

MANGO DISEASE CLASSIFICATION - SHALLOW CNN OR RESIDUAL CNN? - WHICH IS BETTER?

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ABSTRACT

This study aimed to determine which type of Convolution Neural Network, Shallow or Residual, is better in the classification of 7 diseases. Both models were trained and validated using data from the same dataset. The purpose of this study was to do a comparative analysis between these models after training for 20, 50 and 100 epochs.

Keywords: Mango, Residual Convolutional Neural Network, Shallow Convolutional Neural Network, Convolutional Neural Network, Disease Detection.

I. INTRODUCTION

Mango (*Mangifera Indica*) is a tree belonging to the Anacardiaceae family which holds immense economic and social importance, particularly in the Indian subcontinent. Not only are mangos an important aspect in the culture of the subcontinent but also play an essential role in the region's economy. Millions of farmers and laborers are involved in planting, harvesting and processing mangoes.

India is the largest mango producer in the world, with a production of 22 million metric tons in the 2022-2023 calendar year valued at 48.53 million USD [2].

Across the globe, Thailand, Mexico, the Netherlands, Peru, Brazil and India are the biggest exporters of mangoes while China, the United States and the European Union are the largest importers [3].

Mangoes are prone to various diseases such as Anthracnose, Bacterial Canker, Cutting Weevil, Die Back, Gall Midge, Powdery Mildew and Sooty Mould which are caused by bacteria and viruses

ANTHRACNOSE

For mango, anthracnose symptoms occur on fruits, leaves, panicles and twigs of the plant [4].

Anthracnose leads to the development of black or dark-brown spots on the panicles which result in the death of the flower and very low yield.



Fig 1: Leaf infected by Anthracnose

BACTERIAL CANKER

Bacterial Canker is observed as water-soaked, black to dark brown spots which gradually develop into cankerous, raised spots on fruits. The cankers on fruits gradually ooze out a gummy substance containing

bacterial cells which is highly contagious. The disease also affects the flower stalks which results in flowers and young fruits falling off. [5]



Fig 2: Leaf infected by Bacterial Canker

CUTTING WEEVIL

The most common symptom of a Cutting Weevil infestation is the presence of cut leaves on the ground underneath the mango tree, another characteristic symptom is the presence of leafless, stripped shoots. Adult cutting weevils also cut "windowpanes" in leaves. [5]



Fig 3: Leaf infected by Cutting Weevil

DIE-BACK

The disease is most commonly found in the months of October-November after monsoon rains in India, the characteristic symptom of the disease is the dying back of the twigs of the tree. External evidence of the disease includes the darkening of the bark. This symptom is generally spotted in young, green twigs and is difficult to spot in older branches [5]



Fig 4: Leaf infected by Die-Back

GALL MIDGE

The most prominent symptom of Gall Midge is the occurrence of galls, small wart-like structures upto 4mm in diameter, on the surface of the leaves of an infected mango tree.

The galls can also occasionally appear on the fruit as well as the stem of the tree. The presence of these galls greatly reduces the ability of the leaves to take part in photosynthesis. [5]



Fig 5: Leaf infected by Gall Midge

POWDERY MILDEW

The characteristic symptom of Powdery Mildew is the white, powdery fungal growth on the leaves as well as the fruits of the plant, Powdery mildew results in the dropping of flowers of the plant as well as the young fruit. [5]



Fig 6: Leaf infected by Powdery Mildew

SOOTY MOULD

Sooty Mould is characterised by the growth of black mould on the leaf lamina. The growth is black and velvety thin. This disease harms Mango trees by covering the entire surface of the tree thus inhibiting photosynthesis. [5]



Fig 7: Leaf infected by Sooty Mould

II. RELATED WORKS

Plant diseases and infections have been plaguing humanity for centuries, for a long period of time, humans were reliant on their vision to detect and identify plant diseases. However, with the implementation of Machine Learning and Neural Networks in the field of plant disease detection, it has become much easier to identify these diseases. Previous research has been done in the detection of plant diseases in various plants such as Cassava, Grapes, Mangoes, Apples, Rice, Tomatoes, Corn, Cotton, etc.

