforts on prediction of diseases in various fruits and crops [4,5]. Manual plant disease monitoring is time-consuming since that require huge labor and error-prone [6]. Recently, image processing-based automated methods for identifying and recognizing illnesses in horticulture have been created. The researchers employ image processing to determine the position, colour, form, scale, and limits of the sick component. A range of new strategies are used for pre-processing and disease symptom segmentation in plants. Various image processing approaches were used to address issues associated with naked eye inspection in an agricultural field. Several present techniques in the agricultural business address

segmentation of distinct crop components such as fruits, stems, and leaves, as well as removing and recognizing various illnesses and stress regions. Traditional image processing algorithms work well when a large number of training

examples are not available to process. The fusion of background and object regions, similarities and morphologies extracted during feature extraction are some of the difficulties associated with plant disease diagnosis [7-10]. As a result, these difficulties in feature extraction have been effectively solved by modern artificial intelligence (AI) techniques.

Detection of plant diseases using computer vision and AI can help to lessen disease effects and overcome the limitations of continuous human monitoring. In recent years, the expansion of Machine Learning (ML) techniques has permitted a plethora of applications in a variety of fields. By imitating human learning activities, ML systems aim to gain real-world information

independently. A lot of research have recently been dedicated to applying ML approaches to various crops in the agriculture sector [11,12]. Machine learning in agriculture has the potential to be applied to a wide range of applications, from detecting weeds and diseases to predicting crop output and quality, to gathering data, providing insights, and making predictions about livestock production. For example, many ways for classifying plant diseases using DL techniques have been suggested. Nonetheless, many contemporary techniques need extensive training/testing or have low accuracy, which may restrict real-time use. Given the circumstances, an adequate model for plant disease classification is required.

Convolutional neural network (CNN) is a well-known neural network design that has been utilized effectively

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for a wide range of computer vision problems in a variety of industries. CNN architecture and its variants have been utilized by researchers to classify and identify plant diseases [13-15]. CNNs have been used in categorization and prediction and have exhibited superior prediction ability when compared to other techniques such as SVM or RF [16,17]. Deep neural networks were also discovered to outperform other approaches in plant disease recognition. However, improved accuracy comes at a cost, CNNs must be scaled up broader, deeper, and/or higher resolution, which necessitates new architectures with more parameters, leading in prohibitively expensive training and testing. Various compact CNNs have been presented thus far in order to strike a balance between accuracy and computing cost. Still, the performance of such a technique could be enhanced [18,19]. To address the major shortcomings of existing CNN methods, two new deep neural network families, Efficient Net and ResNet, have been developed in this research. The main contribution of this paper are as follows:

- In crop disease prediction, ensemble ResNet and Efficient Net models employs a compound scaling mechanism with preset ratios of all three dimensions of crop images that aid in increasing both computing performance and accuracy in the identification of crop diseases.
- To improve the crop disease prediction performance without noise and perceptual incompleteness, non-linear weighted fuzzy mean filtering and Modified U-Net has been used in preprocessing and segmentation steps that provide super resolute image with segmenting diseased region.

The content of the paper is organized as follows: Section 2 presents the related work; the novel solutions are presented in section 3; the implementation results and its comparison are in section 4 and section 5 concludes the paper

2.Related Work

Agarwal et al [20] identified disease in tomato leaves using a convolution neural network-based technique. This model consists of three convolution layers, three max pooling layers, and then two fully linked layers. According to the experimental results, the suggested model performs better than the pre-trained models VGG16, InceptionV3, and Mobile Net. The suggested model's average classification accuracy is 91.2% for the 9 disease and 1 healthy class, ranging from 76% to 100% depending on the class. However, there is a need to improve the model by using a larger number of images with different cropping. Also, there is a need to enhance the same model on the same dataset because the testing accuracy is low. To detect Bacterial Spot disease in peach plants using leaf photos, a hybrid model based on CNN and Convolution Auto encoder (CAE) network has been proposed by Bedi et al [21], however, it may be used to detect any plant disease. The experiments in this study utilize leaf images from peach plants from a publicly accessible dataset called Plant Village.

The proposed hybrid model needs fewer training parameters than other methods in the literature. As a result, there is a significant reduction in the time needed to train the model for automatic plant disease detection and the time needed to diagnose the illness in plants using the trained model. However,

in this technique, only 9,914 training parameters are used, which is significantly less than the amount of training parameters used in state-of-the-art systems. Dai et al [22] presented DATFGAN a generative adversarial network with topology fusion and dual attention. This network can transform blurry photos into sharp, high-resolution ones. Additionally, the proposed network's weight-sharing method can significantly reduce the number of parameters. Experimental results show that DATFGAN outperforms state-of-the-art methods in terms of visual appeal. Additionally, identification tasks are used to evaluate the tested images. However, larger image datasets like Image Net are not used to train the neural network model. Xiong et al [23] provided a technique using automatic image segmentation and deep learning on a bigger dataset for identifying diseases affecting cash crops. The Grab Cut algorithm-based Automatic Image Segmentation Algorithm (AISA) is designed to automatically remove background information from images while preserving disease areas. A sizable number of cropped images are added to Plant Village, and the Mobile Net CNN model is selected as the deep learning model. The AISA processes the images before using them to extract disease features, greatly reducing calculations and guaranteeing that the crop leaf's disease features can be extracted precisely. However, additional study is required to advance this work, including defining the disease's various stages of development and broadening the type of crop disease. Sampathkumar et al [24] provided the Cognitive Fuzzy C-Means (CFCM) algorithm to distinguish the suspicious zone from the normal region, and the Cross Central Filter (CCF) technique to remove noise from the image. The evaluation is being done in light of the diseases that have affected the apple trees and the rice crop. The performance study shows that the suggested design performs better than the other filters and segmentation methods. However, there is a need to include 10-fold cross-validation technique to validate the categorization procedure. In order to create an IoT system for crop fine-grained disease identification, deep learning and IoT technologies were combined by Hu et al [25]. After that, automatically identify agricultural illnesses and give farmers a diagnosis. A multidimensional feature compensation residual neural network (MDFC-ResNet) model for precise disease diagnosis is presented in this system. Species, coarse-grained disease, and fine-grained disease are the three dimensions that MDFC-ResNet detects in, and it builds a compensation layer that employs a compensation technique to fuse the results of multidimensional recognition. However, impact of making treatment recommendations is not considered based on best practices. From the analysis, [20] have low testing accuracy and training parameters in [21] is significantly low. [22] is not trained using larger image datasets and [23] not consider defining the disease's many stages of development. In [24], there is a need to validate the categorization procedure and in [25], impact of making action based on diseased state is not considered. Hence, there is a need to present a novel model to strike a balance between accuracy and computing cost which is explained in the next section.

