```
pip install mahotas
```

```
     Requirement already satisfied: mahotas in /usr/local/lib/python3.10/dist-packages (1.4.14)
     Requirement already satisfied: numpy in /usr/local/lib/python3.10/dist-packages (from mahotas) (1.25.2)
```

```
#-----------------------------------
# GLOBAL FEATURE EXTRACTION
#-----------------------------------
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import MinMaxScaler
import numpy as np
import mahotas
import cv2
import os
import h5py

#--------------------
# tunable-parameters
#--------------------
images_per_class       = 800
fixed_size             = tuple((500, 500))
train_path             = r"/content/drive/MyDrive/sharunplant/archive/dataset/train"
h5_train_data          = r"/content/drive/MyDrive/sharunplant/train_data.h5/train_data.h5"
h5_train_labels        = r"/content/drive/MyDrive/sharunplant/train_labels.h5"
bins                   = 8
```

```
# Converting each image to RGB from BGR format

def rgb_bgr(image):
    rgb_img = cv2.cvtColor(image, cv2.COLOR_BGR2RGB)
    return rgb_img
```

```
# Conversion to HSV image format from RGB

def bgr_hsv(rgb_img):
    hsv_img = cv2.cvtColor(rgb_img, cv2.COLOR_RGB2HSV)
    return hsv_img
```

```
# image segmentation

# for extraction of green and brown color


def img_segmentation(rgb_img,hsv_img):
    lower_green = np.array([25,0,20])
    upper_green = np.array([100,255,255])
    healthy_mask = cv2.inRange(hsv_img, lower_green, upper_green)
    result = cv2.bitwise_and(rgb_img,rgb_img, mask=healthy_mask)
    lower_brown = np.array([10,0,10])
    upper_brown = np.array([30,255,255])
    disease_mask = cv2.inRange(hsv_img, lower_brown, upper_brown)
    disease_result = cv2.bitwise_and(rgb_img, rgb_img, mask=disease_mask)
    final_mask = healthy_mask + disease_mask
    final_result = cv2.bitwise_and(rgb_img, rgb_img, mask=final_mask)
    return final_result
```

```
# feature-descriptor-1: Hu Moments
def fd_hu_moments(image):
    image = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)
    feature = cv2.HuMoments(cv2.moments(image)).flatten()
    return feature
```

```
# feature-descriptor-2: Haralick Texture
def fd_haralick(image):
    gray = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)
    haralick = mahotas.features.haralick(gray).mean(axis=0)
    return haralick
```

```
# feature-descriptor-3: Color Histogram
def fd_histogram(image, mask=None):
    image = cv2.cvtColor(image, cv2.COLOR_BGR2HSV)
    hist  = cv2.calcHist([image], [0, 1, 2], None, [bins, bins, bins], [0, 256, 0, 256, 0, 256])
    cv2.normalize(hist, hist)
    return hist.flatten()
```

```
# get the training labels
train_labels = os.listdir(train_path)

# sort the training labels
train_labels.sort()
print(train_labels)

# empty lists to hold feature vectors and labels
global_features = []
labels          = []
```

```
['diseased', 'healthy']
```

```
# loop over the training data sub-folders
for training_name in train_labels:
    # join the training data path and each species training folder
    dir = os.path.join(train_path, training_name)

    # get the current training label
    current_label = training_name

    # loop over the images in each sub-folder
    for x in range(1,images_per_class+1):
        # get the image file name
        file = dir + "/" + str(x) + ".jpg"

        # read the image and resize it to a fixed-size
        image = cv2.imread(file)
        image = cv2.resize(image, fixed_size)


        # Running Function Bit By Bit

        RGB_BGR       = rgb_bgr(image)
        BGR_HSV       = bgr_hsv(RGB_BGR)
        IMG_SEGMENT   = img_segmentation(RGB_BGR,BGR_HSV)

        # Call for Global Fetaure Descriptors

        fv_hu_moments = fd_hu_moments(IMG_SEGMENT)
        fv_haralick   = fd_haralick(IMG_SEGMENT)
        fv_histogram  = fd_histogram(IMG_SEGMENT)

        # Concatenate

        global_feature = np.hstack([fv_histogram, fv_haralick, fv_hu_moments])



        # update the list of labels and feature vectors
        labels.append(current_label)
        global_features.append(global_feature)

    print("[STATUS] processed folder: {}".format(current_label))

print("[STATUS] completed Global Feature Extraction...")
