```
from google.colab import drive
drive.mount('/content/drive')
```

Mounted at /content/drive

!unzip /content/drive/MyDrive/Tomato

Streaming output truncated to the last 5000 lines. inflating: Tomato/Tomato healthy/image (342).JPG inflating: Tomato/Tomato healthy/image (343).JPG inflating: Tomato/Tomato healthy/image (344).JPG inflating: Tomato/Tomato healthy/image (345).JPG inflating: Tomato/Tomato healthy/image (346).JPG inflating: Tomato/Tomato healthy/image (347).JPG inflating: Tomato/Tomato healthy/image (348).JPG inflating: Tomato/Tomato healthy/image (349).JPG inflating: Tomato/Tomato healthy/image (35).JPG inflating: Tomato/Tomato healthy/image (350).JPG inflating: Tomato/Tomato healthy/image (351).JPG inflating: Tomato/Tomato healthy/image (352).JPG inflating: Tomato/Tomato healthy/image (353).JPG inflating: Tomato/Tomato healthy/image (354).JPG inflating: Tomato/Tomato healthy/image (355).JPG inflating: Tomato/Tomato healthy/image (356).JPG inflating: Tomato/Tomato healthy/image (357).JPG inflating: Tomato/Tomato healthy/image (358).JPG inflating: Tomato/Tomato healthy/image (359).JPG inflating: Tomato/Tomato healthy/image (36).JPG inflating: Tomato/Tomato healthy/image (360).JPG inflating: Tomato/Tomato healthy/image (361).JPG inflating: Tomato/Tomato healthy/image (362).JPG inflating: Tomato/Tomato healthy/image (363).JPG inflating: Tomato/Tomato healthy/image (364).JPG inflating: Tomato/Tomato healthy/image (365).JPG inflating: Tomato/Tomato healthy/image (366).JPG inflating: Tomato/Tomato healthy/image (367).JPG inflating: Tomato/Tomato healthy/image (368).JPG inflating: Tomato/Tomato healthy/image (369).JPG inflating: Tomato/Tomato healthy/image (37).JPG inflating: Tomato/Tomato healthy/image (370).JPG inflating: Tomato/Tomato healthy/image (371).JPG inflating: Tomato/Tomato healthy/image (372).JPG inflating: Tomato/Tomato healthy/image (373).JPG inflating: Tomato/Tomato healthy/image (374).JPG inflating: Tomato/Tomato healthy/image (375).JPG inflating: Tomato/Tomato healthy/image (376).JPG inflating: Tomato/Tomato healthy/image (377).JPG inflating: Tomato/Tomato healthy/image (378).JPG inflating: Tomato/Tomato healthy/image (379).JPG inflating: Tomato/Tomato healthy/image (38).JPG inflating: Tomato/Tomato healthy/image (380).JPG inflating: Tomato/Tomato healthy/image (381).JPG inflating: Tomato/Tomato healthy/image (382).JPG inflating: Tomato/Tomato healthy/image (383).JPG

```
inflating: Tomato/Tomato healthy/image (384).JPG
      inflating: Tomato/Tomato healthy/image (385).JPG
      inflating: Tomato/Tomato healthy/image (386).JPG
      inflating: Tomato/Tomato healthy/image (387).JPG
      inflating: Tomato/Tomato healthy/image (388).JPG
      inflating: Tomato/Tomato healthy/image (389).JPG
      inflating: Tomato/Tomato healthy/image (39).JPG
      inflating: Tomato/Tomato healthy/image (390).JPG
      inflating: Tomato/Tomato healthy/image (391).JPG
      inflating: Tomato/Tomato healthy/image (392).JPG
      inflating: Tomato/Tomato healthy/image (393).JPG
      inflating: Tomato/Tomato healthy/image (394)..TPG
import tensorflow as tf
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.preprocessing import image
import numpy as np
import os
import random
from shutil import copyfile
import matplotlib.image as mpimg
import matplotlib.pyplot as plt
import cv2
from google.colab.patches import cv2_imshow
from tensorflow.keras.models import Model, Sequential
from tensorflow.keras.layers import Conv2D, Activation, MaxPooling2D, Dropout, Dense
from tensorflow.keras.layers import GlobalAveragePooling2D, Flatten, BatchNormalizatic
from tensorflow.keras.applications.inception v3 import InceptionV3
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.callbacks import ModelCheckpoint, ReduceLROnPlateau, EarlyStoppi
from keras.utils.np utils import to categorical
to create = [
'leaf disease',
'leaf disease/training',
'leaf disease/testing',
'leaf disease/training/Tomato Bacterial spot',
'leaf disease/training/Tomato Late blight',
'leaf disease/training/Tomato Early blight',
'leaf disease/training/Tomato healthy',
'leaf disease/training/Tomato Yellow Leaf Curl Virus',
'leaf disease/training/Tomato Leaf Mold',
'leaf disease/testing/Tomato Bacterial spot',
'leaf disease/testing/Tomato Late blight',
'leaf disease/testing/Tomato Early blight',
'leaf disease/testing/Tomato healthy',
'leaf disease/testing/Tomato Yellow Leaf Curl Virus',
'leaf disease/testing/Tomato Leaf Mold'
for directory in to create:
```

```
try:
   os.mkdir(directory)
    print(directory, 'created')
  except:
    print(directory, 'failed')
    leaf disease created
    leaf disease/training created
    leaf disease/testing created
    leaf disease/training/Tomato Bacterial spot created
    leaf disease/training/Tomato Late blight created
    leaf disease/training/Tomato Early blight created
    leaf disease/training/Tomato healthy created
    leaf disease/training/Tomato Yellow Leaf Curl Virus created
    leaf disease/training/Tomato Leaf Mold created
    leaf disease/testing/Tomato Bacterial spot created
    leaf disease/testing/Tomato Late blight created
    leaf disease/testing/Tomato Early blight created
    leaf disease/testing/Tomato healthy created
    leaf disease/testing/Tomato Yellow Leaf Curl Virus created
    leaf disease/testing/Tomato Leaf Mold created
def split data(SOURCE, TRAINING, TESTING, SPLIT SIZE):
    all files = []
    for file name in os.listdir(SOURCE):
        file path = SOURCE + file name
        if os.path.getsize(file path):
            all files.append(file name)
        else:
            print('{} is zero length, so ignoring'.format(file name))
    n files = len(all files)
    split point = int(n files * SPLIT SIZE)
    shuffled = random.sample(all files, n files)
    train set = shuffled[:split point]
    test set = shuffled[split point:]
    for file name in train set:
        copyfile(SOURCE + file name, TRAINING + file name)
    for file name in test set:
        copyfile(SOURCE + file name, TESTING + file name)
SOURCE_DIR = "Tomato/Tomato Late blight/"
TRAINING DIR = "leaf disease/training/Tomato Late blight/"
TESTING DIR = "leaf disease/testing/Tomato Late blight/"
split size = .7
enlit data/SOURCE DIR TRAINING DIR TESTING DIR enlit eizel
```

```
SPITE_GAGG(SOURCE_DIR, INAIMING_DIR, IESTING_DIR, SPITE_SIZE)
```