3. Methodology

3.1. Crop disease prediction using Ensemble EfficientNet and ResNet model

Precision agriculture is essential for avoiding financial loss and boosting crop productivity, as well as for the accurate and prompt detection of crop diseases. Because so many crop diseases exhibit distinctive symptoms, it can be challenging to precisely pinpoint diseases in leaves. Therefore, image processing-based computer-assisted tools are essential for the quick and precise detection of crop diseases. Deep learning architectures can be used to detect crop diseases, but there are still some gaps to be filled since it is necessary to develop effective models with fewer parameters that can be trained more quickly without sacrificing performance. Hence a novel filtering that improve the image quality by removing noise and segmentation which is done by using Modified U-Net model that effectively segments the diseased area by rearranging the convolutional layer for upsampling and concatenation with the

Ensemble EfficientNet and ResNet model has been proposed that achieves more effective results by figuring out the relationship between the various scaling dimensions of the baseline network while working within a fixed resource constraint. This leads to uniform scaling of depth, width, and resolution as the model is minimized. Also the stacked residual units in ResNet and swish function instead of ReLU function in EfficientNet B4 and B7 effectively extract feature maps without degradation and multi-collinearity problem. Hence based on these feature map an efficient classification has been performed to predict the crop diseases in maize, wheat, rice and ragi. Furthermore, to enhance the performance of the novel EfficientNet and ResNet model, improvement in preprocessing and segmentation of crop image is required. Hence the preprocessing is performed by Non-linear weighted fuzzy mean corresponding feature map for the contracting path. Hence, the proposed model effectively classifies various crop diseases with high accuracy and low loss.

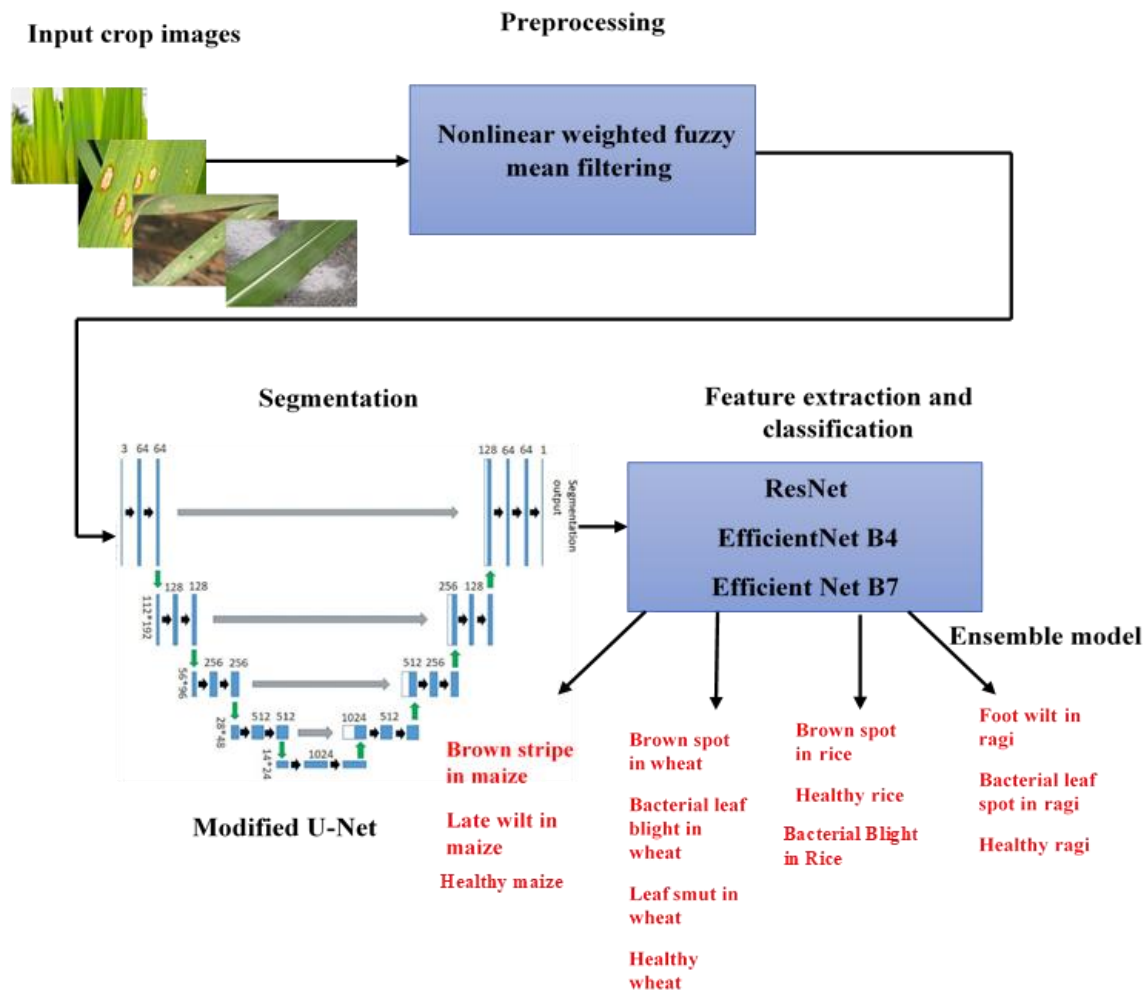


Fig 1. Architecture of Ensemble crop disease identification model

Figure 1 depicts the architecture of ensemble EfficientNet and ResNet model to achieve efficient classification of crop diseases in maize, wheat, rice and ragi. Initially, crop images were given as the input which is preprocessed using non-linear

weighted fuzzy mean filtering and the processed noise free high resolution image is segmented via Modified U-Net. Then, features were extracted from segmented image to aid classification in ensemble model by utilizing compound scaling

mechanism. Hence various crop diseases were identified with high computing efficiency and system performance.

3.2. Ensemble EfficientNet and ResNet model

Ensemble EfficientNet and ResNet model has been proposed to recognize the various diseases in crops in which to improve the recognition accuracy without computational complexity due to the noise and improper segmentation, effective preprocessing and segmentation techniques are incorporated.

3.2.1 Preprocessing

In preprocessing task, Non-linear weighted fuzzy mean (NWFM) filtering approach is used to eliminate the presence of noise in the input image. Consider an noisy input image J sized $M_1 \times M_2$ and grey levels N with working window $M_{i,k}$ and center pixel $y_{i,k}$. The source image is represented as $J = [j(i,k)]_{M_1 \times M_2}$ in which a pixel of source images is denoted as $j(i,k) \in \{0,1, \dots, N-1\}$ for $0 \leq i \leq M_1 - 1$ in addition to $0 \leq k \leq M_2 - 1$. On the discourse universe of $\{0, \dots, N-1\}$, several fuzzy sets are defined in order to denoise the source image. Each fuzzy set corresponds to a source image's abstract grayscale pixel. A specific pixel's membership rank is shown as "very dark," "dark," "middle," "bright," or "extremely bright," along with the corresponding Membership Function (MF).

