

# **PLANT DISEASE DETECTION-*CONVOLUTIONAL NEURAL NETWORK***

**Main project report submitted to CUSAT in partial fulfillment of the requirements for the award for the degree of**

## **BACHELOR OF TECHNOLOGY IN ELECTRONICS & COMMUNICATION ENGINEERING**

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**BONAFIDE CERTIFICATE**

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## ABSTRACT

When plants and crops are affected by pests it affects the agricultural production of the country. Usually farmers or experts observe the plants with naked eye for detection and identification of disease. But this method can be time processing, expensive and inaccurate. Automatic detection using image processing techniques provide fast and accurate results. This project is concerned with a new approach to the development of plant disease recognition model, based on leaf image classification, by the use of deep convolutional networks.

Advances in computer vision present an opportunity to expand and enhance the practice of precise plant protection and extend the market of computer vision applications in the field of precision agriculture. Novel way of training and the methodology used facilitate a quick and easy system implementation in practice. All essential steps required for implementing this disease recognition model are fully described throughout the p, starting from gathering images in order to create a database, assessed by agricultural experts, a deep learning framework to perform the deep CNN training. This method project is a new approach in detecting plant diseases using the deep convolutional neural network trained and fine-tuned to fit accurately to the database of a plant's leaves that was gathered independently for diverse plant diseases. The advance and novelty of the developed model lie in its simplicity; healthy leaves and background images are in line with other classes, enabling the model to distinguish between diseased leaves and healthy ones or from the environment by using CNN.

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## 1. INTRODUCTION

In this project we are going to explain all the theories involved in this project and then we will also explain the algorithms and its working involved. We are also illustration the output and the generated images using CNN.

We are also going to detect the actual condition of plant with the help of Deep Learning. We summarize our contributions as demonstrating the effective prediction of the CNN.

### 1.1 AIM

Our system aims to automatically identify plant disease prediction. Address this issue by introducing CNN for checking the actual condition of image. We approach this by training a convolutional neural network and predicting the source of an image.

### 1.2 OBJECTIVE

The principal objectives of **plant disease detection** are:

- To design such system that can detect crop disease and pest accurately.
- Create database of insecticides for respective pest and disease.
- To provide remedy for the disease that is detected.

### 1.3 PURPOSE

This project is a new approach in detecting plant diseases using the deep convolutional neural network trained and fine-tuned to fit accurately to the database of a plant's leaves that was gathered

independently for diverse plant diseases. The advance and novelty of the developed model lie in its simplicity; healthy leaves and background images are in line with other classes, enabling the model to distinguish between diseased leaves and healthy ones or from the environment by using CNN.

## **1.4 SCOPE**

When plants and crops are affected by pests it affects the agricultural production of the country. usually farmers or experts observe the plants with naked eye for detection and identification of disease. But this method can be time processing, expensive and inaccurate. Automatic detection using image processing techniques provide fast and accurate results. This paper is concerned with a new approach to the development of plant disease recognition model, based on leaf image classification, by the use of deep convolutional networks.

## **2. REQUIREMENT ANALYSIS**

### **2.1 FUNCTIONAL REQUIREMENTS**

#### **2.1.1 INPUT FILE REQUIREMENTS**

- The input file should be a image.

#### **2.1.2 TRAINING SYSTEM REQUIREMENTS**

Main parts of the program:

1. The Dataset
2. Image Preprocessing and Labelling



### 3. Neural Network Training

All parts depend heavily on deep learning algorithms to generate models that can perform their specific functions.

Training the deep convolutional neural network for making an image classification model from a dataset was proposed. Tensor Flow is an open source software library for numerical computation using data flow graphs. Nodes in the graph represent mathematical operations, while the graph edges represent the multidimensional data arrays (tensors) communicated between them.

## 2.1.3 USERS OF THE SYSTEM

### USERS

- Users can upload any image.
- Can get the result as plant health status.

## 2.2 NON-FUNCTIONAL REQUIREMENTS

### Hardware Requirements

The Hardware Requirements to perform this task are:

- Intel i3 processor
- 2 GB RAM
- 512 MB hard disk

### Software Requirements

The software requirements of this are as follows:

- VS Code
- Anaconda Platform
- Google Collab
- Tensorflow 1.15.3-GPU (newer versions will be incompatible)
- Other Python dependencies: numpy, pandas, sklearn, matplotlib, tensorflow, opencv, pillow, skimage, etc

**VS Code:** Visual Studio Code is a streamlined code editor with support for development operations like debugging, task running, and version control.

It aims to provide just the tools a developer needs for a quick code-build-debug cycle and leaves more complex workflows to fuller featured IDEs, such as Visual Studio IDE.

**Anaconda Platform:** Anaconda is a open-source distribution of the Python and R programming languages for scientific computing (data science, machine learning applications, large-scale data processing, predictive analytics, etc.), that aims to simplify package management and deployment..

**Tensorflow 1.15.3-GPU:** TensorFlow GPU support requires an assortment of drivers and libraries

#### Other dependencies

- **NumPy:** NumPy is a Python library used for working with arrays. It also has functions for working in domain of linear algebra, fourier transform, and matrices.
- **OpenCV-Python:** OpenCV-Python is a library of Python bindings designed to solve computer vision problems.
- **Cryptography:** cryptography is a package which provides cryptographic recipes and primitives to Python developers
- **Cython:** Cython is an optimising static compiler for both the Python programming language and the extended Cython programming language (based on Pyrex). It makes writing C extensions for Python as easy as Python itself.

**Reliability:** This software will be developed with machine learning, feature engineering, and deep learning techniques. So, in this step, there is no certain reliable percentage that is measurable.

Also, user-provided data will be used to compare with results and measure reliability. With recent machine learning techniques, user gained data should be enough for reliability if enough data is obtained.

**Usability:** It should be user-friendly and should require the least effort to operate.

**Portability:** The system is made using Python, which is platform-independent and can be transported to other services with minimum effort.

**Flexibility:** It is the effort required to modify an operational program. The whole system should be made using independent modules so that any changes done in one module should not affect the other one and new modules can be added easily to increase the functionality

**Maintainability:** Maintenance is one form of change that typically is done after software development has been completed.