Previous work in the detection of plant diseases has utilised deep learning architectures based on AlexNet, VGG, GoogleNet, InceptionV3. In [6], Rangarajan et al. used pretrained AlexNet and VGG16 net to classify 6 tomato diseases and healthy plants, and obtained an accuracy of 97.29% for VGG16 net and an accuracy of 97.49% for AlexNet.

Nachtigall et al. utilised multiple CNN architectures to classify 5 apple diseases and healthy leaves [7] . They achieved an accuracy of 97.3% with the AlexNet architecture. The performance of CNNs were compared with MLPs (Multilayer Perceptron) and experts in the fields of Soil, Plant Pathology, Plant Nutrition, Crop science and Environmental Management. The CNNs outperformed both MLPs and experts as they had an accuracy of 77.3% and 71.9% (average) respectively. The highest expert accuracy was 93.3%.

In [8], Rangarajan et al. used a pre-trained VGG16 network to classify 5 eggplant diseases. They utilised 3 different colour spaces for the images they used, that is, HSV, grayscale, and YCbCr. They achieved the highest accuracy of 99.4% with the RGB as well as the YCbCr images. The images for this project were collected through mobile phone cameras in both field and laboratory conditions. Surprisingly, the network obtained a higher classification accuracy with field images rather than laboratory images.

This is in contrast to the study performed by Ahmad et al [9]. In the study they identified 4 tomato diseases using several pre-trained deep learning models such as VGG16, VGG19, InceptionV3. InceptionV3 gave the best performance accuracy of any model and performed better on images taken in laboratory conditions than in field images, it gave an accuracy of 99.60% and 93.70% on laboratory and field images respectively.

Previous studies in the field of plant disease detection have also relied on custom CNN models to detect diseases. In [10] Li et al. used shallow CNN models (SCNN) along with classic machine learning classifiers such as Random forests and Support Vector Machines to show the viability of shallower models. They attempted to classify 4 Maize diseases using 2000 images from the PlantVillage dataset and achieved an accuracy of 94%. Wang et al. attempted to classify Apple Black Rot images using Shallow CNNs with just a couple of layers and fewer filters [11], they achieved the highest validation accuracy of >70% with a 8 layer Convulational network.

The studies above can be summarised as follows:

Table 1: showcasing prior research into the field of Plant Disease Detection

Author	Model Architecture	Classes	Plant	Accuracy
Rangrajan et al.	AlexNet, VGG16	6	Tomato	97.29%, 97.49%
Nachtigall et al.	Multiple CNN architectures	5	Apple	97.3%
Rangarajan et al.	VGG16	5	Eggplant	99.4%
Ahmad et al.	VGG16, VGG19	4	Tomato	99.6%
Li et al.	Shallow CNN + Random Forests/SVMs	4	Maize	94%
Wang et al.	Shallow CNN	1	Apple	70%+

III. METHODOLOGY

DATA

The data for this project was obtained from the MangoLeadBD dataset from Mendeley Data[12]. The dataset contains 4000 images belonging to 8 classes (Anthracnose, Bacterial Canker, Cutting Weevil, Die Back, Gall Midge, Powdery Mildew, Sooty Mould and Healthy). Each of the 8 classes contains 500 images. The images have been obtained through mobile phone cameras. Out of the 4000 images, 1800 are of distinct leaves whereas the rest have been prepared by zooming and rotating. The images have been collected from four mango orchards in Bangladesh, namely the Sher-e-Bangla Agricultural University orchard, the Jahangir Nagar

orchard, the Udaypur Village Mango Orchard, and the Itakhola village mango orchard. The dataset was published on August 31st, 2022.

IMAGE PREPROCESSING

The images in the dataset are all rectangular, RGB images. Some very simple data augmentation techniques were employed before the images were fed to both the Shallow CNN and Residual CNN model.