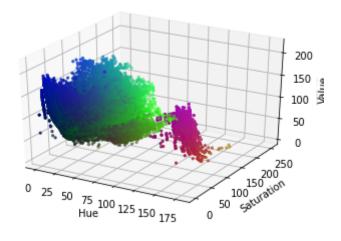
```
SOURCE DIR = "Tomato/Tomato Bacterial spot/"
TRAINING DIR = "leaf disease/training/Tomato Bacterial spot/"
TESTING DIR = "leaf disease/testing/Tomato Bacterial spot/"
split size = .7
split data(SOURCE DIR, TRAINING DIR, TESTING DIR, split size)
SOURCE DIR = "Tomato/Tomato Early blight/"
TRAINING DIR = "leaf disease/training/Tomato Early blight/"
TESTING DIR = "leaf disease/testing/Tomato Early blight/"
split size = .7
split data(SOURCE DIR, TRAINING DIR, TESTING DIR, split size)
SOURCE DIR = "Tomato/Tomato healthy/"
TRAINING DIR = "leaf disease/training/Tomato healthy/"
TESTING DIR = "leaf disease/testing/Tomato healthy/"
split size = .7
split data(SOURCE DIR, TRAINING DIR, TESTING DIR, split size)
SOURCE DIR = "Tomato/Tomato Yellow Leaf Curl Virus/"
TRAINING DIR = "leaf disease/training/Tomato Yellow Leaf Curl Virus/"
TESTING DIR = "leaf disease/testing/Tomato Yellow Leaf Curl Virus/"
split size = .7
split data(SOURCE DIR, TRAINING DIR, TESTING DIR, split size)
SOURCE DIR = "Tomato/Tomato Leaf Mold/"
TRAINING DIR = "leaf disease/training/Tomato Leaf Mold/"
TESTING DIR = "leaf disease/testing/Tomato Leaf Mold/"
split size = .7
split data(SOURCE DIR, TRAINING DIR, TESTING DIR, split size)
data dir = "leaf disease/training"
classes = os.listdir(data_dir)
classes
    ['Tomato Yellow Leaf Curl Virus',
     'Tomato healthy',
     'Tomato Bacterial spot',
     'Tomato Late blight',
      'Tomato Early blight',
      'Tomato Leaf Mold']
img = cv2.imread('/content/leaf disease/testing/Tomato Bacterial spot/image (100).JPC
hsv = cv2.cvtColor(img, cv2.COLOR BGR2HSV)
```

```
from mpl_toolkits.mplot3d import Axes3D
from matplotlib import cm
from matplotlib import colors

pixel_colors = hsv.reshape((np.shape(hsv)[0]*np.shape(hsv)[1], 3))
norm = colors.Normalize(vmin=-1.,vmax=1.)
norm.autoscale(pixel_colors)
pixel_colors = norm(pixel_colors).tolist()
```

```
h, s, v = cv2.split(hsv)
fig = plt.figure()
axis = fig.add_subplot(1, 1, 1, projection="3d")

axis.scatter(h.flatten(), s.flatten(), v.flatten(), facecolors=pixel_colors, marker=".axis.set_xlabel("Hue")
axis.set_ylabel("Saturation")
axis.set_zlabel("Value")
plt.show()
```



```
from google.colab.patches import cv2_imshow
img = cv2.imread('/content/leaf_disease/testing/Tomato_Bacterial_spot/image (100).JPC
hsv = cv2.cvtColor(img, cv2.COLOR_BGR2HSV)

# find the green color
mask_green = cv2.inRange(hsv, (36,0,0), (86,255,255))
# find the brown color
mask_brown = cv2.inRange(hsv, (8, 60, 20), (30, 255, 200))
# find the yellow color in the leaf
mask_yellow = cv2.inRange(hsv, (21, 39, 64), (40, 255, 255))

# find any of the three colors(green or brown or yellow) in the image
mask = cv2.bitwise_or(mask_green, mask_brown)
```