### 3 DESIGN

#### 3.1 USE CASE:

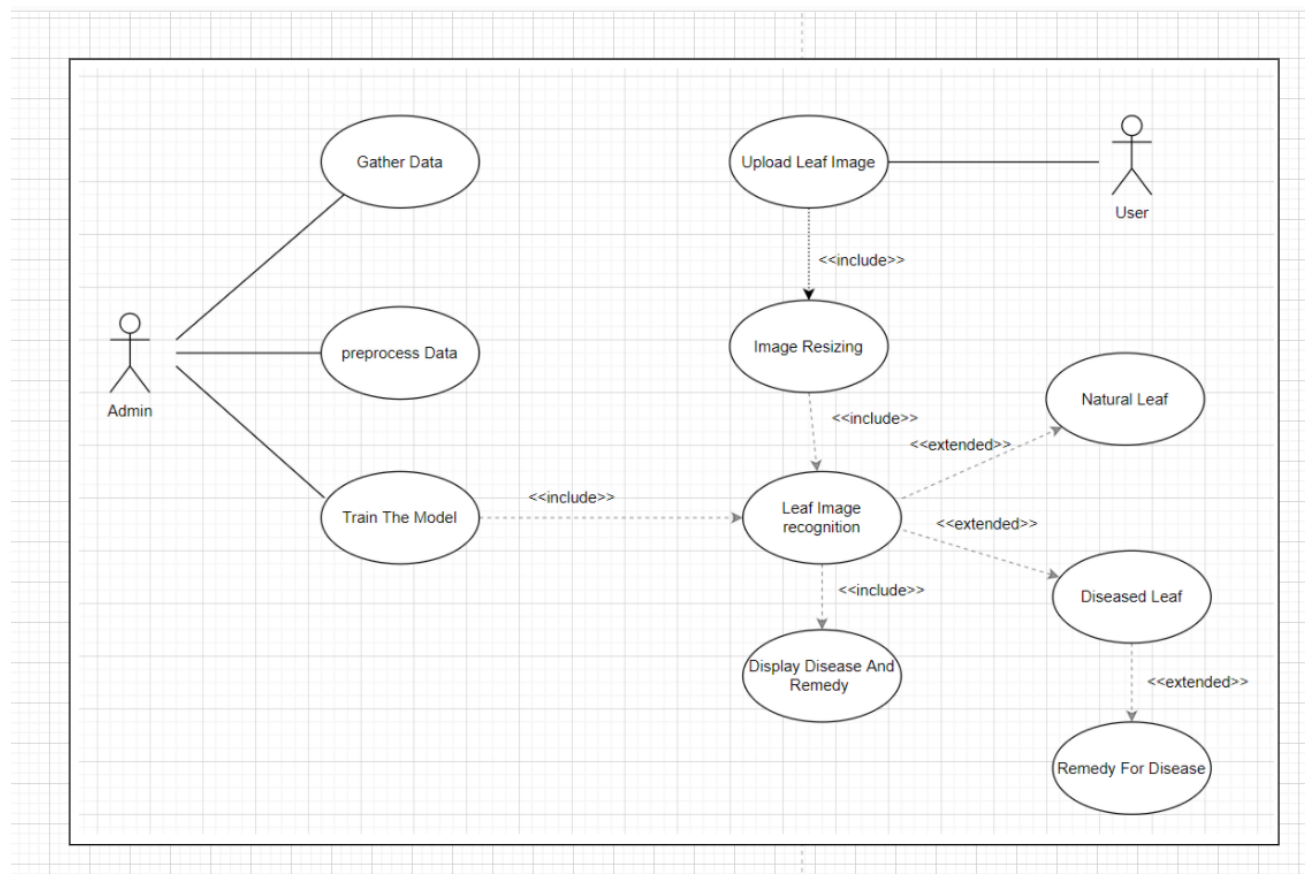


FIGURE 1: USE CASE DIAGRAM

### 3.2 SEQUENCE DIAGRAM:

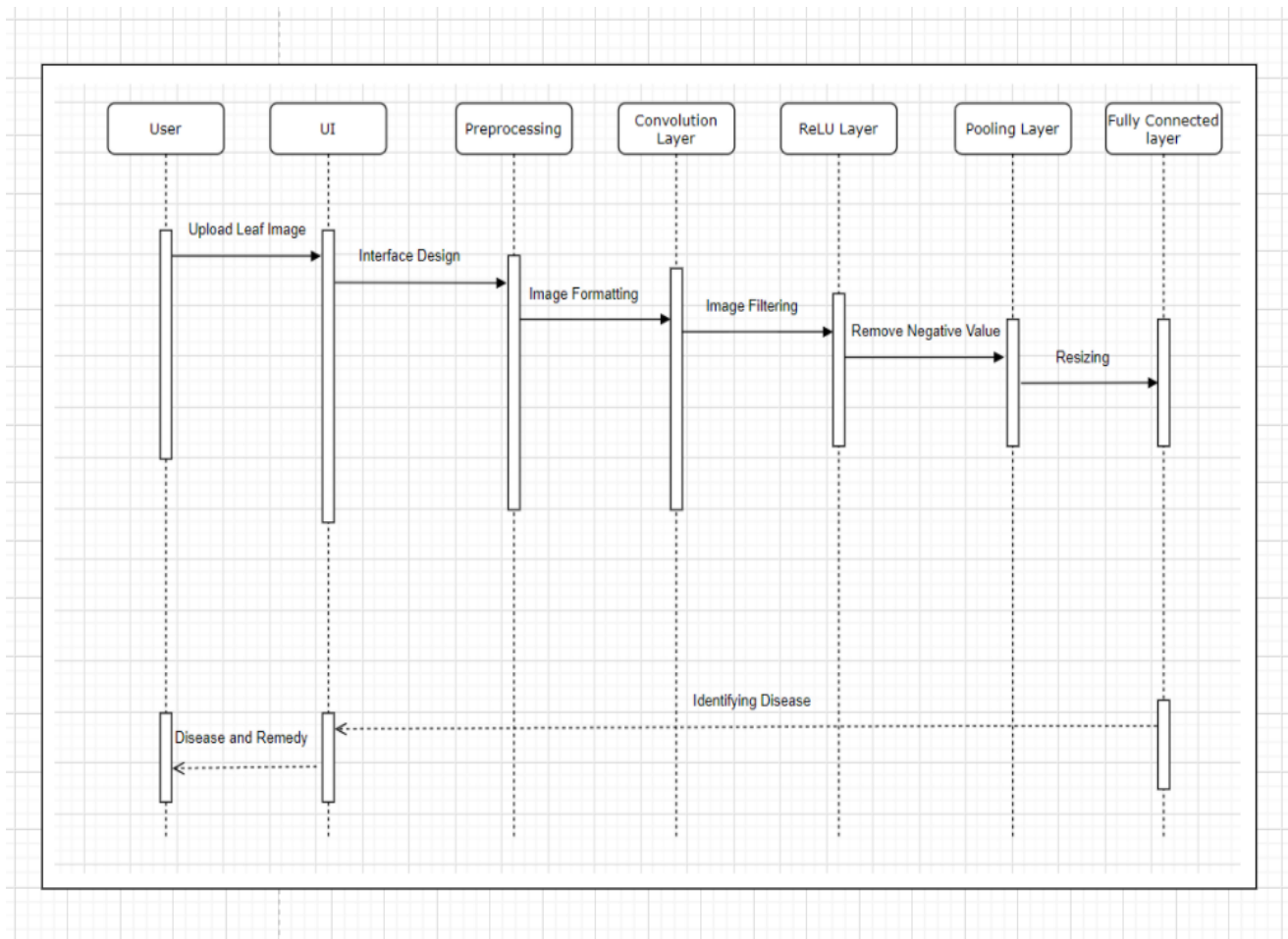


FIGURE 2: SEQUENCE DIAGRAM

## 4. DATA MODEL AND DESCRIPTION

### 4.1 MODEL EXPLANATION

- 1.The input test image is acquired and preprocessed in the next stage and then it is converted into array form for comparison.
- 2.The selected database is properly segregated and preprocessed and then renamed into proper folders.
- 3.The model is properly trained using CNN and then classification takes place.
- 4.The comparison of the test image and the trained model take place followed by the display of the result.
- 5.If there is a defect or disease in the plant the software displays the disease along with the remedy .

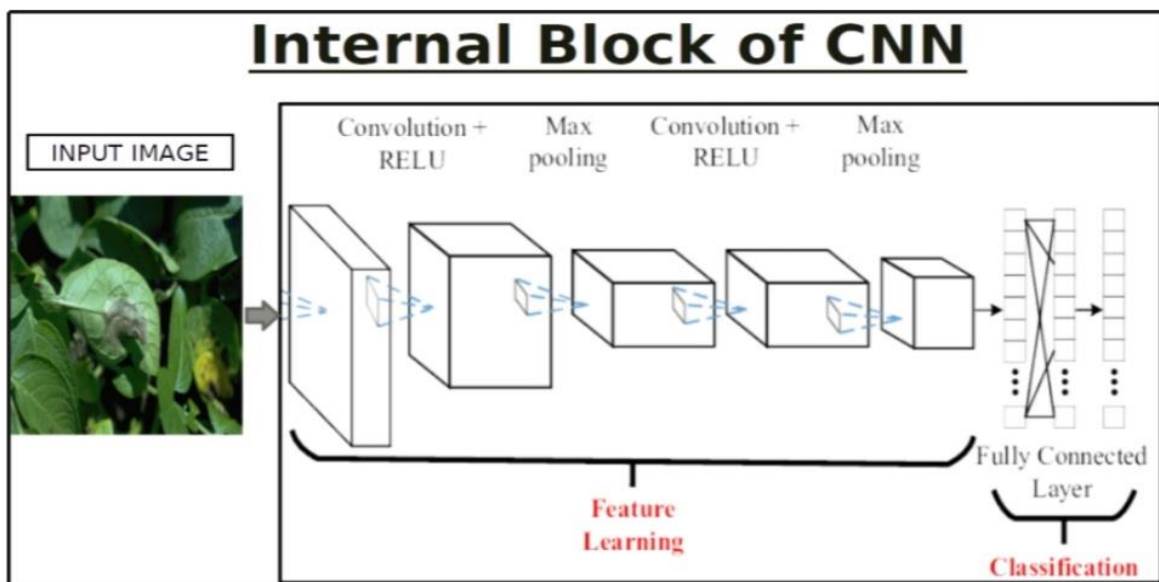


FIGURE 3: MODEL EXPLANATION

### 4.1.1 Deep Learning

Deep learning is a class of machine learning algorithms that uses multiple layers to progressively extract higher level features from the raw input. For example, in image processing, lower layers may identify edges, while higher layers may identify the concepts relevant to a human such as digits or letters or faces.

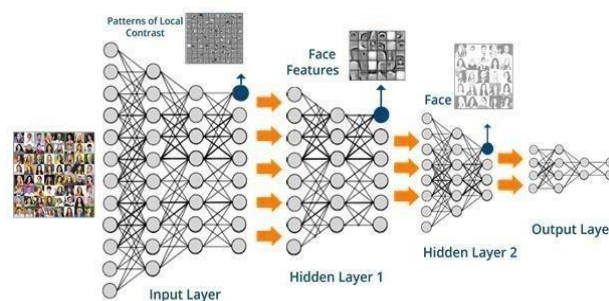


FIGURE 4 DEEP LEARNING MODEL

## 4.2 Database collection:

Initial step for any image processing based project is acquiring proper database which is valid . Most of the time the standard database is preferred but in certain circumstances we do not get proper database .So in such conditions we can collect the images and can form our own database. The database is accessed from crowd AI which is plant disease classification challenge . Data available here is not labeled .So the first task is to clean and label the database. There is a huge database so basically the images with better resolution and angle are selected . After selection of images we should have deep knowledge about the different leaves and the disease they have. Huge research is done from plant village organization repository. Different types of plant images are studied and corresponding . After detail study, labeling is done by segregating the images and with different diseases

### **4.3 Processing and Training the model (CNN):**

The database is Preprocessed such as Image reshaping ,resizing and conversion to an array form. Similar processing is also done on the test image. A database consisting of different plant species is obtained , out of which any image can be used as a test image for the software. The train database is used to train the model (CNN ) so that it can identify the test image and the disease it has .CNN has different layers that are Dense, Dropout, Activation, Flatten,Convolution2D, MaxPooling2D. After the model is trained successfully ,the software can identify the disease if the plant species is contained in the database. After successful training and preprocessing ,comparison of the test image and trained model takes place to predict the disease.