Firstly, all images are resized to a size of 240 by 240 pixels. Both model optimization and model testing were performed on these resized images.

Secondly, all the pixels of the images were divided by 255 to obtain pixels values in the range of 0 and 1 (both inclusive). This was done to reduce magnitude of value the model works with.

Thirdly, all training images are randomly rotated, and flipped horizontally. This augmentation increases the training data the model works with, reduces overfitting and makes the model generalise to the testing data better.

After the collection and preprocessing of the images. The data was split into training and testing data using a (80-20) split ratio. The training images were used to train both the SCNN and RCNN models. Both models utilised a batch size of 16. The classification report, accuracy as well as the Confusion Matrix was obtained for both the models after being trained on the data for 20,50,100 epochs.

IV. MODELING AND ANALYSIS

SHALLOW CONVOLUTIONAL NEURAL NETWORK

For this study, a custom Shallow Convolutional Neural Network (SCNN) was designed using Keras. [13]

Table 2: Shallow Convolutional Neural Network Architecture

Layer Name	Input	Output
Rescaling	(240,240,3)	(240,240,3)
Random Flip	(240,240,3)	(240,240,3)
Random Rotation	(240,240,3)	(240,240,3)
Conv2D 1	(240,240,3)	(240,240,16)
Batch Normalization 1	(240,240,16)	(240,240,16)
MaxPooling2D 1	(240,240,16)	(120,120,16)
Conv2D 2	(120,120,16)	(120,120,32)
Batch Normalization 2	(120,120,32)	(120,120,32)
MaxPooling2D 2	(120,120,32)	(60,60,32)
Conv2D 3	(60,60,32)	(60,60,64)
Batch Normalization 3	(60,60,64)	(60,60,64)
MaxPooling2D 3	(60,60,64)	(30,30,64)
Flatten	(30,30,64)	-57600
Dense 1	-57600	-128
Dense 2	-128	-64
Dense 3	-64	-8

The Shallow Convolutional Neural Network consists of 3 Conv2D layers. The first convolutional layer has 16 filters of size 3 x 3, a ReLU (Rectified Linear Unit) activation and is followed by a Batch Normalization and a 2 x 2 MaxPooling2D layer. The second convolutional layer has 32 filters of size 3 x 3 and a ReLU activation and is followed by a BatchNorm and MaxPooling2D layer of size 2 x 2 as well. The final convolutional layer has 64 filters of size 3 x 3. It is also followed by BatchNorm and MaxPooling2D layers. The output tensor of these 3 Conv2D + BatchNorm + MaxPool layers is of the shape (30,30,64). This tensor is flattened into a tensor of shape

(57600). This tensor is then fed into 3 Dense layers. The first and second fully connected layer have 128 and 64 neurons respectively. Both of these layers feature a ReLU activation function.

The last fully connected layer has 8 output neurons corresponding to the 8 predicted classes (7 diseases and healthy plants) and a softmax activation.