mack - and hituica or/mack mack mallous

```
mask - CVZ.DICWISE_OI(mask, mask_yellow)
```

Bitwise-AND mask and original image res = cv2.bitwise_and(img,img, mask= mask) cv2_imshow(img) cv2 imshow(res) cv2.waitKey(0) cv2.destroyAllWindows()



```
from google.colab.patches import cv2 imshow
   img = cv2.imread('/content/leaf disease/testing/Tomato Yellow Leaf Curl Virus/image (
   hsv = cv2.cvtColor(img, cv2.COLOR BGR2HSV)
   # find the green color
   mask green = cv2.inRange(hsv, (36,0,0), (86,255,255))
   # find the brown color
   mask brown = cv2.inRange(hsv, (8, 60, 20), (30, 255, 200))
   # find the yellow color in the leaf
   mask yellow = cv2.inRange(hsv, (21, 39, 64), (40, 255, 255))
   # find any of the three colors(green or brown or yellow) in the image
   mask = cv2.bitwise or(mask green, mask brown)
   mack = cv2 hitwice or/mack mack vellow)
https://colab.research.google.com/drive/1gTj1baMo\_qceLJiIxG6-E6sm6QLNb\_4T\#scrollTo=Ej7rOwQ48EIc\&printMode=true
```

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```
mask - Cv2.Dicwise_Or(mask, mask_yerrow)
```

```
# Bitwise-AND mask and original image
res = cv2.bitwise_and(img,img, mask= mask)
cv2_imshow(img)
cv2_imshow(res)
cv2.waitKey(0)
cv2.destroyAllWindows()
```