```

```
[STATUS] processed folder: diseased
[STATUS] processed folder: healthy
[STATUS] completed Global Feature Extraction...
```

```
# get the overall feature vector size
print("[STATUS] feature vector size {}".format(np.array(global_features).shape))
```

```
[STATUS] feature vector size (1600, 532)
```

```
# get the overall training label size
print("[STATUS] training Labels {}".format(np.array(labels).shape))
```

```
[STATUS] training Labels (1600,)
```

```
# encode the target labels
targetNames = np.unique(labels)
le          = LabelEncoder()
target      = le.fit_transform(labels)
print("[STATUS] training labels encoded...")
```

```
     [STATUS] training labels encoded...
```

```
# scale features in the range (0-1)
from sklearn.preprocessing import MinMaxScaler
scaler            = MinMaxScaler(feature_range=(0, 1))
rescaled_features = scaler.fit_transform(global_features)
print("[STATUS] feature vector normalized...")
```

```
     [STATUS] feature vector normalized...
```

```
print("[STATUS] target labels: {}".format(target))
print("[STATUS] target labels shape: {}".format(target.shape))
```

```
     [STATUS] target labels: [0 0 0 ... 1 1 1]
     [STATUS] target labels shape: (1600,)
```

```
# Close any previously opened file handles
if 'h5f_data' in locals() and isinstance(h5f_data, h5py.File):
    h5f_data.close()

# Create the HDF5 file
h5f_data = h5py.File(h5_train_data, 'w')
h5f_data.create_dataset('dataset_1', data=np.array(rescaled_features))

```

```
     <HDF5 dataset "dataset_1": shape (1600, 532), type "<f8">
```

```
h5f_label = h5py.File(h5_train_labels, 'w')
h5f_label.create_dataset('dataset_1', data=np.array(target))
```

```
     <HDF5 dataset "dataset_1": shape (1600,), type "<i8">
```

```
h5f_data.close()
h5f_label.close()
```

```
# training
#-----------------------------------
# TRAINING OUR MODEL
#-----------------------------------
import h5py
import numpy as np
import os
import glob
import cv2
import warnings
from matplotlib import pyplot
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.model_selection import KFold, StratifiedKFold
from sklearn.metrics import confusion_matrix, accuracy_score, classification_report
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import SVC
#from sklearn.externals import joblib
from joblib import dump, load


warnings.filterwarnings('ignore')

#--------------------
# tunable-parameters
#--------------------
num_trees = 100
test_size = 0.20
seed      = 9
```

```
train_path =  r"/content/drive/MyDrive/sharunplant/archive/dataset/train"
test_path  = "dataset/test"
h5_train_data    =r"/content/drive/MyDrive/sharunplant/train_data.h5/train_data.h5"
h5_train_labels  = r"/content/drive/MyDrive/sharunplant/train_labels.h5"
scoring    = "accuracy"

# get the training labels
train_labels = os.listdir(train_path)

# sort the training labels
train_labels.sort()

if not os.path.exists(test_path):
    os.makedirs(test_path)

# create all the machine learning models
models = []
models.append(('LR', LogisticRegression(random_state=seed)))
models.append(('LDA', LinearDiscriminantAnalysis()))
models.append(('KNN', KNeighborsClassifier()))
models.append(('CART', DecisionTreeClassifier(random_state=seed)))
models.append(('RF', RandomForestClassifier(n_estimators=num_trees, random_state=seed)))
models.append(('NB', GaussianNB()))
models.append(('SVM', SVC(random_state=seed)))

# variables to hold the results and names
results = []
names   = []

# import the feature vector and trained labels
h5f_data  = h5py.File(h5_train_data, 'r')
h5f_label = h5py.File(h5_train_labels, 'r')

global_features_string = h5f_data['dataset_1']
global_labels_string   = h5f_label['dataset_1']

global_features = np.array(global_features_string)
global_labels   = np.array(global_labels_string)

h5f_data.close()
h5f_label.close()

# verify the shape of the feature vector and labels
print("[STATUS] features shape: {}".format(global_features.shape))
print("[STATUS] labels shape: {}".format(global_labels.shape))

print("[STATUS] training started...")
