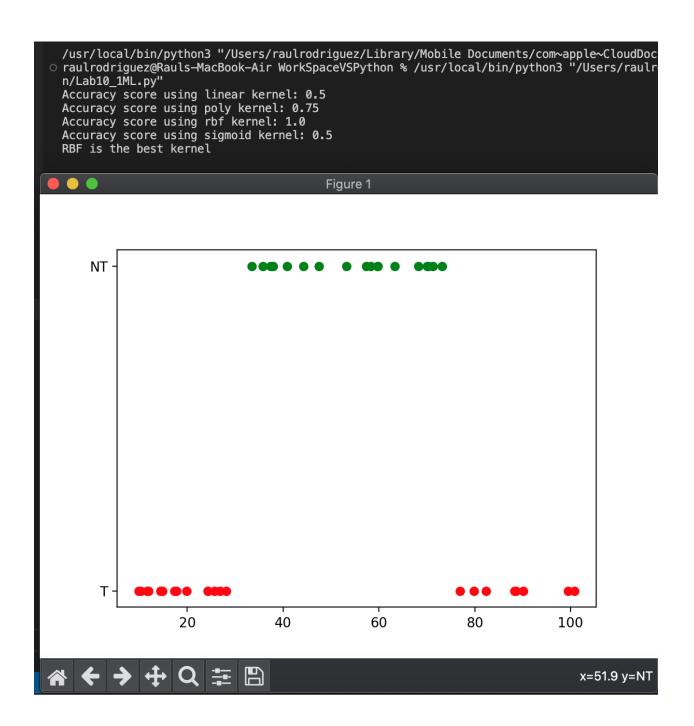
```
import pandas as pd
     import numpy as np
     from matplotlib import pyplot as plt
     from sklearn.linear_model import LogisticRegression
     from sklearn.svm import SVC
     from sklearn.model_selection import train_test_split
     from sklearn.metrics import classification_report, confusion_matrix, accuracy_score, ConfusionMatrixDisplay
     df = pd.read_csv('speedLimits.csv')
     X = np.array(df.Speed)
     y = np.array(df.Ticket)
     X = X.reshape(-1,1)
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     X_train, X_test, y_train, y_test = train_test_split(X, y,test_size=0.1, random_state=0)
     modelSVC = SVC(kernel='linear').fit(X_train, y_train)
     predL = modelSVC.predict(X_test)
     print(f'Accuracy score using linear kernel: {accuracy_score(y_test, predL)}')
modelSVC = SVC(kernel='poly').fit(X_train, y_train)
     predP = modelSVC.predict(X_test)
     print(f'Accuracy score using poly kernel: {accuracy_score(y_test, predP)}')
     modelSVC = SVC(kernel='rbf').fit(X_train, y_train)
     predRBF = modelSVC.predict(X_test)
     print(f'Accuracy score using rbf kernel: {accuracy_score(y_test, predRBF)}')
     modelSVC = SVC(kernel='sigmoid').fit(X_train, y_train)
     predS = modelSVC.predict(X_test)
     print(f'Accuracy score using sigmoid kernel: {accuracy_score(y_test, predS)}')
     print(f'RBF is the best kernel')
     for i in range(len(X)):
         if y[i]=="T":
             plt.scatter(X[i],y[i],c='r')
             plt.scatter(X[i],y[i],c='g')
     plt.show()
```



```
import pandas as pd
import numpy as np
from matplotlib import pyplot as plt
from sklearn.svm import SVC
from sklearn.model_selection import train_test_split
from \ \textit{sklearn.metrics} \ import \ \textit{classification\_report}, \ \textit{confusion\_matrix}, \ \textit{accuracy\_score}, \ \textit{ConfusionMatrixDisplay} \ 
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
names = ['Sample code number', 'Clump Thickness','Uniformity of Cell Size','Uniformity of Cell Shape','Marginal Adhesion',
'Single Epithelial Cell Size','Bare Nuclei','Bland Chromatin','Normal Nucleoli','Mitoses','Class' ]
df = pd.read_csv('breast-cancer-wisconsin.data.csv', names=names)
df=df.replace('?',np.nan)
df=df.dropna()
df=df.drop("Sample code number",axis=1)
X = np.array(df.loc[:, 'Clump Thickness' : 'Mitoses'])
y = np.array(df['Class'])
X = StandardScaler().fit_transform(X)
pca = PCA(n_components=2)
principalComponents = pca.fit_transform(X)
pc1=principalComponents[0:,1]
pc2=principalComponents[0:,0]
 \textbf{X\_train, X\_test, y\_train, y\_test = train\_test\_split(principalComponents, y, test\_size=0.1, random\_state=0)} 
modelSVC = SVC(kernel='linear').fit(X_train, y_train)
y_pred = modelSVC.predict(X_test)
confusionMatrix = confusion_matrix(y_test, y_pred)
print(confusionMatrix)
print(f'Accuracy score: {accuracy_score(y_test, y_pred)}')
for i in range(len(y)):
    if y[i]==2:
         plt.scatter(pc1[i],pc2[i],color='r')
         plt.scatter(pc1[i],pc2[i],color='g')
plt.xlabel("pc1")
plt.ylabel("pc2")
plt.show()
```

