```
import numpy as np
import pickle
import cv2
from os import listdir
from sklearn.preprocessing import LabelBinarizer
from keras.models import Sequential
from keras.layers.normalization 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 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
import matplotlib.pyplot as plt
```

Using TensorFlow backend.

```
In [2]:

EPOCHS = 25
INIT_LR = 1e-3
BS = 32
default_image_size = tuple((256, 256))
image_size = 0
directory_root = '../input/plantvillage/'
width=256
height=256
depth=3
```

Function to convert images to array

```
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
```

Fetch images from directory

```
In [4]:
 image_list, label_list = [], []
 try:
     print("[INFO] Loading images ...")
     root_dir = listdir(directory_root)
     for directory in root_dir :
         # remove .DS_Store from list
         if directory == ".DS_Store" :
              root_dir.remove(directory)
     for plant_folder in root_dir :
          plant_disease_folder_list = listdir(f"{directory_root}/{plant_folder}")
          for disease_folder in plant_disease_folder_list :
             # remove .DS_Store from list
             if disease_folder == ".DS_Store" :
                 plant_disease_folder_list.remove(disease_folder)
         for plant_disease_folder in plant_disease_folder_list:
              print(f"[INFO] Processing {plant_disease_folder} ...")
              plant_disease_image_list = listdir(f"{directory_root}/{plant_folder}/{plant_disease_folder}/")
             for single_plant_disease_image in plant_disease_image_list :
                 if single_plant_disease_image == ".DS_Store" :
                      plant_disease_image_list.remove(single_plant_disease_image)
              for image in plant_disease_image_list[:200]:
                 image_directory = f"{directory_root}/{plant_folder}/{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}")
 [INFO] Loading images ...
 [INFO] Processing Tomato_Septoria_leaf_spot ...
 [INFO] Processing Tomato__Tomato_mosaic_virus ...
 [INFO] Processing Tomato_Late_blight ...
 [INFO] Processing Tomato_Spider_mites_Two_spotted_spider_mite ...
 [INFO] Processing Tomato__Tomato_YellowLeaf__Curl_Virus ...
 [INFO] Processing Tomato_healthy ...
 [INFO] Processing Pepper__bell___Bacterial_spot ...
 [INFO] Processing Potato___healthy ...
 [INFO] Processing Tomato__Target_Spot ...
 [INFO] Processing Tomato_Leaf_Mold ...
 [INFO] Processing Tomato_Bacterial_spot ...
  [INFO] Processing Tomato_Early_blight ...
  [INFO] Processing Potato___Late_blight ...
 [INFO] Processing Potato___Early_blight ...
 [INFO] Processing Pepper bell healthy ...
 [INFO] Image loading completed
Get Size of Processed Image
   In [5]:
 image_size = len(image_list)
Transform Image Labels uisng Scikit Learn's LabelBinarizer
   In [6]:
 label_binarizer = LabelBinarizer()
 image_labels = label_binarizer.fit_transform(label_list)
 pickle.dump(label_binarizer,open('label_transform.pkl', 'wb'))
 n_classes = len(label_binarizer.classes_)
Print the classes
   In [7]:
 print(label_binarizer.classes_)
 ['Pepper__bell___Bacterial_spot' 'Pepper__bell___healthy'
   'Potato___Early_blight' 'Potato___Late_blight' 'Potato___healthy'
   'Tomato_Bacterial_spot' 'Tomato_Early_blight' 'Tomato_Late_blight'
   'Tomato_Leaf_Mold' 'Tomato_Septoria_leaf_spot'
   'Tomato_Spider_mites_Two_spotted_spider_mite' 'Tomato__Target_Spot'
   'Tomato__Tomato_YellowLeaf__Curl_Virus' 'Tomato__Tomato_mosaic_virus'
   'Tomato_healthy']
   In [8]:
 np_image_list = np.array(image_list, dtype=np.float16) / 225.0
```

```
In [9]:
print("[INFO] Spliting data to train, 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] Spliting data to train, test
 In [10]:
aug = 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")
 In [11]:
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

model.summary()

Layer (type)	Output =====	Shape 	Param # ======
conv2d_1 (Conv2D)	(None,	256, 256, 32)	896
activation_1 (Activation)	(None,	256, 256, 32)	0
batch_normalization_1 (Batch	(None,	256, 256, 32)	128
max_pooling2d_1 (MaxPooling2	(None,	85, 85, 32)	0
dropout_1 (Dropout)	(None,	85, 85, 32)	0
conv2d_2 (Conv2D)	(None,	85, 85, 64)	18496
activation_2 (Activation)	(None,	85, 85, 64)	0
batch_normalization_2 (Batch	(None,	85, 85, 64)	256
conv2d_3 (Conv2D)	(None,	85, 85, 64)	36928
activation_3 (Activation)	(None,	85, 85, 64)	0
batch_normalization_3 (Batch	(None,	85, 85, 64)	256
max_pooling2d_2 (MaxPooling2	(None,	42, 42, 64)	0
dropout_2 (Dropout)	(None,	42, 42, 64)	0
conv2d_4 (Conv2D)	(None,	42, 42, 128)	73856
activation_4 (Activation)	(None,	42, 42, 128)	0
batch_normalization_4 (Batch	(None,	42, 42, 128)	512
conv2d_5 (Conv2D)	(None,	42, 42, 128)	147584
activation_5 (Activation)	(None,	42, 42, 128)	0
batch_normalization_5 (Batch	(None,	42, 42, 128)	512
max_pooling2d_3 (MaxPooling2	(None,	21, 21, 128)	0
dropout_3 (Dropout)	(None,	21, 21, 128)	0
flatten_1 (Flatten)	(None,	56448)	0
dense_1 (Dense)	(None,	1024)	57803776
activation_6 (Activation)	(None,	1024)	0
batch_normalization_6 (Batch	(None,	1024)	4096
dropout_4 (Dropout)	(None,	1024)	0
dense_2 (Dense)	(None,	15)	15375
activation_7 (Activation)	(None,	15)	0
Total params: 58,102,671 Trainable params: 58,099,791 Non-trainable params: 2,880			