The fuzzy subsets of an image's intensity feature are retrieved from its histogram, and it also contains a knowledge base about NWFM approach. In order to determine the image's intensity feature in NWFM, fuzzy subsets are used which is given in equation (1),

$$F(y) = \begin{cases} N(v_{NL} - y) & \text{for } y \leq v_{NL} \\ L\left(\frac{y - v_{NL}\alpha_{NL}}{\beta_{NL}}\right) & \text{for } y \geq v_{NL} \end{cases} \quad (1)$$

where, $\alpha_{NL} > 0$, $\beta_{NL} > 0$ and $N(x) = L(x) = \max(0, 1 - x)$ that is N and L has the same texture and structure and also $F(y)$ is employed as a triplet of $(v_{NL}, \alpha_{NL}, \beta_{NL})$. Thereby, determined L uncorrupted pixels from the image and restore the corrupted pixels in weighted mean filter. Once there are enough

uncorrupted pixels, estimate the denoised value using the set L pixel intensities. An inverse distance weighting function is used to weight the elements of L , giving closer pixels more weight and pixels farther away less weight. Following that, the weights are normalized so that their sum is 1. As a result, the central pixel's denoised value is given by

$$y_{i,j}^{new} = \frac{1}{M} \sum_{y_n \in L} W_n y_n \quad (2)$$

In equation (2), W_n denotes the weight for a neighbour uncorrupted pixel y_n and M denotes the normalizing term. Thus, the input images are converted into noise-free super-resolute images by using Non-linear weighted fuzzy mean filtering approach that solves high-level vision problem and perception incompleteness. Then to effectively segment the preprocessed images, Modified U-Net model is used which is explained in the next subsection.

3.2.2 Segmentation

Segmentation of crop image regions with distinctly identifying diseased region is performed by Modified U-Net. A contracting path with four encoding blocks is followed by an expanding path with four decoding blocks in the Modified U-Net model. Two sequential 3×3 convolutional layers make up each encoding block, which is then followed by a downsampling max pooling layer with a stride of two. The decoding blocks consist of two 3×3 convolutional layers, a transposed convolutional layer for upsampling, and concatenation with the relevant feature map from the contracting path. The decoding block uses three convolutional layers rather than two in the modified U-Net architecture. The modified decoder consists of an upsampling layer, two 3×3 convolutional layers, a concatenation layer, and a final 3×3 convolutional layer. The architecture of modified U-Net model to perform effective segmentation is shown in figure 2

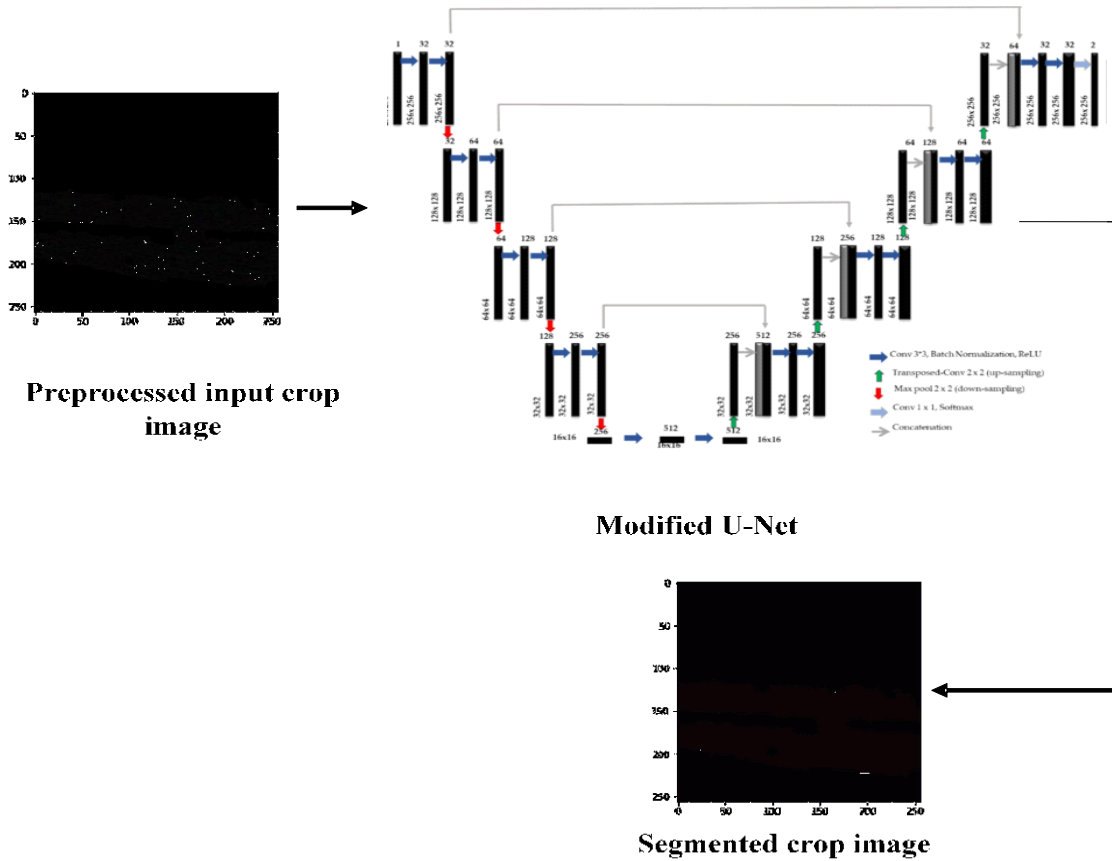


Fig 2. Modified U-Net for crop image segmentation

The preprocessed crop images are given to the contracting path of modified U-Net in which after performing convolution operation, batch normalization and dropout is added. In order to prevent the network from overfitting, the dropout layer randomly deactivated some neurons in the hidden layer, normalizing the outputs of the convolutional layer to have a mean of zero and a standard deviation of one. In the first convolutional block, there are 16 filters, these are doubled in the following three blocks to total 128 filters in the final convolutional block. In order to perform segmentation, this contracting path captures the context or semantics of the preprocessed crop image. It extracts features that have information about the preprocessed crop image using convolutional and pooling layers. The deep or high-level features of the image are obtained during this process, and the size of the feature map is reduced, but the network forfeits the spatial or location data in which those features are located.

The decoder uses up-convolution layers to add spatial information to the segmentation image while recovering the size of the feature map from the encoder's extracted features. The contracting path's coarse contextual data is transferred to the upsampling path through skip connections. In order to retrieve the lost data and give the decoder access to the low-level features created by the encoder layers, skip connections are used. The inputs to the intermediate layers of the decoder

are concatenated with the intermediate outputs of the encoder at the appropriate points. In combination with contextual information from the contracting path, this makes precise localization possible. Thereby achieves effective segmentation results in segmenting diseased location in crop images. Then to classify the various types of diseases in crop images, a novel Ensemble EfficientNet and ResNet model has been used which is explained in the next subsection.

3.2.3 Feature extraction and Classification

The segmented image is input into the Ensemble EfficientNet and ResNet model, which successfully determines the feature vectors during the feature extraction process. This ensemble model created a number of enhancements for training these parameters mainly with their activation function to provide non-linearity. Typical activation function in this ensemble model includes swish function and ReLU function. The models such as ResNet, EfficientNet B4 and EfficientNet B7 are used to develop the ensemble model. The feature extraction and classification task performed by each model has been provided. ResNet model handles automatic feature extraction in addition to classification. As a result, ResNet model eliminates the need for a separate feature extraction method. The ResNet architecture with four stage connection for crop disease prediction has been shown in figure 3.