## 5.PROGRAM CODE

### Convolution Neural Network

#### ➤ Code for Importing the Libraries:

```
import numpy as np
import pickle
import cv2
import os
import matplotlib.pyplot as plt
from os import listdir
from sklearn.preprocessing import LabelBinarizer
from keras.models import Sequential
from tensorflow.keras.layers import BatchNormalization
from keras.layers.convolutional import Conv2D
from keras.layers.convolutional import MaxPooling2D
from keras.layers.core import Activation, Flatten, Dropout
, Dense
from keras import backend as K
from keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.optimizers import Adam
from keras.preprocessing import image
from keras.preprocessing.image import img_to_array
from sklearn.preprocessing import MultiLabelBinarizer
from sklearn.model_selection import train_test_split
```

### ➤ **LOAD DATASET:**

```
# Dimension of resized image
DEFAULT_IMAGE_SIZE = tuple((256, 256))

# Number of images used to train the model
N_IMAGES = 100

# Path to the dataset folder
root_dir = '/content/drive/MyDrive/PlantVillage'

train_dir = os.path.join(root_dir, 'train')
val_dir = os.path.join(root_dir, 'val')
```

We use the function `convert_image_to_array` to resize an image to the size `DEFAULT_IMAGE_SIZE` we defined above.

```
def convert_image_to_array(image_dir):
    try:
        image = cv2.imread(image_dir)
        if image is not None:
            image = cv2.resize(image, DEFAULT_IMAGE_SIZE)

            return img_to_array(image)
    else:
        return np.array([])
```

```

except Exception as e:
    print(f"Error : {e}")
    return None

```

Here, we load the training data images by traversing through all the folders and converting all the images and labels into separate lists respectively.

```

image_list, label_list = [], []

```

```

try:
    print("[INFO] Loading images ...")
    plant_disease_folder_list = listdir(train_dir)

    for plant_disease_folder in plant_disease_folder_list:
        print(f"[INFO] Processing {plant_disease_folder} ...")
        plant_disease_image_list = listdir(f"{train_dir}/{plant_disease_folder}")

        for image in plant_disease_image_list[:N_IMAGES]:
            image_directory = f"{train_dir}/{plant_disease_folder}/{image}"
            if image_directory.endswith(".jpg")==True or image_directory.endswith(".JPG")==True:
                image_list.append(convert_image_to_array(image_directory))
                label_list.append(plant_disease_folder)

    print("[INFO] Image loading completed")
except Exception as e:

```

```

    print(f"Error : {e}")

# Transform the loaded training image data into numpy array
np_image_list = np.array(image_list, dtype=np.float16) / 225.0
print()

# Check the number of images loaded for training
image_len = len(image_list)
print(f"Total number of images: {image_len}")

```

### Examine the labels/classes in the training dataset

```

label_binarizer = LabelBinarizer()
image_labels = label_binarizer.fit_transform(label_list)

pickle.dump(label_binarizer, open('plant_disease_label_transform.pkl', 'wb'))
n_classes = len(label_binarizer.classes_)

print("Total number of classes: ", n_classes)

```

### ➤ Augment and Split Dataset:

```

augment = ImageDataGenerator(rotation_range=25, width_shift_range=0.1,
                             height_shift_range=0.1, shear_range=0.2,
                             zoom_range=0.2, horizontal_flip=True,
                             fill_mode="nearest")

```

Splitting the data into training and test sets for validation purpose.

```
print("[INFO] Splitting data to train and test...")
x_train, x_test, y_train, y_test = train_test_split(np_image_list,
image_labels, test_size=0.2, random_state = 42)
```

## ➤ Build Model:

Defining the hyperparameters of the plant disease classification model.

```
EPOCHS = 25
STEPS = 100
LR = 1e-3
BATCH_SIZE = 32
WIDTH = 256
HEIGHT = 256
DEPTH = 3
```

Creating a sequential model and adding Convolutional, Normalization, Pooling, Dropout and Activation layers at the appropriate positions.

```
model = Sequential()
inputShape = (HEIGHT, WIDTH, DEPTH)
chanDim = -1
```

```

if K.image_data_format() == "channels_first":
    inputShape = (DEPTH, HEIGHT, WIDTH)
    chanDim = 1

model.add(Conv2D(32, (3, 3), padding="same", input_shape=inputShape)
)
model.add(Activation("relu"))
model.add(BatchNormalization(axis=chanDim))
model.add(MaxPooling2D(pool_size=(3, 3)))
model.add(Dropout(0.25))
model.add(Conv2D(64, (3, 3), padding="same"))
model.add(Activation("relu"))
model.add(BatchNormalization(axis=chanDim))
model.add(Conv2D(64, (3, 3), padding="same"))
model.add(Activation("relu"))
model.add(BatchNormalization(axis=chanDim))
model.add(MaxPooling2D(pool_size=(2, 2)))
model.add(Dropout(0.25))
model.add(Conv2D(128, (3, 3), padding="same"))
model.add(Activation("relu"))
model.add(BatchNormalization(axis=chanDim))
model.add(Conv2D(128, (3, 3), padding="same"))
model.add(Activation("relu"))
model.add(BatchNormalization(axis=chanDim))
model.add(MaxPooling2D(pool_size=(2, 2)))
model.add(Dropout(0.25))
model.add(Flatten())
model.add(Dense(1024))
model.add(Activation("relu"))
model.add(BatchNormalization())
model.add(Dropout(0.5))

```

```
model.add(Dense(n_classes))
model.add(Activation("softmax"))

model.summary()
```

## ➤ Train Model:

We initialize Adam optimizer with learning rate and decay parameters.

Also, we choose the type of loss and metrics for the model and compile it for training.

```
# Initialize optimizer
opt = Adam(lr=LR, decay=LR / EPOCHS)

# Compile model
model.compile(loss="binary_crossentropy", optimizer=opt, metrics=["accuracy"])

# Train model
print("[INFO] Training network...")
history = model.fit_generator(augment.flow(x_train, y_train, batch_size=BATCH_SIZE),
                             validation_data=(x_test, y_test),
                             steps_per_epoch=len(x_train) // BATCH_SIZE,
                             epochs=EPOCHS,
                             verbose=1)
```

## ➤ Evaluate Model:

Comparing the accuracy and loss by plotting the graph for training and validation.

```
acc = history.history['accuracy']
val_acc = history.history['val_accuracy']
loss = history.history['loss']
val_loss = history.history['val_loss']
epochs = range(1, len(acc) + 1)

# Train and validation accuracy
plt.plot(epochs, acc, 'b', label='Training accuracy')
plt.plot(epochs, val_acc, 'r', label='Validation accuracy')
plt.title('Training and Validation accuracy')
plt.legend()

plt.figure()

# Train and validation loss
plt.plot(epochs, loss, 'b', label='Training loss')
plt.plot(epochs, val_loss, 'r', label='Validation loss')
plt.title('Training and Validation loss')
plt.legend()
plt.show()
```

Evaluating model accuracy by using the evaluate method.



```
print("[INFO] Calculating model accuracy")
scores = model.evaluate(x_test, y_test)
print(f"Test Accuracy: {scores[1]*100}")
```

### ➤ Save Model:

```
# Dump pickle file of the model
print("[INFO] Saving model...")
pickle.dump(model, open('plant_disease_classification_model
.pkl', 'wb'))

# Dump pickle file of the labels
print("[INFO] Saving label transform...")
filename = 'plant_disease_label_transform.pkl'
image_labels = pickle.load(open(filename, 'rb'))
```

### ➤ Test Model:

We write the following predict\_disease function to predict the class or disease of a plant image.

We just need to provide the complete path to the image and it displays the image along with its prediction class or plant disease.