```

```
[STATUS] features shape: (1600, 532)
[STATUS] labels shape: (1600,)
[STATUS] training started...
```

```
# split the training and testing data
(trainDataGlobal, testDataGlobal, trainLabelsGlobal, testLabelsGlobal) = train_test_split(np.array(global_features),
                                                                                          np.array(global_labels),
                                                                                          test_size=test_size,
                                                                                          random_state=seed)

print("[STATUS] splitted train and test data...")
print("Train data  : {}".format(trainDataGlobal.shape))
print("Test data   : {}".format(testDataGlobal.shape))
```

```
[STATUS] splitted train and test data...
Train data  : (1280, 532)
Test data   : (320, 532)
```

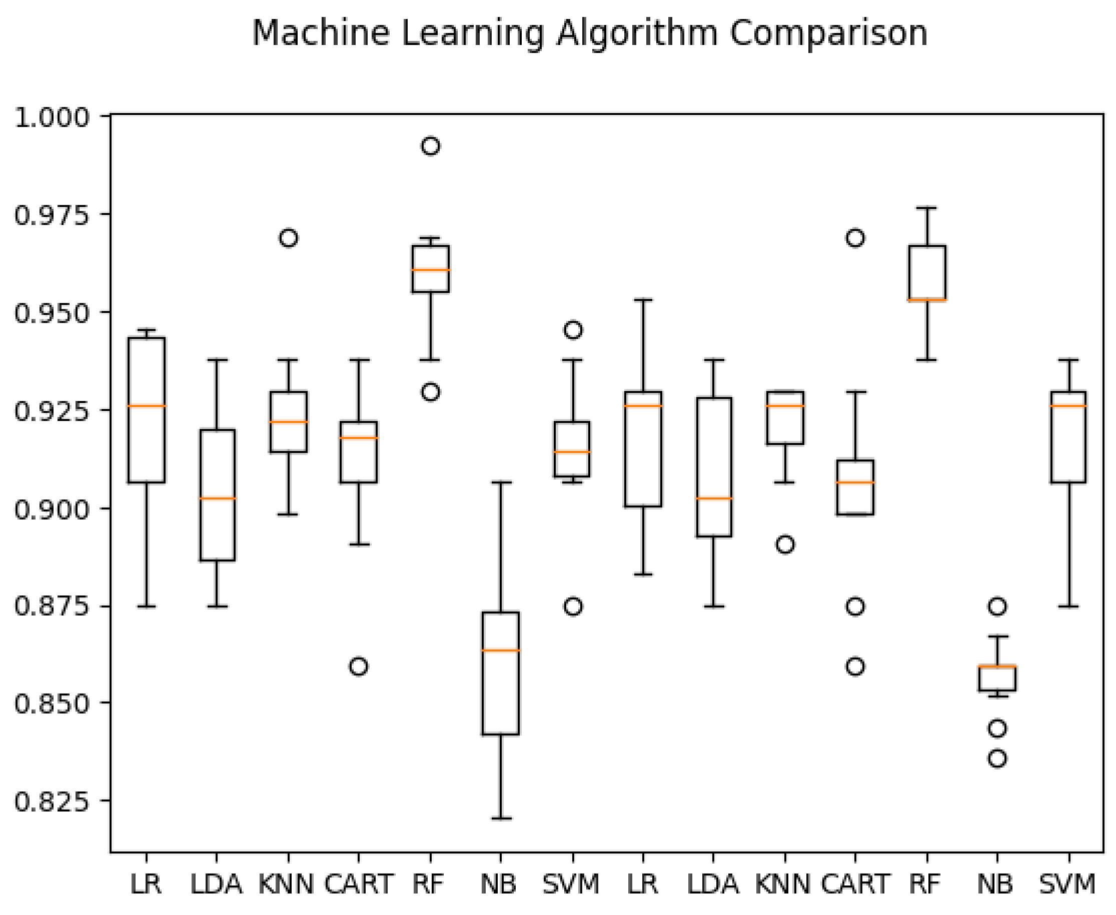
```
print(trainDataGlobal)
```

```
[[0.97973956 0.         0.         ... 0.01058888 0.12693628 0.96573219]
 [0.90470961 0.03308547 0.03047729 ... 0.01058886 0.12692807 0.96573214]
 [0.92166131 0.01766604 0.03559807 ... 0.01058994 0.12737134 0.96573262]
 ...