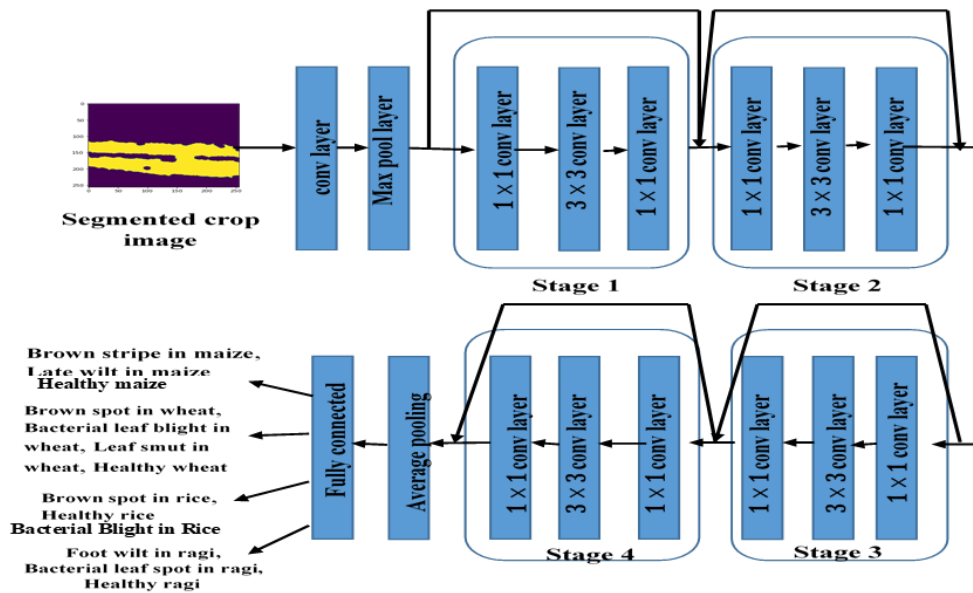


Fig 3. ResNet architecture in crop disease prediction

The segmented crop images are given to ResNet that are processed by residual blocks and skip connection to effectively extract features such as edges, swell, leaf burn, brown spots, and color change thereby precisely classify various crop diseases in maize, wheat, rice and ragi. Residual block employs skip connections to address the grand vanishing issue. Connections that omit one or more layers are known as shortcut connections. The residual shortcut ensures network integrity if the regular connection's coefficient converges to zero during the training process. By enabling users to choose these shortcuts as needed, the alternative connections enhance the network. This architecture was created by introducing skip connections to a plain-34-layer convolutional neural network. This model

improves accuracy while using a small amount of data and saves time in detecting crop diseases. Then, in proposed ensemble model, Efficient Net B4 and Efficient Net B7 are included to further improve the accuracy in the prediction of crop diseases.

In Efficient Net B4, three dimensions of magnification are balanced in terms of network width, network depth, and image resolution. As a result, Efficient Net B4 obtains three-dimensional magnification using the compound scaling method, and then balances the three dimensions of model depth, width, and resolution to obtain the final prediction accuracy and efficiency improvement. The schematic view of Efficient Net B4 for crop disease prediction has been shown in figure 4.

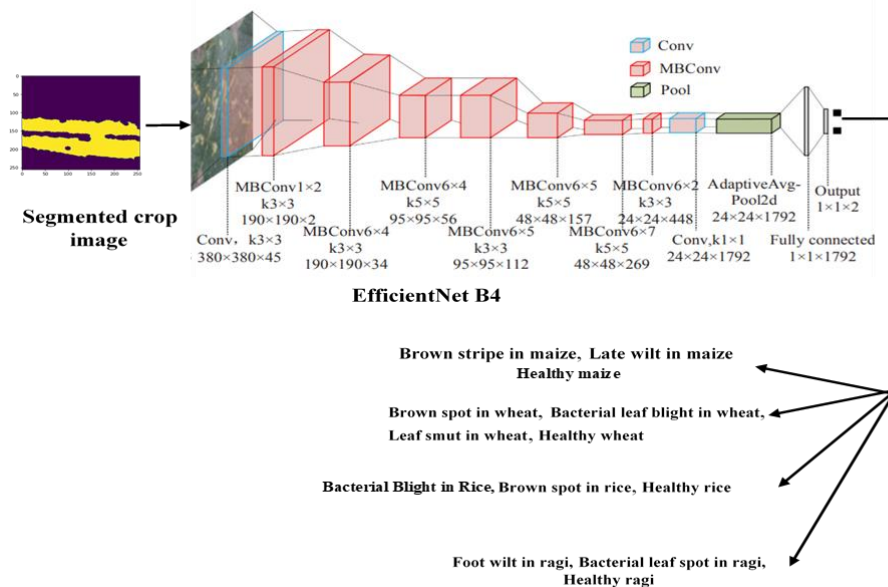


Fig 4. Architecture of EfficientNet B4 in crop disease prediction

The input segmented image is processed through convolution layers to efficiently extract feature maps with balancing the neural network parameters via rescaling mechanism. These scaled feature maps are pooled in the adaptive with finding the

average pixel values by utilizing adaptive average pooling layer. The output of the final Pooling layer is flattened and fed into the fully

connected layer as the input. This layer multiplies the input by a weight matrix, followed by the addition of a bias vector and perform classification based on features extracted by previous

layers. The final classification output of various crop diseases including brown spot, leaf wilt and bacterial leaf is given to the output layer that displays the crop diseases with high accuracy.