RESIDUAL CONVOLUTIONAL NEURAL NETWORK

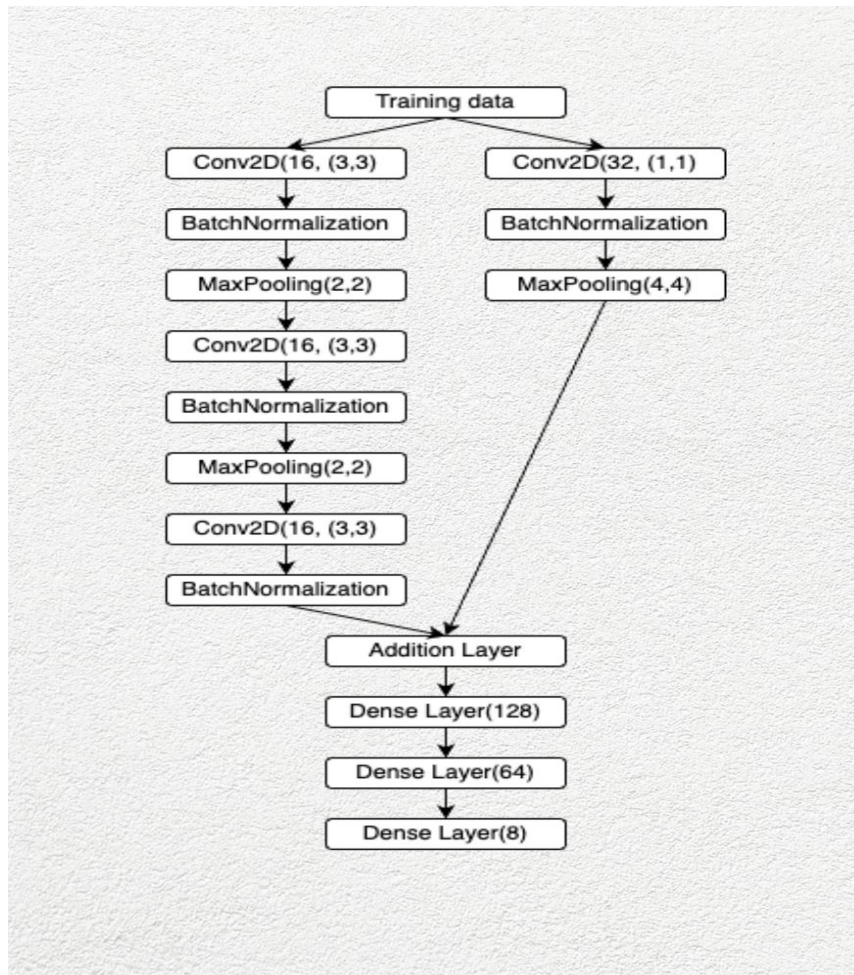


Fig 8: Residual Convolutional Neural Network Architecture

This model was designed using Keras [13]The model features a split architecture, one branch of the Residual Convolutional Neural Network features 3 Conv2D layer with 32 filters of size 3 x 3 and activation ReLU. All 3 layers are followed by a Batch Normalization layer. The first and second Conv2D layers are followed by MaxPooling layers of size 2 x 2. The other branch of the network features one Conv2D layer with 32 filters of size 1 x 1. This layer is then followed by a MaxPooling2D layer of size 4 x 4 to ensure images are of the same size as the images in the other branch. Finally, both these branches are combined using the Add layer from Keras. These tensors are then fed to 3 Dense layers of 128, 64, and 8 neurons respectively. The first two fully connected layers feature a ReLU activation whereas the last dense layer utilises a softmax activation function.

V. RESULTS AND DISCUSSION

Table 3: Confusion Matrix for SCNN (70 Epochs)

	Anthraco	Bacteri	Cutting	Die	Gall	Healthy	Powdery	Sooty
	nose	Canker	Weevil	Back	Midge		Mildew	Mould
Anthraco	95	0	0	0	0	0	0	0
Bacteri	0	98	0	0	0	0	0	0
Canker								

Cutting Weevil	0	0	103	0	0	0	0	0
Die Back	3	0	0	111	0	0	0	0
Gall Midge	0	1	0	0	90	2	0	0
Healthy	0	0	0	0	0	97	0	0
Powdery Mildew	1	0	0	0	0	0	104	0
Sooty Mould	0	0	0	0	0	1	1	93

Table 4: Classification Report for SCNN (70 Epochs)

Class Name	Precision	Recall	F1-Score	Support
Anthracnose	0.9595	1	0.9793	95
Bacterial Canker	0.9898	1	0.9949	98
Cutting Weevil	1	1	1	103
Die Back	1	0.9736	0.9866	114
Gall Midge	1	0.9677	0.9836	93
Healthy	0.97	1	0.9847	97
Powdery Mildew	0.9904	0.9904	0.9904	105
Sooty Mould	1	0.9789	0.9893	95
Weighted Avg	0.9890	0.9887	0.9887	

Table 3 and 4 illustrate the Confusion Matrix as well as the Classification report for the Shallow Convolutional Neural Networks. The SCNN achieves its best validation accuracy of 98.875% after being trained for 70 epochs. The validation accuracy of the SCNN gradually increases as it is trained for more epochs as evident by the increase of the accuracy from 92% at 20 epochs to 95.25% at 50 epochs and subsequently 98.875% at 70 epochs. Fig 9 illustrates the same.