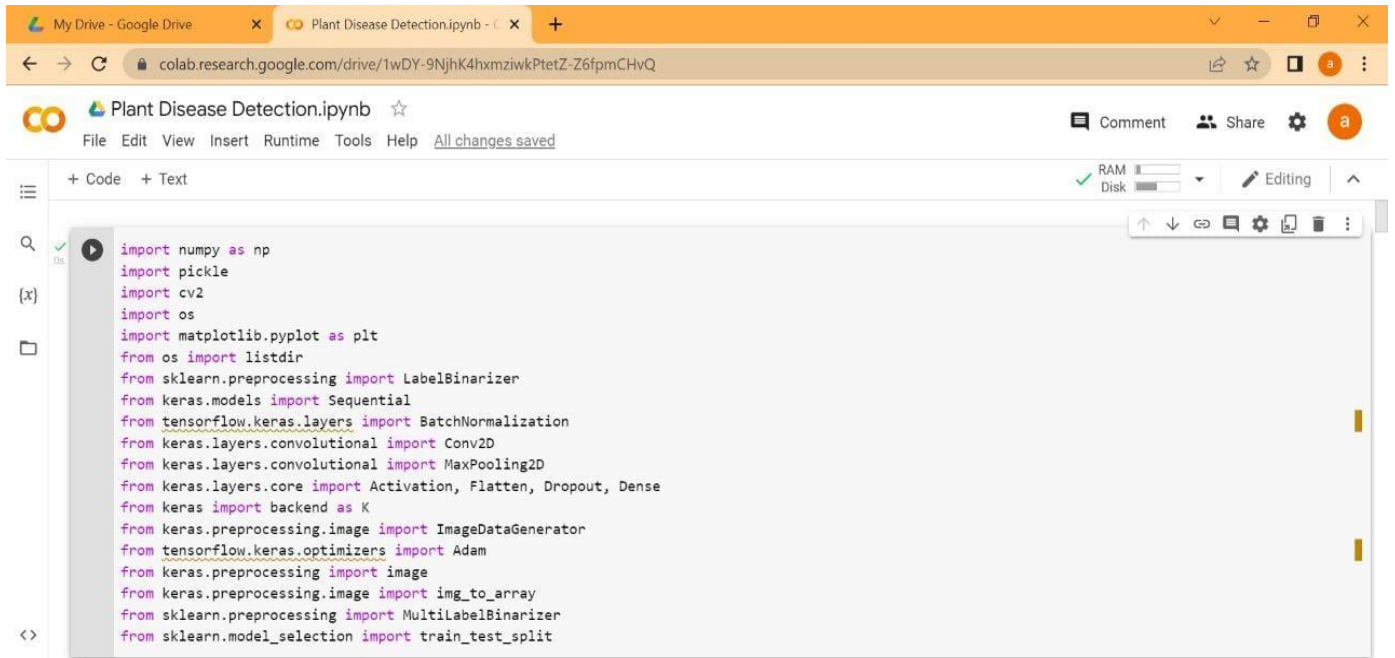
```
def predict_disease(image_path):
    image_array = convert_image_to_array(image_path)
```

```
np_image = np.array(image_array, dtype=np.float16) / 225.0
np_image = np.expand_dims(np_image,0)
plt.imshow(plt.imread(image_path))
result = model.predict_classes(np_image)
print((image_labels.classes_[result][0]))
```

For testing purposes, we randomly choose images from the dataset and try predicting class or disease of the plant image.

```
predict_disease('/content/drive/MyDrive/PlantVillage/val/Apple__Black_rot/0139bc6d-391c-4fd1-bcae-cc74dabfddd7__JR_FrgE.S 2734.JPG')
```

## 6.TESTING



The screenshot shows a Google Colab notebook interface. The browser tab is titled 'Plant Disease Detection.ipynb'. The notebook's title bar also says 'Plant Disease Detection.ipynb'. The code editor contains the following Python code for importing libraries:

```
import numpy as np
import pickle
import cv2
import os
import matplotlib.pyplot as plt
from os import listdir
from sklearn.preprocessing import LabelBinarizer
from keras.models import Sequential
from tensorflow.keras.layers import BatchNormalization
from keras.layers.convolutional import Conv2D
from keras.layers.convolutional import MaxPooling2D
from keras.layers.core import Activation, Flatten, Dropout, Dense
from keras import backend as K
from keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.optimizers import Adam
from keras.preprocessing import image
from keras.preprocessing.image import img_to_array
from sklearn.preprocessing import MultiLabelBinarizer
from sklearn.model_selection import train_test_split
```

**Fig 1:Importing the Libraries**

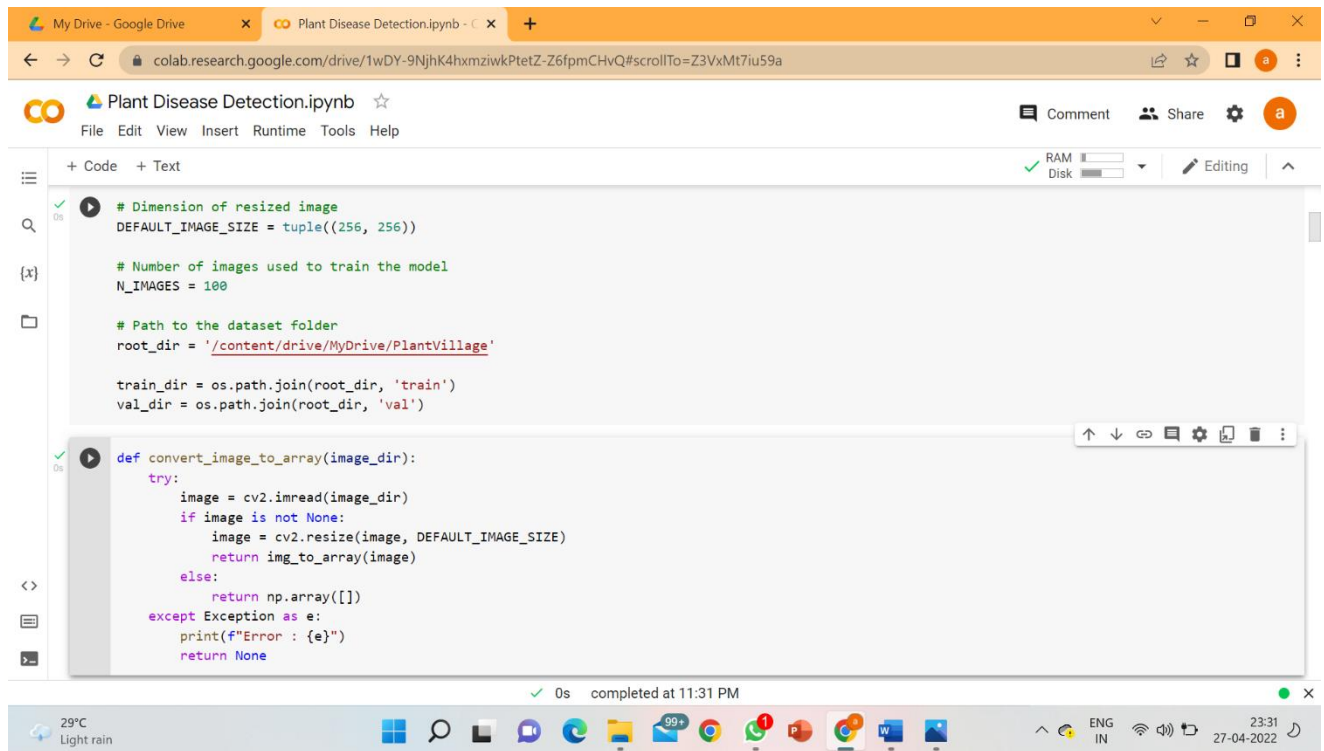


Fig 2

```
image_list, label_list = [], []

try:
    print("[INFO] Loading images ...")
    plant_disease_folder_list = listdir(train_dir)

    for plant_disease_folder in plant_disease_folder_list:
        print(f"[INFO] Processing {plant_disease_folder} ...")
        plant_disease_image_list = listdir(f"{train_dir}/{plant_disease_folder}/")

        for image in plant_disease_image_list[:N_IMAGES]:
            image_directory = f"{train_dir}/{plant_disease_folder}/{image}"
            if image_directory.endswith(".jpg")==True or image_directory.endswith(".JPG")==True:
                image_list.append(convert_image_to_array(image_directory))
                label_list.append(plant_disease_folder)

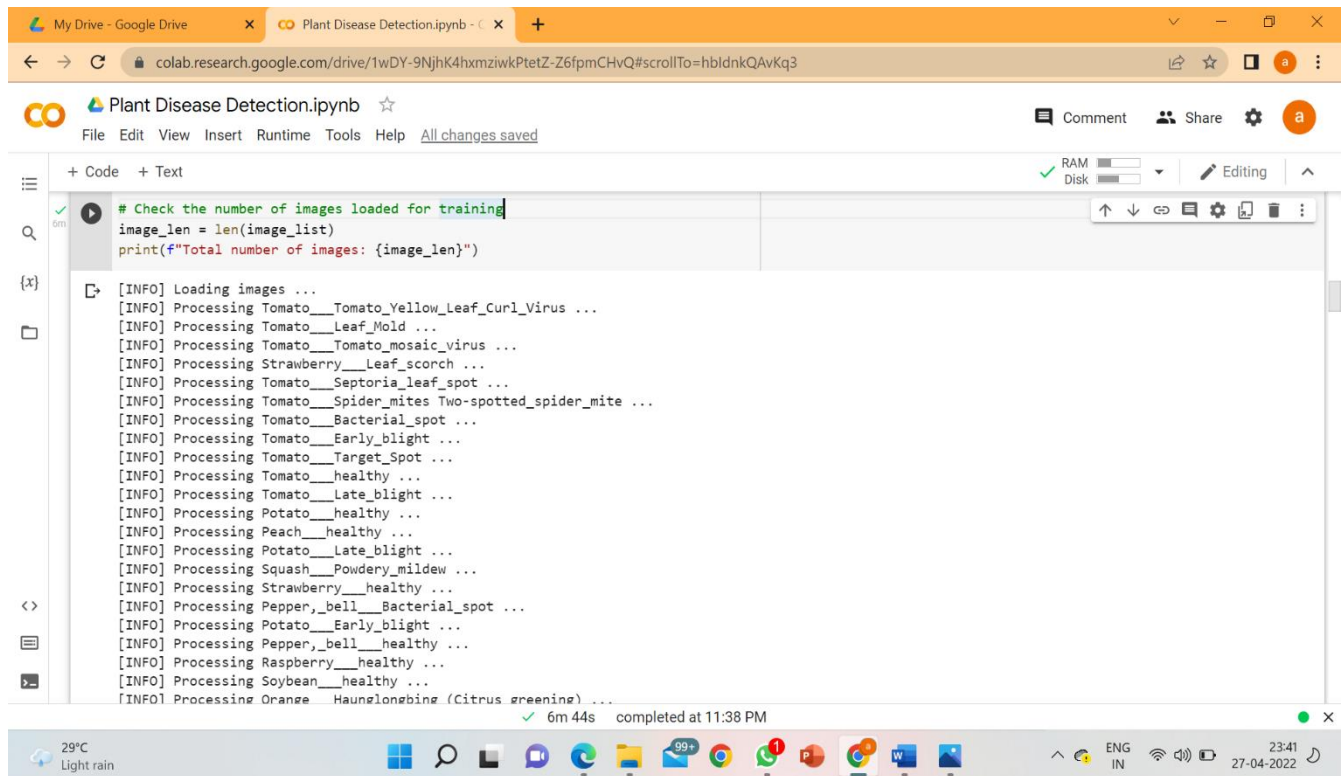
    print("[INFO] Image loading completed")
except Exception as e:
    print(f"Error : {e}")

# Transform the loaded training image data into numpy array
np_image_list = np.array(image_list, dtype=np.float16) / 225.0
print()
```