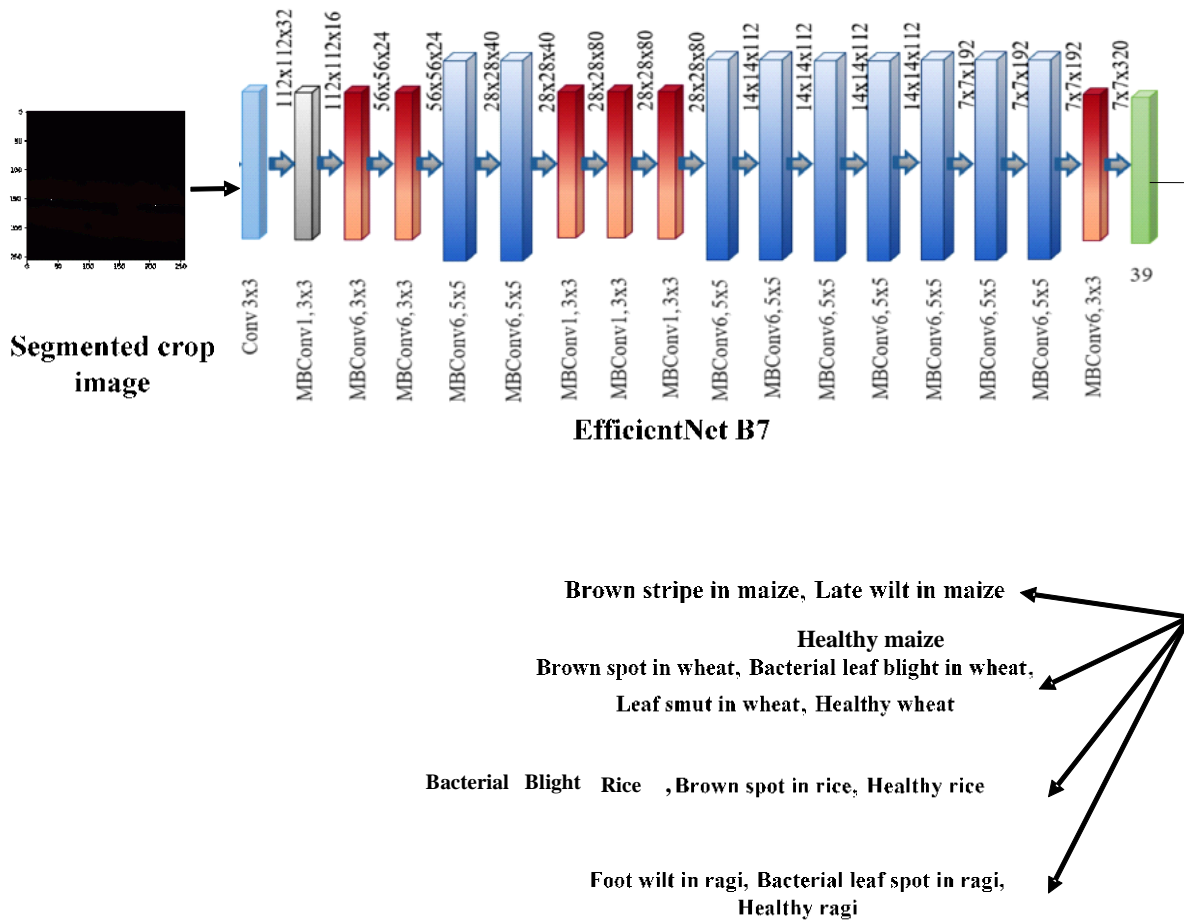


Fig 5. Schematic view of EfficientNet B7

In Efficient Net B7 model, swish activation function $t(k) = \max(0.001 \times k, k)$, a new activation function is used to ignore incorrect predictions brought on by multi-collinearity. When the model is shrunk, uniformly sharing width, resolution, and depth yields more effective results. Figure 5 depicts the architecture of Efficient Net B7's crop disease prediction system.

Since the blocks are composed of a layer that expands and then compresses the channels, between bottlenecks in MBConv, blocks with significantly fewer channels than expansion layers process the input segmented crop image using direct connections. As the layer's design separates, the calculation is reduced by k^2 , where the 2D convolution window's width and height are represented by the kernel size k . EfficientNet B7 model is mathematically depicted in equation (3) as,

$$E = \sum_{y=1,2,3\dots n} W_y^{t_y} (Z_{(a_y, b_y, c_y)}) \quad (3)$$

where W_y denote the mean of the layer and t_y is the variance of y . (a_y, b_y, c_y) represents the shape input in the Z tensor with respect to the layer y . The image inputs are changed from

256 × 256 × 3 to 224 × 224 × 3. The layers are scaled with a proportional ratio optimized using equation (4) in order to increase model accuracy.

$$\max_{x,y,z} = \text{acc}(E(x, y, z)) \quad (4)$$

$$E(x, y, z) = \sum_{y=1,2\dots n} W_y^{t_y} (Z_{(s.a_y, s.b_y, s.c_y)}) \quad (5)$$

In Equation (4), x, y , and z represent the height, width, and resolution. Equation (5) depicts a number of layers used in the model as well as parameter details. These scaled features are further pooled and given to flatten fully connected layer in order to perform efficient classification of various crop diseases in crop images.

Overall, Ensemble Efficient Net and ResNet model for Crop Disease identification has been presented to recognize the diseases in crop image by removing the noise and enhancing image quality with segmenting diseased region in the preprocessing and segmentation steps. Then, features were extracted from these images to predict the crop diseases using Ensemble Efficient Net and ResNet model. The next section

explains the result obtained from an Ensemble Efficient Net and ResNet model for Crop Disease Identification in detail.

4. Results and Discussions

This section includes a thorough analysis of the implementation outcomes, as well as information on how well the suggested system performs and a section of comparisons to make sure the suggested system can be used in agriculture.

4.1 Data Collection

The images of the crop diseases were collected from the agricultural fields of Karnataka State, India, and were validated by agricultural experts. The camera model used was Canon EOS 1500D 24.1 Digital SLR Camera with 24.1 megapixels to capture each image. The sub-image comprising the lesion is acquired manually for each image, and afterward, the image with too low intensities and the blurred image are disposed of, and the number of images is increased by changing the angle and adequately cutting. Afterward, a database of all types of diseases was compiled and a total of 1950 images were used. These collected images include different classes with various types of crop diseases and healthy crops. The exact number of images in each class has been shown in Figure 6.

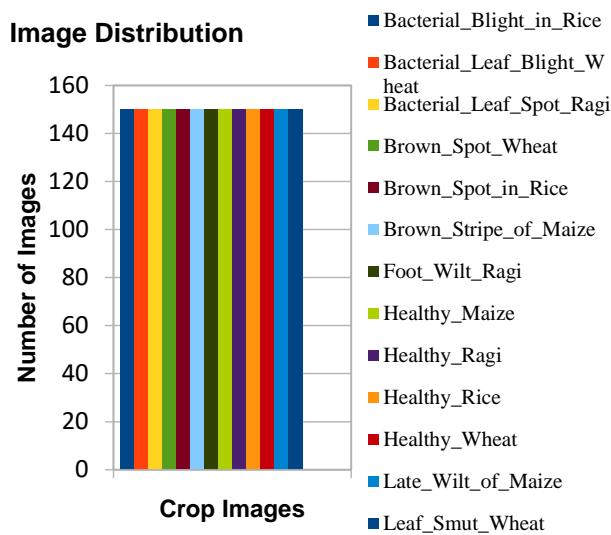


Fig 6. Number of crop images in different classes

From the above figure 6, it is clear that the crop categorizes such as brown stripe in maize, late wilt in maize, brown spots in wheat, bacterial leaf blight in wheat, leaf smut in wheat, healthy wheat, brown spots in rice, healthy rice, foot wilt in ragi, bacterial leaf spot in ragi and healthy ragi have the appropriate number of crop images containing 150 images for each class. The images is spilt into ratio of 70 % for training, 10 % for validation and 20 % for testing.



Fig 7. Sample images collected from crop field

Figure 7. represents the sample crop images collected from Crop fields and it includes images in healthy condition as well as in diseased condition. The sample image has four different crops namely maize, wheat, rice and ragi with more than one disease in each crops.