 [0.77039234 0.         0.         ... 0.01058886 0.12693296 0.96573218]
 [0.96965597 0.         0.         ... 0.01058989 0.1271198  0.96574232]
 [0.98389776 0.19183335 0.15462199 ... 0.01058898 0.12695993 0.96573136]]
```

```
# 10-fold cross-validation loop
for name, model in models:
    kfold = KFold(n_splits=10, random_state=seed,shuffle=True)  # Set shuffle to True
    cv_results = cross_val_score(model, trainDataGlobal, trainLabelsGlobal, cv=kfold, scoring=scoring)
    results.append(cv_results)
    names.append(name)
    msg = "%s: %f (%f)" % (name, cv_results.mean(), cv_results.std())
    print(msg)

# boxplot algorithm comparison
fig = pyplot.figure()
fig.suptitle('Machine Learning Algorithm Comparison')
ax = fig.add_subplot(111)
pyplot.boxplot(results)
ax.set_xticklabels(names)
pyplot.show()
```

```
LR: 0.916406 (0.021833)
LDA: 0.907813 (0.019702)
KNN: 0.920312 (0.012500)
CART: 0.906250 (0.027951)
RF: 0.957031 (0.013189)
NB: 0.857031 (0.010511)
SVM: 0.916406 (0.020086)
```



```
clf  = RandomForestClassifier(n_estimators=num_trees, random_state=seed)
```

```
clf.fit(trainDataGlobal, trainLabelsGlobal)
```

```
▾        RandomForestClassifier
RandomForestClassifier(random_state=9)
```

```
y_predict=clf.predict(testDataGlobal)
```

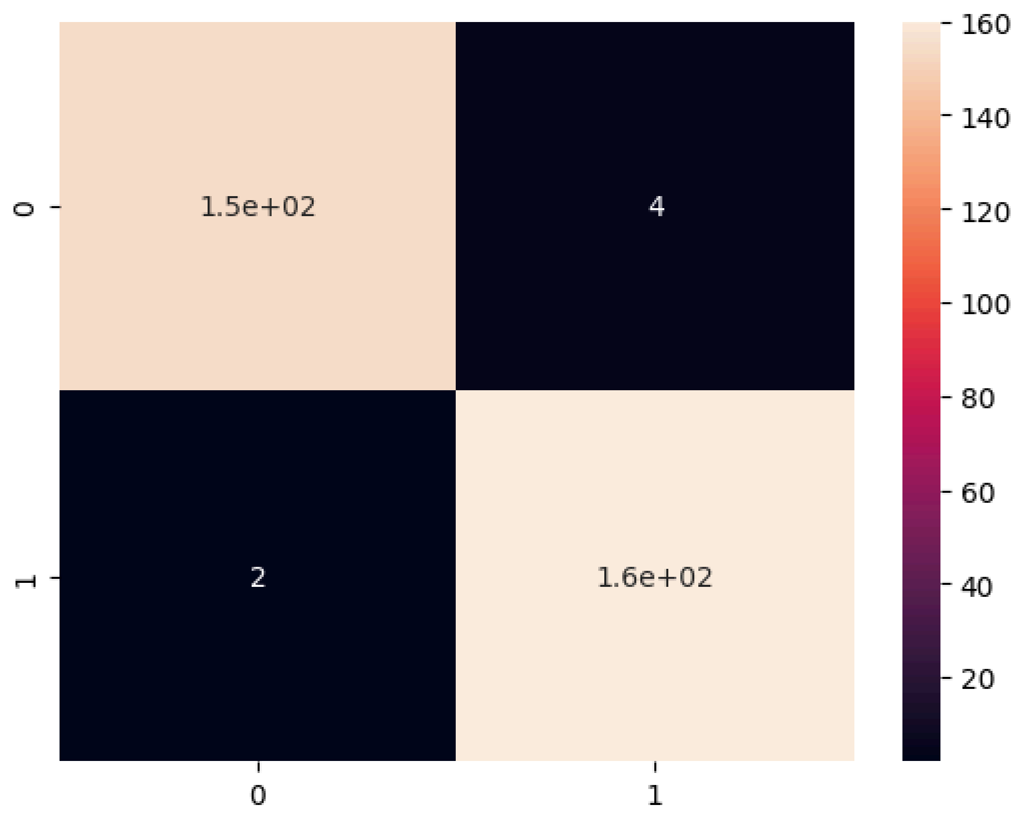
```
print(y_predict)
```

```
[1 1 1 0 0 1 1 1 0 0 1 1 0 0 0 1 1 1 1 1 1 1 0 1 0 0 0 0 0 0 1 1 1 0 1 0 1
 1 1 0 1 0 0 0 1 0 0 0 0 0 1 0 1 0 0 1 1 1 0 1 0 0 1 0 0 0 1 1 1 0 0 0 1 0
 0 1 0 1 1 0 1 1 0 1 1 1 1 0 0 1 1 1 1 1 1 1 1 1 1 1 0 0 1 1 1 0 1 1 0 1 0
 1 0 0 1 1 0 1 0 1 1 0 0 0 0 0 0 0 1 0 1 1 0 1 0 1 0 0 0 1 1 0 0 0 1 1 0 0
 0 1 0 1 0 1 0 0 1 1 0 0 0 1 0 1 0 1 0 1 0 0 1 0 1 0 0 0 0 0 1 1 0 0 1 0 0
 1 1 1 1 0 1 1 1 0 1 0 0 0 0 1 0 1 0 0 0 1 0 0 1 1 0 0 1 1 1 1 0 1 1 1 0 0
 1 0 1 1 0 0 0 0 0 1 1 0 1 1 1 1 0 1 0 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 1 1
 1 1 1 1 1 1 0 1 0 1 0 1 0 0 0 0 1 0 0 1 0 1 1 1 1 0 1 1 1 1 1 1 1 1 0 1 1
 1 1 1 0 0 0 0 0 0 0 1 0 0 1 0 0 1 1 0 0 1 1 0 0]
```

```
cm = confusion_matrix(testLabelsGlobal,y_predict)
```

```
import seaborn as sns
sns.heatmap(cm ,annot=True)
```

```
<Axes: >
```



```
print(classification_report(testLabelsGlobal,y_predict))
```

```
              precision    recall  f1-score   support