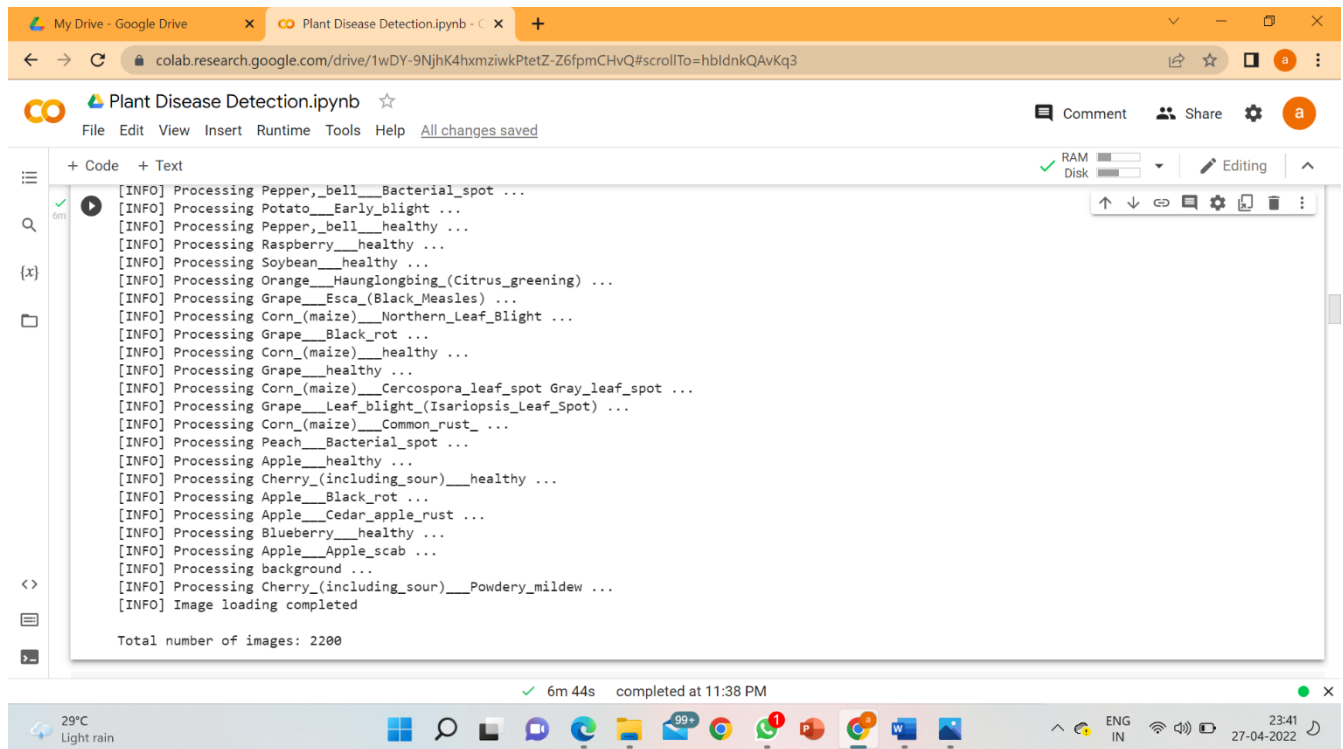
6m 44s completed at 11:38 PM

**Fig 3**

**Fig 2 & Fig 3: Loading Dataset and resizing the image**

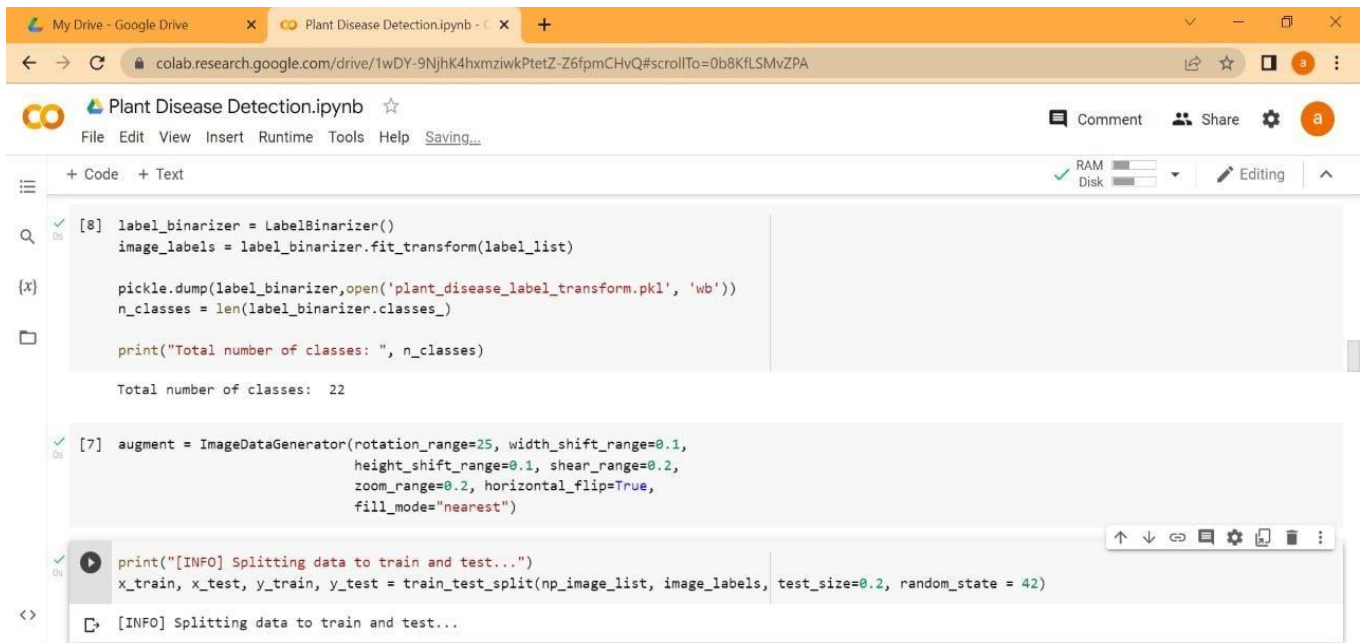


**Fig 4**



**Fig 5**

**Fig 4 & Fig 5: Checking the number of images loaded for training**



```
[8] label_binarizer = LabelBinarizer()
image_labels = label_binarizer.fit_transform(label_list)

pickle.dump(label_binarizer, open('plant_disease_label_transform.pkl', 'wb'))
n_classes = len(label_binarizer.classes_)

print("Total number of classes: ", n_classes)

Total number of classes: 22

[7] augment = ImageDataGenerator(rotation_range=25, width_shift_range=0.1,
                                height_shift_range=0.1, shear_range=0.2,
                                zoom_range=0.2, horizontal_flip=True,
                                fill_mode="nearest")

[9] print("[INFO] Splitting data to train and test...")
x_train, x_test, y_train, y_test = train_test_split(np_image_list, image_labels, test_size=0.2, random_state = 42)

[INFO] Splitting data to train and test...
```