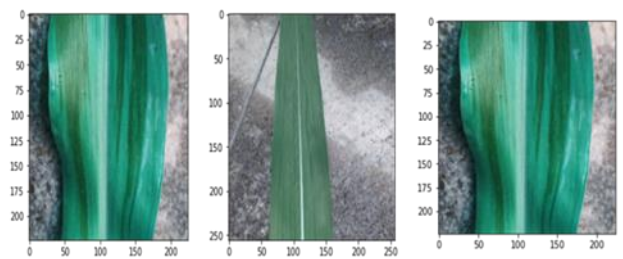


Fig 8. Preprocessed crop images

4.2 Simulated output of proposed model

The crop images have been preprocessed, segmented and classified to categorize using the proposed techniques and the output obtained from each techniques were explained in this section.

Figure 8. represents the simulated output obtained after preprocessing the input crop images. The preprocessing has been done by using Non-linear weighted fuzzy mean filtering in which fuzzy set has been implemented based on image feature intensity. The obtained preprocessed image is noise free and in high resolution

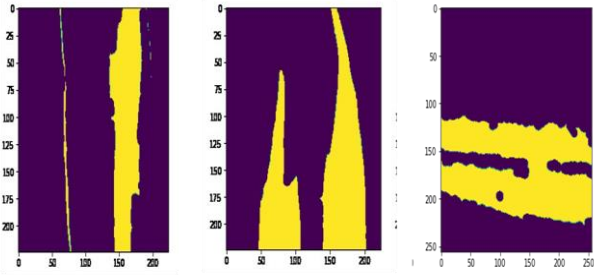
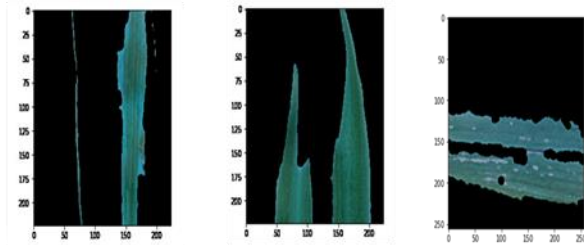


Fig 9. Segmented crop images

The simulated output obtained after segmenting the preprocessed crop images is shown in Figure 9. The preprocessed image has been segmented by using Modified U-Net in which contracting and expanding path extract feature map to segment the diseased regions and the loss of spatial information is removed by using skip connections.



ig 10. Feature extraction in crop images

The simulated output of feature extraction process has been shown in Figure 10. in which the segmented image is given to the ensemble model that effectively extracts features without requiring any additional modules. The features such as edges, swell, leaf burn, brown spots, and color change are extracted by implementing Convolution and MBConv layers in the proposed ensemble model.

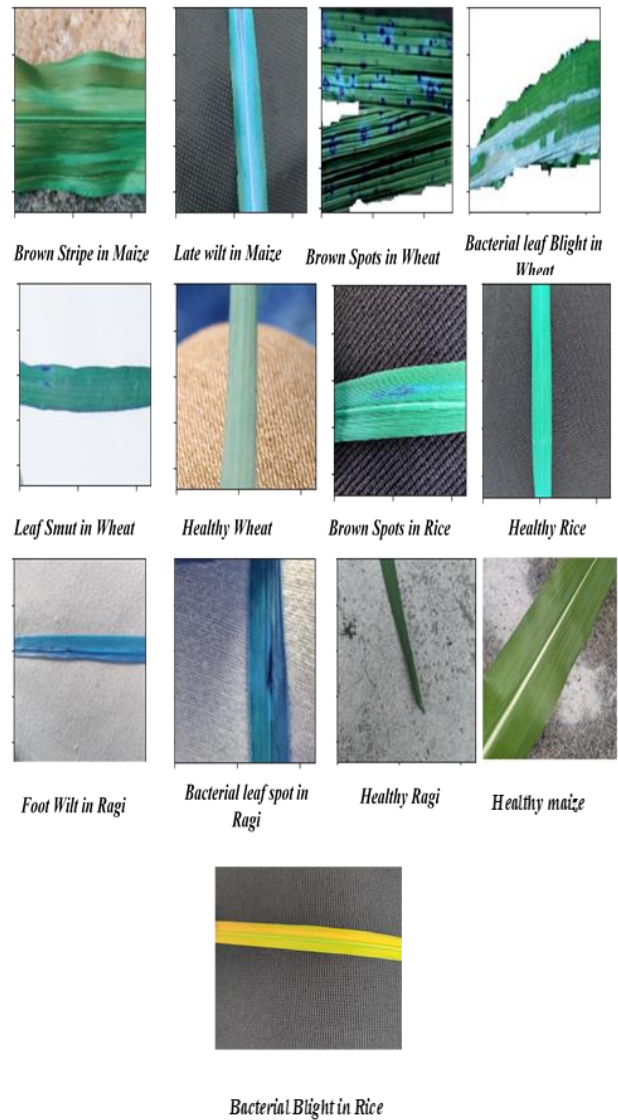


Fig 11. Simulated classification output of ensemble models

The simulated classification output of proposed ensemble model such as ResNet, Efficient Net B4 and Efficient Net B7 has been shown in Figure 11. These ensemble model precisely classify multiple crop diseases in maize, wheat, rice and ragi with processing the extracted feature maps in the flattened fully connected layer with ReLU and swish activation function.

4.3 Performance analysis of proposed model

The performance of the proposed ensemble model and the achieved outcome is explained in detail in this section.

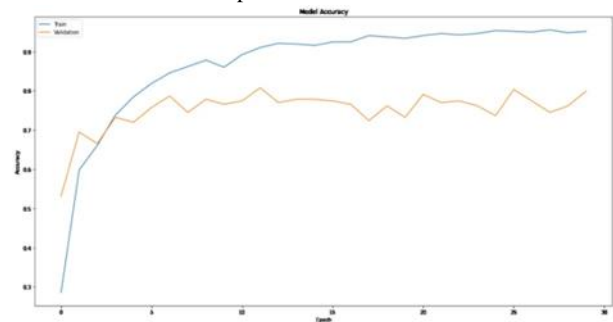


Figure 12. Accuracy of ResNet Model

The overall accuracy of the ResNet model during training and validation is shown in Figure 12. The accuracy was determined by varying the number of epochs from 1 to 30. ResNet model attains the maximum accuracy value of 0.94 and 0.79 during training and validation respectively. Additionally, during training and validation, ResNet achieves minimum accuracy values of 0.6 and 0.55, respectively. The accuracy of ResNet increases with increase in the number of epochs. The accuracy of ResNet is improved by using residual block shortcut connection that ensures network integrity.