```
In [13]:

opt = Adam(lr=INIT_LR, decay=INIT_LR / EPOCHS)
# distribution
model.compile(loss="binary_crossentropy", optimizer=opt,metrics=["accuracy"])
# train the network
print("[INFO] training network...")
```

[INFO] training network...

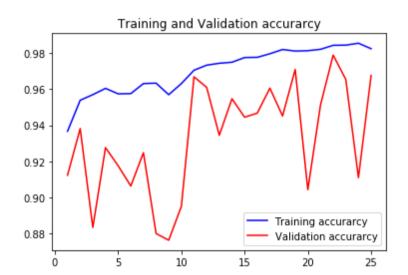
```
In [14]:
```

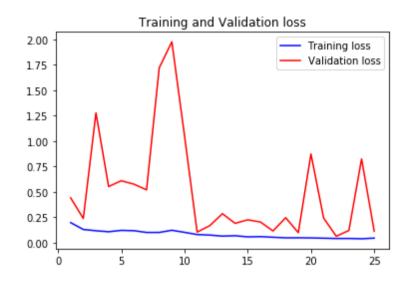
```
history = model.fit_generator(
   aug.flow(x_train, y_train, batch_size=BS),
   validation_data=(x_test, y_test),
   steps_per_epoch=len(x_train) // BS,
   epochs=EPOCHS, verbose=1
  )
```

```
Epoch 1/25
Epoch 2/25
Epoch 3/25
Epoch 4/25
Epoch 5/25
Epoch 6/25
Epoch 7/25
Epoch 8/25
Epoch 9/25
Epoch 10/25
Epoch 11/25
Epoch 12/25
Epoch 13/25
Epoch 14/25
Epoch 15/25
Epoch 16/25
Epoch 17/25
Epoch 18/25
Epoch 19/25
Epoch 20/25
Epoch 21/25
Epoch 23/25
Epoch 24/25
Epoch 25/25
```

Plot the train and val curve

```
In [15]:
acc = history.history['acc']
val_acc = history.history['val_acc']
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 accurarcy')
plt.plot(epochs, val_acc, 'r', label='Validation accurarcy')
plt.title('Training and Validation accurarcy')
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()
```





Model Accuracy

plt.show()

```
In [16]:

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

Save model using Pickle

```
In [17]:
# save the model to disk
print("[INFO] Saving model...")
pickle.dump(model,open('cnn_model.pkl', 'wb'))
```

[INFO] Saving model...