           0       0.99      0.97      0.98       158
           1       0.98      0.99      0.98       162

    accuracy                           0.98       320
   macro avg       0.98      0.98      0.98       320
weighted avg       0.98      0.98      0.98       320
```

```
from sklearn.metrics import accuracy_score
accuracy_score(testLabelsGlobal, y_predict)
```

```
0.98125
```

```
import joblib

# Assuming 'clf' is your trained model
joblib.dump(clf, 'trained_model.pkl')
```

```
['trained_model.pkl']
```

```
import cv2
import numpy as np
import joblib

# Load the trained model
clf = joblib.load('trained_model.pkl')

# Define preprocessing functions
def preprocess_image(image):
    # Resize the image to the same size used during training
    image = cv2.resize(image, (500, 500))
    # Convert image to RGB (if it's not already in RGB format)
    #image = cv2.cvtColor(image, cv2.COLOR_BGR2RGB)
    # Perform any other preprocessing steps here if necessary
    return image

def extract_features(image):
    # Extract features using the same feature extraction functions used during training
    # You can reuse fd_hu_moments, fd_haralick, and fd_histogram functions from your code
    rgb_bgr_image = rgb_bgr(image)
    bgr_hsv_image = bgr_hsv(rgb_bgr_image)
    segmented_image = img_segmentation(rgb_bgr_image, bgr_hsv_image)
    feature_vector = np.hstack([fd_histogram(segmented_image), fd_haralick(segmented_image), fd_hu_moments(seg
    return feature_vector

# Load a sample image
```

```
sample_image_path = "/content/drive/MyDrive/check/dis1.png"
sample_image = cv2.imread(sample_image_path)

# Preprocess the sample image
preprocessed_sample_image = preprocess_image(sample_image)

# Extract features from the preprocessed sample image
sample_image_features = extract_features(preprocessed_sample_image)

# Reshape features to match the input shape expected by the model
sample_image_features = sample_image_features.reshape(1, -1)

# Use the loaded model to make predictions
prediction = clf.predict(sample_image_features)

# Print the prediction
if prediction == 0:
    print("The sample image is predicted to be diseased.")
else:
    print("The sample image is predicted to be healthy.")
```

```
The sample image is predicted to be diseased.
```