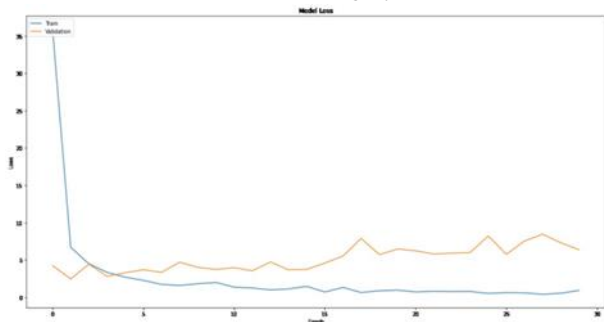


Fig 13. Loss of ResNet Model

The overall loss of the ResNet model during training and validation is shown in Figure 13. The loss was determined by varying the number of epochs from 1 to 30. ResNet model attains the minimum loss value of 14% during training and validation respectively. The loss of ResNet is reduced by using alternative connections by allowing to select the shortcuts as required.

	precision	recall	f1-score
Bacterial_Blight_in_Rice	0.91	1.00	0.95
Bacterial_Leaf_Blight_Wheat	1.00	1.00	1.00
Bacterial_Leaf_Spot_Ragi	1.00	0.47	0.64
Brown_Spot_wheat	0.79	0.83	0.81
Brown_Spot_in_Rice	1.00	1.00	1.00
Brown_Stripe_of_Maize	0.78	1.00	0.88
Foot_Wilt_Ragi	0.53	0.64	0.58
Healthy_Maize	0.81	0.89	0.85
Healthy_Ragi	0.91	0.67	0.77
Healthy_Rice	0.80	1.00	0.89
Healthy_Wheat	1.00	1.00	1.00
Late_Wilt_of_Maize	1.00	0.67	0.80
Leaf_Smut_wheat	0.88	1.00	0.94
accuracy			0.86
macro avg	0.88	0.86	0.85
weighted avg	0.88	0.86	0.86

Fig 14. Classification report of ResNet model

The classification report of ResNet model in predicting multiple disease has been shown in Figure 14. Precision, recall, and f1-score have macro average values of 0.88, 0.86, and 0.85, respectively, while the weighted average values are 0.88, 0.86, and 0.86, respectively.

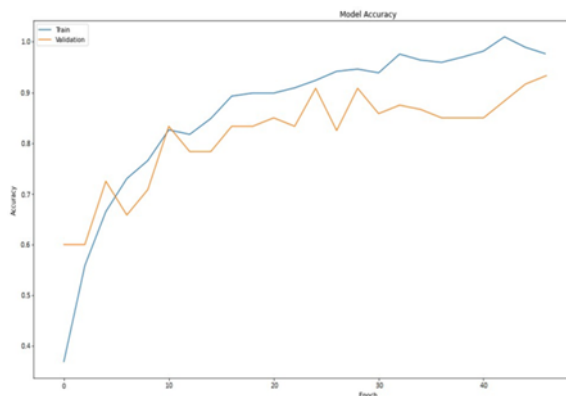


Fig 15. Accuracy of EfficientNet B4

Figure 15. depicts the overall accuracy of Efficient Net B4 model and the accuracy was calculated for epochs values from 1 to 50. The Efficient Net B4 model's maximum and minimum accuracy values during training and validation are 0.99 and 0.9 as well as 0.58 and 0.6 respectively. The more epochs there are, the more accurate the Efficient Net B4 model is. By using a rescaling mechanism to balance the neural network parameters, the Efficient Net B4 model's accuracy is increased.

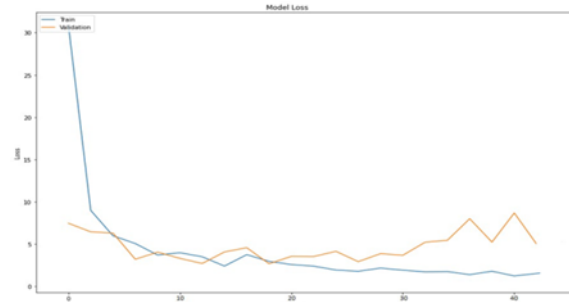


Fig 16. Loss of EfficientNet B4

Figure 16. depicts the overall loss of Efficient Net B4 model and the loss was calculated for epochs values from 1 to 50. Efficient Net B4 model has the minimum loss value of 4% and 9% during training and validation respectively. The loss of Efficient Net B4 model is improved by the addition of a bias vector.

	precision	recall	f1-score
Bacterial_Blight_in_Rice	0.90	0.95	0.93
Bacterial_Leaf_Blight_Wheat	1.00	1.00	1.00
Bacterial_Leaf_Spot_Ragi	0.86	0.71	0.77
Brown_Spot_wheat	1.00	0.91	0.95
Brown_Spot_in_Rice	0.85	1.00	0.92
Brown_Stripe_of_Maize	1.00	1.00	1.00
Foot_Wilt_Ragi	0.80	0.86	0.83
Healthy_Maize	0.88	1.00	0.93
Healthy_Ragi	1.00	0.87	0.93
Healthy_Rice	1.00	1.00	1.00
Healthy_Wheat	1.00	1.00	1.00
Late_Wilt_of_Maize	0.94	0.81	0.87
Leaf_Smut_wheat	0.94	1.00	0.97
accuracy			0.93
macro avg	0.94	0.93	0.93
weighted avg	0.94	0.93	0.93

Fig 17. Classification report of EfficientNet B4

The classification report of Efficient Net B4 model in predicting multiple disease has been shown in Figure 17. Precision, recall, and f1-score have macro average values of 0.94, 0.93, and 0.93, respectively, and their weighted average values are 0.94, 0.93, and 0.93, respectively.

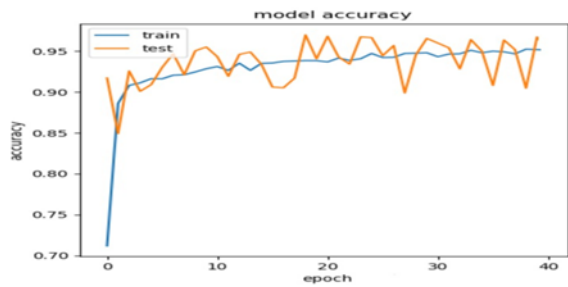


Fig 18. Accuracy of Efficient Net B7

The overall accuracy of the Efficient Net B7 model during training and validation is shown in Figure 18. The accuracy was determined by varying the number of epochs from 1 to 40. Efficient Net B7 model attains the maximum accuracy value of 0.95 and 0.98 during training and testing respectively. Also, EfficientNet B7 model attains a minimum accuracy value of 0.85 and 0.92 during training and testing respectively. The accuracy of EfficientNet B7 model increases with increase in the number of epochs. The accuracy of EfficientNet B7 model is improved by using swish activation function instead of ReLU activation function.