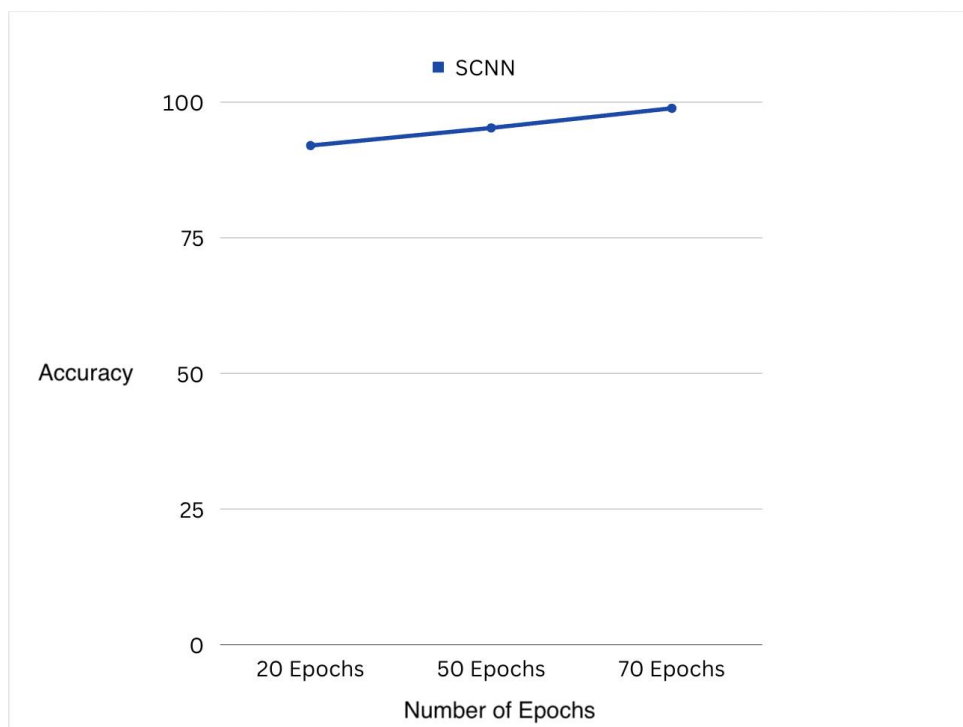


Fig 9: Accuracy over number of epochs for SCNN

Table 5: Confusion Matrix for RCNN (70 Epochs)

	Anthracnose	Bacterial Canker	Cutting Weevil	Die Back	Gall Midge	Healthy	Powdery Mildew	Sooty Mould
Anthracnose	96	0	0	1	0	0	1	0
Bacterial Canker	0	90	0	0	1	0	0	1
Cutting Weevil	0	0	93	0	0	0	0	0
Die Back	0	0	0	117	1	0	0	0
Gall Midge	4	2	0	0	91	0	0	2
Healthy	0	2	0	0	0	98	0	1
Powdery Mildew	0	0	0	0	2	0	98	1
Sooty Mould	0	1	0	0	1	0	5	85

Table 6: Classification Report for RCNN (70 Epochs)

Class Name	Precision	Recall	F1-Score	Support
Anthracnose	0.96	0.9795	0.9696	98
Bacterial Canker	0.9473	0.9782	0.9625	92
Cutting Weevil	1	1	1	99
Die Back	0.9915	0.9915	0.9915	118
Gall Midge	0.9479	0.9191	0.9333	99
Healthy	1	0.9702	0.9849	101
Powdery Mildew	0.9423	0.9702	0.956	101
Sooty Mould	0.9444	0.9239	0.934	92
Weighted Avg	0.9676	0.9675	0.9674	

Table 5 and 6 illustrate the Confusion Matrix and the Classification report for the Residual Convolutional Neural Network. The RCNN also achieves its highest accuracy of 96.75% when trained for 70 epochs. The RC NN achieves an accuracy of 84.25% when trained for 20 epochs and an accuracy of 95.75% when trained for 50 epochs. Fig 10 illustrates the same.