**Fig 6: Examining the labels/classes in the training dataset and splitting the data into training and test sets for validation purpose**



```
[10] EPOCHS = 15
      STEPS = 100
      LR = 1e-3
      BATCH_SIZE = 32
      WIDTH = 256
      HEIGHT = 256
      DEPTH = 3

model = Sequential()
inputShape = (HEIGHT, WIDTH, DEPTH)
chanDim = -1

if K.image_data_format() == "channels_first":
    inputShape = (DEPTH, HEIGHT, WIDTH)
    chanDim = 1

model.add(Conv2D(32, (3, 3), padding="same", input_shape=inputShape))
model.add(Activation("relu"))
model.add(BatchNormalization(axis=chanDim))
model.add(MaxPooling2D(pool_size=(3, 3)))
model.add(Dropout(0.25))
model.add(Conv2D(64, (3, 3), padding="same"))
model.add(Activation("relu"))
```

3s completed at 12:08 AM

Fig 7

```
model.add(BatchNormalization(axis=chanDim))
model.add(Conv2D(64, (3, 3), padding="same"))
model.add(Activation("relu"))
model.add(BatchNormalization(axis=chanDim))
model.add(MaxPooling2D(pool_size=(2, 2)))
model.add(Dropout(0.25))
model.add(Conv2D(128, (3, 3), padding="same"))
model.add(Activation("relu"))
model.add(BatchNormalization(axis=chanDim))
model.add(Conv2D(128, (3, 3), padding="same"))
model.add(Activation("relu"))
model.add(BatchNormalization(axis=chanDim))
model.add(MaxPooling2D(pool_size=(2, 2)))
model.add(Dropout(0.25))
model.add(Flatten())
model.add(Dense(1024))
model.add(Activation("relu"))
model.add(BatchNormalization())
model.add(Dropout(0.5))
model.add(Dense(n_classes))
model.add(Activation("softmax"))

model.summary()
```

Model: "sequential"

3s completed at 12:08 AM

**Fig 8**

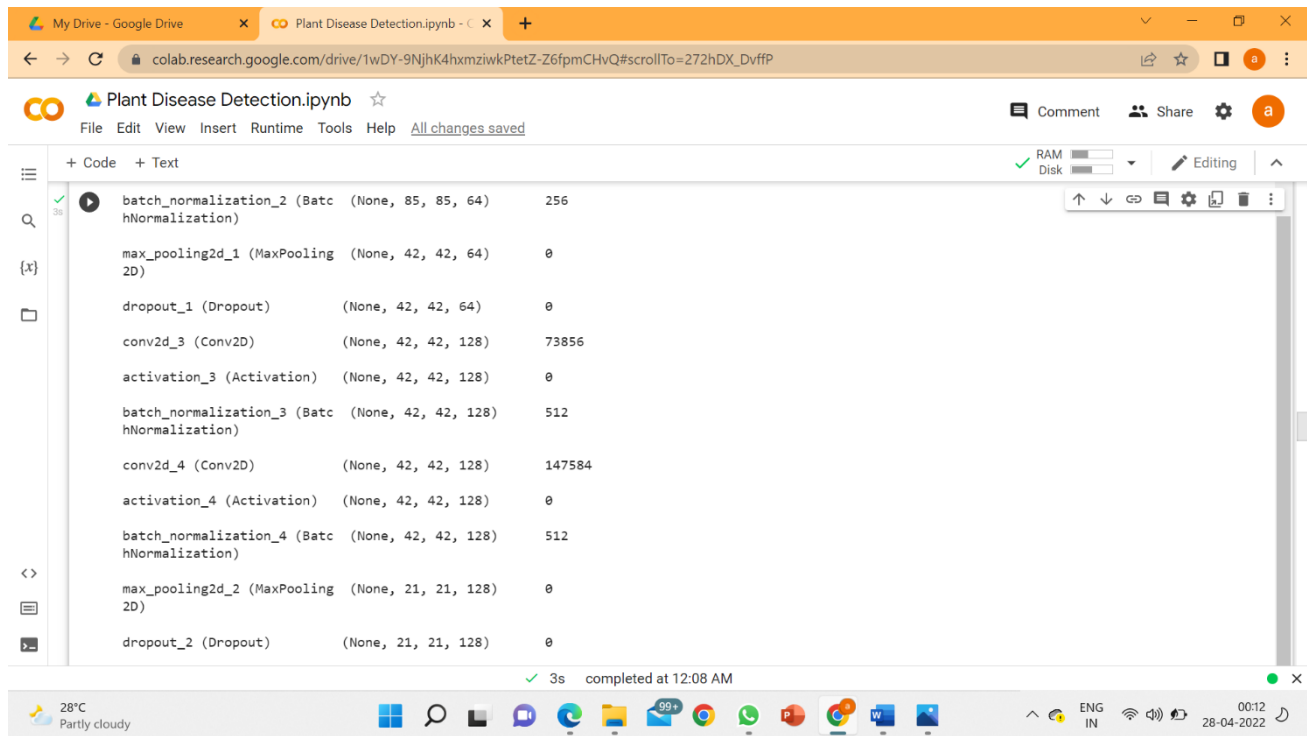
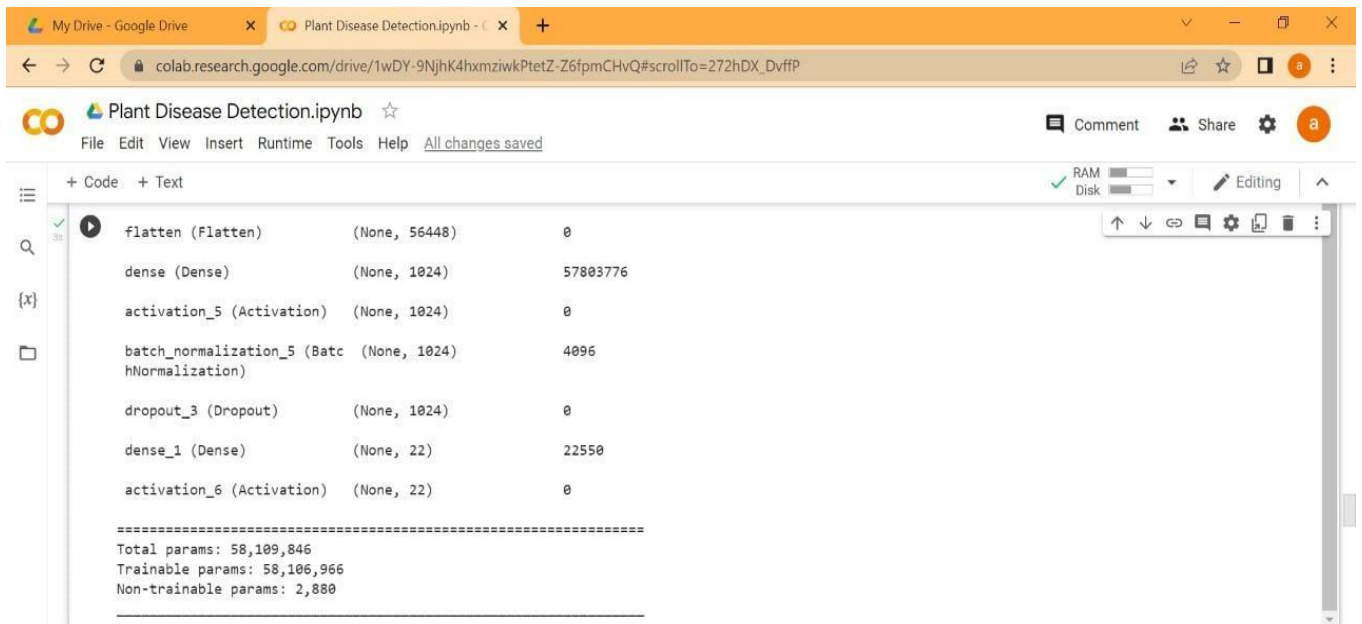


Fig 9



**Fig 10**

**Fig 7,8,9 and 10: Building model by defining the hyperparameters and creating a sequential model and adding different layers at appropriate positions**

The screenshot shows a Google Colab notebook interface. The browser tabs at the top include 'My Drive - Google Drive' and 'Plant Disease Detection.ipynb - C'. The address bar shows the URL 'colab.research.google.com/drive/1wDY-9NjhK4hxmziwkPteZ-Z6fpmCHvQ'. The notebook title is 'Plant Disease Detection.ipynb'. The menu bar includes 'File', 'Edit', 'View', 'Insert', 'Runtime', 'Tools', and 'Help'. The toolbar shows 'Comment', 'Share', and a settings icon. The code editor contains the following Python code:

```
opt = Adam(lr=LR, decay=LR / EPOCHS)

# Compile model
model.compile(loss="binary_crossentropy", optimizer=opt, metrics=["accuracy"])

# Train model
print("[INFO] Training network...")
history = model.fit_generator(augment.flow(x_train, y_train, batch_size=BATCH_SIZE),
                             validation_data=(x_test, y_test),
                             steps_per_epoch=len(x_train) // BATCH_SIZE,
                             epochs=EPOCHS,
                             verbose=1)
```

The output of the code execution is shown in the terminal area:

```
/usr/local/lib/python3.7/dist-packages/keras/optimizer_v2/adam.py:105: UserWarning: The `lr` argument is deprecated, use `learning_rate` instead.
  super(Adam, self).__init__(name, **kwargs)
[INFO] Training network...
/usr/local/lib/python3.7/dist-packages/ipykernel_launcher.py:12: UserWarning: `Model.fit_generator` is deprecated and will be removed in a future vers:
  if sys.path[0] == '':
Epoch 1/15
55/55 [=====] - 31s 543ms/step - loss: 0.0517 - accuracy: 0.8398 - val_loss: 0.3039 - val_accuracy: 0.3568
Epoch 2/15
55/55 [=====] - 29s 529ms/step - loss: 0.0514 - accuracy: 0.8335 - val_loss: 0.3761 - val_accuracy: 0.3864
Epoch 3/15
55/55 [=====] - 29s 532ms/step - loss: 0.0473 - accuracy: 0.8460 - val_loss: 0.0628 - val_accuracy: 0.7818
Epoch 4/15
```

The status bar at the bottom indicates '0s completed at 1:03 AM'. The system tray shows the temperature as 27°C, 'Partly cloudy', and the time as 01:04 on 28-04-2022.