```
validation dir = 'leaf disease/testing'
training generator = train datagen.flow from directory(training dir,
                                                  target size=(256, 256),
                                                 batch size=batch size,
                                                 class mode='categorical')
valid generator = valid datagen.flow from directory(validation dir,
                                             target size=(256, 256),
                                            batch size=batch size,
                                            class mode='categorical',
                                            shuffle=False)
    Found 8477 images belonging to 6 classes.
    Found 6220 images belonging to 6 classes.
class dict = training generator.class indices
print(class dict)
    {'Tomato Bacterial spot': 0, 'Tomato Early blight': 1, 'Tomato Late blight': 2,
target names = list(class dict.keys())
print(target_names)
    ['Tomato_Bacterial_spot', 'Tomato_Early_blight', 'Tomato_Late_blight', 'Tomato_Lot
train num = training generator.samples
valid num = valid generator.samples
model = tf.keras.models.Sequential([
    tf.keras.layers.Conv2D(16, (3,3), activation='relu', input shape=(256, 256, 3)),
    tf.keras.layers.MaxPooling2D(2, 2),
    tf.keras.layers.Conv2D(32, (3,3), activation='relu'),
    tf.keras.layers.MaxPooling2D(2,2),
    tf.keras.layers.Conv2D(32, (3,3), activation='relu'),
    tf.keras.layers.MaxPooling2D(2,2),
    tf.keras.layers.Conv2D(64, (3,3), activation='relu'),
    tf.keras.layers.MaxPooling2D(2,2),
    tf.keras.layers.Conv2D(64, (3,3), activation='relu'),
    tf.keras.layers.MaxPooling2D(2,2),
    tf.keras.layers.Flatten(),
    tf.keras.layers.Dense(512, activation='relu'),
    tf.keras.layers.Dropout(0.2),
    tf.keras.layers.Dense(6, activation='softmax')
```

```
model.summary()
```

Model: "sequential"

Layer (type)	Output	Shape	Param #
conv2d (Conv2D)	(None,	254, 254, 16)	448
max_pooling2d (MaxPooling2D)	(None,	127, 127, 16)	0
conv2d_1 (Conv2D)	(None,	125, 125, 32)	4640
max_pooling2d_1 (MaxPooling2	(None,	62, 62, 32)	0
conv2d_2 (Conv2D)	(None,	60, 60, 32)	9248
max_pooling2d_2 (MaxPooling2	(None,	30, 30, 32)	0
conv2d_3 (Conv2D)	(None,	28, 28, 64)	18496
max_pooling2d_3 (MaxPooling2	(None,	14, 14, 64)	0
conv2d_4 (Conv2D)	(None,	12, 12, 64)	36928
max_pooling2d_4 (MaxPooling2	(None,	6, 6, 64)	0
flatten (Flatten)	(None,	2304)	0
dense (Dense)	(None,	512)	1180160
dropout (Dropout)	(None,	512)	0
dense_1 (Dense)	(None,	6)	3078
Total params: 1,252,998 Trainable params: 1,252,998 Non-trainable params: 0	=====		======

```
Epoch 2/47
Epoch 3/47
Epoch 4/47
Epoch 5/47
Epoch 6/47
Epoch 7/47
67/67 [=============] - 289s 4s/step - loss: 0.3369 - accuracy:
Epoch 8/47
Epoch 9/47
Epoch 10/47
Epoch 11/47
Epoch 12/47
Epoch 13/47
Epoch 14/47
Epoch 15/47
Epoch 16/47
Epoch 17/47
Epoch 18/47
Epoch 19/47
Epoch 20/47
Epoch 21/47
Epoch 22/47
Epoch 23/47
Epoch 24/47
Epoch 25/47
Epoch 26/47
Epoch 27/47
Epoch 28/47
Epoch 29/47
Epoch 30/47
```

```
model.save('trained model.h5')
image_path = "image (14).JPG"
new_img=image.load_img(image_path, target_size=(256,256))
img= image.img to array(new img)
img=np.expand dims(img, axis=0)
img = img/255
img class = model.predict classes(img)
prediction = model.predict(img)
print(img class)
d = prediction.flatten()
j = d.max()
for index, item in enumerate(d):
    if item == j:
        class name = target names[index]
print(class name)
    [1]
    Tomato Early blight
image path = "image (1289).JPG"
new img=image.load img(image path, target size=(256,256))
img= image.img to array(new img)
img=np.expand dims(img, axis=0)
img = img/255
img class = model.predict classes(img)
prediction = model.predict(img)
print(img class)
d = prediction.flatten()
j = d.max()
for index, item in enumerate(d):
    if item == j:
        class name = target names[index]
print(class name)
    [4]
    Tomato Yellow Leaf Curl Virus
history = history
print(history.history.keys())
    dict keys(['loss', 'accuracy', 'val loss', 'val accuracy'])
acc = history.history['accuracy']
val acc = history.history['val accuracy']
loss = history.history['loss']
val loss = history.history['val loss']
```