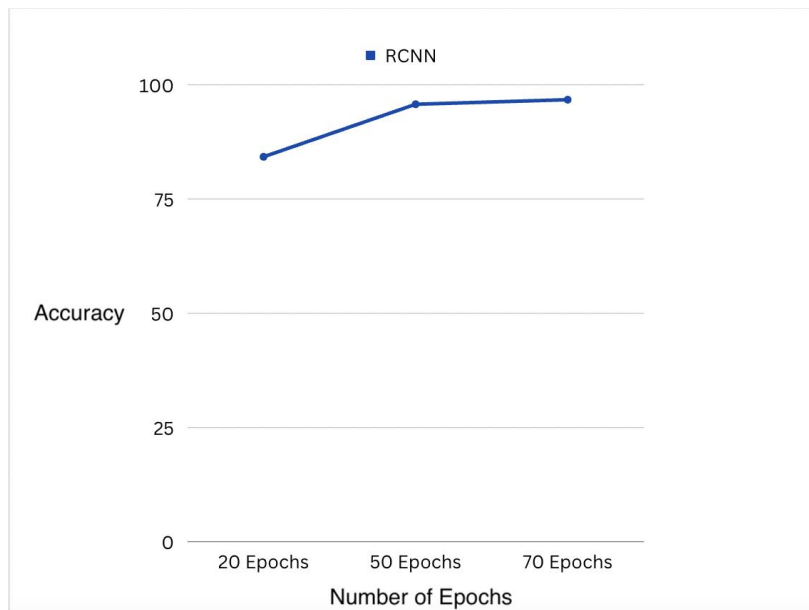


Fig 10: Accuracy over number of epochs for RCNN

As evident by Fig 9 and 10, the SCNN has a higher validation accuracy as compared to the RCNN by a margin of 2.125% overall. While the SCNN is better at classification of leaves infected with Anthracnose, Bacterial Canker, Gall Midge, Powdery Mildew and Sooty Mould; the RCNN model is better at prediction of leaves infected with Die Back and healthy leaves. This comparison has been done on the basis of the F1 score of both these models at prediction of these diseases. Both the models achieved a F1 score of 1 during classification of leaves infected with Cutting Weevils.

VI. CONCLUSION

This study proposes 2 deep learning architectures (Shallow Convolutional Neural Networks and Residual Convolutional Neural Networks) for the detection of 7 Mango diseases and Healthy plants through leaf images. Out of these 2 models, the SCNN outperforms the RCNN at 20 and 70 epochs whereas the RCNN outperforms the SCNN at 50 epochs. The highest accuracy achieved in this study was 98.875% using the SCNN after it was trained for 70 epochs. This performance demonstrates the viability of deep learning in the detection of mango diseases which cause millions of dollars of damage annually.

THREATS TO VALIDITY

There are a few threats to validity to consider:

1. The data obtained from Data Mendeley could be misclassified resulting in incorrect training and classification of diseases.
2. This study's reliance on the Tensorflow library for the construction, training as well as the evaluation of the models could be a source of inaccuracy
3. Suboptimal model design by the author could lead to lower accuracy than possible on the dataset available.

CONFLICT OF INTEREST

The author declares that there are no conflicts of interest in the publication of this paper.

VII. FUTURE WORK

In the future, different deep learning networks such as CapsNets and pre-trained models such as VGG16, AlexNet, VGG19, LeNet can be utilised on this dataset to compare the performance of these models with the 2 models discussed in this study. Furthermore, the testing of the models on field images could validate their potential use as mobile based applications to detect mango diseases in rural regions.

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