Fig 11

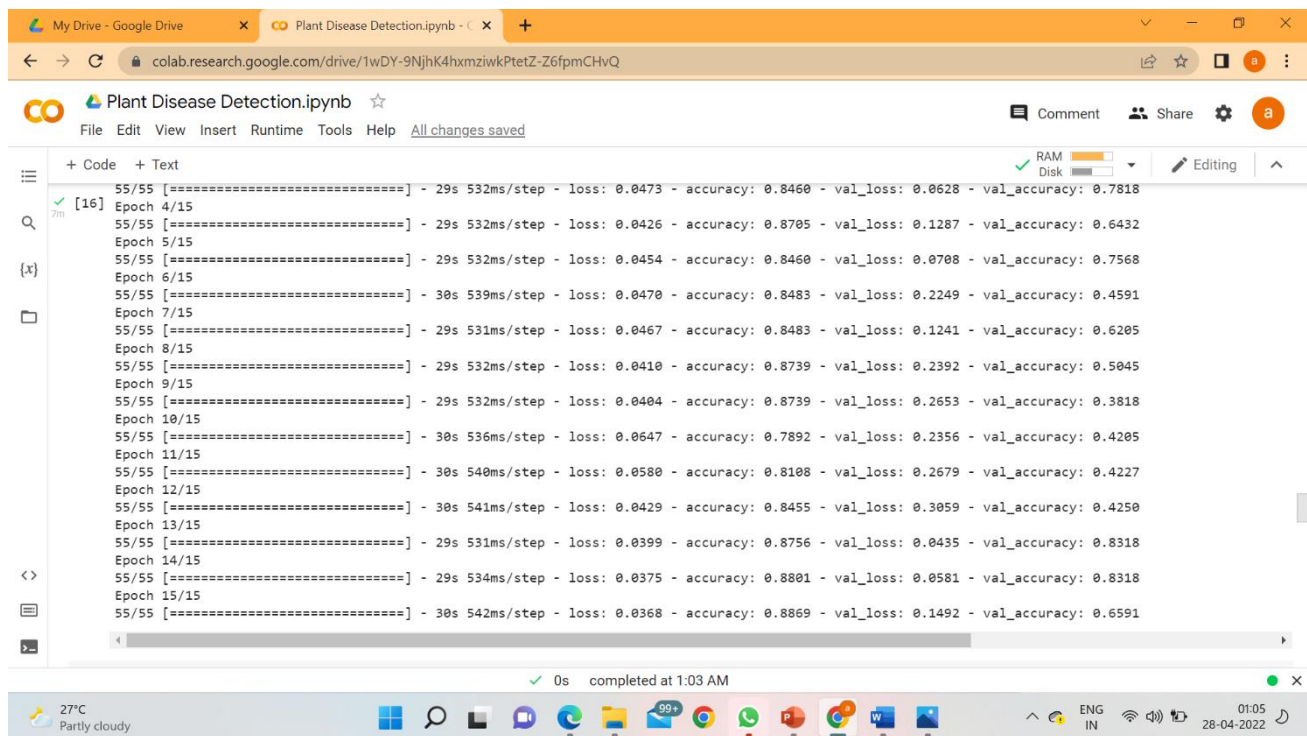
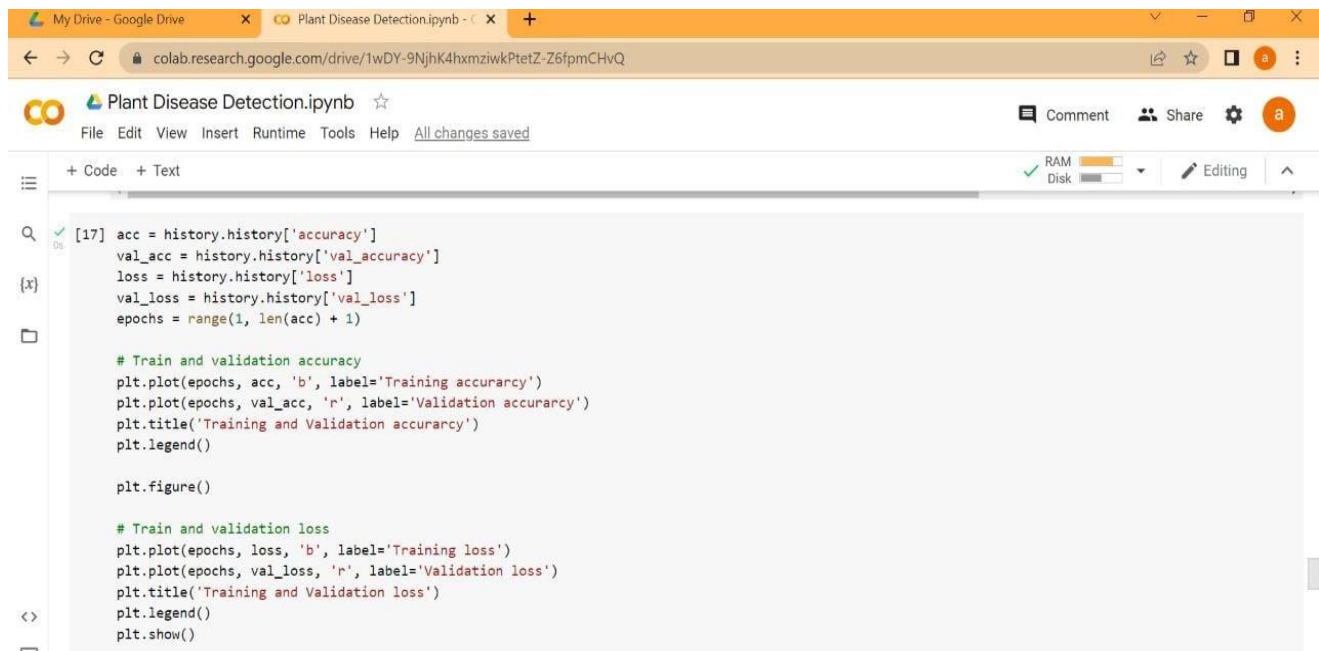