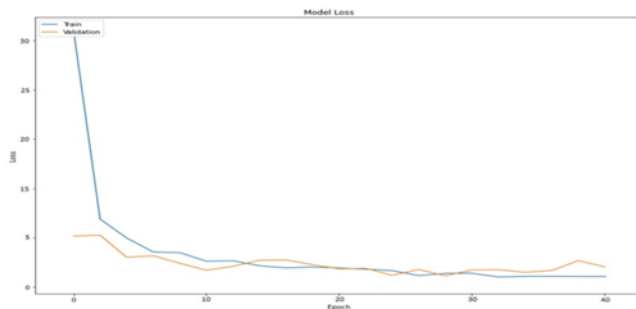


Fig 19. Loss of EfficientNet B7

The overall loss of the Efficient Net B7 model during training and validation is shown in figure 19. The loss was determined by varying the number of epochs from 1 to 40. Efficient Net B7 model attains the minimum loss value of 3% and 4% during training and testing respectively. The loss of Efficient Net B7 model is reduced by using MBConv bottlenecks which includes direct connections.

	precision	recall	f1-score
Bacterial_Blight_in_Rice	1.00	1.00	1.00
Bacterial_Leaf_Blight_Wheat	1.00	1.00	1.00
Bacterial_Leaf_Spot_Ragi	0.88	0.82	0.85
Brown_Spot_Wheat	1.00	0.91	0.95
Brown_Spot_in_Rice	1.00	1.00	1.00
Brown_Stripe_of_Maize	1.00	1.00	1.00
Foot_Wilt_Ragi	0.80	0.86	0.83
Healthy_Maize	0.93	1.00	0.97
Healthy_Ragi	1.00	1.00	1.00
Healthy_Rice	1.00	1.00	1.00
Healthy_Wheat	1.00	1.00	1.00
Late_wilt_of_Maize	1.00	0.90	0.95
Leaf_Smut_Wheat	0.94	1.00	0.97
accuracy			0.96
macro avg	0.96	0.96	0.96
weighted avg	0.96	0.96	0.96

Fig 20. Classification Report of Efficient Net B7

The classification report of Efficient Net B7 model in predicting multiple disease has been shown in Figure 20. Precision, recall, and f1-score have macro average values of

0.96, 0.96, and 0.96, respectively, and their weighted average values are 0.96, 0.96, and 0.96, respectively.

4.4 Comparison result of proposed ensemble model

This section highlights the proposed model performance by comparing it to the outcomes of existing approaches such as SVM, DT, LR, and KNN [26,27] and showing their results based on various metrics.

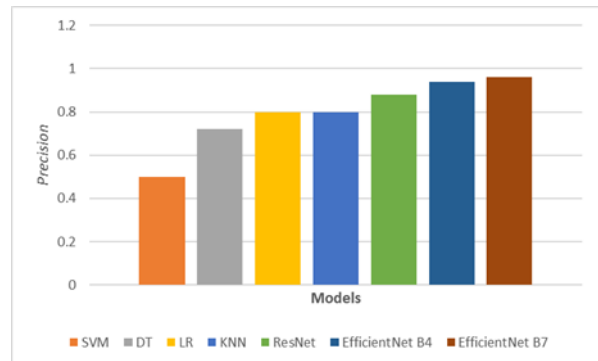


Fig 21. Comparison of precision

The comparison of precision of proposed ensemble models with existing techniques such as SVM, DT, LR, and KNN is shown in Figure 21. The precision of proposed ensemble models attains the maximum value of 0.88, 0.94 and 0.96 respectively whereas the precision of existing techniques such as SVM, DT, LR, and KNN are 0.50, 0.72, 0.80 and 0.88 respectively. Hence, the precision of proposed ensemble model is high whereas the precision of SVM is low.

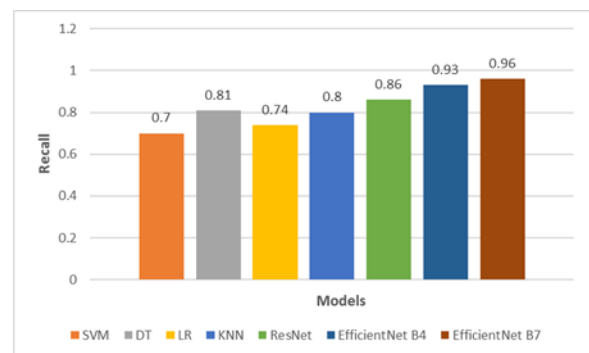


Fig 22. Recall Comparison

Figure 22. shows a comparison of the recall of proposed ensemble model with existing techniques such as SVM, DT, LR, and KNN. The recall of proposed ensemble model attains a maximum value of 0.86, 0.93 and 0.96 respectively whereas the recall of SVM is 0.7, DT is 0.81, LR is 0.74, and KNN is 0.8. Hence the proposed ensemble model has the highest recall, whereas SVM has the lowest recall.

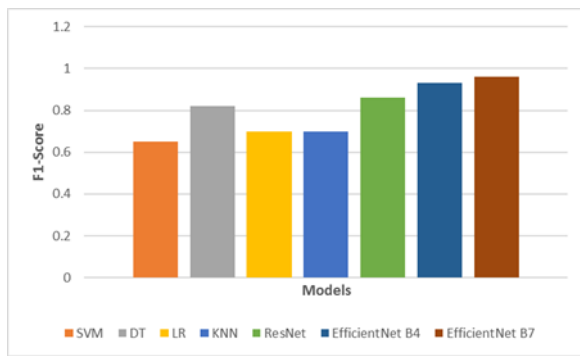


Fig 23. Comparison of F1-Score

The comparison of F1-Score of proposed ensemble models with existing techniques such as SVM, DT, LR, and KNN is shown in Figure 23. The F1-Score of proposed ensemble models attains the maximum value of 0.86, 0.93 and 0.96 respectively whereas the F1-Score of existing techniques such as SVM, DT, LR, and KNN are 0.65, 0.86, 0.699 and 0.7 respectively. Hence, the F1-Score of proposed ensemble model is high whereas the F1-Score of SVM is low.

Overall, the proposed Ensemble Efficient Net and ResNet model for Crop Disease identification outperforms the existing techniques such as SVM, KNN, DT and LR with high precision of 0.88, 0.94, 0.96, high recall of 0.86, 0.93, 0.96 and high f1-score of 0.86, 0.93 and 0.96 respectively due to the usage of progressive activation function and skip connection in feature extraction.

5. Conclusion

An Ensemble Efficient Net and ResNet model for Crop Disease identification in crop images obtained from crop field has been presented in this research to solve the issues in diagnosis of multiple crop diseases in a single leaf and also enhancing the preprocessing and segmentation processes to further improve the prediction performance. The prediction accuracy level is improved using Ensemble Efficient Net and ResNet model due to the incorporation of blocks in direct shortcut connection and advanced activation functions and then, the performance of this ensemble model is further improved by Non-linear weighted fuzzy mean filtering and Modified U-Net. Hence, multiple crop diseases have been identified even for single crop image without any noise, graphics, improper segmentation and with accurate feature extraction and classification. The result obtained from Ensemble Efficient Net and ResNet model for Crop Disease identification outperforms existing techniques with high precision of 0.88, 0.94, 0.96, high recall of 0.86, 0.93, 0.96 and high f1-score of 0.86, 0.93 and 0.96. In future work, the proposed model will be used for vegetables diseases identification and classification that will be helpful for farmers to obtain better yield productivity.

Conflicts of interest

The authors declare no conflicts of interest.

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