```
epochs = range(1, len(loss) + 1)
#accuracy plot
plt.plot(epochs, acc, label='Training Accuracy')
plt.plot(epochs, val_acc, label='Validation Accuracy')
plt.title('Training and Validation Accuracy')
plt.ylabel('Accuracy')
plt.xlabel('Epoch')
plt.savefig(fname='Training_Validation Accuracy')
plt.legend()
plt.figure()
#loss plot
plt.plot(epochs, loss, label='Training Loss')
plt.plot(epochs, val_loss, label='Validation Loss')
plt.title('Training and Validation Loss')
plt.xlabel('Epoch')
plt.ylabel('Loss')
plt.legend()
plt.savefig(fname='Training Validation Loss')
plt.show()
```

```
Tarinian and Malidakian Alancas.
from sklearn.metrics import confusion matrix
from sklearn.metrics import classification report
from sklearn.metrics import accuracy score
from sklearn.metrics import roc curve, auc
from sklearn.metrics import roc auc score
from sklearn import preprocessing
     Q 0./1 //
Y pred = model.predict(valid generator, valid num // batch size+1)
y pred = np.argmax(Y pred, axis=1)
print('Confusion Matrix')
print(confusion matrix(valid generator.classes, y pred))
print('Classification Report')
target names = ['Tomato Bacterial spot', 'Tomato Early blight',
                'Tomato Late blight', 'Tomato Leaf Mold',
                'Tomato Yellow Leaf Curl Virus', 'Tomato healthy']
print(classification report(valid generator.classes, y pred,
                            target names=target names))
    Confusion Matrix
     [[762 14 1 0
                         0
                             01
     [ 0 361
                 1
                         0
                             21
                     0
                   1
        1 28 645
                             41
           7
               0 333
                             01
                     0 483
                 0
            0
                 0
                     0
                         0 58811
    Classification Report
                                    precision
                                                recall f1-score
                                                                     support
            Tomato Bacterial spot
                                         0.99
                                                    0.98
                                                              0.98
                                                                         777
               Tomato Early blight
                                         0.87
                                                    0.99
                                                              0.93
                                                                         364
                Tomato Late blight
                                         1.00
                                                    0.95
                                                              0.97
                                                                         679
                  Tomato Leaf Mold
                                         1.00
                                                    0.98
                                                              0.99
                                                                         340
    Tomato Yellow Leaf Curl Virus
                                         1.00
                                                    0.97
                                                              0.99
                                                                         496
                    Tomato healthy
                                         0.99
                                                    1.00
                                                              0.99
                                                                         588
                                                              0.98
                                                                        3244
                          accuracy
                         macro avq
                                         0.97
                                                    0.98
                                                              0.98
                                                                        3244
                      weighted avg
                                         0.98
                                                    0.98
                                                              0.98
                                                                        3244
all labels = ['Tomato Bacterial spot', 'Tomato Early blight', 'Tomato Late blight',
       'Tomato Leaf Mold', 'Tomato Yellow Leaf Curl Virus', 'Tomato healthy']
fig, c ax = plt.subplots(1,1, figsize = (12, 8))
def multiclass roc auc score(y test, y pred, average="macro"):
    lb = preprocessing.LabelBinarizer()
    #lb = LabelBinarizer()
    lb.fit(y_test)
    y test = lb.transform(y test)
    y pred = lb.transform(y pred)
```

```
for (idx, c_label) in enumerate(all_labels): # all_labels: no of the labels
       fpr, tpr, thresholds = roc_curve(y_test[:,idx].astype(int), y_pred[:,idx])
       plt.xlabel('False Positive Rate')
       plt.ylabel('True Positive Rate')
       plt.legend(loc = 'lower right')
       plt.title('Receiver Operating Characteristic')
       plt.plot(fpr, tpr, label = '%s (AUC:%0.2f)' % (c_label, auc(fpr, tpr)))
   plt.plot(fpr, fpr, 'b-', label = 'Random Guessing')
   plt.savefig(fname='roc auc')
   return roc_auc_score(y_test, y_pred, average=average)
# calling
valid generator.reset() # resetting generator
y pred = model.predict(valid generator, verbose = True)
y pred = np.argmax(y pred, axis=1)
multiclass roc auc score(valid generator.classes, y pred)
    26/26 [======== ] - 21s 791ms/step
    No handles with labels found to put in legend.
    0.9874785226766131
```