Fig 12

Fig 11 ,12: Training the model



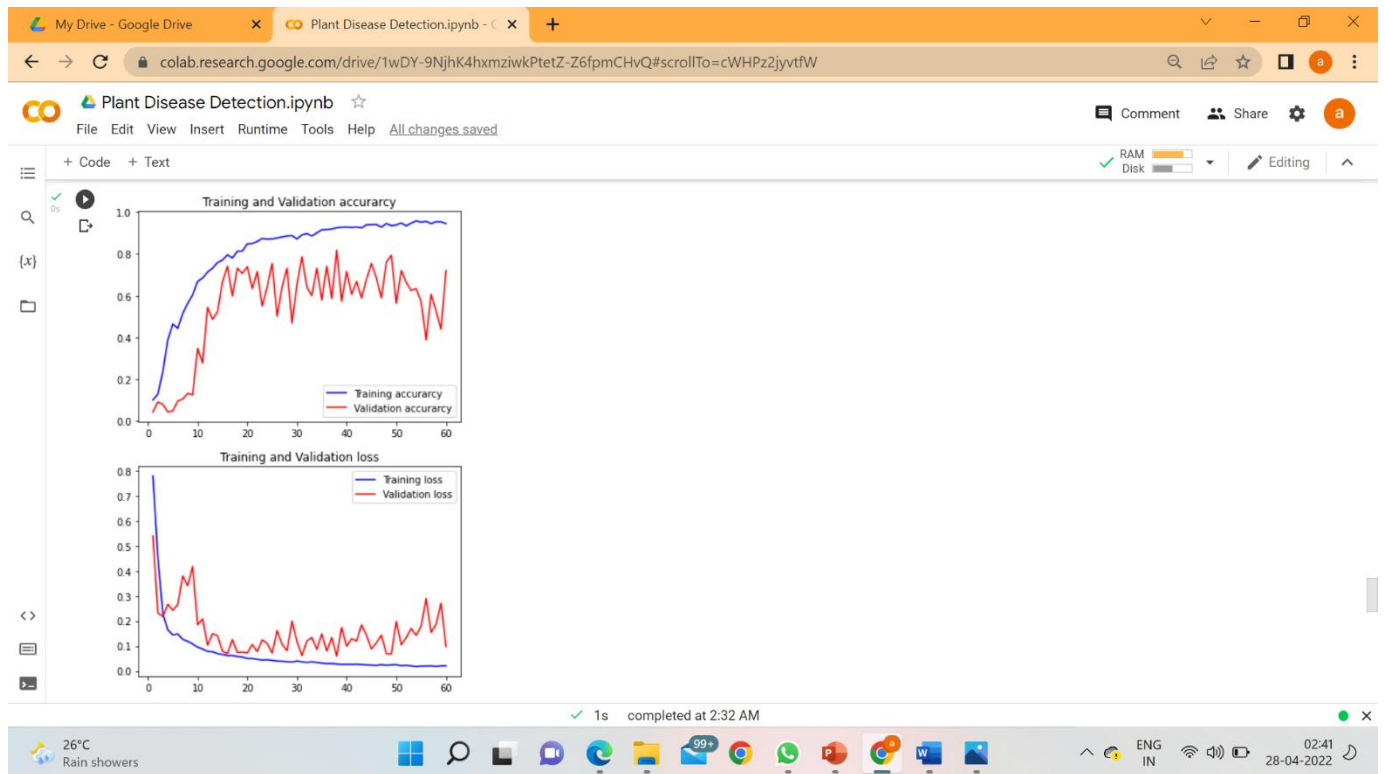
```
[17] acc = history.history['accuracy']
      val_acc = history.history['val_accuracy']
      loss = history.history['loss']
      val_loss = history.history['val_loss']
      epochs = range(1, len(acc) + 1)

      # Train and validation accuracy
      plt.plot(epochs, acc, 'b', label='Training accuracy')
      plt.plot(epochs, val_acc, 'r', label='Validation accuracy')
      plt.title('Training and Validation accuracy')
      plt.legend()

      plt.figure()

      # Train and validation loss
      plt.plot(epochs, loss, 'b', label='Training loss')
      plt.plot(epochs, val_loss, 'r', label='Validation loss')
      plt.title('Training and Validation loss')
      plt.legend()
      plt.show()
```

**Fig 13**



**Fig 14**

**Fig 13,14: Comparing the accuracy and loss by plotting the graph for training and validation**

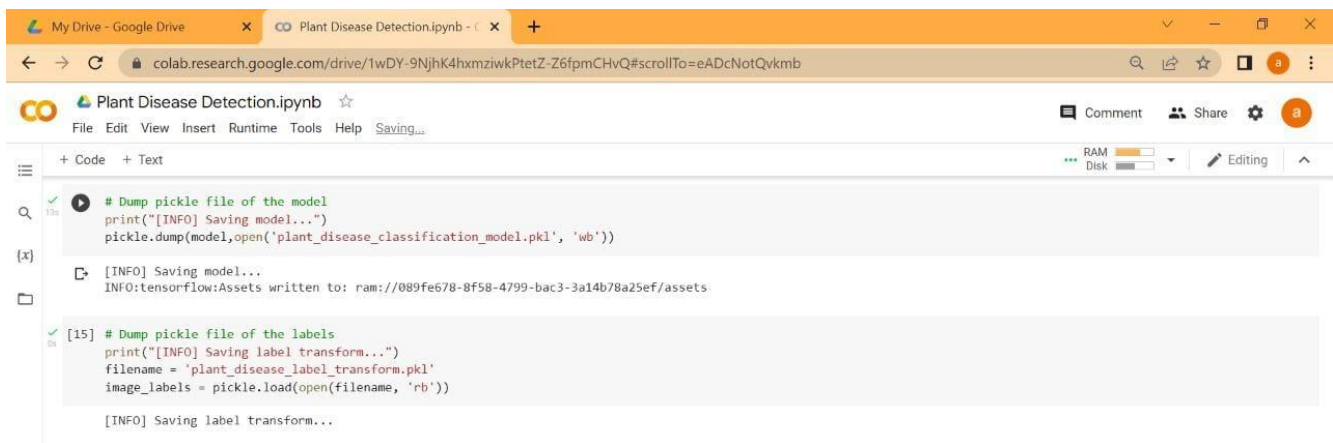




```
print("[INFO] Calculating model accuracy")
scores = model.evaluate(x_test, y_test)
print(f"Test Accuracy: {scores[1]*100}")
```

[INFO] Calculating model accuracy  
14/14 [=====] - 1s 63ms/step - loss: 0.0975 - accuracy: 0.7205  
Test Accuracy: 72.04545736312866

**Fig 15: Evaluating model accuracy by using the evaluate method**



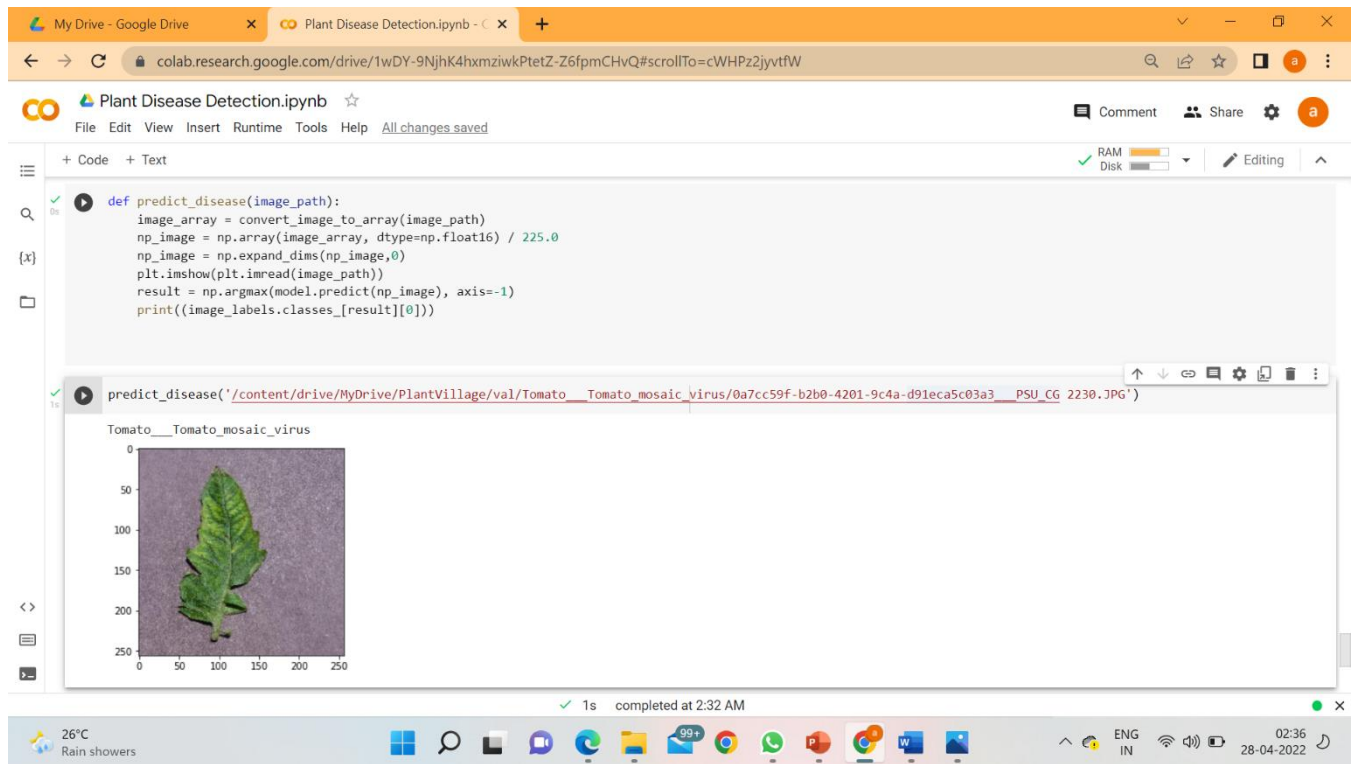
```
# Dump pickle file of the model
print("[INFO] Saving model...")
pickle.dump(model, open('plant_disease_classification_model.pkl', 'wb'))
```

[INFO] Saving model...  
INFO:tensorflow:Assets written to: ram://089fe678-8f58-4799-bac3-3a14b78a25ef/assets

```
[15] # Dump pickle file of the labels
print("[INFO] Saving label transform...")
filename = 'plant_disease_label_transform.pkl'
image_labels = pickle.load(open(filename, 'rb'))
```

[INFO] Saving label transform...

**Fig 16: Saving the model**



**Fig 17: Predicting the disease and printing output result**

## **8. CONCLUSION**

The proposed system is developed taking in mind the benefits of the farmers and agricultural sector .The developed system can detect disease in plant and also provide the remedy that can be taken against the disease. By proper knowledge of the disease and the remedy can be taken for improving the health of the plant .The proposed system is based on python and gives an good accuracy The system can be installed and accesing of crop fields can be done easily.

## 9. REFERENCES

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