```
from google.colab import drive
drive.mount('/content/drive')
    Drive already mounted at /content/drive; to attempt to forcibly remount, call
!unzip /content/drive/MyDrive/Tomato
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
from glob import glob
from tensorflow.keras.applications.inception v3 import InceptionV3
from tensorflow.keras.applications.resnet v2 import ResNet152V2
from tensorflow.keras.applications.efficientnet import EfficientNetB7
from tensorflow.keras.applications.resnet50 import ResNet50
from tensorflow.keras.applications.inception resnet v2 import InceptionResNetV2
from tensorflow.keras.models import Model, Sequential
from tensorflow.keras.layers import Conv2D, Activation, MaxPooling2D, Dropout, Dens
from tensorflow.keras.layers import GlobalAveragePooling2D, Flatten, BatchNormaliza
from tensorflow.keras.applications.inception v3 import InceptionV3
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.callbacks import ModelCheckpoint, ReduceLROnPlateau, EarlySto
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'
```

```
01/10/2021
                                    TransferLearning_ResNet50.ipynb - Colaboratory
   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 = .8
   split data(SOURCE DIR, TRAINING DIR, TESTING DIR, split size)
```

```
https://colab.research.google.com/drive/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i\#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff\&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug8i#scrollTo=wzW6ik4ML3Ff&printMode=true/17njSNLReXzaKpvJ0JSlngXHcyrsKug9i#scrollTo=wzW6ik4ML3Ff&printMode=true/17njSNLReXzaKpvJ
```

SOURCE DIR = "Tomato/Tomato Bacterial spot/"

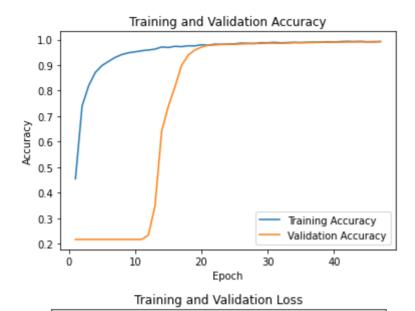
```
TRAINING DIR = "leaf disease/training/Tomato Bacterial spot/"
TESTING DIR = "leaf disease/testing/Tomato Bacterial spot/"
split size = .8
split data(SOURCE DIR, TRAINING DIR, TESTING DIR, split size)
SOURCE DIR = "Tomato/Tomato Early blight/"
TRAINING DIR = "leaf disease/training/Tomato Early blight/"
TESTING DIR = "leaf disease/testing/Tomato Early blight/"
split size = .8
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 = .8
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 = .8
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 = .8
split data(SOURCE DIR, TRAINING DIR, TESTING DIR, split size)
data dir = "leaf disease/training"
classes = os.listdir(data dir)
classes
    ['Tomato Early blight',
     'Tomato healthy',
     'Tomato Bacterial spot',
      'Tomato Late blight',
     'Tomato Leaf Mold',
     'Tomato Yellow Leaf Curl Virus'
train datagen = ImageDataGenerator(rescale=1./255,
                                   shear range=0.2,
                                   zoom_range=0.2,
                                   width shift range=0.2,
                                   height shift range=0.2,
                                   fill mode='nearest')
valid datagen = ImageDataGenerator(rescale=1./255)
batch size = 128
training dir = 'leaf disease/training'
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 8283 images belonging to 6 classes.
    Found 4693 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
train num = training generator.samples
valid num = valid generator.samples
# from keras.applications import ResNet50
# from keras.optimizers import Adam,SGD
# from keras.models import Sequential
# model = Sequential()
# # Sequential needed for add method
# model.add(ResNet50(include top = False, pooling = 'avg' ,weights = 'imagenet'))
# model.add(Dense(6, activation='softmax'))
# model.layers[0].trainable = False
# model.compile(tf.keras.optimizers.Adam(0.001), loss='categorical crossentropy', m
def add new last layer(base model, nb classes):
   x = base model.output
   x = GlobalAveragePooling2D()(x)
   x = Dense(512, activation='relu')(x)
   predictions = Dense(nb classes, activation='softmax')(x)
   model = Model(base model.input, predictions)
   return model
base model = ResNet50(weights='imagenet', include top=False) #include top=False exc
model = add_new_last_layer(base_model, 6)
```

```
model.compile(tf.keras.optimizers.SGD(0.001), loss='categorical_crossentropy', metr
```

```
history = model.fit(
 training generator,
 steps per epoch=train num//batch size,
 epochs=47,
 verbose=1,
 validation data=valid generator,
 validation steps=valid num//batch size
)
 Epoch 1/47
 64/64 [============== ] - 173s 3s/step - loss: 1.7272 - accurac
 Epoch 2/47
 64/64 [============== ] - 167s 3s/step - loss: 1.0637 - accurac
 Epoch 3/47
 Epoch 4/47
 Epoch 5/47
 Epoch 6/47
 Epoch 7/47
 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
 64/64 [=========== ] - 167s 3s/step - loss: 0.0721 - accurac
```

```
Epoch 25/47
    64/64 [============= ] - 167s 3s/step - loss: 0.0685 - accurac
    Epoch 26/47
    64/64 [============= ] - 167s 3s/step - loss: 0.0639 - accurac
    Epoch 27/47
    64/64 [============= ] - 167s 3s/step - loss: 0.0646 - accurac
    Epoch 28/47
    64/64 [============== ] - 168s 3s/step - loss: 0.0625 - accurac
    Epoch 29/47
    64/64 [============= ] - 168s 3s/step - loss: 0.0570 - accurac
    Enoch 20/47
import pickle
filename = 'ResNet50 model.pkl'
pickle.dump(history.history, open(filename, 'wb'))
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 ResNet50')
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 Resnet50')
plt.show()
```



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

Coni	Eusi	on Ma	trix			
[[11	L14	2	1	0	0	0]
[3	492	9	0	0	7]
[0	4	995	0	0	2]
[2	2	3	491	0	1]
[3	0	0	0	735	0]
[0	0	0	0	0	827]]
Classification			on Re	port		

	precision	recall	f1-score	support
Tomato_Bacterial_spot	0.99	1.00	1.00	1117
Tomato_Early_blight	0.98	0.96	0.97	511
Tomato_Late_blight	0.99	0.99	0.99	1001
Tomato_Leaf_Mold	1.00	0.98	0.99	499
Tomato_Yellow_Leaf_Curl_Virus	1.00	1.00	1.00	738
Tomato_healthy	0.99	1.00	0.99	827
accuracy			0.99	4693
macro avg	0.99	0.99	0.99	4693
weighted avg	0.99	0.99	0.99	4693

```
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 InceptionV3')
    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)
```

37/37 [======] - 20s 539ms/step No handles with labels found to put in legend. 0.9936486042745774

Receiver Operating Characteristic

