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               """veg data.ipynb
              Automatically generated by Colaboratory.
              Original file is located at
                         https://colab.research.google.com/drive/1EyjsABIaXDXTPgUeZJgEBKqYVryamZZi
               .....
              from tensorflow.keras.preprocessing.image import ImageDataGenerator
               train_datagen=ImageDataGenerator(rescale=1./255,zoom_range=0.2,horizontal_flip=Tru
              e,vertical_flip=False)
              test datagen=ImageDataGenerator(rescale=1./255)
              x_train=train_datagen.flow_from_directory(r"C:\Users\maris_q3mm6nk\Desktop\FILES\d
               ata_for_ibm\Fertilizers_Recommendation_ System_For_Disease_ Prediction\Dataset
              Plant Disease\Veg-dataset\Veg-dataset\train_set",target_size=(128,128),
                                                                                                                            class_mode='categorical',batch_size=24)
               x\_test=test\_datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\FILES\datagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Desktop\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_directory(r'C:\Users\maris\_q3mm6nk\Gatagen.flow\_from\_
               a_for_ibm\Fertilizers_Recommendation_ System_For_Disease_ Prediction\Dataset Plant
               Disease\Veg-dataset\Veg-dataset\test_set', target_size=(128,128),
                                                                                                                            class_mode='categorical',batch_size=24)
               from tensorflow.keras.models import Sequential
              from tensorflow.keras.layers import Dense,Convolution2D,MaxPooling2D,Flatten
              model=Sequential()
               model.add(Convolution2D(32,(3,3),input_shape=(128,128,3),activation='relu'))
              model.add(MaxPooling2D(pool_size=(2,2)))
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#

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model.add(Flatten())
model.summary()
model.add(Dense(300,activation='relu'))
model.add(Dense(150,activation='relu'))
model.add(Dense(9,activation='softmax'))
model.compile(loss='categorical_crossentropy',optimizer='adam',metrics=['accuracy'
])
len(x_train)
1238/24
\verb|model.fit(x_train,steps_per_epoch=len(x_train),validation_data=x_test,validation\_s|\\
teps=len(x_test),epochs=10)
model.save('vegetabledata.h5')
import numpy as np
from tensorflow.keras.models import load_model
from tensorflow.keras.preprocessing import image
model=load model('vegetabledata.h5')
img=image.load_img(r"C:\Users\maris_q3mm6nk\Desktop\FILES\data_for_ibm\Fertilizers
Recommendation System For Disease Prediction\Dataset Plant Disease\Veg-
dataset\Veg-dataset\test_set\Potato___Early_blight/b817817e-a6b1-4123-88e7-
db98b453ce17___RS_Early.B 6880.jpg")
img
x=image.img_to_array(img)
img=image.load_img(r"C:\Users\maris_q3mm6nk\Desktop\FILES\data_for_ibm\Fertilizers
_Recommendation_ System_For_Disease_ Prediction\Dataset Plant Disease\Veg-
dataset\Veg-dataset\test_set\Potato___Early_blight/b817817e-a6b1-4123-88e7-
db98b453ce17___RS_Early.B 6880.jpg",target_size=(128,128))
img
x=image.img_to_array(img)
```

```
x=np.expand_dims(x,axis=0)
y=np.argmax(model.predict(x),axis=1)
x_train.class_indices
index=['Pepper,_bell___Bacterial_spot','Pepper,_bell___healthy','Potato___Early_bl
ight','Potato___Late_blight','Potato___healthy','Tomato___Bacterial_spot','Tomato__
__Late_blight','Tomato___Leaf_Mold','Tomato___Septoria_leaf_spot']
index[y[0]]
img=image.load_img(r"C:\Users\maris_q3mm6nk\Desktop\FILES\data_for_ibm\Fertilizers
_Recommendation_ System_For_Disease_ Prediction\Dataset Plant Disease\Veg-
dataset\Veg-dataset\test_set\Potato___Early_blight/b817817e-a6b1-4123-88e7-
db98b453ce17___RS_Early.B 6880.jpg",target_size=(128,128))
x=image.img_to_array(img)
x=np.expand_dims(x,axis=0)
y=np.argmax(model.predict(x),axis=1)
index=['Pepper,_bell___Bacterial_spot','Pepper,_bell___healthy','Potato___Early_bl
ight','Potato___Late_blight','Potato___healthy','Tomato___Bacterial_spot','Tomato_
__Leaf_Mold','Tomato___Septoria_leaf_spot']
index[y[0]]
```